TNH
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TROPICAL NATURAL HISTORY

Department of Biology, Faculty of Science, Chulalongkorn University

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Aim and Scope: Tropical Natural History is a journal publishing original research, review and interactive natural history. Manuscripts considered include papers on experimental biology, systematic, ecology, paleontology, and the interaction of organisms with their environment.

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Literature Cited: Include only published or in-press articles. Dissertations resulting from graduate studies and non-serial proceedings of conferences/symposia are to be treated as books. References should be referred to in the text as **Red and Blue (2000)**, **Red et al. (2000)** for 3, or more authors or **(Red, 2000; Blue and Red, 2000; Red et al., 2000)** in the parentheses. All literature cited in the text must be listed alphabetically in the following formats:

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Book: Red, A.A. and Blue, B.B. 2000. Title of Book, Publisher name and location, number of pages (e.g. 123 pp).

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17th World Congress of Malacology

18-24 July 2010
Royal Phuket City Hotel
Phuket, Thailand

Abstract

Edited by:
Somsak Panha
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THE SCIENTIFIC SYMPOSIUM

The WCM is an opportunity for malacologists from throughout the world to get together to discuss their research. There are thematic symposia, open contributed sessions and a poster session with posters on display for the duration of the congress. Note: a maximum of 1 oral and 1 poster per presenting author. Several thematic symposia are as follows:

ECOLOGY, EVOLUTION AND BIOLOGY OF FRESHWATER BIVALVES

Arthur Bogan North Carolina Museum of Natural Sciences, MSC 1626, Raleigh, NC 27699-1626, USA. **E-mail:** arthur.bogan@ncmail.net
Walter Hoeh Department of Biological Sciences, Kent State University, Kent, OH 44242, USA. **E-mail:** whoeh@kent.edu

Freshwater bivalves are found in 19 families with major radiations in the Sphaeriidae and the six families in the Order Unioniformes. The unioniform bivalves are the most endangered group of animals in the World largely because deforestation, dams and pollution are degrading their aquatic habitats. The purpose of this symposium is to bring together researchers working on freshwater bivalve ecology, evolution, reproduction, genetics and biology at all levels of organization. The symposium will be representative of the wide range of research questions being addressed and will be structured to produce a world wide overview of current freshwater bivalve research.

THE BIOLOGY AND EVOLUTION OF LIMPETS

Alan Hodgson Department of Zoology and Entomology, Rhodes University, Grahamstown 6140, SOUTH AFRICA. **E-mail:** A.Hodgson@ru.ac.za

The aim of this symposium is to provide a forum for the discussion of recent findings on all aspects of the biology and evolution of limpets. Previous meetings, held in London and Millport, were highly successful, and it is hoped that the 2010 symposium will build on this success and stimulate more research on these ecologically important molluscs. Speakers at this year's symposium include David Lindberg, Mark Davies, Ross Coleman, Gray Williams, Tomoyuki Nakano, Takenori Sasaki, Doug Eernisse and Alison Haynes. Presentations will cover a variety of topics including the use of limpets as model animals, limpet ecology, evolution and phylogeny, as well as adaptations (behaviour, physiology & morphology). Papers from the symposium will be published (subject to normal peer review) in an issue of Malacologia. For any further details, e-mail Alan Hodgson (Organizer).

EVOLUTION OF THE BIVALVIA

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Paula M. Mikkelsen Paleontological Research Institution, 1259 Trumansburg Road, Ithaca, NY 14850, USA. **E-mail:** pmm37@cornell.edu.

Evolution of the Bivalvia - This symposium explores the current issues and developments in bivalve phylogeny, systematics, and biodiversity studies. Organized in the context of the ongoing Bivalve Tree-of-Life project (www.bivatol.org), presentations by BivAToL and non-BivAToL workers will address the composition and interrelationships of the major clades as well as the position of the Bivalvia within the Mollusca, developments in the study of organ systems for assessing bivalve systematics, novel paleontological findings related to the topic, and evolutionary biodiversity studies focusing on bivalve faunas.

COMMUNITY ECOLOGY OF TROPICAL FOREST LAND SNAILS

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Over recent decades there has been an increasing interest in exploring the diversity and composition of tropical forest land-snail communities. Much of this research has been carried out in West and East Africa and in South and Southeast Asia, and studies completed to date encompass a variety of scales, ranging from studies of single sites to those of multiple assemblages in altitudinally- and/or vegetationally-diverse geographical areas. These studies have shown that tropical forest land-snail communities are highly species-rich, taxonomically broad based and often dominated by rare species. Many species have geographically-localized distributions, and habitat loss is the major threat to many forest-living snails. The purpose of this symposium will be to bring together researchers working on the community ecology of tropical forest land snails. The session will be representative of the full range of research questions being currently explored by researchers from across the globe, and will therefore provide a broad overview of the current state of knowledge in the field.

THE LAST 50 YEARS OF MALACOLOGY: SPECIALIZATION, METHODOLOGICAL TRANSFORMATION AND GLOBALIZATION

Robert Hershler Smithsonian Institution, Department of Invertebrate Zoology, P.O. Box 37012, Washington DC. 20013, USA. **E-mail:** HershlerR@si.edu
David R. Lindberg Department of Integrative Biology, University of California, Berkeley, CA 94720-3140, USA **E-mail:** drl@Berkeley.edu

As the 1950s began the study of molluscs differed little from the preceding 100 years. The choice of morphologic characters and the techniques and optics that were used to resolve them differed little from the time of Dall, Fischer, Gray, Lankester, Pelseneer, Troschel and von Ihering. However, changes were being ushered in as the great exploring expeditions and surveys began to wind down and the volume of material coming into museums decreased, and the encyclopedic knowledge and broad systematic coverage of earlier workers was replaced by increasing taxonomic specialization. Between 1950 and 2000 staggering methodological advances took place, including the advent of scanning and transmission electron microscopy, confocal imaging, electrophoresis and then direct sequencing of nucleotides, digital imaging and quantitative analysis of morphology, *in situ* gene expression, and sequencing of complete genomes. The analysis of systematic/evolutionary data also became more sophisticated as phenetics, multivariate analysis, and cladistics became part of the research enterprise. The advent of personal computers facilitated the organization of collection data and enabled the exploration of biodiversity and biogeographical patterns in a matter of minutes. The discovery of living Monoplacophora, hydrothermal vent and seep taxa, and high volume sampling of supposedly well-known habitats brought a sense of exploration and discovery back into the field. Malacology also took huge steps in entering the conservation arena on a global scale during this time period. Malacological journals and societies proliferated and their contributors, readership, and membership extended well beyond regional and national borders. This period also saw the shifting of malacological centers from long-established groups and institutions to new venues around the world, as well as the arrival of the World Wide Web and e-mail that brought workers into almost instantaneous contact regardless of their geographical proximity. This symposium will examine this incredible period in our field with presentations including, but not limited to, reviews of the changes that have occurred in researchers and the taxon and habitat breadth of their study groups, methodological and research approaches, journals, societies and publication patterns, the role and position of malacology in our museum and universities; and discussions of steps that need be taken to ensure the continued vigor and success of our discipline over the next 50 years. This symposium will also provide the opportunity to recognize colleagues who have played major roles in advancing malacology during this extraordinary period.

STUDIES ON OPISTHOBRANCHS MOLLUSCS

Manuel Malaquias Bergen Museum of Natural History, NORWAY.
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E-mail: tgosliner@calacademy.org

Opisthobranch molluscs have received considerable attention during the past years by a growing and enthusiastic research community. This symposium aims to bring together all those interested in the various aspects of opisthobranch biology and evolution, from development to behaviour, systematics and phylogenetics, palaeontology and biogeography, genomics and ecology, etc. We expect the symposium to be a forum of discussion of the latest advances as well as a platform to establish strategies and collaborations that could lead to a fast resolution of old and new questions on opisthobranch research. The symposium is sponsored by The Malacological Society of London and authors are encouraged to consider submitting their contributions to the Journal of Molluscan Studies (deadline to be announced). Manuscripts that pass the peer-review process will be published together as a collection of papers from the symposium.

EMERGING MOLLUSCAN MODELS: BIOLOGICAL QUESTIONS IN THE 21ST CENTURY

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The Mollusca encompasses a diverse assemblage of species with diverse life history strategies making them fascinating subjects of study. With new emerging technologies in genome science and cell biology, new molluscan models are emerging in the scientific community at large to address a broad range of biological questions ranging from the evolution of torsion, metamorphosis, biomineralization, innate immunity and the understanding of memory and learning behavior, amongst others. Four molluscan genome projects from two classes (Gastropoda and Bivalvia) are close to completion, and many more EST initiatives are underway. These new data will transform the approaches used in molluscan research both in the field and in the laboratory. The time is ripe for a synthetic effort by the molluscan research community to bring together experts working at different scales of biological organization (i.e. molecular, cellular, organismal).

EVOLUTIONARY ECOLOGY AND GENETICS OF MOLLUSCAN POPULATIONS

Takahiro Asami Department of Biology, Shinshu University, Matsumota 390-8621, JAPAN.
E-mail: asami99@shinshu-u.ac.jp

Evolution proceeds at the level of and within populations. To explore the evolutionary implications of diversity and to conserve evolutionarily significant units, it is crucial to understand evolutionary trajectories and mechanisms. Ecological and genetic diversity can be maintained within populations and/or established through cladogenesis by means of speciation between populations. This symposium aims to examine the evolutionary processes and mechanisms that generate diversity within and between populations and to understand the pattern of intra- and inter-specific diversity in molluscs, which pose an extremely unique and diverse array of morphology, ecology, behavior and reproduction compared with other animals. For that reason, the title is not limited within any particular groups of molluscs. This symposium will trigger and illuminate interdisciplinary interest and approaches for understanding of the evolutionary biology of molluscs. Keywords are polymorphism, speciation, reproductive isolation, adaptation, convergence and divergence, and evolutionary ecology and genetics.

THE SYSTEMATICS OF ASIAN LAND SNAILS

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With a few notable exceptions, land snails of Asian countries were neglected for many years and some Asian countries have never had more than descriptions of a few opportunistically collected specimens. This situation has changed dramatically in the past few years and we have entered a new age of land snail research in the region. An urgent need that is being addressed is to develop a sound foundation in country based alpha taxonomy and country based faunal guides, supported by national reference collections. However, national laws restricting access to specimens and limiting exchange of material across national boundaries can be major obstacles to regional studies. In bringing together contributions from a wide geographical range in Asia this symposium will provide a timely presentation of current work and hopefully provide an opportunity to explore the potential for building on the current level of international collaboration.

MOLLUSC AQUACULTURE

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Worldwide, aquaculture has increased at an average compounded rate of 9.2% per year since 1970, compared to only 1.4% for captured wild fish and 2.8% for terrestrial farmed meat production systems. Fish production, including marine and inland water production, has decreased tremendously due to various factors such as overexploitation and habitat degradation. Mollusc aquaculture is an important and rapidly expanding area of the world aquaculture production with currently the majority of production coming from natural populations. However, increasingly the wild stocks are approaching or have exceeded maximum sustainable yields. The production of seed through hatchery propagation is beginning to be recognized as a viable alternative as it will secure seed supply as well as to enable production of pure genetically-selected strains with desirable characteristics suited to particular conditions. This symposium aims to serve as a platform of discussion with the emphasis on aquaculture technology applied to commercially important mollusc species, including edible and pearl oysters, mussels, scallops and abalone, and new hatchery and grow-out technologies, such as juvenile production, production cycles and management practices, nutrition and feeding, the prevention, diagnosis and treatment of common mollusc diseases, and the post-harvest handling and marketing. Hopefully, this symposium will also serve as the catalyst and opportunity for international collaboration.

COUNTDOWN 2010: TOWARDS A GLOBAL FRESHWATER ASSESSMENT OF THREATENED SPECIES

Mary Seddon Shell Life, Bracken Tor, Saxongate, Okehampton, Devon EX20 1QW. **E-mail:** Mary@mollusca.org.uk
Helen Temple IUCN Species Programme, Cambridge, UK.
Will Darwall Freshwater Biodiversity Unit Manager, IUCN Species Programme, Cambridge, UK. **E-mail:** William.Darwall@iucn.org

IUCN Freshwater Biodiversity programme and the SSC Mollusc Specialist Group have been assessing the conservation status of various regional freshwater faunas over the last 5 years. In 2010 two major regions will be completed enabling a review of the freshwater molluscs, dragonflies, fish, crabs and selected plant groups. These form the first comprehensive overviews of the status of these faunas. Various tools have also been developed to assist local communities assess and manage their freshwater resources. This session will present the results of the various regional surveys in Africa and Asia, compare the regional status of the

faunas with other faunistic groups, identify sources of the major threats and propose measures for conservation planning within these regions to ensure that loss of biodiversity is minimised as part of the CBD and UN Millenium Goal targets. Others working on National level threat assessments of freshwater molluscs are welcome to join this symposium.

REPRODUCTION AND MATING SYSTEMS IN HERMAPHRODITIC MOLLUSCS

Kurt Jordaens Evolutionary Ecology Group, University of Antwerp, Antwerp 2610, BELGIUM. **E-mail:** kurt.jordaens@ua.ac.be
Joris Koene Animal Ecology, Faculty of Earth and Life Science, VU University, Amsterdam, 1081HV, THE NETHERLANDS. **E-mail:** joris.koene@falw.vu.nl

Hermaphroditic molluscs show a remarkable variation in fitness-related life history characteristics. Yet, pinpointing the factors that explain this variation proves very difficult. For example, variation in mating systems range from obligate outcrossing to predominant selfing, with various levels of in- and outbreeding depression. Moreover, hermaphroditic molluscs are notorious for their promiscuous sexual behaviours, which often include the use of bewildering and enigmatic reproductive organs that appear to be under strong sexual selection. This symposium aims at exploring the variety of factors that determine life history characteristics in hermaphroditic molluscs and should stimulate and guide further research in this area. We, therefore, welcome contributions in the fields of sexual behaviours, sexual selection, mating system evolution and life history strategies and other topics related to reproduction.

SPECIATION: INSIGHTS FROM INSULAR ISOLATION TO GLOBAL PATTERNS

Matthias Glaubrecht Museum of Natural History Berlin, Leibniz Institute for Evolutionary and Biodiversity Research at the Humboldt University, Berlin 10115, GERMANY. **E-mail**: matthias.glaubrecht@mfn-berlin.de

Darwin's “mystery of the mysteries” - the origin of new species and, as a consequence, multiplication of species - still remains at the forefront of current evolutionary biology research, as speciation ultimately results in biological diversity. While geographic distribution and spatial isolation are the crucial factors in allopatric speciation (sensu Ernst Mayr), which is still considered an important mechanism in many cases, alternative explanations for speciation have increasingly gained support over the last decade. Among the most prominent factors discussed, particularly in the context of radiations, is adaptive divergence in concert with specialization, suggesting that ecology is driving speciation. With an ever increasing armamentarium of molecular genetic tools for exploring the genetic structure of populations and species, the mystery has become many and its potential solutions have multiplied as further complexities are being uncovered.

This symposium aims at bringing together various approaches, based either on phylogenetic pattern, fossils or microevolutionary studies, building on evidence from land, freshwater and the marine realm, in order to evaluate the most important current battlegrounds in speciation studies.

CONFERENCE VENUE

The WCM will start with an icebreaker on Sunday, July 18th 2010. Conference sessions will be organized in several parallel sessions on Monday, Tuesday, Thursday and Friday. All sessions will be held in the Royal Phuket City Hotel conference rooms, which including 4 follow rooms: Room 1 (BALLROOM I), Room 2 (BALLROOM II), Room 3 (NAKHA), and Room 4 (RAYA). Morning and afternoon breaks will be served at the Grand Ballroom Hall, where the place of the posters session. Lunches will be served in the hotel restaurants at 1st and 19th floors. The poster session will be held on Tuesday late afternoon/evening and will include a reception with wine, beers and typical Thai herb beverages and Thai sweets. Wednesday is a free day during which participants can discover the many historical and beautiful places in Phuket. They can also join one of the optional congress trips or do whatever they want. The conference farewell dinner at a venue on the Andaman coast will be held on Friday evening.

Oral and Poster instructions: The oral presenter that using a digital presentation in particular should load their presentation at the preparation room (BON) at least 3 hours before the talk. The poster session will be held on Tuesday evening, and the authors should stand with their posters during the session.

CONFERENCE PROGRAM

Sunday, 18th July: Registration starts from 10:00 to 16:00. Welcome Icebreaker will be held at Kata Beach Hotel from 17:30 to 20:00. Buses leave the conference venue at 16:30 and return at 20:00.

Monday, 19th July: Registration starts from 08:00, opening ceremony begin at 09:00-10:00, and scientific sessions start from 10:00 to 17:00.

Tuesday, 20th July: Registration starts from 08:00, scientific sessions from 09:00 to 16:30 Three-hour poster session is planned for Tuesday evening (from 17:00 - 20:00) at the Grand Ballroom Hall, presenters to discuss their work with conference participants.

Wednesday, 21st July: Free day or optional trips

Thursday, 22nd July: Registration starts from 09:00, scientific sessions from 09:00 to 17:30.

Friday, 23rd July: Registration starts from 09:00, scientific sessions from 09:00 to 15:00. General assembly and closing ceremony from 15:00-16:30. Conference dinner will be held at Kata Beach Hotel from 17:30 to 22:00. Buses leave at 16:30 from the Royal Phuket City Hotel and return at 22:00.

CONFERENCE SCHEDULE

World Congress of Malacology
Phuket, Thailand, 18-24 July 2010

Sunday 18th July 2010:

Registration	10:00-16:00
Poster preparation	10:00-16:00
Icebreaker (Kata Beach Hotel)	16:30-20:00

Monday 19th July 2010

Registration	08:00-17:00
Opening ceremony	09:00-10:00
Scientific sessions (Oral)	10:00-17:00
UM Council meeting	16:00-17:00

Tuesday 20th July 2010

Registration	08:00-17:00
Scientific sessions (Oral)	09:00-17:00
Poster session	17:00-20:00

Wednesday 21st July 2010

Congress tours	

Thursday 22nd July 2010

Registration	09:00-16:00
Scientific sessions (Oral)	09:00-17:00

Friday 23rd July 2010

Registration	09:00-12:00
Scientific sessions (Oral)	09:00-15:00
UM Council meeting	14:00-15:00
General Assembly and Closing ceremony	15:00-16:30
Farewell dinner	16:30-22:00

SCHEDULE

	18 July 2010
10:00-16:00	**REGISTRATION AND POSTER PREPARATION**
16:30-20:00	**ICEBREAKER**

	19 July 2010			
09:00-10:00	**OPENING CEREMONY (BALLROOM I)**			
	Room 1 **BALLROOM I**	**Room 2** **BALLROOM II**	**Room 3** **NAKHA**	**Room 4** **RAYA**
10:00-12:30	Emerging Molluscan	The Last 50 Years of Malacology	Opisthobranch	Biology and Evolution of Limpets
12:30-13:30	**Lunch**			
13:00-17:00	Emerging Molluscan	The Last 50 Years of Malacology	Opisthobranch	Biology and Evolution of Limpets

	20 July 2010			
09:00-12:00	Open Session I	The Last 50 Years of Malacology	Opisthobranch	Freshwater Bivalves
12:00-13:00	**Lunch**			
13:00-17:00	Open Session I	Reproduction and Mating Systems	Asian Land Snails	Freshwater Bivalves
17:00-20:00	**POSTER SESSION**			

	21 July 2010 CONGRESS TOUR

	22 July 2010			
09:00-12:00	Open Session II	Evolutionary Ecology and Genetics	Speciation	Evolution of Bivalvia
12:00-13:00	**Lunch**			
13:00-17:00	Open Session II	Evolutionary Ecology and Genetics	Speciation	Evolution of Bivalvia

	23 July 2010			
09:00-12:00	Open Session III	Evolutionary Ecology and Genetics	Ecology of Land Snails	Aquaculture
12:00-13:00	**Lunch**			
13:00-15:00	Open Session III	Countdown 2010	Ecology of Land Snails	Aquaculture
15:00-16:30	**GENERAL ASSEMBLY AND CLOSING CEREMONY**			
16:30-22:00	**FAREWELL DINNER**			

Monday 19 July, 2010

Room 1 (BALLROOM I)

Emerging Molluscan Models: Biological Questions in the 21st Century

MÓNICA MEDINA, SANDIE DEGNAN AND SAM LOKER

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09:50-10:00	**Symposium Introduction**	
10:00-10:30	Genomic Innovation and Evolution of the Molluscan Shell **Bernard M. Degnan**	1
10:30-11:00	Phylogenetic and Transcriptomic Analyses of Complex Character Trait Evolution in Cephalopods **Todd H. Oakley, Annie R. Lindgren and M. Sabrina Pankey**	2
11:00-11:20	**Coffee/Tea**	
11:20-11:50	Scallop Eyes as a Model for Evolutionary Change from Developmental to Macroevolutionary Timescales **Jeanne M. Serb**	3
11:50-12:20	The Snail *Ilyanassa* as a Model for Asymmetric Cell Division and the Evolution of Development **David Lambert**	4
12:20-13:30	**Lunch**	
	CHAIR: SANDIE DEGNAN	
13:30-14:00	Tradeoffs between Host Selection and Environmental Adaptation: What Experimental Evolution Can Tell Us in a Squid-luminous Bacterium Mutualism **Michele K. Nishiguchi**	5
14:00-14:30	Bridging the Eco-Devo Divide: Molecular Ecology of Larval Settlement in a Tropical Abalone **Sandie M. Degnan**	6
14:30-15:00	Emerging Frontiers of Molluscan Genomics: from Phylogeny to Memory Mechanisms **L. L. Moroz**	7
15:00-15:30	*Biomphalaria* and Its Trematode Parasites: A Model Host-Parasite System with Medical Relevance **Eric S. Loker**	8
15:30-15:50	**Coffee/Tea**	
	CHAIRS: MÓNICA MEDINA AND SAM LOKER	
15:50-16:10	Mega-hemocyanin: A New Character System for Assessing Phylogeny of the Cerithioidea (Caenogastropoda) **Bernhard Lieb, Ellen E. Strong, Wolfgang Gebauer, M. G. Harasewych and Jürgen Markl**	9
16:10-16:30	Exploring the Endocrine System of *Potamopyrgus antipodarum* (Freshwater Mudsnail) **Daniela Stange, Ralf Horres and Jörg Oehlmann**	10

16:30-16:50 Preclinical Trials for the Development of an Anticancer Complementary Medicine from Muricid Whelks
Kirsten Benkendorff, Chantel Westley, Richard Le Leu and Catherine Abbott……………………………………………………………… **11**
16:50-17:10 Growth-Related Gene Expression in *Haliotis midae*: Analysis of Transcriptome Sequence Data Using Next Generation Sequence Technology and Quantitative Real-Time PCR
Mathilde van der Merwe and Rouvay Roodt-Wilding……………………….... **12**
17:10-17:30 The Slipper Snail, *Crepidula:* A Model System for the Evolution of Life Histories and Development
Rachel Collin, Jonathan J. Henry and Frédérique Viard…………………... **13**
17:30-17:50 Molluscan Biomineralization: A Comparative Genomics Approach
Bishoy Hanna, Christian Voolstra and Monica Medina…………………….. **14**
17:50-18:10 Comparative Analysis of Gene Expression for Convergent Evolution of Camera Eye between Octopus and Human
Kazuho Ikeo and Takashi Gojobori………………………………………… **15**
18:10-18:30 Giant Clams (Tridacnidae) Host Basal Lineages of the Symbiotic Dinoflagellate, Symbiodinium
Michele Weber……………………………………………………………... **16**

Monday 19 July, 2010

Room 2 (BALLROOM II)

The Last 50 Years in Malacology: Specialization, Methodological Transformation and Globalization

ROBERT HERSHLER AND DAVID LINDBERG

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	SYMPOSIUM INTRODUCTION **CHAIR:** DAVID LINDBERG	
09:50-10:00	**Symposium Introduction**	
10:00-10:20	Advances in Visualizing Molluscan Structure	
	Carole S. Hickman……………………………………………………...……………	**17**
10:20-10:40	Malacology in the Molecular Age	
	M. G. Harasewych……………………………………………………….……………	**18**
10:40-11:00	The Impact of Cladistic Methodology in Molluscan Research	
	Rüdiger Bieler……………………………………………………………………..	**19**
11:00-11:20	**Coffee/Tea**	
11:20-11:40	Measuring and Modeling Molluscan Morphology: The Legacy of D'Arcy Thompson	
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11:40-12:00	Exploring New Habitats, from Deep-sea to Ancient Lakes: The *Galathea* Legacy and the Transformation of the 'Linnean Apostles'	
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12:00-12:20	A Complicated Relationship with Our New Yearning for Metadata Sources in the 21st Century	
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	Robert Hershler and Robert Cowie…………………………….………………	**23**
	THE ORGANIZATIONS AND PEOPLE **CHAIR:** ROBERT HERSHLER	
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	Edmund Gittenberger……………………………………………………….…...	**25**
14:30-14:50	Publishing in Malacology: Past, Present, and Future Trends	
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	Philippe Bouchet…………………………………………………………….………	**27**
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Monday 19 July, 2010
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Studies on Opisthobranchs Molluscs
MANUEL MALAQUIAS, JUAN LUCAS CERVERA AND TERRY GOSLINER

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	CHAIR: TERRY GOSLINER	
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10:00-10:20	The Long Way to Diversity – a Current View on the Phylogeny and Evolution of Heterobranchia (Mollusca: Gastropoda) **Annette Klussmann-Kolb, Katrin Göbbeler, Vanessa Grätz and Angela Dinapoli**	36
10:20-10:40	Reducing an Enigma: Placing the Vermiform Rhodopomorpha (Gastropoda) in a Phylogeny **Nerida G. Wilson, Katharina Jörger and Michael Schrödl**	37
10:40-11:00	The End of the Guessing Game? Origin and Evolution of Acochlidia (Gastropoda: Heterobranchia) **Katharina M. Jörger and Michael Schrödl**	38
11:00-11:20	**Coffee/Tea**	
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11:40-12:00	The First Molecular Phylogeny of Cladobranchian Opisthobranchs (Mollusca, Gastropoda: Nudibranchia) **Marta Pola and Terrence M. Gosliner**	40
12:00-12:20	Evolution of the Scylllaeidae (Nudibranchia: Dendronotina) with a Revision of *Notobryon* **Terrence M. Gosliner and Marta Pola**	41
12:20-13:30	**Lunch**	
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13:50-14:10	Are the Sacoglossans *Elysia timida*, *Bosellia mimetica* and *Thuridilla picta* (Gastropoda: Opisthobranchia) Truly Amphiatlantic Species? A Molecular Approach **Leila Carmona, Terrence M. Gosliner, Marta Pola, Manuel António E. Malaquias and Juan Lucas Cervera**	43
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14:50-15:10 Functional Chloroplasts in Metazoan Cells: Evolution in Sacoglossa (Opisthobranchia)
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CHAIR: BENOÎT DAYRAT

15:30-15:50 Secondary Metabolites versus Kleptocnides in Cladobranchia (Nudibranchia: Gastropoda)
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15:50-16:10 120 Years After Strubell: 3D Microanatomy and Biology of the Limnic Acochlidian Slug *Strubellia* Odhner, 1937
Bastian Brenzinger, Timea P. Neusser, Katharina M. Jörger and Michael Schrödl…………………………………....................................... **48**

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Monday 19 July, 2010

Room 4 (RAYA)

The Biology and Evolution of Limpets

ALAN HODGSON

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10:00-10:20	Limpets as Models for Exploring Behaviour and Its Constraints **Mark Davies**…………………………………………………………………	**56**
10:20-10:40	Limpet Aggregation: Causes Not Consequences **Ross Coleman**…………………………………………………………...……	**57**
10:40-11:00	Responses of Limpets to Thermal Stress in a Changing World: What We Know and What We Need to Know **Gray A. Williams, Yunwei Dong, David Morritt, Ng Wai-Chuen and Maurizio de Pirro**……………………………………….……………………	**58**
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17:30-17:50 Interactive 3D-Anatomy and Affinities of Bathysciadiidae (Gastropoda: Cocculinoidea), Deep-sea Limpets Feeding on Decaying Cephalopod Beaks
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Tuesday 20 July, 2010

Room 1 (BALLROOM I)

Open Session I

SOMSAK PANHA

CHAIR: SOMSAK PANHA

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09:20-09:40	Research on Micro Molluscs at the Zoölogisch Museum Amsterdam with Some Bizarre Examples **Robert G. Moolenbeek**	**75**
09:40-10:00	The Taiwan Malacofauna Database and Shell-Culture Diversity **Wen-Lung Wu**	**76**
10:00-10:20	New Generation Sequencing and Molluscs: A Leap Forward **Sónia Andrade, Caitlin Feehery, Freya Goetz, Stephen Smith, Nerida Wilson, Gonzalo Giribet and Casey Dunn**	**77**
10:20-10:40	**Coffee/Tea**	
10:40-11:00	Mollusca Aplacophora – Clade or Grade? **Christiane Todt and Christoffer Schander**	**78**
11:00-11:20	Molecular Phylogeny of Aplacophoran Molluscs: Inferences from Mitochondrial Genes **Nina T. Mikkelsen, David Osca Ferriol, Christoffer Schander and Christiane Todt**	**79**
11:20-11:40	The Nervous System of *Scutopus ventrolineatus* (Caudofoveata): A Study Using Histology and 3D-reconstruction **Emanuel Redl Thomas Schwaha, Christiane Todt, Christoffer Schander and Luitfried Salvini-Plawen**	**80**
11:40-12:00	Development of the Excretory System in a Polyplacophoran **Natalie Baeumler, Gerhard Haszprunar and Bernhard Ruthensteiner**	**81**
12:00-13:00	**Lunch**	
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The Last 50 Years in Malacology: Specialization, Methodological Transformation and Globalization

ROBERT HERSHLER AND DAVID LINDBERG

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KURT JORDAENS AND JORIS KOENE

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TAKAHIRO ASAMI

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Speciation: Insights from Insular Isolation to Global Patterns

MATTHIAS GLAUBRECHT

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RÜDIGER BIELER, GONZALO GIRIBET AND PAULA MIKKELSEN

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ORAL PRESENTATION

Tropical Natural History, Supplement 3, July 2010

Genomic Innovation and Evolution of the Molluscan Shell

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The rapid appearance of disparate molluscan forms during Lower Cambrian leaves open the possibility that shells evolved in parallel and independently in at least some classes. To test this proposition we sequenced >12,000 expressed sequence tags (ESTs) from the nacre-forming region of the mantles of the vetigastropod *Haliotis asinina* and the bivalve *Pinctada maxima*. Despite both species having highly lustrous nacre, we find extensive differences in their EST sets. This is particularly pronounced in the genes encoding secreted proteins that may localize to the organic shell matrix, with less than 15% of being shared between *H. asinina* and *P. maxima*. We also detect differences in other extracellular proteins involved in shell formation. For example, chitin-processing genes are expressed in *P. maxima*, but not in *H. asinina*, consistent with calcification proceeding differently in these species. These differences extend to comparisons within the Gastropoda (*Haliotis* vs. *Lottia*), and across three species of *Pinctada*, suggesting that the molluscan shell forming secretome is rapidly evolving. Despite these large-scale differences, *H. asinina* and *P. maxima* both secrete proteins with repetitive low complexity domains (RLCDs). *P. maxima* RLCD proteins – e.g. the shematrins - are predominated by silk/fibroin-like domains, which are absent from the *H. asinina* dataset. These results are consistent with shell formation in bivalves and gastropods having a long period of independent evolution. The prevalence of RLCD proteins in both EST sets suggests these transcriptomes have either evolved in parallel, evolving from a deeply homologous ancestral mantle, or evolved convergently from separate soft-bodied ancestors of these molluscan classes. The presence of RLCD proteins in other metazoans, such as echinonoids, suggests that selective forces for such proteins have acted across the Metazoa during the evolution of disparate biocalcification strategies.

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Phylogenetic and Transcriptomic Analyses of Complex Character Trait Evolution in Cephalopods

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An important question in evolutionary biology is to what extent the same genes are used in the convergent origin of similar phenotypes. Understanding this question requires a good knowledge of phylogenetic relationships and data on the genetic basis of convergent traits. We are examining convergent traits in cephalopods by studying their phylogenetic relationships and by using transcriptome sequencing to determine genes expressed two separate trait systems: light organs - the light-producing and directing organs of bioluminescent cephalopods, and corneas – the transparent tissue covering cephalopod eyes that is derived developmentally from ectodermal skin. To clarify relationships among cephalopods and test for phylogenetic homology of these traits, we generated a MySQL database comprised of all available molecular data for approximately 450 taxonomic units. We then analyzed this concatenated super-matrix dataset using parsimony, likelihood and Bayesian methods under a variety of alignments, parameter-schemes, and sub-matrices. Results support the phylogenetically non-homologous origins of light organs. First, symbiotic light organs (that house luminescent bacteria) evolved at least twice. In addition, our results support the idea that autogenic light organs (where cephalopod proteins catalyze the light reaction) have evolved multiple times. Our results also support phylogenetically non-homologous origins of one-part and two-part cornes in the squid and octopod lineages, respectively. To examine the molecular basis of these convergent phenotypes, we are analyzing gene expression data obtained from 454 pyrosequencing. The bacteriogenic light organ of *Euprymna scolopes* is itself convergent with eyes, and possesses the molecular, biochemical, and physiological capability for light detection. Although we do not currently have evidence that vision genes are also expressed in the phylogenetically non-homologous light organ of *Uroteuthis edulis*, other important genes like reflectins and crystallins are expressed in both the *Uroteuthis* and *Euprymna* organs. As large scale sequencing has become feasible for many traits across taxa, we can now begin to address questions of how entire transcriptomes evolve in convergent traits, to what extent the same or different genes are used, and to what extent rates of molecular evolution vary in association with evolutionary changes in phenotype.

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Scallop Eyes as a Model for Evolutionary Change from Developmental to Macroevolutionary Timescales

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Evolution of the eye is the result of genetic change through modularity, duplication, and co-option of gene networks. To study these processes, it is necessary to go beyond traditional model organisms for a more comprehensive taxonomic representation of the metazoan phylogeny. Yet, despite the number of protostome lineages possessing eyes, only a couple of non-arthropod species have been examined. The scallop (Pectinidae) is an excellent molluscan model to study evolution of the eye as they have 1) two life stages with different visual requirements met by two morphologically distinct eye types; 2) the adult eye has image-forming capabilities and contains two subfamilies of opsins; and 3) an array of species-specific behaviors which may have different visual requirements and are exhibited in a range of photic habitats. Recently, my lab has generated a multigene phylogeny for the Pectinidae that has identified convergent and parallel transitions between behavioral classes (life habit). Here I examine three levels of biological organization, the organism, gene expression profile of the eye, and variation in proteins involved in vision, to determine the degree of repetitive evolution and identify how changes at one level may influence other levels of biological organization.

The Snail *Ilyanassa* as a Model for Asymmetric Cell Division and the Evolution of Development

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As the embryo of the snail *Ilyanassa* reemerges as a model for studies of animal development, molecular tools that have been developed in the last 15 years are complementing a century of descriptive and experimental embryology. The embryo has a number of experimental and practical advantages that make it one of the most capable models for the study of the widely conserved but poorly understood mode of early embryogenesis known as spiralian development. It also has particular advantages for studies of asymmetric cell division and RNA subcellular localization that make it an excellent complement for traditional models of these processes. I will describe spiralian development and *Ilyanassa* as an experimental system. I will then describe recent results that provide the first mechanistic understanding of a key aspect of spiralian development, the generation of developmentally distinct micromere quartets, and discuss the evolutionary implications of these findings.

Tradeoffs between Host Selection and Environmental Adaptation: What Experimental Evolution Can Tell Us in a Squid-luminous Bacterium Mutualism

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The dynamic mutualism between *Vibrio* bacteria and bobtail squids (Cephalopoda: Sepiolidae) has provided a window for observing the mechanisms by which free-living symbiotic *Vibrios* are subject to the selection pressures of both environment and host simultaneously. Abiotic factors (*i.e*., temperature, salinity) certainly have an effect on the competitive dominance of *Vibrio* symbionts that colonize different species of squid host, with secondary colonization events by invading non-native *V. fischeri* occurring. To determine whether a successful infection by a non-native *Vibrio* in a different squid host has specific fitness consequences associated with this switch, we experimentally evolved an isogenic strain of Hawaiian *V. fischeri* ES114 (*V. fischeri* JRM200) into a novel squid host from Australia, *Euprymna tasmanica* over 500 generations in 24 different lineages. Since a "frozen fossil record" of symbionts can be generated, the evolving non-native clone was monitored every 100 generations to determine if its competitive ability had improved relative to native strains of *V. fischeri*. In addition, the relative competitive ability of the derived non-native strain was compared to the ancestral *V. fischeri* ES114 to determine if fitness was improved through adaptation. Non-native *V. fischeri* JRM200 demonstrated rapid adaptation to *E. tasmanica* within 500 generations by serial passage providing evidence that competitive dominance can be neutralized with phenomena such as founder effects due to tight genetic bottlenecks. Further examination of a multiple 500th generation clones by whole genome sequencing has provided intriguing evidence that specific genes are targeted when selection to a novel host is driving bacterial speciation, granting non-native *Vibrios* an opportunity to establish foothold beachheads in foreign *Euprymna* hosts.

Bridging the Eco-Devo Divide: Molecular Ecology of Larval Settlement in a Tropical Abalone

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A huge proportion of marine invertebrates, including many molluscs, have a biphasic lifecycle comprising a planktonic, dispersal phase (the larva) and a benthic, reproductive phase (the adult). Dispersal ends when the larva detects an appropriate environmental cue that induces settlement out of the plankton and metamorphosis into the adult form. Larval experience at settlement can significantly affect adult fitness, and thus population ecology, structure and evolution. The tropical abalone, *Haliotis asinina*, is an ideal mollusc for studying the interplay between ecology and development during this crucial life history transition of settlement and metamorphosis. Building on extensive knowledge of phylogeography, reproduction, embryonic and larval development in this species, we recently have identified a variety of natural algal cues that induce up to 100% of *H. asinina* larvae to metamorphose, and a suite of candidate genes involved in abalone settlement and metamorphosis. Having this unique suite of resources in hand has allowed us to experimentally demonstrate that, although all post-larvae metamorphose in an identical morphological manner, their gene expression profiles differ according to which species of coralline algae is used to induce settlement! Many genes continue to be differentially expressed for at least 40 hours after removal of the algae, clearly demonstrating a substantial carry-over effect of inductive cue on gene expression. Interestingly, many of the effected genes encode proteins that appear to play a role in sensing the external environment. It has long been realised that larval experience prior to and during metamorphosis can significantly affect adult fitness, and our data now highlight gene expression as a mechanism that can mediate between larval and post-larval experiences.

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Emerging Frontiers of Molluscan Genomics: from Phylogeny to Memory Mechanisms

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For more than 70 years Gastropod and Cephalopod molluscs have served as powerful model organisms for comparative biology and neuroscience in particular. They represent a broad spectrum of complexity in their neuronal organizations: from numerically simpler nervous systems with giant identified neurons to one of the most complex brains in the animal kingdom. However, a major limitation in the field has been the lack of genomic information. As the initial steps in this direction, the genomes from three gastropod species (*Aplysia, Lottia* and *Biomphalaria*) have been sequenced. Furthermore, we have sequenced >5,000,000 ESTs/cDNAs from key model gastropod (*Aplysia, Philaplysia, Pleurobranchaea*, *Clione*, *Tritonia*, *Hermissenda, Melibe, Lymnaea,* and *Helisoma*) and cephalopod (*Nautilus*, *Octopus*, *Loligo* and *Rossia*) molluscs. These sequences (derived from developmental stages and various tissues) were assembled and cross-annotated primarily using the extensive transcriptome and genomic information from *Aplysia californica*.

Here, I will present a comparative analysis of these genomes and transcriptomes. *First*, this approach allowed us to identify both evolutionarily conserved neuronal genes and numerous genomic innovations within the phylum Mollusca including novel genes encoding signal molecules such as neuropeptides, prohormones and components of developmental programs. Molluscs have relatively slow evolving genomes allowing us to reveal numerous examples of extensive gene loss and gain across animal phyla (primarily associated with immunity, development and neuronal functions). *Second*, we have implemented several novel approaches that allowed us to characterize nearly all RNAs and epigenomic modifications in single functionally characterized neurons of the feeding and defensive neural circuits. As a result we were able to experimentally address three fundamental problems: (i) the logic controlling regulation of the entire genome in different neurons, (ii) parallel evolution and maintenance of the enormous diversity of neuronal cell lineages (homologous neurons) and (iii) identification of evolutionarily conserved molecular toolkits underlying learning and memory mechanisms. I will illustrate results from this analysis suggesting that injury-associated mechanisms leading to secretion of signal peptides (and related molecules) can be considered as evolutionary predecessors of various forms of memory and as major factors in the appearance of neurons in the first place. Similar evolutionary logic has also been applied to explain complex transcriptome responses following plasticity tests, leading to development of a model for parallel evolution of neurons and plasticity mechanisms.

The established molecular resources and the ability to map gene expression in a diversity of species should allow detailed study of the molluscan phylogeny, a new hypothesis will be discussed here, and evolution of various biochemical, developmental and neuronal systems as well as provide a critical bridge between genes, circuits and behavior in the broad evolutionary context. [Support Contributed By: NIH, NSF, and McKnight Brain Research Foundation].

Biomphalaria and Its Trematode Parasites: A Model Host-Parasite System with Medical Relevance

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The role played by gastropods in transmission of medically important helminths such as schistosomes has provided the impetus to develop new tools and approaches to advance the study of molluscan biology. Studies of *Biomphalaria glabrata* and two of its trematode parasites, *Echinostoma paraensei* and the human-infecting *Schistosoma mansoni*, have helped catalyze the *B. glabrata* genome project, production of BAC libraries and microarrays, and stimulated development and application of reverse genetics approaches. Taking advantage of these tools, the course of trematode development in susceptible snails has been shown to be characterized by a pronounced and persistent down-regulation of snail immune genes. In contrast, three models of snail resistance to trematode infection all show a preponderance of up-regulated immune features, including FREP3 (fibrinogen-related protein 3). The latter is of particular interest because the FREP3 gene is somatically diversified with involvement of gene conversion and point mutation. Application of RNAi using siRNAs targeting FREP3 has been shown to diminish the resistance normally exhibited by adult *B. glabrata* to *E. paraensei*. Use of this model system has also confirmed that exposure of juvenile *B. glabrata* to irradiation-attenuated miracidia of *E. paraensei* renders these snails resistant to challenge with normal miracidia of the same species, a phenomenon called “acquired resistance”. Array profiles of snails with acquired resistance indicate they respond in a distinctive fashion to trematode challenge, with FREP3 a conspicuous part of the response. These studies have also identified a number of other molecules with a potential role in resistance. Our studies point out a role for somatic diversification in invertebrate immune defense and help to explain how heightened levels of responsiveness could be achieved in organisms lacking the anatomical complexity associated with the adaptive immune system of vertebrates. [This study was supported by NIH grant R01AI24340 and NCRR P20RR18754].

Mega-hemocyanin: A New Character System for Assessing Phylogeny of the Cerithioidea (Caenogastropoda)

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The superfamily Cerithioidea is a basal lineage of the Caenogastropoda with marine, brackish and freshwater representatives primarily in tropical and subtropical regions worldwide. Recent molecular and combined morphological and molecular analyses are beginning to converge on a consistent pattern supporting three main clades, but relationships within these clades remain unclear. Recently, we discovered and described a new subtype of the respiratory protein hemocyanin from a member of the superfamily. In addition to the 400 kDa subunit typical for all other gastropod hemocyanins, this new "mega-hemocyanin" contains a large 500 kDa subunit – one of the largest polypeptides ever reported. As hemocyanin sequences have proven to be informative in resolving affinities of a number of molluscan lineages (e.g., Aplacophora, Polyplacophora, Haliotidae), the goal of the present study was to assay the distribution of mega-hemocyanin among other caenogastropods and to explore the utility of this new character system for assessing the phylogeny and affinities of the Cerithioidea.

Of 17 families currently included in the Cerithioidea, we verified expression of mega-hemocyanin in representatives of three freshwater families (Melanopsidae, Pleuroceridae and Thiaridae) and five marine/brackish families (Batillariidae, Cerithiidae, Modulidae, Planaxidae, Potamididae), together representing all three main cerithioidean clades. In contrast, mega-hemocyanin was found to be absent in all the caenogastropod outgroups tested as yet, including members of the Architaenioglossa and Neogastropoda. Thus, mega-hemocyanin appears to be restricted to the Cerithioidea, thereby supporting monophyly of the group as currently conceived. Structural and functional details of mega-hemocyanin in the context of ecophysiological and phylogenetic implications will be discussed.

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Exploring the Endocrine System of *Potamopyrgus antipodarum* (Freshwater Mudsnail)

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Molluscs are becoming more and more popular in scientific research due to their high diversity and importance in aquatic ecosystems. Hence, molluscs are also gaining more attention as ecotoxicological test organisms. The prosobranch, ovoviviparous gastropod *Potamopyrgus antipodarum* responds very sensitive to endocrine disruptors and is therefore proposed as OECD standard test organism. However, the knowledge about the endocrine system of prosobranch gastropods is rather limited, so we investigated the influence of hormones on *P. antipodarum* as well as the existence and regulation of hormone receptors.

We exposed *P. antipodarum* to androgenic (methyltestosterone, triphenyltin) and estrogenic (17α-ethinylestradiol, sewage effluent) substances and determined the reproductive performance of the snails by counting the embryos of each snail. Snails exposed to androgenic substances showed a significant decreased embryo production compared to unexposed snails while snails exposed to estrogenic substances showed a significant increased embryo production. Furthermore we cloned an estrogen receptor analogue and determined a transcriptional up-regulation of this receptor under 17α-ethinylestradiol exposure. Via subtractive hybridization and 454-sequencing more hormonally regulated transcripts were identified which hints at an involvement of steroid hormones and associated pathways in the endocrine system of *P. antipodarum*.

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Preclinical Trials for the Development of an Anticancer Complementary Medicine from Muricid Whelks

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The Muricidae are a family of predatory marine molluscs well known for the production of the dye Tyrian purple. The precursors and pigments of Tyrian purple include bioactive brominated indoles and indirubins which are known to have anticancer and anti-inflammatory activity. The purple dye secretion from muricids is also the source of a homeopathic remedy called *Murex*, which is used for a range of conditions, including cancer. Like most homeopathic remedies, *Murex* has never been tested for biological activity or toxicity. Consequently, our aim was to compare the chemical composition and cytotoxic activities of the *Murex* remedy, against organic extracts from the egg masses of the Australian Muricidae *Dicathais orbita*. Liquid chromatography-mass spectrometry revealed only minor traces of 6 bromoisatin in the *Murex* remedy, whereas *D. orbita* extracts were dominated by tyrindoleninone. Cell proliferation assays revealed no significant anticancer activity in the *Murex* remedy, whereas the *D. orbita* extracts significantly inhibited a range of human carcinoma and lymphoma cell lines. The *D. orbita* extracts were then tested in an *in vivo* preclinical trial for prevention of colon cancer. Enhancement of acute apoptotic response to genotoxic carcinogens was assessed by daily oral administration to mice, at a maximum dose of 1mg/ml. A dose-dependent increase in apoptotic index was observed in the distal colon, with a significant increase detected at an extract dose of 1.0mg/g ($P<0.05$). *Dicathais* extract also appears to confer no major toxic side effects, as all mice consistently gained weight during the trial and colonic crypt height was maintained ($P>0.05$) independent of dose. The protective effect of *Dicathais* extract against colorectal cancer *in vivo* clearly substantiates further research into the development of Muricidae natural products as complementary anticancer medicines.

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Growth-Related Gene Expression in *Haliotis midae*: Analysis of Transcriptome Sequence Data Using Next Generation Sequence Technology and Quantitative Real-Time PCR

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The abalone is a mollusc valued for its flesh, especially in Asian markets. The South African abalone, *Haliotis midae,* is regarded as a high-value species and the local abalone cultivation industry is considered the largest producer outside Asia. The increasing demand for marine shellfish has stimulated research on the biology and physiology of target species, such as abalone. At a fundamental level, investigation of the transcriptome of an organism can be highly informative. To investigate the transcriptome and gene expression, next generation sequencing is emerging as an attractive alternative to microarrays. While high throughput sequencing generates a large amount of information in a short time, quantitative real-time PCR (qPCR) remains the gold standard for nucleic acid quantification.

This paper reports the progress towards elucidation of transcriptome and gene expression data for *Haliotis midae*, generated with Illumina sequencing and qPCR. Fast and slow growing abalone from the same full-sib family were sampled for whole transcriptome sequencing. CLC Genomics Workbench was used to analyse differential expression between the two samples and differentially expressed sequences were BLASTed to public databases, and databases containing growth implicated sequences from closely related mollusc species. A number of relevant sequences were selected and used in qPCR experiments to compare expression between fast and slow growing abalone and fast and slow growing abalone haemocyte cell cultures.

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The Slipper Snail, *Crepidula*: A Model System for the Evolution of Life Histories and Development

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A recent surge in developmental, life history, and genomic research focused on "slipper snail" limpets in the genus *Crepidula* has resulted in the emergence of *Crepidula fornicata* as a *de facto* model system for the evolution of life histories and development. We review recent developments, demonstrating the utility of this genus in diverse studies of evolution and development. Recent studies have resulted in a well-resolved embryonic cell lineage fate map, documented mechanisms for axis determination and D quadrant specification, preliminary gene expression patterns, the application of loss-and gain-of-function assays, as well as the development of ESTs and preliminary genomics work that will promote the use of this system, particularly in the area of developmental biology. These data can be combined with a wealth of comparative information on phylogenetic relationships and updated taxonomy to provide a powerful framework for comparative studies. The extensive variation in mode of development within the family makes the group ideal for comparisons between direct developers and species with planktotrophic development. The numerous studies on larval biology and metamorphosis, primarily in *Crepidula fornicata,* provide a powerful tool for understanding the morphological and physiological changes that take place during metamorphosis. Recent studies of the nitric oxide synthase pathway combine studies of larval biology with data from genomics to shed light on the mechanisms controlling metamorphosis. Finally a summary of the studies on the life histories of *Crepidula* would not be complete without a discussion of sex change, an area in which we believe that genomics approaches have a lot to offer.

Molluscan Biomineralization: A Comparative Genomics Approach

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Mollusks have always been central to biomineralization research. Yet only a small number of the proteins involved in the process have been identified mainly due to the difficulties in isolation and characterization of such proteins. By trying to tackle the evolutionary origins of metazoan biomineralization via comparative genomic approaches (i.e. transcriptomics) we may able to identify new genes involved in the molluscan biomineralization secretome. In order to test different hypotheses related to the evolution of the biomineralization toolkit we developed a bioinformatics pipeline that we used to identify shared protein families involved in biomineralization related processes across cnidarians, mollusks, echinoderms, and vertebrates. By constructing a comprehensive list of biomineralization proteins from the scientific literature and the Gene Ontology project database AMIGO, we identified all Pfam domains associated with the candidate protein list. Using a combination of the HMMER package and BLAST in whole genome sequences and EST datasets, we were able to look at the distribution of shared families between all these different groups. A web-based database was constructed to cater for all the data generated through the pipeline and is available at http://sequoia.ucmerced.edu/biomin/. Our analysis has allowed the identification of a shared toolkit as well as molluscan specific innovations.

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Comparative Analysis of Gene Expression for Convergent Evolution of Camera Eye between Octopus and Human

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Although the camera eye of the octopus is very similar to that of humans, phylogenetic and embryological analyses have suggested that their camera eyes have been acquired independently. It has been known as a typical example of convergent evolution. To study the molecular basis of convergent evolution of camera eyes, we conducted a comparative analysis of gene expression in octopus and human camera eyes. For this purpose, we conducted transcriptome analysis of the octopus eye, leading to 1052 nonredundant genes that have matches in the protein database. Comparing these 1052 genes with 13,303 already-known ESTs of the human eye, 729 (69.3%) g enes were commonly expressed between the human and octopus eyes. On the contrary, when we compared octopus eye ESTs with human connective tissue ESTs, the expression similarity was quite low. To trace the evolutionary changes that are potentially responsible for camera eye formation, we also compared octopus-eye ESTs with the completed genome sequences of other organisms. We found that 1019 out of the 1052 genes had already existed at the common ancestor of bilateria, and 875 genes were conserved between humans and octopuses. It suggests that a larger number of conserved genes and their similar gene expression may be responsible for the convergent evolution of the camera eye.

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Giant Clams (Tridacnidae) Host Basal Lineages of the Symbiotic Dinoflagellate, *Symbiodinium*

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Symbiodinium are a diverse clade of dinoflagellates that structurally and energetically support coral reef communities through symbiosis with marine invertebrates and protists. Giant clams are a unique group of host organisms. They host symbionts intercellularly and as derived metazoans, they exclusively reproduce sexually so every individual acquires its symbionts from the water column. Although *Symbiodinium* are also found in symbiosis with corals, sponges and foraminifera, these organisms are often clonal and symbionts are passed down through unknown, indiscreet generations. Dinoflagellates sampled from giant clam hosts represent a subset of the *Symbiodinium* population present in the water column over reefs across the Indo-West Pacific at the time of host spawning and larval settling.

Sampling tridacnid populations in the Red Sea, the Indian Ocean and the Pacific Ocean, I identified major patterns in *Symbiodinium* biogeography over the complete distribution of a single host clade. Phylogenetic analysis grouped the symbionts into three well-known, subgeneric clades, A, C and D. Giant clam symbionts were most diverse in Papua New Guinea and along the East African coast. At the extreme eastern ends of the host distribution, clams hosted only ancestral symbiont phylotypes.

Giant clam symbiont diversity was limited compared to coral and foraminifera hosts. The same symbiont phylotypes were identified in clams from disparate localities despite evidence for a variety of diverse types populating alternative hosts organisms. Although these data showed that divergent lineages occasionally associate with giant clams, it may be that these hosts primarily partner with less specific, basal symbiont lineages because the algae are not tightly associated with host cells or because acquiring symbionts at each generation does not allow strong selection regimes to develop. Symbiont populations collected from giant clam hosts reveal evolutionary patterns in the basal lineages from which additional *Symbiodinium* diversity evolves.

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Advances in Visualizing Molluscan Structure

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Molluscan imagery has undergone a series of dramatic revolutions over the past 50 years. The most important advances in visualizing structure and function result from (1) overcoming the physics limitations on resolution by light microscopy with tools that dramatically increase the signal to noise ratio, (2) increased computational power for rapid manipulation of data and display of images, and (3) new methods of specimen preparation. A non-exhaustive list of tools includes (1) scanning electron microscopy, (2) x-ray elemental microanalysis, (3) confocal laser scanning microscopy, (4) fluorescent protein tags, (5) Raman microspectroscopy, (6) digital photography and videography, (7) computer simulation of coiled shells and pigmentation patterns, (8) fiber optics and fiber optic video transmission from remotely operated vehicles, (9) atomic force microscopy, (10) x-ray computed tomography. In all instances the primary value of the images is not in their beauty, detail, resolution, or speed of acquisition, but in the new questions that they have stimulated and the new research agendas they have launched.

My personal "top ten" list of fruitful applications of new technology is: (1) structure and function of the molluscan radula, (2) form, function, and development of the gastropod larval shell, (3) shell ultrastructure in general and nacre in particular, (4) biomineralization, (5) form and function of the gastropod velum, (6) early development of musculature and nervous system, (7) simulation and analyses of molluscan morphospaces, (8) biology of deep-sea chemosymbioses, (9) growth line formation and interpretation, (10) functional chemistry of byssal thread cuticle. The most elegant research proceeds from using multiple tools and finding new ways to exploit or extend their existing capabilities for visualization.

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Malacology in the Molecular Age

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Like most branches of Invertebrate Zoology, Malacology in the first half of the 20th century was a field dominated by qualitative, descriptive narratives of new taxa, new anatomical and embryological observations, and new evolutionary scenarios. The field of Biochemistry was in its infancy and numerous methodological developments focused on discoveries and detailed analyses of myriad reactions and metabolic pathways within cells. The rediscovery of Mendel's work in the early 20th century presaged the development of mathematical theories of population genetics and natural selection. The discovery that one gene produces one enzyme was made in 1941. In 1953, Watson and Crick documented the double-helix structure of DNA and its role in the genetic transfer of information from one generation to the next. The first complete sequence of a mitochondrion was published in 1981, of a free living organism in 1995, and of a human in 2001. The first "synthetic genome" was created in 2010.

This paper chronicles the staggering pace of new advances in the ability to decipher and quantify information contained in biological molecules and the numerous applications of these forensic techniques in the field of Malacology. The rapid proliferation of discoveries has ushered in an era of quantitative and experimental biology and hypothesis testing that has blurred former distinctions between biology and the physical sciences.

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The Impact of Cladistic Methodology in Molluscan Research

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As in all other branches of organismal biology, the introduction and application cladistic (phylogenetic systematics) approaches had a profound effect on the field of malacology in the past decades. Cladistics, an approach focusing on shared derived characters, is now accepted as the best method available for phylogenetic analysis, providing an explicit and testable hypothesis of organismal relationships and predicting organismal properties. The history, development, and impact of cladistic approaches in molluscan research are traced and compared to other fields of biology, and some key philosophical and practical issues (interpreting anagenesis; translating cladograms into classifications) are addressed.

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Measuring and Modeling Molluscan Morphology: The Legacy of D'Arcy Thompson

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The geometry of molluscan shells has fascinated humans since the earliest formulations of mathematics. Archimedes, Descartes, Bernoulii, and Sir D'Arcy Thompson all formulated equations to quantitatively describe spiral forms and these equations have figured prominently in subsequent models of shell growth. Beginning in the 1960s there was renewed interest in modeling molluscan shell growth, and studies included both fossil and living taxa and addressed both the theoretical and realized patterns of shell form and morphospace occupation. Modeling of molluscan shell growth peaked in the 1980s, and although they appear to be a topic of limited investigation today, there still remains substantial potential in modeling approaches, especially in understanding the occupation of molluscan morphospace in lineages and through time. Morphometric studies of molluscs also predate the last century, but it was during the latter half of the 1900s that morphometric analyses became more robust. Beginning in the 1960s regression analyses of molluscan shell measurements explored allometric relationships between shape and size. These studies were quickly followed by analyses using multivariate approaches. In the late 1970s analyses based on the formalization of D’Arcy Thompson’s Cartesian coordinate system, which previously was a mostly descriptive representation of transformations between forms, became possible, as computer programs provided the analytical power to superimpose and compare landmark data among numerous individuals. These techniques have become collectively known as geometric morphometrics and have provided new insights and descriptions of molluscan morphology. Morphometric methods are not limited to only studies of the molluscan shell and have been used to study numerous molluscan structures and parts, including embryos, radulae, and even sperm.

Exploring New Habitats, from Deep-sea to Ancient Lakes: The *Galathea* Legacy and the Transformation of the 'Linnean Apostles'

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Scientists' interest in the past is intimately tied up with their interest in the future. Hence, this presentation aims at surveying the exploration of new habitats over the past half century, and highlighting some of the milestones, I investigate what we actually gained and learned from those expeditions, what the implications of the new insights were, and whether and how they changed our perception and the position of malacology over the last 50 years.

Admittedly from a subjective perspective (of someone being born too late to have any influence on these advances or to be involved with more than the latest developments), I will ask (i) whether and how malacology and the way we do explorations has actually changed during this period. Are there, and what are the methodological advances, and how did these contribute and/or change our understanding of molluscs from various regions of the biosphere? How did, if at all, the way we perform expeditions change? Convinced that not so much only new data but instead new concepts contribute most to the advances of a scientific discipline and research field, I will also ask (ii) whether and which new concept(s) facilitated the - proclaimed - transformation of malacology.

Marking the begin of these past 50 years, the (second) Danish "*Galathea*" expedition 1950-52 found a place in history as a most successful scientific exploration, with living monoplacophorans discovered in the deep-sea. Reviewing other expeditions into equally "new" (but often biologically old) habitats, such as e.g. hydrothermal vents and cold seeps in the deep-sea, but also those exploring ancient lakes and rivers, artesian springs and archaic mountains on islands and continents, I will make an attempt to document core activities and agendas, evaluate major advances and accomplishments, and identify key contributions and contributors, calling some of them truly 'Linnean apostles'.

A Complicated Relationship with Our New Yearning for Metadata Sources in the 21st Century

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We worry about taxonomists dying off, yet we live in a time of unprecedented awareness of global biodiversity, and also awareness of the systematic documentation and classification of information of all types. Museum scientific collections are physical databases that record large volumes of multi-faceted data on zoological specimens. In some ways, the interaction of a scientist with a collection is the same as interrogating a computer database. Part of the complexity of specimens' data is that the variety of use and applications of specimens has changed and grown over the last fifty years and longer. The forces that promote such changes are both technological and ideological. The ability to extract new kinds of data from old specimens arises from technology (molecular genetic sequences, or new kinds of imaging techniques), or the prevailing trends in larger scientific discourse that prompt new questions. So a single specimen that was collected with taxonomy in mind also lends itself to studies of diversity, range shifts, or trophic structure. Information technology and its use in digitising collections make the data of the physical specimens more available to a wider audience of potential users. It has also given rise to a new modern enthralment with metadata, or data that summarise datasets, as an interesting end in themselves. These web-based projects (mainly taxonomic) have produced a raft of compendia and 'resources' referred to by acronyms, from the ABCD Schema to WoRMS. This presentation will review the history of malacological 'metadata', and attempt to pay tribute to some of the most important international data products for malacology. This history is not a genealogy of competing web-based taxonomic search engines, but an investigation over the last 50 years of the way that we use collections (another kind of tactile database) and how collections of specimens and data will continue to provide the fundament for the broad scope malacology.

Molluscan Conservation 1960-2010

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Numerous species of molluscs, especially those living in nonmarine environments, have become increasingly imperiled (or extinct) in many parts of the world since 1960 and "molluscan conservation" has developed into a critically important component of malacology during this time span. We provide a brief overview of the history of this emerging discipline. We discuss the current state of molluscan conservation and review some of the positive and egregious developments that have taken place during the past 50 years. We also highlight some of the major publications and new focal areas of endeavor in molluscan conservation (e.g. captive propagation, translocation, use of molecular genetics) and analyze publication trends (using Biological Abstracts and Web of Science). The results of this analysis suggest that while a specialty journal may be needed to help accommodate and bring together the burgeoning body of literature in this field (making it more readily accessible), molluscan conservation would also benefit from more frequent publication of reviews and other major papers in high impact journals, thereby drawing more attention to the severe plight of many species. We also acknowledge those colleagues who have played important roles in the growth and development of this discipline over the past 50 years.

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A Brief History of Malacological Meetings, Symposia, and Workshops Since 1930, with an Emphasis on the Last 50 Years

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Malacology gatherings are a classic example of scientific networking: an opportunity to meet new colleagues, renew acquaintances, give presentations on our research, and learn about the projects of others. There have been vast changes in malacological societies, meetings, symposia and workshops since 1930, not only in terms of numbers of events, but also the increased specialization of topics and inter-disciplinary approaches to research.

The two senior authors examined the *Zoological Record*, and other digital and non-digital forms of communication within the malacological community, in order to obtain data on malacological meetings, symposia, and workshops. Not included in this analysis are the meetings of shellfisheries associations, mariculture and aquaculture groups, or shell collector's organizations. We present here the summary of these data and discuss trends over time, particularly the increasing number of symposia and workshops as part of the regular meetings of malacological societies, and an initial rise followed by a decline in the frequency of stand-alone symposia and workshops.

Malacological meetings, symposia, and workshops are an important part of our discipline. Whether large or small, local or international, these gatherings reflect the increased globalization of malacology. These presentations also demonstrate both the increasing specialization in terms of issues and taxa studied, and the substantial improvements in research methodologies over the last half-century.

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Unitas Malacologica and Malacology Evolving Together

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The Unitas Malacologica Europaea started at a birthday party of the Dutch Malacological Society. At that occasion a small group of European museum curators, specialized in malacology, contributed to a symposium. All participants considered the meeting very stimulating and agreed that more regular, international, malacological congresses should be organized in the future, and that's what happened.

The first UME congress was in London, in 1962, to be followed later on by meetings at three year intervals. Very soon the participants of the UME came from all over the world. Reflecting this globalization, the original name was adapted to the present Unitas Malacologica. The society evolved in many aspects. English became the formal language, both at the general meeting and in the symposium sessions. Malacology was represented in a broader sense, far beyond descriptive museum taxonomy. The number of presentations increased considerably, leading to unmanageable voluminous UM Proceedings, that could no longer be published. An important event was the very first UM congress outside Europe, in the USA, and the decision to have the meetings in Europe only at six-year intervals. Many new initiatives were developed, such as the start of a Trust Fund, and the availability of modest travel grants. A Newsletter was issued to ensure better contacts in the malacological world in between the congresses. The current outcome is that the UM is complementary to the local malacological societies in promoting and stimulating world-wide connections. This year's malacological congress in Phuket sets again the stage for future new challenges.

Publishing in Malacology: Past, Present, and Future Trends

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The worldwide technological advances of the past 50 years have transformed how we read, how we conduct research, and as a consequence, how we publish. In 1950, there were only 23 active malacological journals. There was no internet, no email, and no personal computers; the photocopy machine had only just been invented. Malacologists bought books and journals, wrote letters, joined clubs and societies, and attended scientific meetings, but projects were either small in scope or took a long time to complete. Spurred on by a combination of post-WWII prosperity and globalization (including eased international travel), subsequent decades saw a dramatic increase in the number of available malacological serials: 43 in 1960, 93 in 1970, 139 in 1980, 190 in 1990, and 217 in 2000. Society participation (membership and meeting attendance) tracked this 40-year phenomenon closely, and these parallel metrics are only now beginning to wane.

Today, we have 229 active malacological serials, still a huge number for a single discipline, but the number of new titles per year has slowed to a trickle. Malacology and all sciences are conducted radically differently now than in 1950, or even 1980, with ever-increasing reliance on and ease of accessing electronic media and communication. We email from our cell phones, teleconference, prefer pdfs and e-books to hard copies, often choose broader impact journals over malacological titles, and submit and review manuscripts online. Serials publishers have changed accordingly, adopting desktop publishing, electronic subscriptions, e-journals, and digitization projects (such as BioOne and the Biodiversity Heritage Library). This vast transformation is compelling us to rethink the form and nature of academic publishing – from the peer-review process, to tenure review criteria, to the very meaning of the word "published."

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The Last 50 Years: The “Taxonomic Impediment” Challenged

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Conventional wisdom views taxonomists as a declining commodity, and laments a by-gone era of "taxonomic abundance", when taxonomical expertise was plentiful enough to cope with the needs of biodiversity discovery and species descriptions. The current insufficient amount of taxonomical knowledge for science, conservation and management is embodied in the expression "taxonomic impediment", a term that has become a buzz word in science policy as well as in *Convention on Biological Diversity* circles. The lifetime of *Unitas Malacologica* since its foundation happens to coincide with this perceived shift from "taxonomic abundance" to "taxonomic impediment". However, examination of discovery curves and new species authorship does not support the notion of a crash in taxonomic expertise. In fact, if we go back to 80 years ago, there has never been as many new molluscan species descriptions as there are today, and there has never been as many molluscan taxonomists as today. In this respect, the 1960s resembled the 1930s much more than they resemble the 1990s. Where does this perception of "taxonomic impediment" come from, then? In the last 50 years, standards in species descriptions have on the average significantly improved, and the professional duties of academic scientists have become much more diversified, accounting for a real erosion in new species descriptions from academically employed taxonomists. Simultaneously, current sampling programmes and modern collecting techniques yield many times as many specimens and species than in the 1930-1960s, and new observation approaches (SEM, sequencing) are disclosing a world of small, rare and/or cryptic species completely unimagined by our predecessors. We have a "taxonomic impediment" because we have come to realize the magnitude of what is left to discover, describe and name, not because taxonomists are an endangered species.

The Past 50 Years in European Malacology–A Personal View

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It is a hopeless task to present a fair overview on European malacology. Accordingly, I can only present a personal view, how I myself as a malacogist have been influenced by certain working groups and institutions.

In the 1960ies European malacology was dominated by the "Reading School" of Vera Fretter and Alistair Graham. Indeed, "British Prososbranchs" (1962) was my bible during University education (1975-1981). I grew up within the "Austrian School" of Vienna mainly influenced by Oliver Paget, Ferdinand Starmühlner, and Luitfried von Salvini-Plawen: Olli showed me the value of museum collections, Ferry made me familiar with classic anatomy and histology, and Luitfried (my supervisor for Ph.D) introduced me into molluscan phylogeny. After my Ph.D-Thesis I built up an international network in order to get specimens of deep-sea limpets: Among the European colleagues Anders Warén from the Stockholm Riksmseet and Phillippe Bouchet from the Paris Museum were particularly helpful. Both often worked together and represent (my view) the top of European deep-water taxonomy. Major events during my period (1987-1994) at Innsbruck were my habilitation paper on gastropod phylogeny (1988) and the Centenary meeting of the Malacological Society of London (1993). Both events established my relation to the group of the British Museum of Natural History around John Taylor and David Reid, who were responsible also for the Journal of Molluscan Studies, THE leading European journal of malacology. After my call to Munich (1995) I got contact to the Friedrich-Held-Gesellschaft, were in particular Gerhard Falkner introduced me to the taxonomical problems of continental molluscs. The CLECOM-list is the permanent heritage of his group. Last but not least my whole malacological life has been accompanied by the UNITAS-Congresses, which start as European meetings, but now – as malacology as a discipline – have become a truly global exercise.

Last 50 Years of Southern South American Malacology: A Tale of Setbacks and Progress

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The past 50 years of southern South American history were marked by political movements that dramatically impacted scientific production. Knowledge of the molluscan fauna increased in the early 1960's and a number of regional catalogues were published. Several national and other institutions contained small research centers - e.g., J. Parodiz and A. Carcelles and recently P. Penchaszadeh, at the Museo Argentino de Ciencias Naturales "Bernardino Rivadavia"; M. I. Hylton-Scott and later Z. J. A. de Castellanos at the Museo de La Plata – but their initial isolation prevented the high standard and rich productivity that characterizes modern regional malacology.

Brazil has been the fastest growing country on the continent in terms of malacology over the past few decades, with several prominent workers (e.g. E. C. Rios, Museu Oceanografico de Rio Grande; W. Narchi and O. Domaneschi, Instituto de Biociencias da Universidade de São Paulo; J. W. Thomé, Pontificia Universidade Catolica do Rio Grande do Sul; L. Paraense, Instituto "Oswaldo Cruz" founding what is known as Brazilian Malacology. The Sociedad Malacológica del Uruguay has been publishing the Comunicaciones for more than 50 years and the Museo Nacional de Historia Natural, Universidad de la República and Dirección Nacional de Recursos Acuáticos have been active centers of research where M. A. Klappenbach and V. Scarabino are among the most productive researchers. Chile has been a leader in marine aquaculture and contains several important research centers as The Estación Costera de Investigaciones Marinas and productive researchers (e.g. J. C. Castilla; C. S. Gallardo, Universidad Austral; C. Osorio, Facultad de Ciencias de la Universidad de Chile; J. Stuardo, Universidad de Concepción). The Sociedad Malacológica de Chile has been active since 1979. The Congreso Latinoamericano de Malacologia (CLAMA), which has met every three years since 1991, has been the most significant event in South America.

The last 50 years of malacology in the south of South America were characterized by advances based on personal efforts that due to economical and political crisis, the absence of long lasting scientific programs, and paucity of personnel produced periods of low productivity relative to other regions.

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Significant Developments in African Malacology During the Last 50 Years

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African Malacology is still very much in the discovery and documentation phase. Discovery remains a priority and I highlight significant initiatives in this regard. In terms of documentation, the last 50 years has seen a good deal of progress in certain sectors, but much remains to be done. Historically most of the molluscan material collected in Africa was sent to overseas institutions and even today few African countries have scientifically significant reference collections of their molluscan fauna. South Africa, where there was strategic rationalization of collections in the 1980s, is an exception. The strong marine biology research focus at the University of Cape Town and more recently also at Rhodes University has made a seminal contribution to our knowledge of the systematics and biology of marine molluscs. The study of Africa's terrestrial molluscs is dominated by the output of a few productive individuals, but large parts of the continent remain very poorly surveyed and the taxonomy/systematics of many groups is woefully inadequate. In proportion to their diversity, Africa's freshwater molluscs have received far greater attention, largely due to their importance as vectors of human parasites. Even so, species discrimination remains problematic.

Modern approaches to systematics, including more holistic phylogenetic analyses, are helping to place African molluscs in a global context. Insights gained from DNA sequence data have made an enormous contribution to our understanding of the origins and relationships of the fauna on both global and regional scales. Freshwater taxa have been a notable focus in this regard, particularly with reference to the systematics of parasite vectors and the endemic gastropod radiations in the Rift Valley lakes.

Externally-funded initiatives designed to build capacity and promote mollusc conservation within Africa have achieved a degree of success, particularly in the freshwater sector, but it remains a reality that, with the exception of some centres of expertise in South Africa, most of the groundbreaking work done on African molluscs has been, and continues to done by malacologists working elsewhere.

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Advances in Malacology in the Recent Fifty Years: Japan and Other Asian Regions

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Asia is a large mollusc-rich area, ranging from the tropical Indo-West Pacific to the subarctic zone. To understand the changes in study methods and interests in Asian Malacology over the last 50 years, we traced the history of Japanese molluscan studies, and compared it with that of other Asian regions. In all countries Malacology started out with taxonomical descriptions of local faunae. Finding and describing new species was also of central importance during that phase. With the development of taxonomy, however, more focused scientific research began. The following major changes took place between 1960 and 2010. 1. Phylogenetic analysis followed α-taxonomy. Cladistics was accepted in the 1990s, and molecular phylogeny became the most common method in phylogenetics. 2. In molecular work, isozyme analysis by electrophoresis was widely adopted in early years, but then largely replaced by DNA sequence analysis. 3. Chromosome studies (karyotype analysis) were also popular earlier, but declined after the 1980s. 4. Anatomical and histological studies improved with the use of SEMs, TEMs and new staining methods. Cutting-edge developmental studies were combined with gene expression experiments. 8. Studies of micromollusca became easier and more reliable with the use of the SEM, starting in the early 1990s. 7. Investigation of shell microstructure was also improved by SEM observation. 8. New findings were made from newly recognized habitats such as hydrothermal vents, cold seeps, submarine caves, sunken wood and bone, and anchialine ponds. 9. Biogeographic studies were advanced by detailed descriptions of fossil records (historical biogeography) and the progress of molecular phylogeny (phylogeography). 10. The number of introduced species increased in terrestrial, freshwater and shallow-water environments, especially since the 1980s. 11. Conservation biology and endangered species also attracted wide attention. Red lists or red data books have been published by various organizations. 12. Databases and DNA barcording have emerged as new fields for the 21st century.

Australasian Malacology – the Last 50 Years

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Australia and New Zealand have had a long history of significant malacological research carried out by scientists in museums, universities, government agencies and also by some amateurs. The last 50 years has seen notable advances in our understanding of the diversity and systematics of some previously poorly known components of the fauna such as non-marine molluscs, marine micromolluscs, cephalopods, opisthobranchs and, in the case of New Zealand, the deepwater fauna. New Zealand scientists have also been responsible for leading edge studies in Cainozoic palaeontology, applied aspects of pest control and endangered species conservation. Both countries have research programs in aquaculture and fisheries and have been involved in research on Antarctic and sub-Antarctic molluscs. Australian scientists have programs of world significance in systematics, ecology, evolutionary development, genetics, phylogenetics, bioprospecting and other investigations for medicines and other useful products. Access to information on molluscs has been helped by some significant general publications in both countries with the most important being the Southern Synthesis treatment of Mollusca in 1988. While the New Zealand fauna (~ 4600 known species) has been checklisted for many years, the Australian fauna (~ 16,000 species) is only now in the process of being comprehensively catalogued. The major museums in both countries have, or are in the process of having, their collection databases on line. The relatively small malacological community is represented by a single professional society (*The Malacological Society of Australasia*) which produces a specialist journal, *Molluscan Research* (jointly published with *The Society for the Study of Molluscan Diversity* in Japan since last year) and holds a regional meeting every three years.

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The Conservation Status of the Land Snails of the World: Endangered Unless Documented Safe, or Safe Unless Documented Endangered?

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Huge progresses have been made over the last 50 years regarding tools allowing to study the biology, genetics, biogeography of molluscs. However, there is a great imbalance between the complexity and accuracy of these new technologies applied to the study of molluscs and the very little we know about the actual survival in the field of most mollusc species. Our 2007 study showed that the number of known mollusc extinctions is almost double that of the IUCN Red List: information from the literature and the experts revealed 288 previously unlisted cases of extinct species. Given this, the present study investigates biases and limits of our knowledge in mollusc extinctions due to the Taxonomic Impediment. Focusing on a random sample of 200 land snail species taken regardless of their conservation status, we assessed how up-to-date is our knowledge on their survival in the field. All available references on these species were scanned, and experts were consulted world-wide. These two phases of data collection allowed to gather all the available information on these species in order to rule on their conservation status. Emphasis was put on separating primary from secondary information in the literature. Biases on the availability of information related to geographical areas, experts' nationalities and periods, imbalance between published information and unpublished information known only from the experts also became apparent. We thus found out that the proportion of references containing primary information (by comparison with the total number of references consulted) ranged from 34% for Oceanian species to 61% for European species. We also found out that for more than 45% of our species the last primary information dated from before 1950, this figure reaching 60% for Asian or Oceanian species. Despite the large array of new technologies and scientific tools malacologists can now use, bibliographic research and field work remain compulsory in order to answer the basic question: are the species still there?

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Resolving Old Questions in Mollusc Phylogenetics with New EST Data

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Molluscs are one of the most diverse groups of animals and arguably the animal phylum with the largest body plan disparity. In addition, molluscs include many economically and medically important species. Despite great general interest, the internal mollusc phylogeny has been particularly difficult to resolve with confidence using morphology or traditional molecular approaches. The objectives of the present study are to investigate the relationships among the molluscan classes using a phylogenomic approach, including the development of new software that will allow anyone in the community to apply the same phylogenomic methods to other groups of organisms. New Expressed Sequence Tag (EST) are being collected from a total of 64 widely sampled molluscs using new high-throughput sequencing technologies with the aim of producing a well-resolved phylogeny of the group. This will answer critical questions about the origin of the mollusc body plan, such as whether or not the common ancestor of living molluscs was segmented, and establish how many times a true shell has been gained and lost. This work will provide a valuable foundation for future studies of mollusc phylogeny, both by developing a well resolved backbone for the addition of further species to resolve finer scale relationships, and by contributing more than a billion bp of new sequence data that will greatly inform the selection of genes for molecular phylogenies. The new trees to be generated, and the sequence data themselves, will impact many aspects of our knowledge of mollusc biology. Preliminary results of the 454 sequencing approach will be presented. [This project is supported by NSF collaborative grants DEB-0844596/0844652/0844881].

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Relationships of Philippine Species of the Genus *Turris* (Turridae: Neogastropoda) Based on Comparative Analysis of Radular Morphology and Molecular Markers

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The family Turridae is known to be one of the most diverse and taxonomically problematic groups of marine gastropods. Various attempts to revise the phylogeny of the family have led to 9 to 13 subfamilies being proposed within Turridae to accommodate more than 5000 recent species.

Recent molecular studies on the phylogeny of the Turridae have revealed that the problems in the taxonomy of the family are even more complex; not only subfamilies, but also some well-established genera which were thought to be well understood will require revision and redefinition.

Turris, Röding, 1798, the type genus of the family Turridae, and the type species, *Turris babylonia* (Linnaeus, 1758) have been revised on the basis of radular morphology and molecular markers (CO1, 12S, 16S). We analyzed specimens conventionally assigned to 10 species of the genus *Turris*. Our results reveal that these species form two separate, well-supported clades, provisionally assigned to two different subgenera. Five of the species belong to the subgenus *Turris (s.s.)* Röding 1798: *T. babylonia,* (Linnaeus, 1758) *T. crispa,* (Lamarck, 1816) *T. dollyae,* (Olivera, 1999) *T. normandavidsoni* (Olivera, 1999), *T. spectabilis* (Reeve, 1843) and *T. totiphyllis* (Olivera, 1999); these comprise a well-defined monophyletic clade. Four species clearly do not belong to *Turris* (*s.s*) and form a more loosely delineated group provisionally designated the subgenus *Annulaturris* Powell, 1966: *T. annulata,* (Reeve, 1843), *T. cryptorrhaphe* (Sowerby, 1825), *T. undosa* (Lamark, 1816), *T. cristata,* Vera-Pelàez *et. al*., 2000, and *T. nadaensis*, Azuma, 1973. For three latter species, which are known to be quite difficult for distinguishing from each other, clear criteria on delimitation has been established.

The specimens traditionally assigned to *T. babylonia* were found to comprise complex encompassing more than one species. The taxonomic revision of the complex has led to the description of the new species (*T. assyria*).

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The Long Way to Diversity – a Current View on the Phylogeny and Evolution of Heterobranchia (Mollusca: Gastropoda)

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Heterobranchia are one of the most speciose and morphologically as well as ecologically diverse groups of Gastropoda with partly poorly resolved phylogenetic relationships. Traditionally Heterobranchia comprise several taxonomic entities labelled "lower Heterobranchia" (e. g. Valvatoidea, Rissoelloidea, Architectinicoidea, Pyramidelloidea, Orbitestelloidea) as well as the well defined Euthyneura including Opisthobranchia and Pulmonata. Current molecular systematic studies continuously challenge previous morphology-based classifications, especially with regards to the monophyly of Opisthobranchia and Pulmonata.

Our efforts in the last few years have concentrated on unraveling phylogenetic relationships of major heterobranch subgroups. We particularily focussed on basal taxa as well as non-nudipleuran Opisthobranchia and Eupulmonata. Our molecular studies, based on multilocus datasets of nuclear and mitochondrial genes reveal monophyly of Heterobranchia but non-monophyletic Opisthobranchia and Pulmonata. Sacoglossa and Acochlidiacea are more related to Pulmonata than to the rest of Opisthobranchia, whereas Pyramidellidae cluster well supported within Pulmonata.

The phylogenetic hypotheses have been used to infer evolutionary ages of the Heterobranchia and its subclades, as well as to enlighten questions regarding historical biogeography and evolution of morphological and ecological traits.

Although we have made a large step forward to understanding phylogenesis in Heterobranchia molecular systematic studies of these gastropods are still hampered by the lack of equally suitable markers across the diversity of taxa. Future efforts should focus on detection of novel markers providing better phylogenetic signal to infer more robust phylogenetic hypotheses in order to shed light on the still unknown mysteries of heterobranch evolution.

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Reducing an Enigma: Placing the Vermiform Rhodopomorpha (Gastropoda) in a Phylogeny

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Rhodopemorpha is a turbellarian-like group of gastropods thought to have Euthyneuran affinities. The group consists of two genera *Rhodope* and *Helminthope*, both of which live interstitially, and are seldom seen. Modifications for a mesopsammic lifestyle have been extreme, and rhodopids lack a foot, mantle cavity, gill, heart, radula and cephalic tentacles, and a reduced kidney and digestive system. This lack of morphological characters has hampered the phylogenetic placement of Rhodopemorpha. Their nomenclatural history has been varied, and the most recent classification of Gastropoda (Bouchet and Rocroi, 2005) places the group as a family in Nudibranchia. To date, no molecular data have been available for rhodopids, and we have addressed this by generating novel data for the group. We collected a number of putative new species of rhodopids as well as *Rhodope veranii*, *Rhodope roskoi* and *Helminthope psammobionta*. We then sequenced mitochondrial markers COI and 16S rDNA, and nuclear 28S rDNA and 18S rDNA, and analysed available data from a wide range of heterobranch taxa. Although a fully resolved tree for the Heterobranchia is still lacking, the Rhodopemorpha can be confidently placed outside the Euthyneura, as sister to a shelled group.

The End of the Guessing Game? Origin and Evolution of Acochlidia (Gastropoda: Heterobranchia)

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As traditional order of the “Opisthobranchia” the enigmatic, mainly mesopsammic Acochlidia look back on a long history of controversial taxonomic placements, among others influenced by convergent adaptation to the meiofaunal habitats. Analysing specimens of 11 of 12 acochlidian genera (representing 6 of 7 acochlidian families) in a comprehensive euthyneuran taxon sampling with special focus on minute aberrant slugs, our multi-locus molecular study places Acochlidia in a pulmonate relationship, as sister to Eupulmonata. Previous hypotheses of “opisthobranch" relationships of Acochlidia or a common origin with other meiofaunal Euthyneura are clearly rejected by our data. Potential morphological synapomorphies are critically evaluated, currently neither contradicting nor supporting molecular results. Evolutionary pathways leading to the aberrant acochlidian morphology are discussed.

The robust phylogenetic hypothesis on the phylogeny of Acochlidia based on molecular markers and in congruence with previous morphological analyses is the base to trace the evolution of this formerly enigmatic taxon. The position of the amphibious and insectivorous Aitengidae *incerta sedis* in relation to Acochlidia is discussed. Flexibility in habitat choice (from marine meiofaunal, to limnic benthic and semi-terrestrial) within Acochlidia is highlighted and the evolutionary key features are discussed.

Acochlidian divergence times are estimated to Mesozoic Jurassic using a relaxed molecular clock approach. These relatively old splits and recent findings of a high level of cryptic speciation might indicate that known acochlidian species form just the tip of the iceberg concerning acochlidian diversity.

A Praise of Taxonomic Monographs: The Discodoridid Sea-Slugs (Gastropoda: Nudibranchia) as a Case Study

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Taxonomic monographs, because they are comprehensive and synthetic, represent one of the most rigorous ways to publish taxonomic work. However, fewer and fewer taxonomists make the decision of publishing monographs. One of the reasons is that the quantitative metrics of our “productivity” (e.g., used for academic advancement) are largely inadequate for taxonomic work in general, and monographs in particular. Other reasons shall be discussed as well. Regardless, monographic revisions are critically needed because they are the only way to revise comprehensively the taxonomy of taxa (i.e., examining all type and non-type material, re-evaluating the entire literature, addressing the status of all names, describing new taxa, reconstructing supra-specific phylogenetic relationships, etc.). A taxonomic monograph of the discodorid sea-slugs, (Gastropoda, Nudibranchia) recently published by the author (March 2010) and freely-available as a PDF on the website of the *Proceedings of the California Academy of Sciences*, will be presented. With 403 pages and 382 plates, it comprehensively revises the genus *Discodoris* and some of its closely related taxa, such as *Peltodoris* and *Anisodoris*. Also, reasons why monographic works should continue to be published by taxonomists, regardless of the lack of support and recognition we might encounter from outside our field, will be discussed.

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The First Molecular Phylogeny of Cladobranchian Opisthobranchs (Mollusca: Gastropoda: Nudibranchia)

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The first molecular phylogeny is presented for the highly diverse, opisthobranch molluscan Cladobranchia. This study, the most comprehensive for Cladobranchia to date, used new sequences of two mitochondrial and one nuclear genes for 95 specimens from 22 families and 38 genera with a species of Pleurobranchoidea as outgroup. Although our results do not resolve all the relationships within the Cladobranchia, there are significant findings that have implications for the systematics of the Cladobranchia. Cladobranchia represents a monophyletic group within the Nudibranchia with the exception of a clade containing species of *Melibe*. These species share a deletion of four codons in the COI gene that may account for their strong divergence from the remainder of the Cladobranchia. Bornellidae is the sister group to the rest of Cladobranchia, but this relationship is weakly supported. A series of well-supported clades within Cladobranchia show little structure as to their relationships to each other in the current analysis. The relationships of *Tethys* and Hancockidae to other Cladobranchia remain unresolved. *Pseudobornella orientalis* is here transferred to *Dendronotus* as *D. orientalis*. With this systematic change Bornellidae and Dendronotidae are now monophyletic. *Lomanotus* appears as the sister group to a monophyletic Aeolidida, but this relationship is not strongly supported. Scyllaeidae is monophyletic in the present study with *Scyllaea* being sister taxon to *Notobryon*. The Proctonotidae are monophyletic and are clearly nested in the Cladobranchia. Dotoidae is monophyletic when *Pinufius* is included in this clade. *Doriodomorpha* is sister taxon to the Arminidae. Within Arminidae, *Dermatobranchus* and *Armina*, as they are presently constructed, are not monophyletic. In this study, *Marianina rosea* is nested within Tritoniidae, thus we consider Aranucidae, and its synonym Marianinidae, as a junior synonym of Tritoniidae to preserve the monophyly of Tritoniidae.

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Evolution of the Scylllaeidae (Nudibranchia: Dendronotina) with a Revision of *Notobryon*

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The Scyllaeidae represent a relatively small clade of dendronotoid nudibranchs. The most commonly reported species, *Notobryon wardi* Odhner, 1936, has been reported to occur from the tropical Indo-Pacific and from temperate South Africa. Two additional species of *Notobryon* have been described from Japan, but the systematics of Notobryon have not been reviewed using modern systematic tools, including comprehensive morphological studies and molecular phylogenetics. Specimens of *Notobryon* were examined from the tropical eastern Pacific, several localities in the Indo-Pacific and from temperate South Africa. Additionally, representatives of the other two scyllaeid taxa, *Scyllaea* and *Crosslandia* were studied. Our molecular phylogenetic studies clearly indicate that Scyllaeidae is monophyletic. *Notobryon* is also monophyletic and is the sister group of *Crosslandia* plus *Scyllaea*. The molecular data also clearly indicate that within *Notobryon*, at least three distinct species are present, two of which are presently undescribed. Genetic distance data for the cytochrome oxidase subunit I indicate that eastern Pacific and South African exemplars are 10-20% divergent from Indo-Pacific exemplars of *Notobryon wardi*. Our morphological studies clearly corroborate our molecular findings and differences in external and internal morphology distinguish closely related species. Specimens from each major geographical area clearly have distinct penial morphology and there are at least two sympatric species present in southern Japan. These studies clearly reinforce the view that Eastern Pacific, Indo-Pacific and temperate biotas consist largely of distinct faunas, with only a minor degree of faunal overlap.

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Turning Haeckel's Law Up Side Down? Morphology, Phylogeny and Evolution of Corambid Sea Slugs (Gastropoda: Euthyneura)

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Nudibranch mollusks of the genus *Corambe* differ from most other Doridoidea by having ventral rather than dorsal anus and gills. For these and other features, corambids for a long time were considered as an archaic, or at least an enigmatic or aberrant group. Herein we present a 3D-anatomical description of a new corambid species from tropical Peru, together with a revision of other corambids. Parsimony analysis of a comparatively large and quality-checked structural character set confirms an onchidoridid origin of monophyletic corambids. The well-resolved and overall highly supported ingroup topology indicates the potential of careful morphology-based phylogenetic analyses, especially for groups with rare or hard to obtain members that are elusive to molecular systematics. The robust and plausible phylogenetic hypothesis on corambids also allows for reconstructing character evolution in considerable detail. Evolutionary traits of mantle and gill complexes in adult corambids are compared with partly novel ontogenetic data on other dorids: progenetic corambids "recapitulate" such early juvenile dorid stages – turning Haeckel's law up side down.

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Are the Sacoglossans *Elysia timida*, *Bosellia mimetica* and *Thuridilla picta* (Gastropoda: Opisthobranchia) Truly Amphiatlantic Species? A Molecular Approach

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Amphiatlatic distribution in marine organisms raises controversy in many marine zoological groups with ongoing discussions whether species in both sides are the same or different biological entities. Geographical isolation coupled with factors such as dispersal capacity of larvae and/or adults, food availability, and patterns of ocean surface currents, can hamper gene flow between these allopatric populations challenging the view of amphiatlantic distributions. Furthermore, molecular systematics has showed the potential for cryptic speciation whereas the impact of shipping and aquaculture trade, are important known vectors of introduction of exotic marine species.

Concerning the opisthobranchs, few contributions have tested these relationships in a molecular framework. *Elysia timida, Bosellia mimetica* and *Thuridilla picta* are three sacoglossan opisthobranchs with an amphiatlantic status. Distance and Bayesian analyses of partial DNA sequences of mitochondrial (COI and 16S) and nuclear (H3 and 28S) genes have been performed. The results showed that *E. timida* and *B. mimetica* are likely truly amphiatlantic species and raises the possibility that western Atlantic “populations” are the product of a recent introduction. The results suggest the need for reassessing the taxonomic status of *E. cornigera*, *E. papillosa*, and *Bosellia* spp. from the Caribbean. Moreover, individual-gene and concatenated analyses do not recover the monophyly of the genus *Bosellia)*. Finally, the phylogenies support that *Thuridilla picta* from the eastern Atlantic and *T. hopei* so far unequivocally regarded as distinct species are the same taxon.

Two alternative hypotheses, related with its amphiatlantic status, are proposed: 1) *T. picta/hopei* is a single and truly amphiatlantic species with a genetic marked difference between western and eastern Atlantic populations that maybe under a process of differentiation (speciation) or 2) *T. picta/hopei* represents two distinct species geographically isolated but closely related both genetically and morphologically. Both hypotheses imply nomenclatural consequences.

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Worldwide Diversity and Speciation of *Haminoea* Gastropods (Opisthobranchia: Cephalaspidea): Preliminary Results

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Haminoea are a tropical and temperate worldwide genus of shallow-water cephalaspidean gastropods leaving in coastal lagoons, estuaries, rocky shores, and coral reefs, usually associated with seagrass or algae.

The systematics of the genus is still largely based on shells, which are all very similar both in colour and shape, rendering a very confusing taxonomy. Twenty species have been named in the Eastern Atlantic (EA), 15 in the Western Atlantic (WA), 12 in the Eastern Pacific (EP) oceans, and 64 in the Indo-West Pacific (IWP). Nonetheless, recent faunistic inventories and taxonomic works combining shells and anatomical characters recognized no more than eight and three species in the EA and WA, respectively, four in the EP, and nine in the IWP.

In this work an integrative taxonomic approach combining shells, anatomy, morphology, SEM analysis, ecology, fossil record, and multi-gene molecular phylogenetic hypotheses, are used to revise the systematics and infer the historical biogeography and diversification patterns of the group.

Radula, gizzard plates, male reproductive system, and coloration patterns are good characters for species recognition, but the latter can show remarkable intraspecific variability. Preliminary single- and concatenated-gene phylogenies are shown. Both point towards higher species diversity than that currently recognized. The first insights into the origin and diversification patterns of the group are given and discussed.

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Molecular Systematics and Global Phylogeography of the Pelagic Nudibranch Genus *Glaucus*

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Ecological transitions from benthos to pelagos are as rare in terms of number of phyla (11) as the transition from marine to terrestrial environments. One example of such a transition is the aeolid genus *Glaucus*, the only truly pelagic nudibranch. Using highly-specialized gastric cavities to store gulped air bubbles, members of this genus drift passively at the ocean surface for their entire adult lives. The genus currently comprises two species: *G. atlanticus*, which has a global distribution, and *G. marginatus*, known from the Pacific. To date, a convincing benthic sister lineage has not been identificd by morphological means; to that end, I will present a molecular phylogeny of *Glaucus* with other aeolidioideans. Initial molecular analyses place *Glaucus* sister to Favorininae, which is broadly consistent with Miller's (1974) taxonomy. The second component of this research is part of a larger project examining the global phylogeography of the neuston community. Previous studies indicate that continental landmasses (*e.g.* for the epineustonic insect genus *Halobates*) and strong equatorial currents (*e.g.* for microscopic zooplankton) present varying, taxon-specific barriers to gene flow. Molecular analyses of the cosmopolitan *G. atlanticus* and Indo-Pacific *G. marginatus* show strikingly different patterns: *G. atlanticus* exhibits modest variation in the Pacific and Indian basins, which is contained within the variation in the North Atlantic, three gyre systems away. Migration analyses show significant uni-directional migration from the North Atlantic to the Pacific and Indian basins, with non-signifcant back migration to the North Atlantic. In *G. marginatus,* on the other hand, there are three highly divergent co-occurring mitochondrial lineages in the Pacific basin, which may represent cryptic species. This is the first phylogeographic analysis of macroscopic neuston from adjacent subtropical gyres, and it indicates that genetic isolation by continental landmasses and equatorial currents varies within-genus.

Functional Chloroplasts in Metazoan Cells: Evolution in Sacoglossa (Opisthobranchia)

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Functional chloroplasts (kleptoplasty) only occur among Metazoa in the gastropod taxon Sacoglossa. These kleptoplasts are diet-derived and are maintained intracellularly in the slug's digestive epithelium. However, photosynthetic ability varies widely among sacoglossans; some species have no plastid retention while others survive for months solely on photosynthesis. We distinguish three levels of photosynthetic activity: (1) no functional retention; (2) short-term retention lasting about one week; and (3) long-term retention for over a month. A survey of photosynthetic ability among Sacoglossa and of their diets is given and related to phylogeny.

We found that among the Sacoglossa, functional chloroplast retention is derived, and an apomorphy of the taxon Plakobranchoidea. However, long-term chloroplast retention evolved independently in four species of Plakobranchoidea. Surprisingly, the degree of chloroplast retention is not correlated with host alga (plastid donator), and many species feed on different algae. Since food source was unknown for the long-term species *Plakobranchus ocellatus*, stored chloroplasts were DNA bar-coded using the plastid *tufA* gene; results indicate that *P. ocellatus* feeds on different ulvophycean algae than other sacoglossans expressing long-term retention.

Secondary Metabolites versus Kleptocnides in Cladobranchia (Nudibranchia, Gastropoda)

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The lack of a physical defence in soft bodied animals led to the evolution of diverse alternative defensive strategies. In the nudibranch taxon Cladobranchia two strategies are known, although information is sketchy and rare: sequestration or *de novo* synthesis of secondary metabolites and incorporation of functional cnidocysts. Cladobranchia feed on a high variety of cnidarian species, which commonly exhibit a functional cnidom for capturing prey organisms or for defence. However, this is not the case for many soft corals (Octocorallia), which seem to produce defensive natural products instead. In contrast, Hydrozoa are usually considered to exhibit a functional cnidom, but nearly nothing is known about their ability to produce natural products.

In this contribution, first results on the defence mechanisms for several cladobranch species are shown in relation to their food organisms. According to our knowledge on cladobranch phylogeny and food organisms, a preliminary evolutionary scenario of defensive strategies will be outlined.

120 Years After Strubell: 3D Microanatomy and Biology of the Limnic Acochlidian Slug *Strubellia* Odhner, 1937

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The heterobranch Acochlidia is the only known group of slugs that exhibit a radiation into freshwater streams. The genera *Acochlidium* and *Strubellia* were the first of the group to be discovered by the Austrian naturalist Strubell in 1892, on the island of Ambon (Amboina) in the Indonesian Moluccas archipelago. Since then, these genera of relatively large-bodied species (compared to the otherwise tiny marine mesopsammic acochlidians) have been shown to be widespread in streams of South-East Asian and Western Pacific tropical islands.

We examined the original *S. paradoxa* and specimens from the Solomon Islands and Vanuatu. Three-dimensional reconstruction of the anatomy from series of semithin sections revealed a complex copulatory apparatus with clear evidence for proterandry, and elaborate circulatory and excretory systems with apparent morphological adaptations to the freshwater habitat, resembling the condition found in the coastal mesopsammic *Pseudunela*. Further characters detected and so far unknown in Acochlidia include a small osphradium, several new nerves and a 'cephalic gland' above the cerebral ganglia.

Live and SEM observations of Solomon Islands specimens showed the species to be specialized for feeding on the reinforced egg capsules of syntopic neritids by employing elongated median teeth with serrated margins and possibly a grid of spicules above the radula as a counter.

Population genetics show three distinct clades among the genus, separating the Ambon *S. paradoxa* from the Solomon Islands/Vanuatu populations, next to a population in Sulawesi known from only a single specimen.

Comparative Study of the Crop in the Carnivorous Opisthobranchs *Philinopsis depicta* and *Aglaja tricolorata* (Cephalaspidea: Aglajidae)

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Cephalaspideans include carnivorous and herbivorous species, being suitable to investigate relationships between these diets and morphofunctional features of the digestive system. Herbivory is considered the plesiomorphic condition in cephalaspideans, with carnivory having arisen two or three times within this taxon. Therefore, in carnivorous cephalaspideans the ancestral digestive system had to be adapted to a new diet. Specimens of *P. depicta* and *A. tricolorata* were collected in the south coast of Portugal and their crops processed for light and electron microscopy. The crop of *P. depicta* contains two high ridges creating a channel between them, extending from the middle of the crop to the posterior oesophagus. This channel is lined by a ciliated epithelium, but the outer surface of those ridges and the crop wall in general are lined by a non-ciliated epithelium covered by a thin cuticle. Large mucus-secreting cells are present in the crop epithelium, except in the ciliated channel. Their secretion is stained by PAS reaction for polysaccharide detection and alcian blue at pH 2.5 for carboxylic polysaccharides. However, negative results were obtained with alcian blue staining at pH 1 and the tetrazonium coupling reaction, indicating absence of sulphated polysaccharides and proteins, respectively. The crop of *A. tricolorata* does not have ridges; instead the lining epithelium forms deep infolds. Secretory cells are not present in the crop and the non-ciliated lining epithelium is covered by a thick cuticle. However, secretory eosinophilic cells exist in the region between the anterior oesophagus and crop. These cells stain with PAS and tetrazonium coupling reactions, but not with alcian blue. In spite of the differences, in the crop of both carnivorous species a dense network of blood vessels is located below the epithelium. So far, a similar network of blood vessels was not reported in the oesophagus or crop of herbivorous opisthobranchs.

Spatiotemporal Expression Patterns of Mantle Secreting Genes Throughout Larval Development in *Aplysia californica*

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The ability to construct mineralized structures has contributed to the evolutionary success of many animal phyla. Molluscs are a good example, well-known for their great diversity in shell morphologies. The molluscan mantle is the organ responsible for shell formation through the controlled secretion of shell proteins and the synthesis and deposition of calcium carbonate minerals. Even though molluscan shells have been extensively studied, very little is known about how the developmental programs are regulated. The California Sea Hare, *Aplysia californica* (Opisthobranchia: Anaspidea), provides a good system to examine the molecular basis of shell formation as there are readily available developmental stages through hatchery populations, as well as a growing number of genomic and developmental tools. Here we analyze eleven candidate biomineralization genes during early developmental stages (trochophore, early pre-hatching veligers and stage 1 veligers) of shell production in *A. californica.* These genes were putatively assigned to biomineralization processes based on transcriptional profiles from *A. californica* developmental microarray data. Six of these genes are ribosomal proteins that are specific to the mantle, while four of these are evolutionarily ancient transcripts that have been previously described from the mantle of other molluscs and an unknown gene with no identity to known proteins. All eleven genes display specific spatiotemporal expression patterns during shell fabrication. The expression patterns of these eleven genes provide insight to how the molecular machinery in biofabrication of the molluscan shell is controlled; from a broad expression (in trochophores) to a spatial refinement of expression as the progression of the shell takes place. The presence of both conserved and potentially lineage-specific transcripts during all stages of shell production suggests that there is a core set of mantle-secreting genes (provided by a shared metazoan ancestor) and novel proteins that are needed for the diversity and distinctive nature of molluscan shell forms.

The Food Habit of *Kalinga ornata* (Nudibranchia: Doridina: Anadoridoidea: Polyceridae)

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Field experiments of the food of *Kalinga ornata* (Nudibranchia: Doridina: Anadoridoidea: Polyceridae) were conducted. *Kalinga ornata* fed on six species of Ophiuroidea which were presented for our field experiment, those were *Ophiothrix exigua*, *O. nereidina*, *O. panchyendyta*, *Ophioplocus japonicus*, *Ophiactis savignyi* and *Macrophiothrix longipeda*. *K. ornata* sucked and swallowed ophiuroids whole in cases when the prey was small. The predator bit off the preys arm in cases when the prey was big. Although *K. ornata* was interested in some other echinoderms, it did not feed on them. All other prey items were ignored by *K. ornata*.

The ophiuroid spicules were found in the feces from the specimen reared in the aquarium, indicating that the seaslugs really digested the preys they had eaten in the field experiments. The present results strongly suggest that *K. ornata* feeds exclusively on ophiuroids in nature.

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Arms Race in Increasing Trophic Levels: An Example from a Nudibranch-sponge Association

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The selection by counterpart pressure in predator-prey relations is amongst the main factors that promotes evolution. Opisthobranch molluscs are an interesting study case on this subject. As they evolved, opisthobranchs underwent progressive shell loss, paving the way to the acquisition of new defensive strategies, including chemical defenses, which are related to their trophic specialization. In order to prey on chemically defended species, opisthobranchs entered in an arms race, developing means to detoxify and/or excrete harmful compounds, which led to the sequestration of those compounds and their self-defensive use, a by-catch escalation of defenses. Here we aim to understand whether or not the opisthobranch predator is better protected than its chemically defended prey, using as predator-prey model a nudibranch (*Hypselodoris cantabrica*) and the sponge it preys on (*Dysidea fragilis*), and from which it obtains deterrent chemical compounds. In order to do so, specimens of both species were collected in two sites along the Portuguese coast. Defensive compounds were extracted, analyzed and used in palatability tests. Some variability in the concentration of the obtained crude extracts was observed in both species. Although the compounds found in nudibranchs were also present in the sponges, the nudibranchs had a larger concentration of crude extract than the sponges, probably due to a progressive accumulation of the compounds. The palatability tests revealed a more effective deterrent activity in the nudibranchs' extracts. In this instance, significant rejection rates were observed at lower concentrations than those necessary for the sponge extracts to have the same effect. We concluded that the predator is chemically better protected than its prey, which suggests that its acquisition of chemical defenses consisted not only in a defensive escalation but also in an upgrade compared to preys' defenses.

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Spatial Distribution of Opisthobranchs on Subtidal Soft Bottoms at the Ensenada de Baiona (Galicia, NW Iberian Peninsula)

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The Galician rias (NW Spain) are a special type of estuarine system characterised by the presence of a great variety of sedimentary substrata inhabited by particularly rich benthic faunas. Molluscs are an important component of benthic assemblages in subtidal sediments of the rias, both in terms of abundance and biomass. In many cases, gastropods inhabiting those sediments have a great influence on the populations of other benthic animals, particularly those acting as grazers, predators or scavengers. Nevertheless, specific studies on composition and distribution of gastropod assemblages in general, and of opisthobranchs, in particular, are scarce when compared to those devoted to other components of the benthic macroinfauna; in many occasions, those are integrated within more general studies also including polychaetes, crustaceans and bivalves. In this communication, the distribution and composition of the opisthobranch fauna inhabiting subtidal sediments of the Ensenada de Baiona (Galicia, Spain) is described by means of quantitative sampling done at 21 sites. A total of 336 individuals representing 10 opisthobranch species and 6 families were found. The family Retusidae was the most diverse in number of species (4), followed by Philinidae (3); *Cylichnina umbilicata* was the most abundant species. Multivariate analyses done on abundance data showed that the distribution and composition of the opisthobranch fauna has a high correlation with that of sedimentary types. In turn, the distribution of sediments at the Ensenada de Baiona is determined by local patterns of hydrodynamism and different exposure to oceanic swell.

Opisthobranch Fauna from West Coast of India

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Opisthobranchs are fascinating molluscs with species diversifying not only in colors but also in their specificity of feeding habit and habitat.

Opisthobranchs are among the least studied molluscs in India and the work done on opisthobranch fauna is little and patchy. Though India has over 8000 km large coastline, two oceanic archipelagos with diverse habitats such as coral reefs, sandy shores, rocky patches, mangroves as well as large mud flats, records of Indian opisthobranchs are very less.

Five sites were selected for the preliminary rapid assessment which began in 2008 on the west cost of India. Of the five sites, three sites namely Lakshadweep, Ratnagiri and Gulf of Kutch where work was done intensively. Two sites namely Malvan and Mumbai where two rapid assessments were carried out.

During the one year survey we were able to record 155 species of opisthobranchs from various families. Of these, 118 are new records to India and 11 species still need identification and validation. The paper presents a brief review of the work done in 2008-2009 by the authors.

During the present study, authors recorded opisthobanch species belonging to 37 Families and 74 genera of which 35 genera are newly recorded in India.

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Opisthobranch Molluscs Collected in Shallow Water at Ghizo Island, Solomon Islands

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Opisthobranch molluscs were collected as part of the research project undertaken by the Marine Invertebrates section of the Zoological Museum in Copenhagen in connection with the Galathea 3 Expedition. The research group took deep-sea samples along transects in the Solomon Sea from the naval vessel “Vædderen” (The Ram) and afterwards collected shallow water samples from the waters around Ghizo Island in the Solomon Islands.

Samples were collected between 30 December 2006 and 6 January 2007 from several habitats: sandy beach with steep slope, sheltered sandy beach with dense seaweed and seagrass, sandy beach with coral heads, small mangrove with boulders and soft sandy sediment, and a few samples taken by SCUBA divers from coral reefs. Most specimens were found by sorting through collected seaweeds or coral rubble.

The most common species was the sea hare *Stylocheilus striatus*. Another common species was the sacoglossan *Elysia (Elysiella) pusilla*, which is associated with the calcareous alga *Halimeda* spp. In total we found about 10 species of Cephalaspidea (Aglajidae were most common); about 10 species of Sacoglossa (Elysiidae were most common); 3 species of Aplysiomorpha; and about 5 species of Nudibranchia were collected (a few more were seen, but not collected). Also a few species of Pyramidellidae were found. Only one or two species of sacoglossans appear to be undescribed. A single specimen of the recently described *Ercolania kencolesi* Grzymbowski, Stemmer and Wägele, 2007, which lives inside the alga *Boergesenia* sp., was found. Most of the species have wide Indo-West Pacific distributions.

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Limpets as Models for Exploring Behaviour and Its Constraints

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Limpets move over measurable scales, can be followed (though not always easily), are not compromised by sexual activity, often have a fixed or localised resting point between bouts of feeding, (indeed resting zones and feeding zones are often spatially separate), and examples can usually be found of foraging in essentially two-dimensional space. Shouldn't this make them ideal models for studying the drivers for animal foraging, from which we can extrapolate?

Considerable effort has been expended in determining the spatial and temporal patterns of foraging in limpets. Perhaps even more effort has been expended in speculating about the drivers of the patterns recorded. Early studies were mostly anecdotal and inconclusive: much variability was noted at a range of spatial, temporal and taxonomic scales. Later studies were systematic and scientific but also inconclusive, noting even more variability than the early studies. Consequently a rigid classification of behaviour is impossible to produce and few generalisations can be made, though I will try. A constraint to understanding is the size of datasets: many published works represent a snapshot of limpet activity, typically have low sample sizes, and are temporally and spatially localised. Nevertheless, what is emerging, in some species, is the existence of endogenous rhythms that can be overridden extremely easily by small-scale exogenous factors. Since establishing patterns in behaviour patterns is difficult, recent examples of both conformity and plasticity in behaviour will be discussed. The question of the utility of limpets as models will be returned to and the use of *in silico* methods explored.

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Limpet Aggregation: Causes Not Consequences

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Ecologists have to try and explain how patterns of distribution are associated with, and have consequences for, ecological processes. Limpets are important animals in this respect as they are one of the few whose behaviour and ecology is known to have direct ecosystem consequences; in fact, we have quantified this. Yet there is much to explain about limpet behaviour, in particular, what may cause the spatial arrangement of limpets.

Limpets are known to form aggregations. Such limpet groups are reasonably abundant yet neither group membership nor location of the groups is constant. Additionally, limpets can choose to join or leave groups and they often do; being a singleton at one time and grouped the next. Classically such behaviours have been associated with some sort of risk-benefit trade-off based on food supply vs. risk from the environment. I will discuss the evidence for these ideas and show that from experiments I have done, that these explanations may not be sufficient. There is another dimension to this behaviour. Limpets may be aggregating or not as a result of social interactions and I will discuss what evidence is needed to critically evaluate the social context of limpets being in groups.

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Responses of Limpets to Thermal Stress in a Changing World: What We Know and What We Need to Know

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The Patellogastropods (marine limpets) are abundant on rocky shores around the world where they play a key role in regulating community structure. Attached to the rock surface via their muscular foot and conical shell, limpets are especially vulnerable to thermal stress as they are unable to isolate themselves from the external environment. As a result, many species risk mortality during emersion and mass deaths have been recorded during extreme weather conditions. As many species are living close to their thermal tolerances, limpets provide an excellent model to investigate how intertidal species can tolerate and adapt to thermal stress, especially given predicted climate warming scenarios. Specific behaviour patterns determine the environment that limpets must face during emersion. Some species return to fixed locations on the rock surface where their shells have become moulded to fit tightly to the rock contours. These homing species are able to seal their shells against the rock surface and gain some degree of isolation from the external environment. Being active during less stressful periods and then seeking refuge in less stressful habitats on vertical surfaces, in crevices or rock pools is common for non-homing species. Despite adopting these cooler habitats, animals still experience hot temperatures and suffer associated increases in body temperature and concomitant increases in heart rate. As animals become more stressed variation in heart activity is seen with periodic acardia and bradycardia until coma is reached in extreme conditions. Associated with increasing body temperatures is desiccation, with animals losing their mantle water and therefore being unable to exchange gases via their gills. This has subsequent effects on the animals haemolymph, which becomes more concentrated as water loss increases and also more acidic. Some species combat these cellular stresses by having high levels of Heat Shock Proteins (HSPs), which are present in the haemolymph (i.e., constitutive HSPs) or by inducing their production. Other protein and enzyme level responses are also seen, although the exact role of many of these are, as yet, unknown. With recent advances in proteomic and genomic techniques it is believed that quantifying these responses will help understand fundamental responses to thermal stress and also shed light on future adaptations that these animals may show to increasing temperatures.

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Oxygen Delivery and Thermal Stress in Tropical Limpets: Testing the Oxygen Limitation Hypothesis

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Understanding of the evolutionary and physiological basis for thermal tolerance of organisms contributes to understanding of how species may respond to climate warming. A general and popular hypothesis (the oxygen limitation hypothesis) proposes that mortality of ectotherms during thermal stress arises from the impairment of the oxygen delivery system and the insufficiency of this system to meet cellular metabolic demand. The theory is based on the presumption that the oxygen delivery system is a derived ‘weak link’ in organismal thermal tolerance, whereas the thermal limits of molecular and cellular functioning usually exceed that of this system. However, tests of the hypothesis mostly concern stenothermal marine ectotherms having a relatively high scope for activity and metabolism. The present investigation explored the generality of the hypothesis by investigating a tropical intertidal limpet, as a model of a eurythermal organism having a relatively reduced scope for activity and metabolic rate. There was little evidence in support of the hypothesis from experiments which compared rate-temperature relationships, Arrhenius breakpoint temperatures (ABTs) and end point temperatures for heart performance (supply) and oxygen consumption (cellular aerobic demand) of limpets held in air and in normoxic and hypoxic seawater. Other physiological and ecological situations in which the oxygen limitation hypothesis is unlikely to apply are discussed in the context of these findings.

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Using the Force: The Tenacity of Limpets

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Limpets are numerically abundant and have important effects on the abundance and distribution of other intertidal organisms on rocky shores. An important measure of performance is their tenacity (i.e. how well they stick onto a surface), which is based on suction and glue-like secretions from their foot. Limpets use this to resist dislodgment from waves and predators. This paper will discuss recent advances in methods used to measure the force of detachment (shear and normal) and the size of the foot. The results of field and laboratory experiments will be used illustrate how these techniques have gained important insights into how natural (avian predators, shore-exposure, height and slope) and anthropogenic stressors (metals, pesticides and modification of habitats) influence the biology of limpets.

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The Physiological and Evolutionary Adaptations of Limpets of Rocky Shore to Environmental Change

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Limpets are cosmopolitan on rocky shores, living at a variety of latitudes and different vertical heights. As such, limpets are good candidates to investigate physiological and evolutionary adaptations against thermal stress and to study the impact of global change on species distributions. Using heart rates (HR), heat shock responses (HSR) and functional and structural properties of cytoplasmic malate dehydrogenases (cMDHs), different strategies were studied among related species with different latitudinal and vertical ranges along the east and west Pacific coasts. Compared to the high-shore *Cellana grata*, *C. toreuma* had a lower Arrhenius break temperature of HR and HR decreased abruptly after 60 min at 40°C. In contrast, *C. grata* maintained regular HR at 40°C for ~4hrs. Varying strategies of Hsp70 expression were recorded in limpets occupying different heights on both temperate (*Lottia* spp., California, USA) and tropical rocky shores (*Cellana* spp., Hong Kong). On temperate shores, high-shore animals (*L. scabra*) had higher constitutive Hsp70 levels than low- and mid-shore species (*L. pelta*, *L. scutum* and *L. digitalis*), possibly as a possible "preparative defense" strategy to tolerate the extreme high-intertidal environment. On tropical shores, however, high-shore species (*C. grata*) showed a positive response to thermal stress. The mid-shore species (*C. toreuma*) possessed two isoforms of Hsp70, but did not exhibit a positive response to thermal stress. The HSR of limpets inhabiting different tidal heights and latitudes are, therefore, complex and related to local thermal habitats. Differences in Km^{NADH} and thermal stability of cMDH between orthologs in *L. digitalis* and *L. austrodigitalis* are only due to a single amino acid substitution, that favours additional hydrogen bonding and reduced conformational entropy. This difference between congeners demonstrates the importance of minor alterations in protein sequence in temperature adaptation and suggests that such variation is important in governing shifts in biogeographic range.

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The *Lottia gigantea* Genome: New Tools, Opportunities, and Insights in Molluscan Research

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Genome sequencing of the patellogastropod *Lottia gigantea* was initiated in 2005 by the Department of Energy Joint Genome Institute and completed in 2006. As part of the Community Sequencing Program, *L.gigantea* was both the first mollusc and first lophotrochozoan to have its genome sequenced and made publicly available. *L. gigantea* is an important model organism in evolution, behavior, life history, ecology, and conservation and its position as a representative of one of the earliest gastropod lineages makes it especially important for documenting gene evolution throughout the Gastropoda. Another advantage is that the *L. gigantea* genome consists of only about 360 mega base pairs and is therefore small relative to other molluscs. Thus, the *L. gigantea* genome sequence provides a foundation for elucidating the evolutionary and ecological success of the species and its lineage and provides a critical point of comparison for understanding the early diversification of animals and their genomes. To date the *L. gigantea* genome has provided insights into the evolutionary dynamics of various gene families, including *Wnt*, *Fox*, *Hox*, and fibrinogen-related proteins, the diversity of neurohormones and neuropeptides, and the rapid evolution of the molluscan secretome involved in shell fabrication and patterning. The *L. gigantea* genome also was critical in identifying the molluscan *nodal* and *Pitx* genes and their role in determining left-right asymmetry and coiling direction in gastropods. The advent of low cost and high speed sequencing technologies have now opened the door to large-scale, sequencing projects by smaller research communities and even individual laboratories. More molluscs will be sequenced with increasing regularity in the near-future, ushering in an exciting new era of comparative genomics in molluscan biology. Soon to be just one of many, a lowly limpet will always retain its distinguished honor of having been first. [The *L. gigantea* genome can be accessed at: http://genome.jgi-psf.org/Lotgi1/Lotgi1.home.html].

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Recent Findings on Aspects of Patellogastropod Limpets Based on the Molecular Data

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With the advent of molecular phylogenetics, the systematics and taxonomy of Patellogastropoda have been greatly improved from levels family to species. At least seven families Eoacmaeidae, Patellidae, Nacellidae, Pectinodontidae, Lepetidae, Neolepetopsidae and Lottiidae are currently recognized in the order. The family Acmaeidae is subdivided into two subfamilies: Acmaeinae and Pectinodontinae. The Acmaeidnae are synonymized with the Lottiidae, and the Pectinodontinae are elevated to the familial rank. The family Eoacmaeidae includes the *Patelloida profunda* group formerly assigned to the Lottiidae. Although more than 2,700 sequences of patellogastropod limpets have been deposited in GenBank to date, most of them are from intertidal Patellidae, Nacellidae and Lottiidae. Deep-water limpets belonging to Pectinodontidae and Lepetidae, and vent or seep associated Neolepetopsidae have only rarely been included in molecular phylogenies.

At the specific level, molecular studies have revealed that intraspecific variation in shell morphology and color are much more common than previously thought. On the other hand, cryptic speciation has been reported in this morphologically simple group.

In this review, I attempt to provide an overview of the phylogeny of Patellogastropoda focusing on the generic and species level relationships within each family based on the recent molecular studies.

Comparative Anatomy, Shell Microstructure and Higher Systematics of Patellogastropoda

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Phylogenetic analysis and higher sytematics of Patellogatropods have greatly advanced in the last two decades. New data have accumulated in anatomical, shell microstructural and molecular characters. Anatomical studies revealed novel characters in the odontophoral cartilages, subradular organ, buccal musculature, salivary glands and ducts, esophageal torsion, circulation pattern, and configurations of kidneys and digestive tracts, in addition to traditional characters such as gills, radular teeth, pallial streaks, osphradia, pallial tentacles, etc. In shell microstructural studies, earlier data were refined by observations with scanning electron microscopes, and some characters were split into more finely defined characters. In addition, crystallographic texture of individual shell layers, describing the arrangement of crystal axes of individual biocrystals, was studied (by EBSD) providing new independent shell characters. In this study we attempted new cladistic analyses at genus level using ca. 50 anatomical and shell microstructural and microtextural characters, and compared the results with those of molecular phylogenetic analyses. The main results can be summarized as follows: (1) Neolepetosidae and Lepetidae are basal in Patellogastropoda. (2) Patellidae and *Nacella* form a clade. (3) Patellidae, *Nacella* and *Cellana* are united as the clade Patelloidea. (4) Eoacmaeidae, Pectinodontidae and Lottiidae constitute another large clade. (5) "Acmaeidae" is included in Lottiidae. These results revealed that the position of some groups is inconsistent between morphological and molecular analyses, especially regarding the positions of the Lepetidae and Eoacmaeidae.

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Phylogeography of the *Scutellastra* Complex

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Scutellastra flexuosa is a widespread tropical limpet found throughout the Indo-West Pacific, mostly intertidally on coralline reef crests. We have collected populations throughout its range from Africa to French Polynesia to examine geographic structure and gene flow within this species. Powell recognized two species in the complex: *Scutellastra exusta* from the Western Indian Ocean and *Scutellastra flexuosa* from predominantly the Pacific Ocean. Molecular results from both mitochondrial and nuclear markers support at least 36 unique clades throughout the currently circumscribed range of the group. Like other non-planktotrophic mollusks such as *Astralium*, *Scutellastra* shows remarkable endemicity throughout the Indo-West Pacific with each isolated archipelago harboring distinct species. Similar to previous findings in *Astralium*, we have recovered sympatric lineages living side-by-side in multiple locations (Vanuatu and Reunion) that remain distinct according to independent genetic markers. Allopatric diversification in tropical reef-associated lineages is the norm among clades tested to date. With an allopatric cryptic multiplier of x18, *Scutellastra* is the poster child among lineages studied so far to address species richness projections for gastropod global diversity.

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Phylogenetic Perspective on the Remarkable Diversification of Western North American Limpets

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The rocky shores of western North America have a stunning diversity of limpet (Lottiidae) species, including over 20 species in California alone. The morphology, biogeography, and ecology of California limpets were the subjects of Avery Test's Ph.D. dissertation research at the University of California during the 1930s. Later she speculated on the most likely speciation mechanisms leading to this impressive species diversity. Unlike her contemporary, Ernst Mayr, whose emphasis on allopatric speciation dominated biology's "Modern Synthesis," Test argued that allopatric speciation could only explain some limpet speciation. She postulated instead that ecological speciation was more frequent, with co-occurring limpets in different microhabitats becoming reproductively isolated and specialized. Some of her key assumptions were later disproven: limpets often migrate between microhabitats and typically free spawn, whereas she thought limpets moved little and might internally fertilize. These newer findings have weakened her scenario, but Test was perceptive in pointing out lingering limitations of the allopatric model. In my lab we are reinvestigating western North America limpets employing DNA sequence comparisons and morphological study. We have compared mitochondrial 16S rRNA (16S) for over 30 species and more than 600 individuals along the coast. We have also sequenced a second gene for over 50 selected limpets representing 17 species: an 830 bp portion of the nuclear gene, cytoplasmic malate dehydrogenase (cMDH). Separate and combined analyses have yielded robust support for three north/south cryptic species pairs unknown to Test; these are likely the results of allopatric speciation events. Judging from the extent of interspecific sequence divergence, even the most recent speciation events still likely predated the Pleistocene, so there has been ample time for current range overlap to reflect secondary expansion. At higher levels, *Lottia* appears to consist of at least four divergent subclades, exemplified by *Lottia gigantea*, *L. scabra*, *L. scutum*, and *L. pelta*.

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The Distribution and the Evolution of the Reproductive System of the Freshwater Limpet *Septaria* (Neritidae)

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Thirteen species of the genus *Septaria* live on stones and boulders in fast flowing streams and rivers in South Asia, South East Asia and tropical Pacific and Indian Ocean islands. Six species have reproductive systems like other freshwater Neritidae, in which the females have a spermatophore sac with spermatophores. The other seven species show gradual modifications leading eventually to loss of a spermatophore sac in females and to smaller males producing free sperms.

The more modified species are found, at the limit of *Septaria*'s range. *S.bougainvillei* and *S. macrocephala* are endemic to Fiji and New Caledonia and *S. taitana* and *S. apiata* to Fench Polynesia. All four species were formally known as *S. porcellana* While *S. taitana* is the only *Septaria* species in the Society Islands and *S.apiata* the only one in the Marquesas, the less isolated Fiji islands have five *Septaria* species. Three have spermatophores and two do not. All five species may live together in the same stream, but each species has a preferred habitat. *S. livida* lives in brackish-water, *S.bougainvillei* and *S. suffreni* are most abundant on boulders further upstream and *S. sanguisuga* and *S. macrocephala* are most abundant on bedrock in swift current.

Phylogenetic analysis of the 13 species divided the genus into two clades. One contained the widespread brackish water species *S. tesselata* and *S. livida,* which is endemic to Fiji and Vanuatu. Both have ecologically dimorphic shells. The rest of the genus is divided into two more clades, those with spermatophores and those without. *Septaria* with spermatophores have spread north and south from South East Asia. *S. sanguisuga* and *S. cumingiania* with complex spermatophores and sexually dimorphic two pronged opercula have a wider distributed than *S. luzonica* and *S. suffreni* with simple spermatophores and one pronged opercula.

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Evolutionary Relationships and Biogeography of the New Zealand Siphonariidae

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The family Siphonariidae is a diverse group of marine pulmonate limpets, commonly known as siphon limpets, with a wide geographical distribution from the tropics through to subantarctic regions. Representatives of the Siphonariidae inhabit all levels of the sea shore from the high tide mark to the shallow subtidal zone and exhibit a range of reproductive strategies from long-lived planktonic larvae to direct development. They are an interesting model group for investigating long-standing questions regarding biogeographical history, the evolution of reproductive strategies, and the role of planktonic larvae in the dispersal of marine species. Siphon limpets are common on rocky shores throughout New Zealand, with seven species distributed across 23 degrees of latitude (29 – 52°S), from the subantarctic islands to the subtropical Kermadec Islands. All four genera within the family (*Siphonaria*, *Benhamina*, *Williamia*, *Kerguelenella*) are represented in New Zealand, and one (*Benhamina*) is not found anywhere else. This study uses molecular phylogenetic analyses to provide insights into the origin and speciation of the family and of the New Zealand species in particular. Samples were collected from New Zealand, Australia, South Africa, South America and the Pacific and a molecular phylogeny was constructed from mitochondrial and nuclear DNA sequences. A range of phylogenetic analyses were used to investigate taxonomic assignments, evolutionary relationships and the biogeographical history of the family.

Defensive Glands in *Trimusculus*, a Comparison with Other Marine Pulmonates

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Trimusculid limpets, like many other marine pulmonates, produce sticky mucus from the dorso-lateral pedal region when attacked by predators. Histology and electron microscopy were used to describe the structure of the glands of *Trimusculus costatus*. Based on the appearance of their secretory products, the epidermis of this species has three types of unicellular gland that stained positively for acidic, neutral and sulphated mucins only. Each gland secretes its contents via a pore between the epithelial cells. Therefore unlike other marine pulmonates (Siphonariidae and Onchidellidae), *T. costatus* does not have large multi-cellular glands encapsulated in a well-developed muscle layer. Rather, the glands, the active ingredients of which are labdane diterpenes, are more similar in structure to those of some opisthobranchs. This information adds further support to the removal of the Trimusculidae from the Siphonarioidea.

Genetic Investigation of an Endemic Complex: The *Cellana strigilis* Subspecies in the New Zealand Subantarctic Islands

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Scattered between 44° and 52°S in the Southern Ocean, New Zealand's subantarctic islands represent some of the most isolated islands on Earth and are composed of six groups: the Auckland, Campbell, Snares, Bounty, Antipodes, and Chatham Islands. The high conservation value of the islands was recognized in 1998 by their designation as a World Heritage Area. Few studies have been conducted at these island groups due to the difficulty of collecting specimens: further research is needed to inform appropriate conservation management of the islands' marine biodiversity. This study focuses on a genetic investigation of the *Cellana strigilis* (limpet) complex. Classified into 6 endemic subspecies using morphological characters, the first genetic investigation of this complex (Cytochrome b mt DNA), showed that the complex is composed of two genetically distinct lineages and revealed little or no genetic variation within each lineage. Here we report the use of two mitochondrial markers (COI and 16S), one nuclear marker (ATPS beta subunit) and RAPDs to investigate the *Cellana strigilis* complex in more detail: we detected pronounced genetic structuring within each lineage, each island having its own genetic identity. Our results are also strikingly congruent with a study on *Durvillea antarctica*, in which the NZ subantarctic islands were proposed as putative refuge area during the Last glaciations Maximum.

Historical Biogeography and Phylogeny of *Nacella* (Patellogastropoda: Nacellidae) along the Southern Ocean

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The Nacellidae (Patellogastropoda) includes two genera *Nacella* and *Cellana* with distributions in the Southern Ocean and the Indo-West Pacific regions, respectively. Species of the genus *Nacella* are distributed in different provinces in the Southern Ocean like Antarctica, Central Chile, the Kerguelen and the Antipodean Provinces. The genus includes only 15 extant species described mainly in terms of morphology and distribution. We performed phylogenetic reconstructions using different methods (MP, ML and MCMC) in 14 species of *Nacella* from different provinces of the Southern Ocean, using different mtDNA (COI, Cytb and 16S) and nucDNA (28S rDNA, Actin and Epic30) sequences. We estimated divergence times in the evolution of *Nacella* using relaxed bayesian methods.

The selected markers clearly discriminate among major lineages of *Nacella* with high bootstrap and posterior probabilities support. Divergence time estimations indicate that the separation of *Nacella-Cellana* took place during the Miocene (between 30 to 14 Ma), a period of major oceanographic and climatic changes in the Southern Ocean. According to our results the diversification of *Nacella* took place in three stages, the appearance of species in different biogeographic regions like Antarctica, South America and Kerguelen between 9 to 6 Ma. A second round of diversification took place between 5.5 to 2.6 Ma and include the origin of the South American species of the genus. The third round of diversification includes an explosive pleistocenic radiation in the Magellan Province. Our results suggest that *Nacella* exhibits great trans-oceanic discontinuities without any evidence of recent or recurrent gene flow between Antarctic and Subantarctic regions. All the species of the Magellan province show extreme low levels of genetic divergence among them, showing an absence of reciprocal monophyly. These results suggest a very recent origin of the species in this province followed by a rapid morphological and ecological diversification. [Thesis projects INACH B_01_07 and CONICYT 24090009 (C.G), projects INACH 02-02 y 13-05 (E.P), IDEAWILD. Ecology and Biodiversity Institute (IEB) ICM-P05-002 y PFB-023-CONICYT].

Comparative Morphology of *Gundlachia* Pfeiffer, 1849 Occurring in the State of Rio de Janeiro, Brazil

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The Ancylidae *sensu latum* are strictly freshwater pulmonate snails, characterized by a pateliform shell. In Brazil the genus *Gundlachia* comprises four nominal species: *G. ticaga* (Marcus and Marcus, 1962); *G. lutzi* Walker, 1925; *G. radiata* (Guilding, 1828); and *G. leucaspis* (Ancey, 1901). We compared the shells and soft parts morphology of *Gundlachia ticaga* (Marcus and Marcus, 1962) and *Gundlachia* sp., the two species of *Gundlachia* found in Rio de Janeiro. Nine morphometric characters considering shell size and shape, as well as carving and apex position were used to morphological evaluation of differences between studied populations. Discriminant analysis was performed to test shell differences among populations, considering shells measurements. Significant differences in shell morphometry were observed. The diagnosis of *G. ticaga* is based on the following characters: elliptical shell aperture; projected rounded apex, on the posterior right quadrant of the shell, flexed to the right sometimes surpassing the right margin; protoconch with an apical depression followed by a small flat area and an area with irregular punctuations; teleoconch with concentric growth lines; radial lines absent or present; anterior right rounded and larger muscle scar, drop-shaped; anterior left muscle scar and posterior muscle scar rounded; ovotest with 15 folicules; seminal vesicle with four or five roundish projections; prostate with four folicules. *Gundlachia* sp. differs from *G. ticaga* by having almost rounded shell aperture and higher; protoconch with an apical depression followed by irregular punctuations, without smooth area; anterior right elliptical muscle scar; ovotestis with five folicules; seminal vesicle with seven saculiform projections. More specimens are being studied to clarity the taxonomic status of *Gundlachia* sp; is it a new criptic species or only a variety?

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Interactive 3D-Anatomy and Affinities of Bathysciadiidae (Gastropoda: Cocculinoidea), Deep-sea Limpets Feeding on Decaying Cephalopod Beaks

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The anatomy of five bathysciadiid limpets including the type species *Bathysciadium costulatum* (Locard, 1898), which all feed on decaying cephalopod beaks in deep waters, has been investigated by means of semithin serial sectioning and interactive, computer-aided 3D-reconstructions.

The small (2-10 mm) limpets have an oval to circular shell often provided with centrifugal periostracum fringes, being provided with a horse-shoe-shaped shell muscle. The large head shows a large copulatory verge at the right side, a pseudoplicatid gill is placed in the shallow mantle cavity. There is a monotocardian heart and a single, left excretory organ. The hermaphroditic genital system is provided with a receptaculum and contains large, yolky eggs and filiform or spiral sperm, the gonoduct is glandular. The bathysciadiid alimentary tract is largely modified. The oral lappets are provided with distinct cuticularized zones and act as suckers. The diagnostic radula is supplied with a single pair of cartilages. The esophageal glands form huge, ramified sacs throughout the animal's body. Its epithelium is characterized by strange "pellets". The very large stomach lacks a gastric shield as well as midgut glands. The narrow intestine is looped and occasionally enlarged, the rectum passes beneath the ventricle. The anterior nervous system is hypoathroid, there are true pedal ganglia, whereas the streptoneurous visceral loop is cord-like. The short cephalic tentacles are smooth. Eyes, osphradia, or epipodial tentacles are lacking, statocysts contain single statoliths.

Differences between species are found in conditions of shell, protoconch, mantle papilla, copulatory organ, receptaculum openings, oral lappets, and rectal histology. The Bathysciadiidae share several synapomorphies with the Cocculinidae, namely the pseudoplicatid gill, a single, left kidney, the hermaphroditic gonad with the single, glandular gonoduct, and the statocysts with single statoliths. Therefore we confirm the clade Cocculinoidea, which is considered to be highly modified offshoot of early gastropods.

Identification Guides for Mollusca: What Do We Have? What Do We Need?

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The Mollusca are considered unanimously as a diverse and renown group of animals but notwithstanding their coverage by identification guides and high-quality popular books lags behind other less species-rich groups like birds, fish, or flowering plants. This generally results in poor levels of identification in ecological studies or environmental impact surveys, whose accuracy relies heavily on the quality of taxonomy.

Common shortcomings of current molluscan guides are discussed. Some possible guidelines regarding exhaustiveness, geographical scope, text, keys and illustrations are proposed following the completion of an exhaustive illustrated guide describing and illustrating 1200 species of Mollusca from southern Spain.

In these times of environmental crisis and unprecedented loss of natural resources, it is urgent that accurate and updated information be formatted and made accessible to a broad range of readers, including experts, policy makers or nature lovers. Conservation issues should be kept in mind, providing the elements for identification of endangered species as well as an overview of the total species diversity.

It is stressed that experienced taxonomists should get involved in the making of identification guides even if this kind of publication does not earn as much recognition as do scientific papers. If accurate, these are long-lasting products (up to several decades) in the scientific literature and largely contribute to the stability of usage given to scientific names.

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Research on Micro Molluscs at the Zoölogisch Museum Amsterdam with some Bizarre Examples

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Studies on micro molluscs can nowadays only be done with the use of a good scanning electron microscope (SEM) and therefore this study is avoided by many malacologists. At the Zoölogisch Museum Amsterdam research on micro molluscs started with studying them from the Netherlands Antilles by De Jong and Coomans in 1988 and the Macaronesian Islands. Research on micro molluscs was continued in the Indian Ocean, in particular around the Sultanate of Oman and later on around the island Mauritius. A few new taxa were already described; more than 100 new taxa are still waiting their description. During recent expeditions to Indonesia, initiated by Naturalis and LIPI, sediment-samples were collected and checked for molluscs. Some bizarre shaped new species of micro molluscs found in these samples will be shown. Collecting by SCUBA-diving may lead to a good overview on the malacofauna living in a local reef system. Unfortunately almost no living specimens were collected so DNA-related studies cannot be done with these samples.

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The Taiwan Malacofauna Database and Shell-Culture Diversity

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The Taiwan Area, an elaborate ecological system, breeds a great diversity of biotas. We approximately generalize the following reasons: Firstly, geographical distribution includes main island and many sub-archipelago islands. Inside this wide range, both characteristics of the tropical and subtropical zone can be found here. Secondly, this island spreads high mountains up to 3,945m and smooth rivers lower to the sea level. Abundant river-basins and forests contain the varied creatures. Furthermore, Taiwan locates at the east edge of the Eurasia Plate. Flat continental shelf forms the Taiwan Strait and continental slope forms the precipitous terrain at the east of Taiwan. These two conspicuous differences cause complicated ocean currents around Taiwan. The Oyashio brings cold water from north to south and the Kuroshio takes warm water from south to north. Similarly happens to mollusks, Taiwan owns more than 3,700 species of shells. Now, we already establish a scientific Database and website as an interface for people who interesting the Taiwan mollusks. The Taiwan Malacofauna Database contains (1) the Catalogue, (2) the Distribution, (3) the Bibliographies, (4) the Curatorial data (5) the Chinese names of the world common shells, and (6) the Shell n. spp. and new records. After this, the author wish to popularize shells into human life, and we begin to study the Shell-Culture (Mollusks and Human relationship). To use the database combining with shells, humanities, and information science would be a way for people to think extensively and study deeply, then also want to popularize the important ideas, Environmental Protection and Wildlifes Conservation. Now people all over the world are available to join us at “Shell, Humanity, and Database” website (http://shell.sinica.edu.tw/).

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New Generation Sequencing and Molluscs: A Leap Forward?

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Next generation sequencing allows for the acquisition of vast amounts of molecular data at a very small cost, including large fractions of transcriptomes or even full genomes. These tools are still in their infancy, though, and there are a variety of technical issues that must be addressed to apply them to phylogenomic problems. These challenges relate both to sequence acquisition and to data analysis. The length of the sequence reads and the amount of sequences per run are also important factors for choosing among existing and emerging technologies. The data can also be used for many other biological studies, including gene expression. In this talk we will discuss some of the protocols and outcomes of these techniques. [This project is supported by NSF collaborative grants DEB-0844596/0844652/0844881].

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Mollusca Aplacophora – Clade or Grade?

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The aplacophoran mollusks (Solenogastres = Neomeniomorpha and Caudofoveata = Chaetodermomorpha) are characterized by a number of common morphological characters, such as their worm-shape, cuticle with sclerites (and no shell), posterior mantle cavity, direct connection between the gonad and pericardial system, and distinctly tetraneural nervous system with a suprarectal commissure. Taking these unifying characters as apomorphies, Aplacophora has been interpreted as a clade and given the systematic rank of a class. Others, in contrast, have been pointing out the numerous differences between the aplacophoran taxa, interpreting the unifying characters as plesiomorphies and doubting an aplacophoran sister group relationship.

In this presentation, the contrasting views on aplacophoran relationships will be outlined and shown in the light of new morphological, developmental and molecular studies. Even though recently published molecular phylogenies show aplacophoran mollusks as closely related to Cephalopoda or Scaphopoda, they are here still seen as basal branches within Mollusca. Based on the profound differences between Solenogastres and Caudofoveata, the use of the term Aplacophora indicating a class-level rank is discouraged.

Molecular Phylogeny of Aplacophoran Molluscs: Inferences from Mitochondrial Genes

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The aplacophoran molluscs Caudofoveata (= Chaetodermomorpha) and Solenogastres (= Neomeniomorpha) are generally considered basal among Mollusca but their relative position to Polyplacophora and “higher” molluscs (i.e., Conchifera) is debated. It is paramount to unravel these relationships in order to understand the evolution of molluscs.

The main objective of our present project is to construct a solid hypothesis for the phylogeny of Caudofoveata and Solenogastres. Both the placement of the taxa relative to other molluscs and the phylogenetic relationships within and between the Caudofoveata and Solenogastres are investigated.

This is the first attempt to reconstruct the phylogeny of aplacophoran molluscs on a broad basis using molecular characters. We present results of phylogenetic analyses based on mitochondrial genes including close to 20 species of Caudofoveata and Solenogastres. In addition, we are exploring other potential sources of phylogenetic information from mitochondrial genes, such as gene order and secondary structures.

The Nervous System of *Scutopus ventrolineatus* (Caudofoveata): A Study Using Histology and 3D-reconstruction

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The caudofoveate *Scutopus ventrolineatus*, an animal of usually about 0.5 to 2 cm in body length, has a widespread distribution covering the whole Eastern Atlantic, the Western Mediterranean Sea and the Southwest Indian Ocean. It can be found – locally with high abundance – in muddy bottoms in depths of about 40 to more than 1200 m. Owing to the anatomy of the radula apparatus and the presence of a ventral suture as a remnant of the foot, *S. ventrolineatus* is thought to be one of the most primitive representatives of Caudofoveata making it an interesting animal for phylogenetic studies.

The nervous system of *S. ventrolineatus* – one of the most promising organ systems in this respect –has been studied previously and is thus well known in its broader features, but these studies were limited to paraffine sections of often suboptimally fixed specimens. This left some open questions concerning mainly the precerebral and the buccal nervous system and the body regions they innervate, as well as the innervation of the organs of the posterior body end.

Here, we present some preliminary results of a study employing semithin serial sectioning of properly fixed material followed by computer-based 3D-reconstruction for the first time to investigate and visualize the nervous system of *S. ventrolineatus*. Our results corroborate most of the data gained by previous studies and contribute to the clarification of the above-mentioned questions. The number of precerebral ganglia, for instance, actually shows an intraspecific variation (as it probably does generally in caudofoveates), in this case between 4 and 5 pairs and their regions of innervation do not follow a “logical” order from dorsal to ventral according to the arrangement of the ganglia themselves with respect to the cerebral ganglion. The phylogenetic implications of our findings will be discussed, along with some methodological remarks.

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Development of the Excretory System in a Polyplacophoran

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As typical for the Mollusca and other trochozoan taxa, the polyplacophoran *Lepidochitona corrugata* (Reeve, 1948) shows two different excretory systems during ontogenesis: the larval-juvenile paired protonephridia and the likewise paired juvenile-adult metanephridial system. The protonephridia exhibit two remarkable features: Firstly, they achieve their peak level of development (size, structural differentiation) during post-larval development. This is exceptional since such organs usually are attributed nearly exclusively to the larval phase of molluscan life cycles. Secondly, protonephridia form voluminous pouch-like differentiations in the duct, previously unknown from molluscan protonephridia. The metanephridial system, consisting of pericardium plus heart and metanephridial nephroduct (“kidney”), is formed during early juvenile development. It is derived from common paired laterally located anlagen, with the nephroduct portion slightly preceding the formation of the pericardium. Podocyte ultrafiltration sites in the pericardium anlagen indicate filtration functionality ways prior to final formation of pericardium and heart. In early developmental stages, ultrafiltration takes place in close proximity to the efferent duct. Hence, the organs here – from the structural perspective – resemble protonephridia rather than a metanephridial system. This totally contradicts earlier accounts on chiton development, where the “kidneys” are reported as being derived from the earlier formed pericardium. Based on the latter data, the molluscan metanephridial system was regarded as independently evolved and non-homologous with those of other trochozoans. Our findings contradict this hypothesis, but suggest homology of (components of) both excretory systems within the Mollusca and with those of other trochozoans, namely the annelids. In *L. corrugata* the protonephridia and the (developing) metanephridial system – which overlap in presence for a substantial period during juvenile development – show striking resemblances. These include the ultrafiltration sites with slits between regularly arranged pedicles or the reabsorptive differentiations (“kidneys”) of the ducts, which show identical histology and cytology.

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You Can't Get There from Here: South Pacific Distributions of Deep Sea Chitons (Mollusca: Polyplacophora: Lepidopleurida)

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This research presents a novel combination of data and methodology to predict connectivity of deep-sea benthic populations, using the known distribution of four species of deep-sea chitons in the south-west Pacific. The study fauna is found on sunken wood from 200 - 1600m, around New Caledonia, Vanuatu, and the Solomon Islands. The species are well defined by multiple morphological characters, and are known to range on sunken wood across the whole of the tropical Pacific. Our model infers larval dispersal capability by combining oceanographic, species distribution and physiological data. Dispersal speed and direction are estimated from ARGO probe data; dispersal times are inferred from comparative (shallow water) and predicted (temperature-based estimate) larval lifespans. Finally, the release locations of the larval particles are based upon species distribution data from deep-sea ecological surveys. This information is combined into a coupled biophysical transport model, which predicts the possible dispersal pathways of larvae. Our analysis shows that direct connectivity is unlikely between the three archipelagos where the deep-sea chitons have been found because the spatial scale of simulated larval dispersal is an order of magnitude too small and dispersal directions carry larvae away from the known populations. In considering mechanisms that could connect the known conspecific populations, we consider the most parsimonious explanation to be a large number of intermediate habitats which have not yet been discovered; our modelling approach can be used to produce testable hypotheses about the density and the likely locations of these intermediate stepping stone populations.

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Serialia or Not Serialia? Adding Three Monoplacophoran Species to a Multigene Approach on Basal Molluscan Phylogeny

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Prior morphological and molecular studies of molluscan phylogeny lead to contradictory results, and the different topologies proposed already count for many of all possible combinations of the eight extant molluscan classes. Molecular systematics ultimately favoured a clade Serialia, including Monoplacophora and Polyplacophora. Violating the apparently well-settled, morphology-based Conchifera concept, the Serialia were opposed by many systematists though. In fact, both recent multigene analyses recovering the Serialia were subject to sequence contamination and relied on a poor monoplacophoran and aplacophoran taxon sampling. Long Cambrian branches, signal erosion and accelerated evolutionary rates of ribosomal DNA in certain taxa were suspected to have hindered inferring natural relationships successfully.

In this study, an existing data set by Wilson and co-workers was further optimised by removing dubious sequences and by adding previously underrepresented taxa, including three further monoplacophoran species. Our data set thus is the first to contain multigene data of more than single representatives of major molluscan clades. Phylogenetic analyses were performed using Maximum Likelihood. Our results confirm that Monoplacophora is monophyletic and shed some new light on the Serialia hypothesis. Future work on additional molecular markers is expected to provide a more robust phylogenetic framework for reconstructing molluscan evolution.

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Variability in Recruitment of an Introduced Mussel *Mytilopsis adamsi* Morrison, 1946 in Haad-kaew Lagoon, Songkhla Lake Basin, South Thailand

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This study aims to gain the knowledge of *Mytilopsis adamsi* Morrison, 1946 (Bivalvia: Dreissenidae) favorite environmental characteristics for the survival and reproduction, and the period of its reproductive activity which guide us to understand the population regulation and dynamics of the species. *Mytilopsis adamsi* is a recently discovered invasive mussel in the brackish part of Songkhla Lake Basin, Thailand. Study on spatial and temporal variability of the *M. adamsi* recruitment, and the correlation between environmental parameters and the recruits were carried out in Haad-kaew Lagoon.

The interaction between seasonal and habitat factors was found. The density of recruits was highest in seasonally-closed lagoon and in the south-east predominant wind season. There were two peaks of intense recruitment. A minor peak was from May to August 2007 in the south-west monsoon season, and a major pulse was from November 2007-March 2008 of the intermediate between the north-east monsoon and the south-east predominant wind. The density of *M. adamsi* recruits was negatively related to salinity, but was positively related to the density of cyanophytes, phytoflagellates, and diatoms. The decrease of salinity in the mid north-east monsoon and low salinity in the south-east predominant wind possibly caused the major peak of recruitment found. The minor peak of recruitment in south-west monsoon was potentially due to the high abundance of *M. adamsi*'s food, phytoplankton, which provided the proper condition for the reproduction.

Population Dynamics and Reproductive Biology of the High Shore Bivalve, *Isognomon* sp. on Sichang Island, Thailand

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The high shore is typically the most stressful environment on tropical rocky shores, as species inhabiting this zone have to endure long periods of emersion and therefore experience severe thermal and desiccation stresses. The high shore bivalve, *Isognomon* sp. is extremely abundant (ca. 3,700 ind./m^2) in cracks and crevices on the high shore of sheltered rocky shores in Sichang Island, Thailand, where study on rocky shore ecology is very few. This paper investigates the seasonal variation in population dynamics and reproductive cycle of the bivalve, with the aim of understanding the strategies it may adopt to survive in this extremely stressful environment. To determine spatial and temporal variation in abundance and distribution, transects were positioned at five different 25 cm heights from mid shore to high shore (2.5 to 3.5m above MSL) on two shores. At each height, abundance of the bivalves was recorded on a monthly basis from April 2009 to March 2010. Patterns showed that the bivalves distributes from 2.75 to 3.25 m above MSL. To investigate variation in population dynamics, > 300 ind. of the bivalve were collected monthly for length frequency measurement. The species appears to have 2 cohorts and the new recruits were observed in November or December. Gonadal development was determined by histological methods in order to obtain information on the bivalves' gametogenic cycle and spawning period. Preliminary data suggest this species is reproductive in July to September, during the rainy season. Results indicate this species is extremely well adapted to living in the high shore, maintaining an abundant, stable and reproductively viable population. Further investigations are underway to determine possible physiological strategies that this species may adopt to allow it to thrive in such a physically stressful environment.

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Gametogenic Cycle, the Number of Spawning Seasons, and the Sizes at the Rate (50%) of Sexual Maturity of the Manila Clam, *Ruditapes philippinarum*, in Western Korea

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The gametogenic cycle and the number of spawning seasons, and the size at rate (50%) of *Ruditapes philippinarum* were investigated by qualitative and quantitative analyses. In qualitative reproductive analysis (histological observations), monthly variations in the gonad index showed a pattern similar to that of the gametogenic cycle. The gametogenic cycle in female and male individuals of this species can be classified into five successive stages: early active, late active, ripe, partially spawned, and spent/inactive stages. The spawning season occurred once per year from June to October. In quantitative reproductive analysis (statistical analysis) using an image analyzer system, the patterns of monthly changes in the portions (%) of the areas occupied by follicles to the ovary area in females (or by spermatogenic stages to the testis area in males) showed a maximum in May and reached the minimum in December to February 2004. From these data, it is apparent that spawning season occurred once a year. Female and male *R. philippinarum* showed a unimodal gametogenic cycle during the year. Shell lengths of sexually mature clams (sizes at the rate (50%) of sexual maturity, RM_{50}) that were fitted to an exponential equation were 18.12 mm in females and 17.16 mm in males (considered to be 1 year old).

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Deviation from Typical Bivalve Sperm Morphology in the *Tellina* and *Strigilla* Species (Bivalvia: Tellinidae)

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The ultrastructure of bivalve spermatozoa can be species-specific and provide valuable taxonomic traits for systematic reviews and phylogenetic reconstructions. Despite the ecological and economic importance of the family Tellinidae, sperm ultrastructural studies of these bivalves are still scant. The spermatozoa ultrastructure of seven species of this family (*Macoma biota*, *M. cleryana, M. constricta*, *Strigilla carnaria*, *S. pisiformis*, *Tellina punicea* and *T. lineata*) was studied in the present work, which aimed to identify characteristics that could be useful for further taxonomic and phylogenetic analyses. The species of the subfamily Macominae studied here produced *primitive-type* spermatozoa, typical of marine invertebrates in which eggs are fertilized in the surrounding water. The Tellininae spermatozoa, which fall in the *modified* category, showed short and conical acrosomes, long and helical nuclei, usually elongated mitochondria in the middle piece and a simple flagellum. In conclusion, our results suggest that analyzing the sperm ultrastructure of the bivalves in the family Tellinidae can help discriminate species and investigate their taxonomic relatedness. We conclude that *primitive* sperm cells are predominant in the subfamily Macominae, whereas *modified* sperm cells occur in high frequencies in the Tellininae subfamily. According to some authors, divergence from the typical bivalve sperm morphology occurs in groups of bivalves in which the mode of fertilization or the type of egg envelope differs from the typical bivalve condition. Can the species of the genera *Tellina* and *Strigilla* studied here produce yolk-rich eggs possibly showing a lecithotrophic development? Further studies will certainly be helpful to answer this question. Ultrastructural analyses of the ovule may reveal a relationship between the size of the sperm head and the characteristics of the egg cell. It has been proposed that spermatozoa with long heads and modified middle pieces usually fertilize thick yolky eggs.

Transcriptome Analysis of the Adult Mirror Eye from the Scallop, *Argopecten irradians*

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Next generation sequencing has quickly grown in popularity as a method for studying a vast array of different systems, from single developmental processes to whole microorganism communities. In particular, non-model systems have benefited from these methods, as they have provided some of the tools needed to explore these systems at a genomic level. One such non-model system is the scallop. Scallops (Pectinidae) are a diverse group of marine bivalves with a unique eye type, a double retina mirror eye. While there have been many studies on the structure of the scallop eye, molecular studies are uncommon. In order to explore the genetics of this unique eye type, we sequenced the eye transcriptome of the bay scallop, *Argopecten irradians,* through the combined use of Sanger and 454 sequencing of a normalized cDNA library. Sanger sequencing yielded 1920 sequences, while 454 sequencing produced >194,000 reads, which were assembled into 3495 continuous sequences (contigs). Assembly of both sets of sequences produced 2993 contigs and 402 single sequences, 66.5% of which were annotated through BLAST. Of those BLAST annotated sequences, 79.3% are unique sequences. Gene Ontology (GO) analysis of the transcriptome shows that the most common gene functions are related to metabolic processes (19%), protein binding (15%), and structure (11%), with 3% of the GO annotated sequences related to vision and/or neural activities. We then compared eye transcriptome databases in order to assess the level of gene expression conservation between the scallop mirror eye and the camera-type eyes found in relatively closely related (octopus) and distantly related (mouse) animals. Through this analysis, we were able to test the hypothesis that similarity of gene expression among eyes depends more on eye type (camera vs. mirror) than phylogenetic relatedness.

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The Development of the FMRFamide-like and 5-HT-Immunoreactive Central Nervous System in Coleoid Cephalopod Mollusks

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As highly intelligent invertebrates, cephalopod mollusks are emerging lophotrochozoan models in cognitive neuroscience and evolutionary developmental biology. Compared to the rather simple central nervous system (CNS) of gastropod mollusks or the complex brain of certain vertebrates or ecdysozoan invertebrates, cephalopods provide further insights into the evolution and development of complex nervous systems. However, cellular and molecular processes involved in cephalopod brain development are still obscure and homologies poorly established. FMRFamide-related peptides (FaRPs) and serotonin (5-HT) are evolutionarily conserved neurotransmitters present in the CNS of many metazoans. Here we present data acquired by immunocytochemistry and gene expression analyses on the development of the decapod *Idiosepius notoides* and preliminary results on *Octopus vulgaris*. In *I. notoides*, the FMRFamide encoding gene *InFMRF* and FaRPs are first expressed in a cluster of cell somata in the palliovisceral ganglia, the future subesophageal mass, during early development when the nascent ganglia are yet hardly discernable. In the supraesophageal mass, *InFMRF* is expressed significantly later during mid-embryogenesis. Compared to *InFMRF*, 5-HT is first expressed much later in cell somata located between the optic ganglia and the palliovisceral mass. Slightly later, 5-HT is found in most brain lobes, the majority of 5-HT-immunoreactive cell somata being located in the subesophageal mass but also in the subvertical and posterior basal, optic, and superior buccal lobes. In hatching squids and adults, 5-HT, *InFMRF*, and FaRPs are expressed throughout most brain lobes. The overall distribution of 5-HT- immunoreactive elements within the CNS of adult *I. notoides* resembles that of adult *Octopus vulgaris* and *Sepia officinalis* in that the superior frontal lobe possesses solely few or no 5-HT-ir cell somata while the superior buccal lobe with many. This study contributes to characterizing neuronal populations by their neurotransmitter and molecular genetic fingerprint in order to establish homologies among cephalopods and eventually other mollusks.

A Preliminary Multi-locus Phylogeny of Sepiidae (Cuttlefish) – Is Our Classification in Order?

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The familly Sepiidae is represented by 117 species within three genera - *Sepia*, *Metasepia* and *Sepiella*. The great bulk of this taxonomic diversity falls within the single genus *Sepia* (107 species), which has been tenatively partitioned into 6 sub-genera. Recent MtDNA work has alluded to the paraphyly of *Sepia*; however, insuffucient taxonomic sampling has hampered robust inference. We present a preliminary multi-locus molecuar phylogeny of Sepiidae, hypothesising the phylogenetic position of 45 taxa. Preliminary results strongly support S*epia* as being paraphyletic and comprising several relatively old lineages. In terms of the current subgeneric classification, four subgenera are not supported. The most striking result is the relataively recent divergence of *Metasepia* spp. within *Sepia* s.s., forming a sister relationship with the *Sepia papuensis* complex. Similarly, recent divergence also underpins the sister relationship between *Sepiella* spp. and members of the *Sepia officinalis* complex. Taken together, our results indicate a need for reassement of the phylogenetic utility of morphological characters currently used in Sepiidae systematics.

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Sex Pheromones: Are Hybrids Superior or Inferior in Mating Success?

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Premating reproductive isolation is necessary for the completion of speciation and coexistence of related species in communities. However, mechanisms for premating isolation are little known in molluscs. Having limited visual or acoustic senses, gastropods would most plausibly reply on chemical cues to recognize conspecifics to mate. However, only few studies have tested the efficacy of sex pheromones for their interspecific discrimination. Even no candidate substance of a mate attractant has been identified in pulmonates as far as I know. For the studies of sexual isolation by pheromones, we developed a bioassay system to evaluate the pheromonal activity of airborne substances secreted by terrestrial pulmonates by using a simple hand-made olfactometer. By using this system, we tested the effectiveness of premating isolation by pheromones between two closely related species of the genus *Bradybaena*. They mate assortatively with conspecifics in mate-choice experiments. When they mate between species, they court and copulate with each other simultaneously and reciprocally. In this study, we found that they release airborne pheromones that attract conspecific adults. Juveniles, however, did not respond to them or attract adults in either species. Thus, these airborne attractants are sex pheromones. Their F_1 hybrids attracted both species but did not respond to the pheromones released by either species or hybrids. Thus, F_1 hybrids must be releasing the sex pheromones of both species but recognize neither substance. Our results demonstrate the behavioral evidence of airborne sex pheromones that function for premating isolation in pulmonates. F_1 hybrids exhibit vigor in sex-pheromone production and breakdown in sex-pheromone sensitivity. This study provides new insights to explore the evolutionary genetics and chemical ecology of sexual isolation by pheromones and how the reproductive success of hybrids depends on population dynamics in hermaphroditic pulmonates.

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Remating and the Role of the Penial Gland in the Terrestrial Slug *Deroceras panormitanum*

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In the mating of *Deroceras panormitanum*, after mutual exchange of sperm each partner everts a large penial gland which deposits a secretion over the partner. Here we use latency to remate as an assay to test two hypotheses (amongst others) for the function of this secretion. The first hypothesis is that it identifies the donor and thus allows slugs to avoid remating with the same partner, potentially to the advantage of both. Slugs collected from the wild were isolated and then allowed to mate under observation with a specified partner. Partners were then either swapped or not and these pairs were provided with repeated opportunities to remate. Latency to remate did not differ significantly between these treatments, yielding no support for the first hypothesis. The second hypothesis is that the secretion acts as an antiaphrodisiac, manipulating the recipient to delay remating, to the advantage of the donor in reducing sperm competition and possibly in increasing the recipient's fecundity. Slugs collected from the wild were isolated and then allowed to mate. After sperm exchange matings were either interrupted so that the partners separated before gland eversion or were allowed to continue and the slugs similarly disturbed after gland eversion and natural separation. There was again no significant difference between treatments in latency to remate, yielding no support for the second hypothesis. In both experiments the proportion of pairs mating was lower in the days soon after the last mating than later; for half the pairs to remate took 3–5 days.

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Replenishment Mechanism of Disposable Penes in a Sea Slug *Chromodoris tinctoria*

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The sea slug *Chromodoris tinctoria* (Opisthobranchia, Nudibranchia), a simultaneous hermaphrodite, autotomizes its penis equipped with backward spines after every copulation and it can copulate again within approximately 24 hours. Why does the sea slug autotomize its penis and how can it copulate again within such s short time from the loss of its penis? Anatomical and histological observations on the morphology of male reproductive organs in cleared wholemount preparations with methyl salicylate and in parrafin sections revealed that the penis was a double ductal organ and the inner duct was coiled loosely. The length of the penis including the coil part was sufficient for three or more times of copulations. Then we measured the cell density and the area of nuclei at the coil part, near the genital orifice part of internal penis, and at the autotomized penis, respectively. The cell density decreased and the area of the nuclei increased in this order. The coil part of the penis is composed of indifferent tissues and they gradually differentiate to "the next penis" available for copulation. *C. tinctoria* has the replenishment mechanism of available penes successively in a short time by compressing and coilng the undifferentiated tissue of the penes. Probably the sea slug has evolved the long penis with backward spines to insert as deep as possible for removing sperm already stored in a partner's sperm receptacle. It seems so difficult to retract such a differentiated penis with spines after copulation that the sea slug may well autotomize the penis.

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Effects of Male Accessory Gland Products on the Great Pond Snail

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Seminal fluid is an important part of the ejaculate of internally fertilizing animals. This fluid contains substances that nourish and activate sperm for successful fertilization. Additionally, it contains components that influence female physiology to further enhance fertilization success of the sperm donor, possibly beyond the recipient's optimum. Although behavioural evidence for such substances abounds, relatively few studies have unravelled their identities, and focus has been exclusively on separate-sex species. I will present our work on the seminal fluid composition of a hermaphrodite, the pond snail *Lymnaea stagnalis*. One newly-identified seminal fluid protein, called Ovipostatin, is found to suppress egg mass production. I will show how this is consistent with previous findings looking at mating costs in this species. Hence, seminal fluid proteins can evolve even when the sexes are combined. More importantly, what is unique to hermaphrodite mating systems is that accessory gland proteins can theoretically also influence the male function of the sperm recipient, I will show that there is indeed another seminal fluid protein that suppresses the amount of sperm transferred by the recipient in a subsequent mating. The latter finding clearly highlights how our understanding of sexual selection is enhanced by considering different mating systems.

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Nocturnal Light Pollution and Chemical Contaminants Alter Reproductive Patterns and Hormone Concentrations of Hermaphroditic Freshwater Snails

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Hermaphroditic, pulmonate snails are widespread and important members of aquatic ecosystems, and may serve as indicator-species when assessing levels of environmental stress. As benthic organisms living in relatively shallow waters, pulmonates may be at risk of exposure to various anthropogenic pollutants, including chemical pollutants in bottom sediments and light pollution from above. Light pollution (artificial light in normally dark nocturnal habitats) may have wide-ranging effects on organisms, including altered behavioral patterns, growth rates, and reproduction. Polychlorinated biphenyls (PCBs), which are organic, industrial chemicals, are known endocrine disruptors and are often found in aquatic sediments. In one experiment, we examined growth and reproduction rates of *Physa acuta* reared under 100 lx diurnal illumination and four different nocturnal lighting treatments (0.0001, 0.01, 1 or 100 lx) for four months. We found a significant time-treatment interaction effect in growth, with *P. acuta* in the 0.01-lx treatment growing the largest. Onset of reproduction differed between the nocturnal treatments; *P. acuta* in the 1-lx treatment laid eggs earlier, and had significantly lower estrogen and higher testosterone concentrations than other treatments. In a second experiment we tested whether exposure to Aroclor 1254®, a common mixture of PCB congeners, influenced reproduction rates, and estrogen and testosterone concentrations of *Helisoma trivolvis*. We maintained snails in either clean water or water containing 56 ppb Aroclor 1254® for two months. *H. trivolvis* exposed to PCBs experienced higher mortality and significantly reduced reproduction rates. While testosterone levels did not differ between the treatment groups, estrogen concentrations were significantly higher in *H. trivolvis* exposed to PCBs. Given the abundance and importance of hermaphroditic molluscs in aquatic ecosystems, it is important to understand how disruptions to the physiology, life-history characteristics, and mating systems affect these species and the communities in which they live.

Haldane's Rule in Hermaphrodites

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Haldane's Rule (HR), which states that "When in the offspring of two different animal races one sex is absent, rare, or sterile, that sex is the heterozygous [heterogametic] sex", is one of the most valuable patterns for understanding generalities about speciation. Since it was defined for gonochoristic taxa with sex chromosomes, hermaphrodites seem to fall outside of the realm of HR studies. However, upon reviewing the malacological literature and interviewing colleagues, we found that in pulmonate land snail hybrid zones, genital defects are present in a number of individuals, and these defects predominantly affect the male parts of the genitalia. This allows a fortuitous possibility to test one hypothesis for explaining HR (faster male evolution) in isolation from its main competing hypothesis (dominance).

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Mating Systems, Inbreeding Depression, and the Timing of Reproduction in Snails

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Theories on mating-system evolution predicts an association between outcrossing and high inbreeding depression (ID). Although this applies to any hermaphroditic organism, large-scale tests have only been performed in flowering plants. Diverse as they may be, flowering plants are just one clade. Moreover, outcrossing in plants is often constrained by the environment (pollinators).

Basommatophorans (a group of pulmonate snails) have very diverse mating systems and offer an opportunity to test the theory on a second clade. We assembled a multi-species dataset using both published and new data. Using this dataset, we provide the second large-scale validation of the theory predicting that selfing/outcrossing coevolves with inbreeding depression (ID). Most species fall either into a highly-outcrossing, high-ID, or into a highly-selfing, low-ID category, with few (if any) intermediates.

We also investigated how the mating system responds to variation in mate availability. We constructed a theoretical model predicting that when ID is high individuals should delay the onset of egg-laying to avoid self-fertilization when they find no mates in the environment. This waiting time (WT) has been observed in the freshwater snai *Physa acuta*, a widespread freshwater snail, and closely matches theoretical expectations. We also showed that WT is genetically variable within and among populations; and that longer WTs are, as predicted, correlated with more intense ID at both scales. Finally our multi-species dataset confirmed that species with the high outcrossing-high ID strategy have positive, significant WT, while it never differs significanty from zero in species in high-selfing, low-ID species. In addition, we identified two different outcrossing strategies: obligate outcrossers unable to produce viable self-fertilized eggs (e.g. *Helisoma* spp.) and preferential outcrossers with positive but finite WT and ID, which can self-fertilize when mates are unavailable. Our results point to clear evolutionary trait syndromes associated with selfing and outcrossing in animals and plants.

Male and Female Investment in the Hermaphroditic Land Snail *Succinea putris* (Gastropoda: Pulmonata: Succineidae): Effects of Social Group Size, Mating Frequency and Body Size

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An individual's sex allocation is predicted to depend on its body size. In addition, sex allocation models for simultaneous hermaphrodites predict a shift toward a more male-biased sex allocation with increasing mating group size. We test these theoretical predictions in the simultaneously hermaphroditic land snail *Succinea putris*. Specifically, (1) effects of social group size, density and body size on the reproductive and sex allocation were examined by assigning juveniles to a certain social group size and density, (2) mating frequency in sexually mature individuals was experimentally manipulated to see whether the number of recent copulations itself may have effects on an individuals reproductive and sex allocation, and (3) we evaluated seasonal variation in reproductive and sex allocation in individuals collected from three natural populations at three periods within the breeding season of the species. In this study, we demonstrate that there exists variation in the reproductive and sex allocation in individuals of the reciprocally mating land snail *S. putris*, such that (1) reproductive allocation between individuals varies in relation to body size, (2) body size greatly affects the relative allocation towards the male and female reproductive organs, viz. smaller individuals allocate relatively more to the male function than larger individuals, (3) seasonal variation is detected in the reproductive and sex allocation of individuals collected from the field, (4) group size affects egg laying behaviour, viz. individuals in larger group sizes showed a lower fecundity and invested less per egg. Additionally, we suggest a trade-off between sperm production and egg investment in *S. putris*: a higher allocation to sperm production resulted in a proportional decrease in egg investment. Our results are in line with predictions of size-dependent sex allocation models.

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Effects of the Breeding System on Life History Traits in Land Snails and Slugs (Pulmonata)

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All pulmonate gastropods are hermaphroditic and (with a few exceptions) can act in both (i.e. male and female) sexual roles. Life history traits such as growth (rate), age at first reproduction, fecundity, fertility, future survival and offspring survival are highly variable within pulmonate species, even among individuals of the same population. Here, we review aspects of the breeding system that influence an individual's life history traits: viz. self-fertilization versus cross-fertilization, mixed mating strategies, geographic variation in breeding system, delayed selfing (i.e. effects of the waiting time), multiple mating and variation in sex allocation strategies. We will show that two or more of these aspects may interact, yet, studies examining interactions are very scarce. Further, there appears a strong discrepancy in the available data between basommatophoran and stylommatophoran species that may partly be attributed to the medical importance of some basommatophoran species which are intermediate hosts of trematode parasites. Finally, the effects of several of the aspects dealt with in this review may be environmentally (e.g. temperature, humidity), age, density and/or genotype dependent, which makes it very difficult to draw general conclusions on the effects of the breeding system (and other factors such as various reproductive behaviours and parasites) on (the evolution of) life history strategies in pulmonate gastropods.

A Decade of Darwin Initiative Projects in Asia

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Darwin Initiative projects seek to utilise British resources for furthering Convention of Biological Diversity objectives in biodiversity rich countries. Beginning in Sri Lanka and later extending to India, Nepal, Thailand, Laos, Malaysia and Vietnam we have worked with local collaborators to help build expertise and resources in partner countries and run extensive 'outreach' projects. A series of land snail faunal surveys have formed the basis for setting up or enhancing local and national reference collections, amassing detailed distribution information and embarking on a wide range of research projects. Some of the questions we ask about a snail fauna are what species, genera and families are present, where do they occur, how are they related, how did they come to be where they are and how do they interact with their physical and living environment. Such questions can be addressed on a wide rang of scales in time and space. For snails to be a focus of research or indeed to receive any attention from ecologists, conservationists, evolutionary biologists, and amateur naturalists, a capacity to identify specimens is needed. If specimens cannot be identified people will move on to look at groups that they can identify. For this reason we have put a lot of effort into producing identification guides ranging from field guides, featuring representative taxa for a region, to comprehensive illustrated guides to a fauna.

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Morphological Variations of *Gyliotrachela hungerfordiana* Species Complex of Langkawi Islands in the Straits of Malacca

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A species complex of micro-landsnails, *Gyliotrachela hungerfordiana*, on scattered limestone outcrops within the Langkawi Islands in the Straits of Malacca was studied. Being the most dominant micro-landsnails from the family Vertiginidae in the Langkawi Islands, the species complex exhibited interesting morphological variation across their distribution in nine sampling localities from the north to the south of these geographically complex islands. Morphological analysis was performed on eight shell measurements of the adult shells namely shell height, shell width, spire width, umbilical width, aperture height, aperture width, tuba length and degree of tuba elevation. Relationships among the morphological variables were examined by principal component analysis on the correlation matrix. The findings from this study showed clustering of populations of *Gyliotrachela hungerfordiana* from different localities denoting northern populations, southern populations and populations in between. The main differences in the shell morphology between these clusters of populations were the shell height and spire width.

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Systematics of Land Snails in Nepal Himalaya: Challenges and Future Opportunities

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Home to the world's highest mountains, the Himalaya is one of 34 global biodiversity hotspots. It covers nearly 750,000 km² and extends over 3,000 kilometres from west to east. Two regions of the Himalaya are recognised, Eastern Himalaya ranges across parts of Nepal, Bhutan, the northeast Indian states of West Bengal, Sikkim, Assam, and Arunachal Pradesh, southeast Tibet (China), and northern Myanmar; the Western Himalaya ranges west of the Kaligandaki river of Nepal across Kumaon-Garhwal, northwest Kashmir, and northern Pakistan.

The systematics of Himalayan land snails began in the 1830s following William Benson's arrival in India. Following Benson other pioneer Asian malacologists Henry and William Blanford, Henry Godwin-Austen, Thomas Hutton, Geoffrey Nevill, Ferdinand Stoliczka and William Theobald produced the baseline studies of the land snail fauna of the Indian subcontinent including the Eastern and Western Himalaya. Gerard Gude and Sylvanus Hanley's compilation work on the South Asian snail fauna was carried out in Britain.

The Nepal Himalaya, extending nearly 1000 km between the Eastern and Western Himalaya, was untouched by all 19th century malacologists. Systematic work in Nepal dates back only to 1973 with a review of Nepalese clausiliids by Nordsieck. Since then about 100 terrestrial molluscs have been identified, of which about 25 percent are new species that have been described by workers outside of Nepal. Taxonomists working within Nepal are greatly handicapped by a lack of access to specialist literature and specimen reference collections, most notably type material. Infrastructure is poorly developed and such problems as an intermittent power supply present added difficulties. Stable resources to deposit mollusc voucher specimens in Nepal are not yet established in museums and universities. Obstructive rules and regulations discourage and sometimes preventing scientific work. The draft of a Biodiversity Act has been ready for many years but it is not yet published and implemented. In the meantime permission to export biological samples for scientific work is invariably withheld by bureaucrats in the government system. A dialogue is under way between scientists and bureaucrats that will hopefully resolve the current impasse.

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Streptaxidae (Pulmonata: Stylommatophora) in Asia: Prospects and Predictions

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Phylogenetic work on Streptaxoidea (Streptaxidae and Diapheridae) allows its historical biogeography to be discussed for the first time. It appears the superfamily is of Laurasian origin while the main expansion and radiation of Streptaxidae into seven or more subfamily-level lineages post-dates Gondwanan fragmentation, despite richness in former Gondwanan landmasses. In the light of this I examine the morphological and phylogenetic diversity of Asian Streptaxoidea. Published data are scant but allow the 17 nominal genera to be assigned to the exclusively Asian Diapheridae (six genera) or pantropical Streptaxidae (nine genera), while two Philippine genera are doubtfully streptaxoid. Karstic northern Vietnam is an Asian centre of genus-level diversity, and includes the streptaxids *Elma* and "*Ennea*" *aliena* (the latter arguably a monotypic genus). Their atypical morphology and far eastern distribution suggest deep divergence from the remaining Asian streptaxids. If this predates the mid-Cenozoic Himalayan orogeny they may constitute additional subfamilies. Significantly or not, they also resemble certain western Indian Ocean endemics. The Indian *Huttonella* arose from the African *Gulella* in the late Cenozoic, suggesting overland or oversea dispersal to Asia. Monophyly of the remaining Asian Streptaxidae is suggested by unusual parietal teeth in the type species of *Perrottetia* (Indian subcontinent) and *Oophana* (Indo-China), and in some species referred to *Haploptychius* and *Indoartemon* (Indo-China) and *Discartemon* (Sundaland). Available data suggests these belong to the pantropical Streptaxinae. These genera, between which "intermediate" forms exist, did not arrive on the Deccan plate and are predicted to post-date the Himalayan orogeny. A phylogenetic hypothesis thus emerges: ((Diapheridae) ((*Elma*) (*Ennea aliena*) (*Gulella* including *Huttonella*) (Streptaxinae including remaining Asian Streptaxidae))). The biogeographic implication is that pre-Himalayan Asian streptaxid phylogenetic diversity was superseded when streptaxids reached tropical Africa, but has been enriched later. The hypothesis is testable by Asian workers, for whom priority taxa and characters are suggested.

Phylogenetic Reconstruction and Shell Evolution of the Subfamily Diplommatininae (Gastropoda: Caenogastropoda: Diplommatinidae)

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The terrestrial micromollusc subfamily Diplommatininae (Gastropoda: Caenogastropoda: Diplommatinidae) has a number of fascinating and unlikely shell shapes that beg evolutionary and functional morphology questions (e.g., *Opisthostoma vermiculum* with its four axes of coiling). This group is also interesting from a biogeography standpoint due to high levels of endemism and the island-like distribution pattern on limestone outcrops. This leads to many conservation concerns as severe disturbance of a single hill can lead to the extinction of a species. Furthermore, there are new species of diplommatinids being found regularly. Unfortunately, the systematics of this group has not been examined in any detail, and no subfamily level phylogeny is currently available, nor has its placement within the Cyclophoroidea been tested.

Here, a molecular phylogenetic reconstruction was undertaken which demonstrated the monophyly of this clade. The outgroup to Diplommatininae appears to be Cyclophoridae + (Cochlostomatinae + Megalostomatinae), such that Cochlostomatinae does not belong in the Diplommatinidae. Four main clades appear within the subfamily, following both chirality and biogeographical patterns. The genus *Opisthostoma* is the only clearly monophyletic genus tested, with *Arinia* appearing as its sister clade. *Palaina* is paraphyletic, containing *Hungerfordia,* as well as some *Diplommatina,* and this clade appears as basal within the Diplommatininae. Morphological measurements were analyzed using both ancestral state reconstruction and a phylogenetic PCA. Ancestral state reconstruction suggests a sinistral origin for this subfamily.

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The Land Snail Genus *Rhiostoma* Benson, 1860

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The land operculate cyclophorid snail genus *Rhiostoma* Benson, 1860 is endemic to Indochina and the Malay Peninsula region. The peculiar appearance of the external breathing tube extending from the final whorl of the shell has given rise to its common name of ‘snorkel snail’. These snails have received little attention beyond the original, largely nineteenth century, descriptions of about 25 species that were based purely on shell characters. After a critical study of type specimens and other reference collections from many museums and examination of recently collected specimens, we recognise 15 previously described species as valid and propose 5 new species. In addition, a large genetic distances value from allozyme variation analysis that is also supported by mt DNA analysis, may represent at least two distinct species within the current concept of *R. housei*.

Karyotypic analysis showed that *Rhiostoma* exhibits similar diploid and haploid numbers to the well-known cyclophorid genus *Cyclophorus* Montfort, 1810. However, *Rhiostoma* karyotypes exhibit differences in the appearance of telocentric and acrocentric chromosomes.

The Systematics, Diversity and Zoogeography of Chinese Enoidea (Gastropoda: Stylommatophora)

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Developed from the studies initiated by Gredler (1884-1898), Ancey (1882-1888), Heude (1882-1890), Sturany (1900), Moellendorff (1884-1901), Preston (1912), Annandale (1924) and some other authors, mostly a century ago, this revision demonstrates that China possesses a rich fauna of enoid species. Described species and subspecies amount to 164 and 40, respectively, and. newly described species and those under description amount to 32. It is clear that many Chinese species are still unknown.

Past determination of Chinese enoids was based largely on shell morphology and anatomical information is needed for most taxa. Fourteen recognized genera (with *Lophauchen* Mlldff moved to the helicoid family Bradybaenidae), in the family Enidae: *Rachis* Albers; in the family Pachnodidae: *Pupinidius* Mlldff, *Serina* Gredler, *Holcauchen* Mlldff, *Clausiliopsis* Mlldff, *Pupopsis* Gredler, *Petraeomastus* Mlldff, *Coccoderma* Mlldff, *Mirus* Albers, *Turanena* Lindholm, *Subzebrinus* Westerlund; and three genera with unclear taxonomic position: *Heudiella* Annandale, *Funiculus* Heude, and *Dolichena* Pilsbry. Nevertheless, to date, shell morphology of taxonomic importance is not sufficiently studied. In recent work the anatomical morphology of the majority of Chinese genera has been compared with related genera.

The lack of comparative data across the wide range of distributions in the region makes it difficult to assess the status of species within China and there are still significant gaps of knowledge within mainland China. The known distribution range of enoids includes Anhui, Beijing, Fujian, Gansu, Guangdong, Guangxi, Guizhou, Hongkong, Hubei, Hunan, Jiangsu, Jiangxi, Shaanxi, Sichuan (with Chongqing), Taiwan, Xinjiang, Xizang (Tibet), and Yunnan; while in the remaining provinces, the situation of enoid diversity is completely unknown. More than 62% of enoid species occur in Gansu and Sichuan (with Chongqing), where both enoid diversity and endemicity are extremely high. For other enoid-distributed regions information is very limited. In a series of recent surveys, no enoids were found on Hainan Island and it is likely that they are absent from the Island. The distribution pattern of revised genera (published and in preparation), i.e. *Pupinidius*, *Pupopsis* and *Serina,* coincides with that of the helicoid family Bradybaenidae. It appears that the region encircling the Qing-Zang Plateau is important for understanding enoid and other stylommatophoran diversity and patterns of distribution.

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Systematics and the Evolution of the Unionida

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Doubt regarding the history of higher level unionoid 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 unionoid phylogeny, especially those dealing with interfamilial relationships, stem principally from an insufficient amount of data. For example, the two largest published analyses of unionoid phylogeny both utilized a total of only 1182 characters. To address this deficiency, DNA sequence data from seven loci representing three genomes (M- and F-mitochondrial and nuclear genomes; 5,243 characters) were combined with 44 non-molecular characters, scored from 132 terminals, and analyzed using Bayesian inference (BI) and maximum parsimony (MP) algorithms. Maximum likelihood (ML) analyses were also performed on the DNA data alone. Both the ML and BI trees indicated, with significant nodal support values, the following relationships among unionoid families: (((Unionidae, Margaritiferidae) (Etheriidae [containing mycetopodids and *Etheria*], Iridinidae)) Hyriidae). This topology supports the recently published subordinal nomenclature proposed by Hoeh and co-authors (Unionoina and Hyrioina) and rejects the traditional, two superfamily nomenclature (Unionoidea and Etherioidea). Furthermore, a cemented unionoid lineage, *Pseudomulleria,* is confirmed as a member of the Unionidae. These phylogenetic relationships indicate that hyriids, rather than margaritiferids, are a product of the basal cladogenic event in the ancestral unionoid lineage. In addition, ML character optimizations strongly support (1) the glochidium as the ancestral unionoid larval type, (2) endobranchial brooding as ancestral for the Unionoida, (3) cementation having evolved independently at least three times within unionoid bivalves and (4) doubly uniparental inheritance of mtDNA (DUI) having been lost in the ancestral etherioid lineage. The following is a phylogenetic classification based on the above tree topology:

- Unionida
  - Hyriidin
    - Hyroinei
      - Hyrioidea
        - Hyriidae

- Unioniidina
  - Unionoinei
    - Unionoidea
      - Unionidae

Community Structure and Environmental Gradients Determine Ecosystem Services Provided by Freshwater Mussel Communities

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Freshwater mussels provide important ecosystem services to streams, but the rates and magnitude of mussel-generated services depend on community structure and environmental conditions. Ecosystem services are the product of the expression of species traits. Mussel species traits (primarily temperature-specific filtration and excretion rates) are correlated with phylogeny, but expression varies with both abiotic (river hydrological and thermal regimes) and biotic conditions (other species in the community). Mussels subsidize river food webs through nutrient excretion that stimulates primary and subsequently secondary production. The amount of nutrients contributed by mussels depends on mussel biomass, species composition, temperature, discharge, and local nutrient conditions. Overall nutrient contributions from the mussel community depend on which species are dominant. However, even common mussel species are declining, leading to shifts in species dominance patterns and thus nutrient recycling. Examining these linkages requires using multiple approaches: small-scale laboratory experiments, mesocosm experiments, field experiments, large-scale, comparative field studies, and models.

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Population Genetics of the Threatened Louisiana Pearlshell (*Margaritifera hembeli*) (Bivalvia: Margaritiferidae)

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This study was initiated to determine the extent of genetic structure and gene flow between populations of the Louisiana Pearlshell (*Margaritifera hembeli* Conrad, 1838). The resulting information could be used in identifying unique or genetically distinct populations of this threatened species and serve as guidelines for future conservation related actions such as hatchery propagation and reintroduction or population augmentation aimed at reversing declines and preventing extinction of this species throughout its range. Species specific microsatellite markers were generated and >200 individuals from 17 populations were genotyped at ten loci. Standard population genetic analyses were performed on the data including examination of how genetic variation was partitioned at different spatial scales (Fst, AMOVA, etc.), as well as tests of migration/gene flow. In addition, analyses based on graph theory were used to test hypotheses of population subdivision that were developed from previous analyses. The results indicate that substantial amounts of gene flow between populations significant genetic structuring exists across the specie range. In particular the Red River appears to present a substantial barrier to gene flow between Northern and Southern populations.

Variability, Function and Phylogenetic Significance of Unionoid Shell Characters

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Freshwater mussels (Unionoida) show a wide variability in various shell features but an understanding of which factors determine which trends in morphology is poor. This study investigates inter- and intraspecific patterns in unionoid shell characters and their potential use for reconstructing (1) environments, (2) characteristics of populations and (3) phylogenies.

Investigation of morphological patterns within three unionoid species from two habitat types of the River Thames, UK, elucidated consistent ecophenotypic trends in maximum shell size, relative adductor size and shape of the dorso-posterior shell margin. These characters may thus have broad ecological significance and considerable utility to palaeontologists, taxonomists and conservation biologists.

Molecular analyses using Amplified Fragment Length Polymorphisms suggested that pronounced differences in shell morphology between populations of the same species were caused by phenotypic plasticity. Observed genetic differences along the River Thames, on the other hand, were consistent with a pattern of isolation by distance and probably reflect limited dispersal via host fish species upon which unionoid larvae are parasites.

While relative shell width was a poor indicator of environment, this character was significantly influenced by allometric growth, sexual dimorphism and trematode parasitism. Detailed investigations on *Anodonta anatina* revealed that differences in the degree of sexual dimorphism between populations may reflect the overarching effect of habitat on morphology.

Interspecific morphological trends and their potential use for reconstructing phylogenies were investigated with regard to two types of shell sculptures. First, a new model of character evolution of umbonal sculptures in the Unionoida was developed by examination of over 150 extinct and modern species. Second, investigation of shell surfaces from specimens of all extant palaeoheterodont (unionoid + trigonioid) families using scanning electron microscopy revealed the presence of three types of periostracal microprojections. Observations on both umbonal and periostracal sculptures indicated considerable functional and phylogenetic significance of these two shell features.

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Fossil Bivalves from Freshwater Quaternary Deposit in Sand-pits of Mun River Basin, Nakhon Ratchasima Province, Northeastern Thailand

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The sandpits in Tha Chang areas of Chalerm Phrakiat District, Nakhon Ratchasima Province, Northeast Thailand are located in a tertiary basin and with Quaternary sediments along the Mun River bank on Khorat Plateau. These areas were utilized as private sand quarries where several fossil remains of vertebrate skeletons, petrified wood were found in late Miocene to Quaternary layers. At least 9 species from 6 genera of freshwater bivalves family Unionidae occurred, including *Chamberlainia* Simpson, 1900, 2 species; *Cristaria* Schumacher, 1815*, Ensidens* Frierson, 1911, 3 spp.; *Hyriopsis* Conrad, 1853, 1 species.; *Pseudodon* Gould, 1844, 2 species. and *Trapezoideus* Simpson, 1900, 1 species. Sizes range from 50 mm to largest size 225 mm. length. All fossil mollusks were collected from a deposit of the Quaternary Period, in Pleistocene Epoch and Pliocene Epoch of Neogene/Tertiary Period,. The fossils were deposited in muddy sand sediments, accompanied by fossil mammals including elephant *Stegodon* spp., rhinoceros, wild cattle, wild pig and reptiles; crocodiles, turtles, reflect the habitats of tropical dry forest and wetlands.

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Acute Salinity Tolerance of the Freshwater Mussel *Westralunio carteri* Iredale, 1934 of South-west Western Australia

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Salinity is a major threat to the conservation of freshwater biota in many ecosystems of Australia, especially in south-western Western Australia (WA) where salt has impacted 9 of 17 (53%) freshwater river basins. Freshwater macro-invertebrates are sensitive to changes in salinity, which is a major threat to their survival. The degree to which salinisation affects particular species has not been thoroughly investigated in Australia. *Westralunio carteri* Iredale, 1934 is the only freshwater mussel species found in south-western WA. It has been listed as Vulnerable on the International Union for the Conservation of Nature Red list of Threatened Species due to population decline resulting from increasing salinisation of and anthropogenic threats to waterways of its natural habitat. In this study, we perform two experiments to test the acute lethality of varying salinity concentrations (0, 1, 2, 3, 4, 5, 10, 15 and 20 g/L) for *W. carteri* to quantify sensitivity. Logistic regression analysis indicates that *W. carteri* has a salinity LC_{50} value of 3.06 g/L and an LC_{95} of 4.06 g/L. Salinities of 4 g/L or more were lethal to 100% of the mussels tested.

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Potomida littoralis Evolutionary History. Slow Evolution or Recent Speciation?

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Studying taxonomy, phylogenetic relationships and population diversity of some molluscs could be an unapproachable task if we only count on morphological data. Different problems as diminutive sizes, simple structures or great morphological variability might impede progress in the knowledge of these taxa. Molecular tools have come to support previous or current studies based on characters that sometimes could present a considerable homoplasy. Moreover, these techniques have, among others, the advantage of providing data that can be compared for different taxa, more or less related. Patterns of distribution, population differentiation or phylogeographical studies can be addressed and data compared for integrating them in a broad framework.

In this study, we deal with the genetic differentiation of *Potomida littoralis* in a wide range of its distribution. Based on the mitochondrial data analysed here, we have tackled its phylogenetic relationships, dispersion ability, biogeographical patterns and evolutionary history. This highly supported monophyletic group showed certain population substructure, and mainly a geographical signal could be found among the samples analysed. The greatest differentiations were found among the Turkish and the rest of populations from Tunisia, Morocco, Spain and France, although we still lack samples from eastern Mediterranean regions. Seemingly, and based on different molecular clock calibrations, the end of the Messinian (end of the Mediterranean salinity crisis) is one of the main periods for the splitting of different lineages.

On the other hand, and centred in the Iberian Peninsula, while for other unionids their evolutionary history is related to the formation of the different basins, *Potomida littoralis* almost show no differentiation. This fact could be explained by a slower mutation rate, a more recent arrival to this area or by a greater mobility of the fish that acts as its glochidia host.

Female-dependent Sex Determination is a Shared Feature of Bivalve Species with Doubly Uniparental Inheritance (DUI) of Mitochondrial DNA

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Several species from a number of bivalve moluscan families are known to have a paternally transmitted mitochondrial genome, along with the standard maternally transmitted one. The main characteristic of the phenomenon, known as doubly uniparental inheritance (DUI), is the coupling of sex and mtDNA inheritance: males have the paternal mtDNA, females do not. In the marine mussel family Mytilidae it is known that paternal mtDNA inheritance and maleness are under maternal control. Here we show that presence of the paternal genome varies dramatically among embryos from seven single females of the fresh water mussel, *Unio delphinus* (Unionidae), since sex and species specific primers were developed. Furthermore, considering possible mistakes along the study, the sex ratio for descendants is not different from the reported one for *Mytilus edulis*, strongly deviated from 1:1 ratio and mostly female-biased (five out to seven females). In spite of this, the number of female-biased and male-biased mothers is not significantly different from 1:1. The finding suggests that maternal control of sex determination (maleness are mother-dependent in Unionidae) and of paternal mtDNA inheritance, which is the situation observed in marine mussels, is a general feature of species with DUI and implies that transmission of the paternal mitochondrial genome is a very old phenomenon. A genetic model for sex determination by females was proposed by Zouros (2000) and Kenchington *et al.* (2009) but this study do not show the molecular way of paternal mtDNA transmission but it can be the beginning of a deeper study about sex determination in freshwater bivalves.

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Freshwater Bivalves (Unionidae) of the Amur River Basin, Russian Far East

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The Amur is the world's ninth longest river (with a total length of 2,824 km and the drainage basin of 1,855,000 square km), forming the border between the Russian Far East and Northeastern China. First notes on freshwater unionids from the Amur River basin in Russia were made by Middendorff (1847) and Schrenck (1867). First revisions were made by Shadin (1938, 1952) and Moskvicheva (1973a, b, c). New important stage was started in 2004 with the Amur River Biodiversity Project. In summary now 13 species from 2 genera of naiads (Nodulariinae, Unioninae) and 14 species from 4 genera of anodontines (Anodontinae) are known from the Amur R. basin (including Ussury River and Khanka Lake) while totally for the Russian Far East 22 naiads species from 2 genera and 42 anodontine species from 7 genera are recognized.

Based on the Project data 3 Red Books were prepared where listed threatened, rare and endangered unionid species from the Amur – 7 for Primorye Territory, 10 for Khabarovsky Territory and 3 for Amurskaya Province. Morphology of larval shells (glochidia) was studied for 8 Amur's species by light and scanning electron microscopy when glochidia of 3 species were firstly investigated.

Since 2007 firstly for the Amur R. basin data on symbiosis between small cyprinid fishes and freshwater unionids were received. Embryos and eggs of lazy gudgeon (Gobioninae) and 3 bitterling species (Acheilognathinae) were found in the gills of *Sinanodonta* spp., *Anemina* spp. (Anodontinae) and *Nodularia* spp. (Nodulariinae) mussels moreover fish species differed in the number of host species used.

Since 2009 first data on relations between water-mites and unionids for the Amur region were received. Water-mites *Unionicola aculeata* and *U. ypsilophora* (both species are the first records for the Russian Far East) were found in the gills of the anodontine bivalves *Amuranodonta* and *Anemina*.

The Rise of the Quagga Mussel – the Fall of the Zebra Mussel?

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Biological invasions are one of the most serious threats for native organisms. A prime example constitutes the zebra mussel *Dreissena polymorpha* (Pallas, 1771), which is known as invasive species in Europe for approximately 200 years. In 2006, the quagga mussel *Dreissena rostriformis bugensis* (Andrusov, 1897) followed its congener into western European inland waters. First reported in the Rhine River in Netherlands, only one year later it already had reached two major rivers in Germany. In North America where both taxa are also invasive, it was shown that in places where they co-occur, the quagga mussel often reduces the number of zebra mussels tremendously or even displaces them. This raises the question if the zebra mussel in central Europe will also be affected by this incoming invader.

In autumn 2009, the presence, abundance and shell size of quagga mussels and zebra mussels were determined in several important western European waterways. Our preliminary findings show that 1) the quagga mussel extended its distribution into all examined inland waters in which the zebra mussel is present, 2) at several localities the number of quagga mussel exceeded the number of zebra mussels by far, and 3) the average shell size of adult zebra mussels decreases with increasing percentage of quagga mussels, while the average size of quagga mussels is not affected by zebra mussels.

These findings indicate that the zebra mussel suffers from the arrival and spread of the quagga mussel in central Europe. Current studies focus on mechanisms of competition between the two invaders based on controlled field studies and aquarium experiments.

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The Relationship between Behaviour and Evolution of the R-Opsin in the Scallop Eye (Bivalvia: Pectinidae)

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Opsin, a seven-transmembrane protein used for vision, initiates the phototransduction pathway of all organisms with image-forming eyes. Changes in the gene sequence can have dramatic effects on protein function by altering an organism's sensitivity to specific wavelengths of light. Scallops are an excellent model to study the molecular evolution of opsin as pectinid species are found in different light environments and exhibit a suite of visually-mediated behaviours. If vision or light-sensitivity are important in an ecological context for scallop species, we predict that variation in opsin protein sequences will be correlated with specific habitats or behavioural categories. We tested our hypothesis using a phylogenetic comparative approach to determine if modifications to r-opsin sequences are correlated with either behavioural categories or changes in habitat. We examined the rhabdomeric opsin (r-opsin), which responds to changes in light intensity and is expressed in the proximal retina of the image-forming eye. Using a molecular phylogeny of the Pectinidae, r-opsin was sequenced from thirty species representing the six known behavioural groups. The vision-related molecular traits, behavioural states and habitat data of the extant species were mapped on the phylogeny and ancestral states were reconstructed for these characters and compared. To examine the molecular evolution of r-opsin, we targeted specific characteristics involved in protein function, such as changes in hydrophobicity and polarity or regions affecting wavelength sensitivity (e.g., the chromophore binding region). While previous research of the molecular evolution of vision generally has been limited to Arthropods and Chordates, our study is an opportunity to broaden vision research in molluscs. This study is one of the first interspecific comparisons of opsin evolution in bivalves.

The COI Gene and Morphological Analysis of Exotic Species, *Mytilopsis sallei*, in Four Bays in the Southeastern Coast, China

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There are four species in gernus *Mytilopsis* (*M. sallei*, *M. adamsi*, *M. leucophaeata* and *M. trautwineana*) in America coast. To ascertain whether the exotic species of mussel in Fujian and Guangdong coast in China belong to *Mytilopsis sallei* or not, whether *Mytilopsis sallei* in Fujian and Guangdong coast in China is the same species or not, thirty-five individuals of *Mytilopsis sallei* in four bays in Fujian and Guangdong coast were collected. Their shell shapes were observed and their COI gene sequences and phylogeny were studied. All the samples in four bays have an apophysis or projection on the lateral margin of its myophore plate. The fragment of COI gene is 546 bp in length. The homology of *Mytilopsis* in four bays in COI gene sequences was 97.88%. The variation rate of bases was 3.8%. The genetic distance ranged from 0.002 to 0.027 among intraspecies and from 0.139-0.745 among interspecies. The comparison with morphology and molecular phylogeny for samples in four bays, they were the same species, as *Mytilopsis sallei*.

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Genetics of Sex Determination in *Mytilus*: A Re-analysis

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Large variation in offspring sex ratio has been known in at least three species of *Mytilus* mussels (*M. edulis*, *M. galloprovincialis* and *M. trossulus*). They are also members of bivalves that show doubly uniparental inheritance of mitochondria (DUI; F mitochondria are inherited from the mother to both sons and daughters as "normal" mitochondria, and M mitochondria from the father to sons only). The relevance of DUI to sex determination and resulting sex ratio variation has been pointed out based on evidence such as behavior of M mitochondria in the developing embryos, similar patterns of inheritance of M mitochondria and of sex ratios, and M- or F-specific DNA sequences. Thus, several models of sex determination have been proposed in *Mytilus*, but they are often mixtures of physiological and genetic mechanisms, and they appear to be too complicated as genetic models.

In this paper, I i) overview the current models of sex determination in *Mytilus* spp., and ii) re-analyze the published data on their sex ratio variation (mainly Saavedra *et al*. 1997 and Kenchington *et al*. 2002) using classical genetic analyses. I try to summarize what we know about their genetics and clarify what are needed to further understand their sex determination.

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Evolutionary Radiation and Biogeography of Mangrove-Associated Molluscs

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Both mangrove plants and their associated molluscs show maximum global diversity in SE Asia, centred in the South China Sea. Few gastropods show an obligate association with mangroves, but these include the Potamididae (30 worldwide species) and *Littoraria* (Littorinidae; 39 species); in addition the Batillariidae (14 species) show a weaker association. A combination of species-level molecular phylogenies, geographical distributions and the fossil record is being used to reconstruct the biogeographic history of these groups. Three processes have contributed to the present distribution and diversity patterns of these molluscs in SE Asia: relictualism, diversification and extinction. All three groups show examples of clades that were once widespread outside the Indo-West Pacific (IWP), but are now restricted to this region. These relicts are concentrated within SE Asia and Australasia. Although diversification of each group has occurred within the IWP, there are notably few examples of allopatric sister species within SE Asia. Instead there are examples in each group of sister-species pairs that are distributed to the north and south of equatorial SE Asia; this implies extinction in the intervening area, in one case (*Batillaria*) supported by fossil evidence. The causes are unclear, but productivity regime may have played a role. The affected species are found only on continental margins with high primary productivity, and are absent from eastern Indonesia and the Banda Sea with oceanic conditions of low productivity. Mangrove-associated molluscs that are more tolerant of low productivity regimes have a wider distribution throughout Indonesia and Australia, and extend into the Indian and Pacific Oceans. The fossil record of other groups reveals examples of large gastropods from high-productivity regimes that have become regionally extinct in the Late Miocene and Pliocene, so this may be a more general phenomenon.

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Sessile Snails, Dynamic Genomes: Gene Rearrangements within the Mitochondrial Genome of a Family of Caenogastropods

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Within the vermetid gastropods we have uncovered major changes in mitochondrial gene order indicative of a surprisingly dynamic genome. Major mitochondrial gene rearrangements have occurred within this family at a scale unexpected for such an evolutionarily young group and unprecedented for any caenogastropod examined to date. We determined the complete mitochondrial genomes of four species and the partial mitochondrial genomes of two others. Each of the six vermetid gastropods assayed possessed a unique gene order. In addition to the typical mitochondrial genome complement of 37 genes, additional tRNA genes were evident in some species. Elevated sequence similarities between isoaccepting leucine tRNAs in several species suggest that tRNA remolding has been rife within this family. Studies of mitochondrial genomes at low taxonomic levels should help to illuminate the dynamics of gene order change, since the telltale vestiges of gene duplication, translocation, and remolding have not yet been erased entirely. Likewise, gene order characters may improve phylogenetic hypotheses at finer taxonomic levels than once anticipated and aid in investigating the conditions under which sequence-based phylogenies lack resolution or prove misleading. [This project is supported by NSF grant DEB- 0841777].

Tentacles in Vetigastropoda - What Can We Learn about All This Sensory Organs?

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Vetigastropoda have different kinds of tentacles in a huge diversity of shape and number. Three main types can be distinguished. [1] Cephalic tentacles covered by sensory papillae; [2] Epipodial tentacles covered by sensory papillae; [3] Epipodial sense organs (ESO). In this study tentacles have been investigated by applying histological semi-thin sectioning, scanning electron microscopy and, in parts, ultrastructural analysis. All three tentacular types show characters for sensory functions. Furthermore, there are a large number of different neck lobes and copulation organs.

Form and shape of the ESO are important systematic characters. Within Vetigastropoda three types of ESOs can be distinguished: Type 1 is a smooth tentacle, not combined with a papillate epipodial tentacle, e.g. in Scissurellidae, Fissurellidae, or Seguenzioidea. In type 2 the ESO is a small papilla at the base of a papillate tentacle. This type is restricted to the Haliotidae and the "trochoid + turbinoid" assemblage. Finally, ESOs might be entirely lacking such as in Pleurotomariidae and several Lepetelloidea.

Also certain *Neomphalina* show epipodial tentacles and *Peltospira operculata* McLean, 1989 has a very special tentacle ring around its foot. Histological and ultra-structural characteristics suggest sensory function. Comparing this structure with the vetigastropod ESO might provide evidence, whether *Neomphalina* should be included to Vetigastropoda or are to be considered as sister taxon.

Forest Snail Faunas from Georgian Transcaucasia: Patterns of Diversity in a Pleistocene Refugium

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Thirty forest sites in Georgia were sampled to obtain inventories of their land snail faunas. The sites, in nine sampling areas, ranged from Batumi near the Turkish border to Lagodekhi near the Azerbaijan border, and included parts of both the Lesser and Greater Caucasus mountains and the Colchic lowlands. Abundance was generally low, and most sites held less than 20 species. 90 species were found overall. Although sites within some sampling areas had very similar faunas, the overall levels of similarity among sites and sampling areas was low, especially when compared with similar forests from northern central Europe. Both climate and geographical position affected similarity; while these were correlated, independent effects of each were detected, and the effect of position alone was stronger. Despite this effect, most species have ranges extending into Turkey or Ciscaucasia, few have very limited ranges, and there is no evidence of patterns of allopatric replacement among congeners. These patterns resemble those seen in faunas from forests in lower latitudes, and suggest a slow build-up of regional diversity by differentiation *in situ,* without the repeated restrictions to a multiplicity of small refugia characteristic of areas where fluctuations in aridity are important. The refugium has remained isolated, and contributed little to the Holocene recolonisation of areas further north.

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Evolution and Extinction of *Chartronella* (Gastropoda): A Case Study from the Uppermost Jurassic of Kutch, India

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Chartronella belonging to the family Paraturbinidae has a long stratigraphic range from Hettangian to Upper Tithonian within the Jurassic. It is a small clade with low speciation rate. Here we describe two new species from the Upper Tithonian beds of Kutch, western India. They are *C. mundhanensis*, the older and *C. lakhaparensis*, the younger. Precise stratigraphic investigation reveals, the older species spans the last three standard European zones (Simplisphinctes to Durangites) of the Tithonian, while they co-occur in a condensed uppermost Durangites Zone. Both species show many morphological similarities which suggest that they constitutes an evolutionary plexus. The younger *C. lakhaparensis* appears to be paedomorphically derived from *C. mundhanensis* by retaining nontuberculate early stage of the ancestor. Evolution appears to be very rapid (confined within a standard ammonite zone), cladogenetic (stratigraphic overlapping of both ancestor and descendent species) and compatible with punctuated model of evolution.

The paedomorphic evolution appears to be in response to progressive shallowing of the basin under a high energy environment when India experienced intense tectonic disturbance. This scenario prompted many macroevolutionary changes in other taxa (e.g. ammonites and trigoniid bivalves). However, this rapid evolution within *Chartronella* was short-lived since the clade soonbecome extinct at the Jurassic-Cretaceous boundary which is considered as a mass extinction boundary.

Challenges and Progress in a Systematic Revision of the Problematic Worm Snail Genus *Dendropoma* (Vermetidae: Gastropoda)

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Vermetid worm snails have been largely neglected by modern evolutionary biology, presumably because of their notoriously perplexing taxonomy, inconsistent shell morphology, derived anatomy and superficial resemblance to other irregularly coiled gastropods and polychaetes. In light of a recent molecular survey revealing a cryptic and apparently morphologically indistinguishable species complex of Mediterranean *Dendropoma*, it is necessary to develop a set of morphological characters capable of reliably differentiating vermetid taxa at the species and genus level. As part of a larger evolutionary analysis of Vermetidae based on morphology, molecules, and sperm ultrastructure, we are conducting a systematic revision of the Caribbean worm snail fauna. We have focused initially on the operculate *Dendropoma* group, which, unlike any other accepted vermetid genera, is monophyletic based on preliminary molecular results. Although there are many available names for the Caribbean region, few are described beyond shell morphology, and even fewer are supported by meaningful synapomorphies. Using a combination of soft-tissue anatomy, operculum and shell morphology (including protoconch structure) we have identified a set of characters which are suitable for use in a systematic revision of this difficult group. In particular, organs of the mantle cavity, including the reproductive system, were found to be informative. A survey of the extremely abundant reef-building species *Dendropoma corrodens* from several locations around the Caribbean rim illustrates many of the issues impeding recognition of species-level diversity in Vermetidae. [This project is supported by NSF grant DEB-0841760].

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Radiation in the Balkan *Bythinella* (Rissooidea)

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Bythinella from Romania, Greece, Bulgaria, Serbia and Montenegro was studied. The anatomical study covered the shell, the penis and the female reproductive organs; in the molecular study mitochondrial cytochrome oxidase subunit I (COI), ribosomal internal transcribed spacer (ITS-1), and ribosomal 18S were considered. In Romania, two sympatric and four allopatric groups of a species rank were found. The occurrence of six species - all of them represented by low numbers of haplotypes that showed high interspecific differences - is explained by: (1) a relatively long history of *Bythinella* in the territory of a Pleistocene glacial refugium; (2) the discontinuous character of this northern refugium, which promoted speciation, but also caused local extinction and subsequent recolonization; (3) unstable, post-glacial microhabitat conditions; (4) the fragmented distribution of the Romanian *Bythinella*. In Greece we distinguished ten groups of a species rank, which were less varied interspecifically than the ones noted in Romania. The pattern that we observed in the Greek *Bythinella*, in which diversity decreased from the north to the south, is in part explained by the geological history of the area. Environmental factors in the past might at first promote vicariant speciation, but later triggered dynamic processes of colonization and recolonization coupled with dispersal over short or (sometimes) long distances, which made it possible, for *Bythinella* to survive in miniature and unstable habitats. The phylogeny inferred for all the *Bythinella* taxa from Romania, Greece, Bulgaria, Serbia and Montenegro showed two big clades. First of them comprised the Romanian, Montenegro, and one Serbian population; the second one (less genetically diversified) consisted of one Serbian and the Bulgarian/Greek populations. We assigned this distinction to isolation by the Dacic Basin (part of the Paratethys). There was only one *Bythinella* species in Bulgaria, which may be assigned to the recent recolonization of this territory from the south.

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Epitoniidae (Mollusca: Gastropoda: Caenogastropoda) Collected During the CANCAP Expeditions in the South-eastern Part of the North Atlantic Ocean

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Forty species of Epitoniidae were identified from 437 samples collected during the CANCAP expeditions (1978-1986) in the south-eastern part of the North Atlantic Ocean and housed at Leiden National Museum of Natural History. Most of 898 studied specimens are empty (96%), young or subadult (69%) shells. Usual benthos sampling and sorting methods seem to be unsuitable to obtain living specimens of these gastropods strictly associated to anthozoans. The species-level taxonomy is reviewed with emphasis on the protoconch species-specific characters. Protoconch size and sculpture seem to be good characters to differentiate species. *Epitonium turnerae* is reported for the first time in the eastern Atlantic. *E. nitidella* and *E. brevissimum* are reported in this part of the Atlantic Ocean, extending their area of distribution. Furthermore, two interesting and most likely non-described species are discussed. Most of species are shared with European or African mainland or with the Canary, Madeira and Cape Verde Islands, and 15% have amphiatlantic distribution, but this percentage may be underestimated. A thorough taxonomical review of north Atlantic Epitoniidae is needed, since some eastern Atlantic species have closely related western counterparts described under different names, and all but one eastern species here studied showed multispiral protoconchs indicating planktotrophic larval development, which might ensure transoceanic dispersal.

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The Genus *Olivancillaria* d´Orbigny, 1840 (Gastropoda: Olividae): Endemic to the Southwestern Atlantic?

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Species included in *Olivancillaria* d´Orbigny, 1840 are mostly known from the Southwestern Atlantic. They usually live in shallow water down to about 50 m depth in the Argentine Malacological Province, ranging from Bahia (Brazil) to Golfo Nuevo (Argentina). Only three species living beyond this area have been assigned to this genus, i.e., *O. acuminata* and *O. nana*, from Mauritania to Angola along the eastern coast of Africa and *O. gibbosa* from the Indian Ocean. However, such a generic placement is at least doubtful. An in-depth revision of all nominal species of *Olivancillaria* from South America was undertaken. Research was focused on the description of each species, analysis of synonymous names, illustration of characters and distribution patterns, together with SEM illustrations of protoconch, shell ultrastructure, radulae, penes, siphon papillae and egg capsules of all known species. Additionally, interspecific shell variation was analyzed using geometric morphometric techniques. Eight living species were recognized as valid: *O. deshayesiana*, *O. vesica*, *O. urceus*, *O. auricularia*, *O. contortuplicata*, *O. orbignyi, O. teaguei* and *O. carcellesi*. All are restricted to the Southwestern Atlantic from Bahia state, Brazil (~12°S) to Chubut province (42°37'S), Argentina, ranging from the intertidal zone down to 70 m depth. A comparison with other genera (e.g., *Agaronia*) suggests that *Olivancillaria* is endemic to Southwestern Atlantic waters.

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Comparing Apples to Apples: Clarifying the Identities of Two New World Ampullariids, *Pomacea canaliculata* and *Pomacea insularum*

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The Ampullariidae (apple snails) are freshwater gastropods and a key group of basal caenogastropods. They play important ecosystem, disease vector and agricultural pest roles and have great potential as models in evolutionary biology. The family is composed of two reciprocally monophyletic lineages, one of Old World taxa, and the other consisting of the more diverse New World ampullariids. The family has never been revised and knowledge of their levels of species diversity remains in a state of confusion, particularly among New World taxa with >250 available species-group names. Few types of the more than 150 possibly valid species have been adequately illustrated or described, most of those based only on general shell features. The taxonomic confusion that is rampant within this group is amply illustrated by two species that have been introduced widely and are difficult to differentiate conchologically, *Pomacea insularum* (d'Orbigny, 1835) and *P. canaliculata* (Lamarck, 1822). Until recently, studies of these invasive snails and their impacts mistakenly referred to both as *P. canaliculata*, which is listed as one of the World's 100 worst invasive species. Difficulty in accurately identifying these species has hampered efforts to prevent their spread and to precisely assess their immense environmental and agricultural impacts. Furthermore, this confusion has made it difficult to evaluate the true range of life-history variation and biogeographic distribution of either species. Only recently, molecular phylogenetic data have been successfully used to separate these species and closely related congenerics. This phylogenetic framework has allowed us to begin developing a clearer understanding of their taxonomically informative characters. Here we present some of the preliminary data illustrating the morphological distinctiveness of these two species. In particular, differences in adult shell morphology, reproductive anatomy, life history and biogeographic distribution allow these two species to be readily distinguished, corroborating our molecular results.

Revisiting the Cerithiidae: More Species, New Clades, Different Lifestyles

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Large, common, and variable. This is the prevailing view on species of Cerithiidae, with fewer than 200 species currently accepted as valid worldwide, but close to 1,000 nominal species. This paradigm has already been challenged in species-poor regions such as the Mediterranean, where the use of molecular characters is revealing taxonomic complexes among species long accepted as examples of common and variable taxa. Massive sampling programs in the West Pacific, coupled with the use of anatomical characters and molecular techniques, are now starting to reveal another world of numerous small, cryptic and/or rare species of Cerithiidae. The traditional distinction between the subfamilies Bittiinae and Cerithiinae is shaken by a clade of Indo-West Pacific near-offshore cerithiids around *Cerithium koperbergi* Schepman, 1907, with cerithiine shell morphology and a combination of cerithiine (lacking epipodial skirt) and bittiine (midgut morphology) anatomical features. Species in the *Cerithium koperbergi* clade are generally small, rare, and live on hard bottoms in coral reef environments, adding an unconventional dimension to the currently accepted view on cerithiid ecology. Despite having a multispiral protoconch indicating planktotrophic larval development, virtually identical specimens from Vanuatu and the Philippines are separated by COI sequence divergences as high as 11%. Taxonomical monographs of cerithiid genera produced in the 1980s and 1990s need to be re-evaluated in the light of newly preserved material, newly explored habitats and newly available techniques. The true diversity of the family Cerithiidae is likely two to three times higher than currently accepted.

Comparative Anatomical Analysis of the *"Parajuga"* (Gastropoda: Cerithioidea) with Notes on Other Asian and North American Pleurocerids

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The Pleuroceridae is widely distributed in Asia and North America but is still a poorly studied freshwater gastropod family. A study of the pallial gonoduct of freshwater cerithioideans from the Russian Far East, China, Korea, and North America was conducted (using histological methods). New important facts were revealed.

Besides the nidamental and albumen glands, there is the pararenal gland in the proximal portion of the lateral lamina of studied genera, except *Elimia*. This gland, located on the level of the seminal receptacle, produces an albumen-mucous secretion.

Inside the spermatophore burses of eastern North American Pleuroceridae special structures (analogous to the seminal receptacles of the other Asian-American pleurocerids) are found. These structures are located an area of the inner walls of the bursa with oriented spermatozoa (*Pleurocera* and *Elimia*), and an inner seminal receptacle opening into the bursa lumen (*Leptoxis*).

In contrast to the reproductive system, kidney and the alimentary and nervous system (phylogenetically important features) of the "*Parajuga*" remained undescribed. To clarify these questions representatives of the genus from the Amur River system are examined morphologically in detail. Using data presented by Ellen Strong with co-authors for *Pleurocera, Elimia, Juga* and *Hua,* a comparative anatomical analysis of "*Parajuga*" from the Amur drainage and the Korean Peninsula was conducted. The analysis indicates some unique characters of the nervous system of the "*Parajuga*" (comparatively long commissure between cerebral ganglion, short radula comprising 70-80 rows) as well as some anatomical features shared with Asian *Hua* and western North American *Juga*.

Based on original and literature data, a preliminary phylogenetic analysis of the studied pleurocerid genera was conducted. The resulting dendrogram supports two main clades – eastern North American Pleurocerinae *s. str.* and Asian-American Semisulcospirinae *s. lato* with low similarity. Within the last clade viviparous genera are the sister-group to oviparous "*Parajuga", Hua* and *Juga*.

The Geographic Scale of Speciation in *Stramonita* (Neogastropoda: Muricidae)

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Stramonita is a relatively small, well-defined genus of muricid marine gastropods limited to the tropical Eastern Pacific and the Atlantic. The type species, *S. haemastoma*, is known to have teleplanic larvae and is estimated to remain in the water column for several weeks. *Stramonita haemastoma* shows regional variation, and this has led to the recognition of five geographical subspecies: *S. h. haemastoma*, from the Mediterranean and Eastern Atlantic to Brazil, *S. h. floridiana*, on the east coast of Florida and in the Eastern Caribbean, *S. h. caniculata* on the west coast of Florida and the Gulf of Mexico, *S. h. rustica* in the Western Caribbean and *S. h. biserialis* in the Eastern Pacific. The protoconch has been shown to be similar across the *S. haemastoma* complex, implying that all subspecies have equally long lived larvae. Within these subspecies, cryptic variation is suspected. For example, *S. h. biserialis* is suggested to be differentiated North/South on a small scale. In the presence of teleplanic larvae, speciation on such a small scale seems paradoxical. Various explanations for this paradox are possible. Actual (or realized) dispersal of *Stramonita* species may be more limited than presently believed, leading to allopatric differentiation. Alternatively, morphological differentiation may not be a reliable indicator of genetic differentiation, and *S. haemastoma* (*sensu lato*) might indeed prove to be a single taxa. It is also possible that ecological speciation could result in geographical speciation on a small scale in the presence of wide dispersal. My results suggest that five species of *Stramonita* are present in the Caribbean, at least three of which occur sympatrically. Gene flow is maintained between Caribbean and Mediterranean populations in at least one species, while no genetic differentiation was found along the Eastern Pacific coast. The implications of these results are discussed.

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Temperature Dependency of Bisphenol a Effects in *Potamopyrgus antipodarum* and a Comparison of Effects in Two Other Molluscs

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Aquatic ecosystems are unintentionally exposed to a huge diversity of chemicals with sewage treatment plant effluents and runoff from agricultural fields, industrial and traffic zones as major sources. Other chemicals are introduced intentionally, like in aquaculture, and have largely unknown impacts on survival, development, fitness and reproduction of aquatic species.

Molluscs, though the second largest clade next to the arthropods, have widely been neglected in environmental risk assessment schemes for chemicals, mainly due to the lack of standardised and broadly accepted test guidelines for molluscs. Furthermore, data on substance-dependent effects on development, behaviour, reproduction or survival has only been marginally collected.

In the framework of the OECD test guidelines program a project was funded by the environmental authorities of Germany and the United Kingdom to prepare a *Draft Detailed Review Paper (DRP) on Mollusc Toxicity Testing*. Potential test designs for an evaluation of chemicals have been proposed and bisphenol A (BPA), a chemical compound in many plastics, was chosen as a reproduction modulating substance for the validation studies.

Therefore, we exposed the ovoviviparous mudsnail *Potamopyrgus antipodarum* to BPA in a four-week semi static test design under different temperature scenarios at 7, 16 and 25 °C, focusing on reproduction and mortality as main endpoints. The aim was to investigate the potential modulation of substance-related effects under varying test conditions like temperature.

We determined a significantly higher number of embryos in the brood pouch in BPA exposed groups, irrespective of the applied temperature scenario. However, at the lower and higher temperature (7 and 25°C) significant effects were observed at lower BPA concentrations when compared to 16°C, the normal culture temperature in laboratory-reared *P. antipodarum*.

Further, we investigated BPA effects on the reproduction of the hermaphroditic pulmonates *Physa acuta* and *Lymnaea stagnalis* and compared the resulting effect concentrations to those of the prosobranch *P. antipodarum*. [We thank the environmental authorities of Germany as well as the United Kingdom for DRP-project funding].

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Onchidiids of Four Genera (Gastropoda: Systellommatophora: Onchidiidae) in Chinese Mainland Inferred from Ecology Morphology Isozyme and Molecular Data

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Onchidiidae (Mollusca: Gastropoda) is a hermaphrodite and there are at least four species of Onchidiidae in coastal areas of China inferred from morphology, habitat, sequence character, genetic distance and system differentiation, respectively *Onchidium struma*, *Platevindex mortoni*, *Paraoncidium reevesii*, and *Peronia verruculata* of which the last three species are new record ones in mainland China. Their ecological habits and external morphology were observed through field investigation and laboratory culture. The main indicators of biological characteristics were measured for statistical analysis. The reproductive system and digestive system of the four species were compared of internal structure after anatomical observation. The results indicate that the living habitats of these four species show a gradient which are respectively from a low tide zone to the high tide zone of the intertidal zone and then to supratidal zone.

Their living habits and the ways of breathing are different because of different habitats. The differences on the external morphology of the four species are significant of which the color of feet and dorsal are different. *Platevindex mortoni* has no dorsal eyes with a gray black or grey white foot and only *Peronia verruculata* has dendritic gills. The internal structure shows that *Platevindex mortoni* has no penis subsidiary gland while *Paraoncidium reevesii* has no penis traction muscles and as same as *Peronia verruculata* which has no anal glands. Foot length and foot width are found as typical indicators in the analysis of biological data of four species. The ratio of the length of pneumostome to posterior and anus to pneumostome is a significant observation indicator in comparison of genera and species. It is correct to divide them into four species after morphological comparison. The special external structure and differences of the internal structure can be one of the main basis for classification in Onchidiidae.

By sequencing segments of 18S rRNA, 28S rRNA, COI and 16S rRNA. The phylogenetic trees indicate that the populations can be divided into 4 subgroups, which are *Peronia*, *Onchidium*, *Platevindex* and *Paraoncidium. Peronia is* the most evolutionary one of all. Perpendicular plate of polyacrylamide gel electrophoresis was used to investigate CAT, SOD, EST of Onchidiidae among six different geographic location species. Analysis the characteristics and distribution of the isozyme and using clustering analysis method, investigate their relationship directly.

To sum up, the comparative study of four species in coastal areas of Mainland China has great significance to basic research in amending new type species and morphological re-description of Onchidiidae. Another *Peronia* sp. and *Onchidella* sp. are still obscure.

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Korean Cave Malacofauna with Emphasis on Troglobitic Carychiids (Pulmonata: Ellobioidea: Carychiidae)

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Limestone caves in South Korea are widely distributed; however, most of them are concentrated in the eastern-central part of the peninsula. The depauperate hypogean malacofauna is represented by both troglophiles (three freshwater species) and true troglobites (one terrestrial and one amphibious species), which are very rare and not often found in Korea. As opposed to trogloxenes which occur in various caves throughout South Korea, hypogean mollusks are restricted to Gangweon Province, where the largest limestone caves, Hwanseon, Baengnyong, Dongdae, and Nodong, are located.

In Korea, at present, only one troglobitic land snail species is known. In January, 2000, molluscs were obtained from the wet muddy walls of Nodong cave, near piles of small limestone fragments, and identified as *Carychium* sp. by Dr. J.-S. Lee. Because of their ecology and shell morphology, these mollusks are re-identified as belonging to the European carychiid troglobitic genus *Zospeum* Bourguignat, 1856. Shell morphology of the Korean specimens is quite varied within the population, as is the case with the European *Zospeum.*

This discovery represents a range extension of the genus to Asia, but with disjunct distribution. Korean specimens, like European representatives of the genus, have squat, conic-ovate shells nearly 2 mm long, which are white, fragile, and transparent, with a parietal denticle in the aperture. Besides the apparent resemblance, however, there are essential differences in shell microsculpture. The shell surface of the Korean specimens, in contrast to other carychiids, is without malleation but finely pitted. Both the protoconch and teleoconch of the Korean *Zospeum* are covered by spiral rows of shallow pores one micron in diameter. In some parts of the shell the pores join together and exhibit dotted spiral grooves.

This distinctiveness of shell microsculpture will probably cause both European *Zospeum* and Asian *Zospeum* sp. n. to be regarded as separate genera. The discovery of a new species of hypogean carychiid demonstrates that the cave malacofauna of the Korean Peninsula is probably more varied than previously believed, and therefore merits further study.

Sarasinula Genus (Gastropoda: Veronicellidae): Analysis of a Complex of Species Based on Mitochondrial Genes (COI and 16S rDNA) and Morphological Data

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Sarasinula species have received attention because of medical and economic problems they cause in tropical and subtropical areas, being absent only in the African region and most of the Oriental region. The penis, which is the main specific diagnostic structure in Veronicellidae, however, is very similar in these species. This has hindered the determination of the species of the genus and generated systematic confusions. In this study, we investigated this complex of species based on analysis of the mitochondrial citochrome oxidase I (COI) and 16S rDNA (622 and 300bp, respectively) and of the penis and penial gland (accessory structure to penis). Evolutionary trees were constructed based on 94 individuals from Venezuela (El Hatillo and Caracas), Colombia (Caldas), Peru (Iquitos and Tonganape) and different regions from Brazil (AM, CE, MG, GO, MT, SC, SP States), including representative of eight other genera of Veronicellidae. Our molecular results strongly supported the *Sarasinula* monophyly and its sister-group relation to the American *Belocaulus willibaldoi* species. They also permitted to identify four monophyletic clades into *Sarasinula*, which probably correspond to S. *marginata* (described to Rio de Janeiro) (form 1), *S. linguaeformis* (described to Quito) (form 2), *S. plebeia* (described to Nova Caledônia) (form 3) and a forth one form (found in south Brazil) (form 4). Our study also strongly supported the clade that grouped the form 2 and 4, which is probably a sister clade of the form 3. The form 1 position changed according to data, although it has been well supported based on COI sequences, as a sister group of the clade that included the other forms. Except for the form 3, that can has penis and penial gland similar to form 2, we could also distinguished these forms by a demarcated difference in the penis and penial gland size and number and length of the penial gland tubules. [Supported by FAPESP].

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Ecotoxicological Assessment of Water Samples and Effluents of Tietê River (SP, Brazil) with Adults and Embryos of *Biomphalaria glabrata* (Say, 1818)

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The insertion of ecotoxicological assays as a tool for environmental assessment is necessary due to large amounts of substances harmful to the environment that, in addition to cause acute toxic effects, it can induce changes in fertility and viability of offspring of exposed populations, through the induction of mutations in germ cells, leading to extinction of species. In this way, new methodologies for monitoring water quality in the freshwater snail *Biomphalaria glabrata* were proposed: acute toxicity assays in adult specimens and embryos in blastula, gastrula, trochophore and veliger stages and dominant lethal test to detect germ cells mutations. The impact of sewage treatment plant upon receiving waters of Tietê River (SP, Brazil) in a highly industrialized region was studied. Five points were chosen: Ponte Nova Dam, 200 meters upstream to the plant, the influent of plant, the effluent treated by plant before discharge in the river and 200 meters downstream to the river discharge. Only the station influent was toxic for adults and embryos. After discharge into the river, treated effluents were not toxic for *B. glabrata* adults and embryos. There was no mutagenicity in any samples. These results show the importance of the sewage treatment plant in reducing acute toxicity of effluents. The efficiency of the *B. glabrata* toxicity test was demonstrated in comparison with standardized bioassays with *Daphnia similis*. Snails showed similar sensitivity to daphnids, demonstrating that *B. glabrata* is a suitable species for monitoring of freshwater and can be integrated in the battery of tests, validated and used to control environmental pollution. [Financial Support: FAPESP, CNPq. Technical Support: SABESP, Suzano, SP].

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Ecological Release and Venom Evolution of a Predatory Marine Snail at Easter Island

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Ecological release is coupled with adaptive radiation and ecological diversification yet little is known about the molecular basis of phenotypic changes associated with this phenomenon. The venomous, predatory marine gastropod *Conus miliaris* has undergone ecological release and exhibits increased dietary breadth at Easter Island. We examined the extent of genetic differentiation of two genes expressed in the venom of *C. miliaris* among samples from Easter Island, American Samoa and Guam. The population from Easter Island exhibits unique frequencies of alleles that encode distinct peptides at both loci. Levels of divergence at these loci exceed observed levels of divergence observed at a mitochondrial gene region at Easter Island. Patterns of genetic variation at two genes expressed in the venom of this *C. miliaris* suggest that selection has operated at these genes and contributed to the divergence of venom composition at Easter Island. These results show that ecological release is associated with strong selection pressures that promote the evolution of new phenotypes.

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Birth, Death, Diversification and Differential Expression of Conotoxin Gene Families of Vermivorous Marine Snails *Conus*

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Predatory marine snails *Conus* use venom comprised of a cocktail of potent neurotoxin, termed conotoxin, to paralyze prey, and different species of *Conus* have unique compositions in their venom. Conotoxins are encoded by many gene families, and even closely related species might have completely different conotoxin genes expressed. This unique phenomenon inspires one interesting question: What drives the origin of unique venom composition among species of *Conus*? The possible explanations are the divergent evolution and differential expression of conotoxin gene families among closely related species of *Conus*. To test these hypotheses, we recovered all A-superfamily conotoxin genes from the genomic DNA of four closely related vermivorous species *C. lividus*, *C. diadema, C. sanguinolentus* and *C. quercinus* by PCR with multiple sets of primers, cloning, screening and sequencing. Three types of putative pseudogenes and four types of conotoxin subtypes are recovered from the genomic DNA, and Bayesian tree shows that frequent duplication, gene death and functional diversification lead to diverse genomic repertoire among closely related species. Positive selections are detected on all the functional conotoxin genes and even on one type of putative pseudogenes.

Expression profiles are obtained by PCR from cDNA, cloning, screening and sequencing in exactly the same condition as in genomic DNA. Partial and differential expression has been proved by comparing the expression profiles with the genomic information. Less than 40% of conotoxin genes in the genome are expressed, and majority of genes expressed among closely related species fall into different clades. These results show that the different venom composition among *Conus* species results from birth, death, divergent evolution, and partial and differential expression of conotoxin genes.

Patterns of Genetic Diversity in Squids with Contrasting Life History in the Humboldt Current System

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Dosidiscus gigas (Ommastrephidae) and *Doryteuthis gahi* (Loliginidae) correspond to the most abundant pelagic squids in the Humboldt Current System (HCS). These species are characterized by contrasting life histories related to spawning and migration behaviours. To determine the population structure and genetic diversity of both species, we collected specimens from different sites in the HCS, and amplified a fragment of the mitochondrial gene Cytochrome c Oxidase I (COI). Molecular analyses in *D. gigas* showed low genetic diversity, absence of population structure and evidence of demographic expansion after the last glacial maximum (LGM). These results suggest that *D. gigas* conforms a single large population characterized by high levels of gene flow along the HCS. For *D. gahi*, COI sequences revealed the presence of two population units in the HCS corresponding to Central Chile and Peru. In the Peruvian unit we detected lower genetic diversity and evidence of demographic expansion corresponding to a date similar to that of *D. gigas*. The Chilean unit exhibited higher levels of diversity, suggesting that it corresponds to an older and stable population. According to these results, we propose that the Peruvian unit of *D. gahi* may have originated from the Chilean population through a founder effect. Changes in distribution ranges and population sizes could be related in both cases to the variations in productivity at a millennium scale along the HCS. Contrasted dispersal and migration capacities of both species could explain the differences in their genetic population structure.

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Phylogeography of *Enteroctopus megalocyathus* (Gould, 1852) (Cephalopoda: Octopodidae) along the Southern South America

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Geological events and global climate changes are recognized as the main drivers of changes in the species distribution range at ecological and evolutionary time scale. Changes in distribution range left genetic signature at the population and species level, which can be detected using phylogeographic approach. In this study we performed a phylogeographic analysis of *Enteroctopus megalocyathus*, widely distributed along Southern South America coast (Chile and Argentina). We amplified the Cytochrome c Oxidase subunit III gene to carry out analysis of genetic diversity, population structure and demographic history. Two population genetic units were detected, corresponding to Chile and Argentina samples. Only one haplotype were shared between Atlantic and Pacific populations and genetic diversity was lower in Chilean samples. Coalescent-based analysis showed that the Chilean unit experienced a recent demographic expansion, while the Argentina unit exhibited signals of an older population. Based on these results, we propose that Chilean population of *E. megalocyathus* originated from Argentinean one through a founder event related with the last glacial-interglacial transition period. These results suggest also a reduced gene flow across the southernmost tip of South America, probably related with the limited dispersal capacity of the supra-benthic paralarvae that characterized this species.

Factors Driving the Population Ecology between Sepiolid Squids and Their Luminous *Vibrio* Symbionts- Why Ecology Matters

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Sepiolid squids (Cephalopoda: Sepiolidae) form mutuatlistic associations with luminous bacteria in the family Vibrionaceae (g-Proteobacteria). The bacteria are harbored in a dynamic light organ complex; the bioluminescence created by the bacteria is used in a behavior known as counter-illumination. Additionally, this association is environmentally transmitted; that is, the bacteria infect their host with each new generation from the surrounding seawater. Thus, specific *Vibrio* bacteria must be capable of accommodating abiotic factors that dictate their fitness outside the squid, as well as the mechanisms that control specificity and host selection while in symbiosis. Interestingly, both sepiolids and *Vibrio* bacteria do not exemplify strict patterns of co-speciation; rather, their populations follow phylogeographical boundaries set by temperature and salinity ranges. Using physiological, genetic, phylogeographical, and GIS predictive measurements, we can better predict how populations of both sepiolids and *Vibrio* change over the course of time, and whether these patterns are influenced by seasonal variation, or more dramatic changes that are linked to larger-scale global changes. Determining whether populations of squid host and symbiotic *Vibrio* bacteria are effected by their environment has direct implications to abiotic selection (and therefore ecology), and the influence of host specificity on driving bacterial speciation in this ecologically important mutualism.

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An Assessment of the Genetic Diversity of *Prestonella* (Mollusca), an Endemic Genus from the Great Escarpment of South Africa

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The genus *Prestonella* is a distinctive component of the southern African terrestrial malacofauna, and is restricted to relictual habitats associated with the southern edge of the Great Escarpment in South Africa. This genus represents the only surviving African element of a Gondwanan Bulimulidae *s.l.* Three species-level taxa referable to the genus *Prestonella* have been described, *P. bowkeri*, *P. nuptialis* and *P. quadingensis*. Two species (*P. bowkeri* and *P. nuptialis*) appear to have very specific habitat requirements, being found almost exclusively on near-vertical rock faces above water courses and on moist, shaded (south-facing) cliffs. The habitat requirements of *P. quadingensis* remain unknown. The distribution of the genus is highly fragmented due to the evident habitat specificity of the species.

An assessment of the phylogeographic diversity of *Prestonella* using the mitochondrial marker COI revealed that there is no gene flow between populations across their distribution range. Due to the large distances between suitable habitats, populations are isolated from each other and each possesses unique genetic diversity. The range of many terrestrial snails is limited due to specific habitat requirements and poor dispersal capacity, and this in turn may prevent terrestrial snails from escaping changing ecological conditions. Thus, owing to their specialized habitat requirements and fragmented distributions, *Prestonella* species are likely to be adversely affected both by land degradation and by the regional aridification anticipated to result from global warming. This highlights the need for careful monitoring and site-specific conservation action plans.

Another Invited Invader – Phylogeography of *Carychium minimum* in Europe, North America and on the Azores

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As a result of the post-Columbian globalization since 1492 more and more non-indigenous species are reported all over the world. Humans themselves act as the best leveler of the world's biota actively or passively dispersing species. No longer hindered by active dispersal barriers such as oceans or mountain ranges, dispersed species can occupy previously inaccessible habitats and become invasive.

A well known example is the 'exchange' of gastropod species between e.g. North America and Europe. In our study we analyzed the phylogeography of a member of the Carychiidae (Pulmonata, Ellobioidea) - the Herald Thorn *Carychium minimum* (O. F. Müller, 1774). The European population structure of this minute terrestrial snail consists of four distinct phylogenetic units. Long standing gene-flow barriers such as different refugial areas during glacial periods can most likely explain such a pattern of genetically isolated units. A climatic niche modeling approach for the time of the Last Global Maximum (21,000 years before present) revealed potential suitable habitats at the Iberian Peninsula, Italy, the Balkan and areas northwards the Alps (cryptic northern refugia), well known refugial areas in Europe. Moreover, two populations, on the Azores and at the East Coast of North America, possess haplotypes which cluster in between a European phylogenetic unit otherwise only restricted to Central-Western Europe. Hence, another passive anthropogenic dispersal for this species seems most likely.

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The Geography of Partulid Tree Snail Diversification: New Insights from Old (Museum) Specimens

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Partulid tree snails are endemic to tropical Pacific oceanic high islands and, though collectively distributed across 10,000 km of Oceania, most species are single island endemics. Their academic study has a distinguished history but it has been seriously disrupted in recent decades by a major wave of extinction and extirpation. Access to museum collections, together with recently collected specimens forwarded by generous colleagues, has allowed us to glean new molecular phylogenetic insights into aspects of their evolutionary history and biogeography. These include the systematic and biogeographic inter-relationships of the genera *Partula* and *Samoana*. Our novel results indicate that the genital anatomy characteristic of *Partula* species may be plesiomorphic and that these two genera have experienced very different biogeographic histories and diversification patterns east of Samoa/Tonga. Based on their respective generic phylogenetic topologies, *Samoana* appears to be a relative newcomer to the eastern archipelagoes (Society, Australs, Marquesas), but has been more adept at both intra- and inter-archipelago colonization. Our Society Island results are inconsistent with the speciation model developed for Moorean and Tahitian *Partula* species: Tahitian taxa stem from multiple colonizing lineages and a large fraction of Tahitian mitochondrial treespace lacks explicit phylogenetic ties to Moorea. Two species, *P. hyalina* and *P. cateriensis*, transgress familial biogeographic norms (have multi-archipelagic distributions and occur on low islands), likely due to prehistoric anthropogenic introductions. Some of these findings have practical implications for partulid conservation.

The Difficulty of Delimiting Species in the Largely Selfing Land Snail Genus *Rumina* (Pulmonata: Stylommatophora)

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The regular occurrence of selfing in hermaphroditic taxa may strongly affect population genetic structuring and may complicate taxonomic interpretations. This is well-illustrated by the predominantly selfing terrestrial snail genus *Rumina* which shows a high degree of colour and shell shape variation. This variation was formerly used to distinguish numerous (sub)species. Although many of these taxa are no longer recognized, 2-3 "species" are still "in use", viz. *Rumina decollata*, *R. saharica*, and *R. paivae*. However, in view of the supposed high prevalence of selfing in *Rumina*, it remains unclear to what extent this morphology-based taxonomic interpretation of *Rumina* is well-founded.

Here we explore this issue by a molecular phylogenetic analysis of 6 gene fragments (ITS1, ITS2, COI, CytB, 12S and 16S) in the genus *Rumina* troughout its native distribution range around the Mediterranean. This revealed several highly divergent clades, separating *R. decollata* and *R. saharica,* and with *R. decollata* being further subdivided in several deep, strongly supported clades that differ in shell shape and body colour, including shell morphs corresponding to *R. paivae*. This suggests that the current interpretation of *Rumina* as a complex of only 2-3 "species" level taxa may be ill-founded, though it remains uncertain to what extent *Rumina* "taxa" in fact represent intraspecific polymorphisms that are structured by sustained selfing. [This work is supported by the FNRS (Belgium) that conceded a FRIA PhD grant to V. Prévot].

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Parapatry in Pilbara *Rhagada* – Something Old or Something New?

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Rhagada species from the Pilbara mainland, like so many Australian camaenids, have relatively small, non-overlapping geographic distributions. Eleven described species of *Rhagada* form a series of geographic replacements from Cape Leveque, in the Kimberly, southwards to Shark Bay. No obvious geographical barriers to dispersal explain the lack of geographical overlap. Current interpretation of the distributions of species of *Rhagada* is based solely on morphological taxonomy, and the lack of overlap has precluded direct tests of reproductive isolation. Our extensive search for areas of transition between morphological forms revealed a sharp cline over less than 10 km between the large, unbanded, coastal species *R. convicta*, and an inland, small, heavily banded undescribed form of *Rhagada*. We are investigating the population genetics of this transition, and the evolutionary history of these distinct forms. To test whether the meeting of the forms is the result of primary or secondary contact, relationships were investigated using two mitochondrial genes (COI and 16s). Phylogenetic analyses and levels of sequence divergence between the two forms indicate secondary contact. Variation of genital morphology was also analysed along the transect, in the context of variation of shell morphology and the underlying phylogenetic relationships. The next stage of this study will be to examine whether gene flow occurs between these distinct forms using microsatellites, to attain some insight as to why parapatry and allopatry are typical in this genus, whether either genitalia or shell morphology are reliable indicators of species relationships, and therefore whether reproductive isolation can be inferred from genitalia in *Rhagada*.

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The *Rhagada* Land Snails of Rosemary Island: a Taxonomist's Nightmare and Evolutionist's Delight

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Snail shells are notoriously variable structures, but the variations need not reflect speciation or common ancestry, and can instead present themselves at the level of the population. Despite these facts, shells form the basis for many taxonomic descriptions. Such is the case on Rosemary Island, a small continental island off the northwest Australian coast, where five species of *Rhagada* land snail were previously described. Although the variation in shell size and shape is extreme, spanning the genus, the descriptions were based on small collections of empty shells. Curious to the true nature of the variation, specifically whether it reflects speciation as suggested by the existing taxonomy, or if it has presented itself at the level of the population, we conducted a detailed study of morphological, molecular and anatomical variation. Although we confirmed the presence of several morphologically distinct groups in the type material used in the original descriptions, we found no such groups in the samples that we collected from 103 populations, instead finding complete continuums of size and shape variation between the extreme forms. We observed very low levels of molecular divergence and no relationship between morphological and molecular variation; not only was there little coherence between populations of the same shape/size within a phylogeny, the morphological variation was distributed among well supported clades. We also found no relationship between morphological and anatomical variation, with discriminant analysis unable to distinguish between four morphologically distinct populations based on measurements of genital structures often examined in taxonomic studies of land snails. Together, these data favour the view that there is a single, morphologically diverse species of *Rhagada* on Rosemary Island. They also demonstrate that extreme morphological variation need not reflect speciation, can evolve rapidly and repeatedly, and can present itself at the level of population without significant genetic or anatomical change.

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Resolving Taxonomic Complications in the Family of Ariophantidae by Using Molecular Marker and Morphological Characteristics: A Preliminary Attempt

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This study is an attempt to resolve the taxonomic complication in the Family Ariophantidae by using nucleotide sequences 16S rRNA gene with the aid of morphological characteristics of the shell. Morphological classification of members of this group can be very confusing. The ariophantids that were used in this study were collected from Langkawi Island located at the Straits of Malacca. Langkawi Island is an isolated island thus any environmental changes in the island will affect the distribution of organisms in it. The initial finding of this study suggested that the genetic approaches are as important as the morphological approach in discriminating land snails species. Even a slight change in the color of the shell may denote a distinct separation in the phylogenetic relationships. However, a few samples were found to be clustered together in a group although they showed slight different in the shell coloration, which denotes that there are possibilities of different morphological adaptation to the same environment. Using morphological characteristics alone can be unreliable but the evolutionary relationships in deeper phylogeny within the group may be confirmed through molecular data.

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Phylogeography of a High Alpine Austrian Endemic: *Cylindrus obtusus* (Gastropoda: Pulmonata: Helicidae)

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Cylindrus obtusus (Helicidae) is a hermaphroditic landsnail, endemic in the Austrian Alps, which is restricted to high elevations (1600 to 2500 m asl) and limestone. As a specialist of high alpine rocky habitats, *C. obtusus* 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. However, genetic distances are small (max. 1.7 %). The microsatellite analysis reveals a high differentiation between the populations implying restriction of gene flow. The highest genetic variability was found in the central populations. 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. Further investigations shall elucidate whether this lack of heterozygotes is caused by selfing and if so, why it occurs at such a high frequency.

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The Snail Genus *Trochulus* (Gastropoda: Pulmonata: Hygromiidae) as an Example for Morphological, Genetic and Ecological Differentiation of Alpine Land Snails

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Both *Trochulus oreinos oreinos* (Wagner, 1915) and *T. o. scheerpeltzi* (Mikula, 1957) are endemics of the north-eastern Austrian Alps. Originally they were regarded as regional subspecies of *Trochulus hispidus* (Linné, 1785), but later *T. oreinos* was raised to species status. We analysed these three taxa morphologically and genetically to evaluate whether a delimitation between them is possible, and, if so, to resolve their phylogenetic relationships. Shell morphological results revealed high similarity between the two *T. oreinos* taxa, and that they are clearly separated from *T. hispidus*. The subspecies *T. oreinos* tends to be smaller than *T. hispidus*, but measures of shell size showed overlapping ranges. In contrast, the length of hairs at the last whorl turned out as a suitable trait to discriminate both *T. oreinos* subspecies from *T. hispidus*. Additionally, the *T. oreinos* subspecies concur with respect to their habitat preferences, as they are both restricted to rocky high alpine grassland, whereas *T. hispidus* is distributed over a wider altitudinal range occurring in moist areas and scrubby perennial herb vegetation near water bodies. While the morphological and ecological results allow clear differentiation between *T. hispidus* and *T. oreinos* only, analyses of the mitochondrial cytochrome oxidase subunit I and 16S rRNA genes revealed high sequence divergences between all three taxa, which indicates that they represent very old lineages. The two *T. oreinos* taxa appear as distantly related sister group, well separated from *T. hispidus*. Whether *T. o. oreinos* and *T. o. scheerpeltzi* should be considered as independent species shall not be decided at the current state of knowledge.

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Cepaea Shell Polymorphism and the Evolution Megalab: Preliminary Analyses on Behalf of the Megalab Steering Group

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The Evolution Megalab, set up by the Open University in the UK for Darwin Year, was designed to involve the public in sampling and scoring the shell polymorphism in populations of *Cepaea nemoralis* and *C. hortensis* across their European ranges via an interactive website. In part, it aimed to see whether there had been changes in morph-frequencies over time, and so a database of all accessible earlier records (from c. 10,000 populations) was also compiled. The Megalab itself generated c. 7,500 records, although some of these (especially for *C. hortensis*) were unreliable. For *C. nemoralis,* preliminary analyses show strong geographical patterns and variation with habitat in both old and new records, and some interaction between them. The patterns in *C. hortensis* are less easy to interpret. Any later conclusions available will be presented, and some lessons about the conduct of such a project considered.

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Local Adaptation in the Land Snail, *Cepaea nemoralis*

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The land snail *Cepaea nemoralis* is highly polymorphic in directly observable shell characters. The underlying genetics of these shell characters is simple, facilitating the demonstration of local adaptation and disruptive selection at individual loci based on morphological data alone. There is a consistent association of shell colour (and therefore gene frequency) and habitat type, implying that natural selection is acting to shape patterns of divergence on a local scale. However, there is a lack of molecular data to support the idea that selection is operating. A genome-wide scan with hundreds of amplified fragment length polymorphism (AFLP) markers may reveal loci that are highly differentiated between divergent populations of *C. nemoralis*. Highly differentiated loci are the signature of natural selection operating in the genome. In addition, mapping these markers in relation to each other and to shell character loci makes it possible to identify and locate regions of the genome under selection – will the region of the genome that harbours the shell colour locus be under selection?

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Rapid Evolution in Unstable Habitats: a Success Story of the Polymorphic Land Snail *Cepaea nemoralis*

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In this study I report on a natural experiment with ten replicates in which rapid, predictable and consistent divergence of *Cepaea nemoralis* populations occurred in response to repeated selection gradient of adjacent open and shaded habitats. While the frequencies of various genetically based phenotypes varied widely among surveyed populations, the changes were consistently towards higher frequencies of dark morphs in the shaded and light morphs in the open habitats, a result attributable to natural selection. There was however no overall variation with habitat. This indicates that without the knowledge of the genetic composition of reference populations it is often not possible to discern selection from random processes. At each site a different morph combination contributed to the divergence of populations indicating that there are many genetic solutions to similar ecological problems; this likely enhances the maintenance of high levels of polymorphism. Adaptation of populations occurred in contemporary time and was fast. In one case where following changes was possible, significant shifts in morph frequencies occurred within just two snail generations (selection coefficients 0.404 and 0.518). High evolvability may be one of the factors contributing to the ecological success of *Cepaea nemoralis*.

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Three Decades of Climatic Selection in the Land Snail *Theba pisana*

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Few continuous, long-term studies have measured the intensity and variability of natural selection within a framework of clear adaptive hypotheses. In the snail *Theba pisana* the proportion of effectively unbanded shells is higher in exposed habitats than in adjacent shrubby areas, which has been explained by microclimatic selection. Comparisons across an ecotone for 33 consecutive years determined the combined effects on morph frequencies of habitat and changes in temperature. The persistent association of shell banding with habitat accounted for 34% of the variation in morph frequencies, but differences among years were also large, representing 25% of the variation. Proportions of effectively unbanded snails were higher following hot, sunny summers, so both spatial and temporal variation support the hypothesis of microclimatic selection. Based on observed rates of change, the mean annual selection on this polymorprhism was about 0.14, but the variance was large, with $s \leq 0.05$ in about half the years, but as high as 0.6. The large variance and frequent reversals in direction of selection indicate a high potential for genetic change, but with little net change in morph frequencies over three decades, highlighting the value of long-term, continuous studies of populations under normal conditions.

Purifying Selection Against Left-right Reversal in the Freshwater Pulmonate *Lymnaea stagnalis*

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The left-right polarity of development has been conserved with no reversed species in most metazoans. Many of them fertilize externally or copulate with the genitalia located in the midline. Thus, their reversed mutants should experience little mating disadvantage, whereas internally-fertilizing snails undergo positive frequency-dependent selection against reversal because of physical difficulties in copulation between dextral and sinistral morphs. Furthermore, left-right reversal should not affect the external features of metazoans, because most of them are symmetric in basic external body plans. Accordingly, the evolution of reversal is most plausibly suppressed through endogenous fitness reduction by reversal. However, the effect of developmental reversal on fitness is not ordinarily distinguishable from the pleiotropic effects of the reversal allele through its zygotic expressions during ontogeny. We achieved testing the effect of developmental reversal on fitness by generating dextral and sinistral snails in *Lymnaea stagnalis* that share the same genomic background by a crossing scheme that exploited maternal inheritance and hermaphroditism. These sinistrals frequently developed lethal anomalies of morphology before hatching. Shell shapes of adult dextrals and sinistrals differed from the mirror image of each other. The polarity genotypes exhibited no pleiotropic effects on hatchability or shell shape. In pulmonates, the direction of early spiral cleavage, instead of maternal substances, epigenetically determines the polarity of whole-body structure. Thus, these results show that purifying selection operates against the genetic reversal of cell configuration in early embryos. In this study, we discovered that sinistral variants do not perform spiral cleavage in the mirror-image of the dextral wild type. The deviation of blastomere configuration by a maternal pleiotropic effect of the reversal gene was responsible for the reduction of embryonic viability resulting in purifying selection against left-right reversal. We discuss the evolutionary implications of these results for understanding the constraint and evolution of left-right reversed species in gastropods.

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Spatial mtDNA Population Genetic Structure and Asymmetric Gene Flow in Two South African Intertidal Gastropods: *Oxystele variegata* and *Oxystele sinensis*

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Oxystele variegata and *O. sinensis* are topshells endemic to the coast of South Africa. They occur on intertidal, rocky shores and have a pelagic larval stage of an unknown duration. We examined the spatial genetic structure and gene flow of the two species using 141 and 165 cytochrome oxidase subunit 1 sequences of *O. variegata* and *O. sinensis*, respectively, collected from eight localities each (from Port Nolloth to Haga Haga) covering most of their geographic range. Analysis of molecular variance and pairwise Φ_{ST} values suggest significant spatial population genetic structure in both species. Two phylogroups were recovered in *O. sinensis*, a south-western one comprising individuals from Wooley's Pool, Betty's Bay and Cape Agulhas, and a south-eastern one consisting of individuals from Herolds Bay to Haga Haga. The same number of phylogroups was found in *O. variegata* with a western phylogroup including Port Nolloth, Hondeklip Bay and Lambert's Bay and a south-eastern one comprising the rest of the localities. No spatial genetic structure was detected within phylogroups in both species, consistent with their having a pelagic larval stage. Coalescent analyses suggest asymmetric gene flow between localities in both species. Gene flow was predominantly westward on the south-west coast but mainly eastward on the south-east coast in *O. sinensis*. In *O. variegata* gene flow was northward on the west coast and similar to that of *O. sinensis* where they occurred together. The spatial genetic structure observed confirms the genetic barriers between the west coast and the south-west coast (around Cape Point), and another one around Cape Agulhas found in previous studies. The gene flow patterns suggest that the north-east flowing Agulhas counter currents predominantly influence dispersal on the south and south-east coasts whereas the Benguela Current, which flows north-westwards, influences dispersal on the west coast.

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Environmental Tolerance, Historical Isolation and Contemporary Currents Influence the Ranges of Species and Intra-specific Clades in the Intertidal Mollusca of Southeastern Australia

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South eastern Australia offers an increasingly well-studied opportunity for untangling the effects of historical isolation, contemporary current flows and endogenous environmental tolerance on species ranges and the distribution of intra-specific genetic variation. For example, isolation induced by landbridge formation across Bass Strait between central Victoria and Tasmania at glacial maxima has been hypothesised as the cause of phylogeographic boundaries in a chiton and a number of gastropods. The lack of structure in the estuarine hydrobiid *Tatea* that we reported at the 2007 WCM is a notable counterexample to the general pattern. In recent studies, we have collected distribution data and DNA sequence information from a pulmonate gastropod (*Siphonaria*), a vetigastropod (*Austrocochlea*) and two mytilid bivalves (*Brachidontes* and *Limnoperna*) to address two principal questions. (1) Is it true that, in this region, marine taxa generally show more phylogeographic structure than estuarine taxa? (2) What phylogeographic structure exists along the eastern coasts of NSW, Victoria and Tasmania? There are major latitudinal changes in faunal composition along these coasts that are apparently independent of oceanographic currents. However, not enough has previously been known about intra-specific regionalization to assess whether the changes in faunal composition are also independent of historical isolation processes.

Our results showed that Bass Strait is associated with phylogeographic structuring in most studied species (except *Brachidontes rostratus*) whether they were marine or estuarine. There was a notable degree of habitat plasticity in intra-specific clades in both *Austrocochlea* and *Limnoperna*.

Little intra-specific phylogeographic structure was observed along the eastern seaboard. For example, none of the three species range boundaries in *Siphonaria* was associated with a phylogeographic boundary. Current patterns along the coast may partly explain the location of some species boundaries but the ranges of most Mollusca in this latitudinal gradient appear to be determined mostly by their tolerance of environmental variability.

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Shell Orientation and Thermal Tolerance in the Singapore Littorinids, *Echinolittorina malaccana* and *E. vidua*

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High-shore littorinids are exposed to thermal stress during low tides and many forms of behavioural responses, such as hiding in crevices, foot withdrawal and mucous attachment, to overcome heat gain have been reported. Shell orientation, whereby individuals aligned themselves to the direction of the sun, had also been observed. This behaviour is, however, not extensively studied. Shell orientation of the high-shore and low-shore tropical littorinids *Echinolittorina malaccana* (n = 280) and *E. vidua* (n = 280) respectively, in Singapore (1°17′N 103°50′E), was studied outdoor during morning low tides in May and June 2008. A sundial was used to determine the orientation of littorinids' shell apexes that point towards the direction of the sun (i.e., in-line orientation) or away from the direction of the sun (i.e., broadside orientation). Temperature difference (TempDiff) between rock surface temperature and that of shell surface (i.e., TempDiff = $T_{rock} - T_{shell}$) of both *Echinolittorina* species was also recorded. Results showed that individuals which had orientated 'in-line' and 'broadside' showed differences in the TempDiff. More 'broadside' *Echinolittorina* species had negative TempDiff than 'in-line' *Echinolittorina* species, indicating that individuals in 'broadside' positions have higher shell temperature than rock temperature and are exposed to higher heat gain due to larger exposed shell area. Interspecific differences in TempDiff, however, may imply differences in thermal tolerance and their capability in thermoregulation between both *Echinolittorina* species. Both 'in-line' and 'broadside' *Echinolittorina malaccana* also have wider ranges of TempDiff and larger differences in the range of TempDiff than that of *E. vidua*, suggesting that high-shore *E. malaccana* has lower heat gain and higher thermal tolerance as compared to that of low-shore *E. vidua*.

Spatial Segregation of Populations in a Mangrove Ecosystem

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We present a mathematical model described by partial differential equations that simulates the evolution of two competing species in a mangrove ecosystem which is characterized by heterogeneous soil salinities. Our model is based in the Shigesada-Kawasaki-Teramoto (SKT) model which simulates the spatial segregation between interacting species. The SKT model includes a so-called cross-diffusion term that models pressures on populations through individual interactions within and between species, in addition to the usual Lotka-Volterra competition terms and a convection term involving an "environmental potential" which indicates spatial preferences of populations. In our contribution, we introduce several variations to the SKT model in order to investigate the process of learning or adaptation of populations to the environment, a mangrove ecosystem, represented by an environmental potential which describes the spatial salt concentration distribution. These variations are centered in the convection term, whose strength of attraction to the low saline regions is assumed to depend on the time a population has already spent in that area (adaptation), and on the growth rate of the Lotka-Volterra term, which we assume varying as a function of the environmental potential, i.e., larger growth rate in better environmental regions. The conclusions of our model are twofold: first, that adaptation in a stable environment enhances segregation and therefore diversity. Second, that rapid adaptation may lead to extinction under catastrophic environmental events. In our presentation, we shall describe biological meanings of these new terms incorporated in our model. We shall also demonstrate with numerical examples the pattern of spatial segregation which our model generates.

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Contrasting Genetic Diversity of *Limnoperna fortunei* (Dunker, 1856) among Cryptogenic and Invasive Populations

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Freshwater ecosystems are prone to be invaded by alien species because of human activity. *Limnoperna fortunei* (Dunker, 1856) is a freshwater mussel native to China and Southeastern Asia that has invaded Hong Kong, Japan, Argentina, Uruguay, Paraguay, Brazil and Bolivia due to human-mediated transportation. *L. fortunei* was first recorded from Taipei before 1922, but without any specimen record. Until 1986, large amount of mussels were found at Chih-Tan Dam (Sindian River, Taipei County). Later, *L. fortunei* was found at Sun Moon Lake (Nantou County) in 1990 and Shihmen Reservoir (Dahan River, Taoyuan County) in 2000. Therefore, *L. fortunei* is thought as a cryptogenic species that can not be classified as native or exotic species in Taiwan. We tried to infer the orgin of Taiwanese *L. fortunei* via analyzing the population genetics. Partial sequences of mitochondrial cytochrome c oxidase subunit I from 321 individuals (265, 32, 24 individuals from Taiwan, Japan and Argentina, respectively) were sequenced. Overall, 25 polymorphic sites (all synonymous mutation) revealed 20 haplotypes. Only one haplotype is presneted among all populations. Specimens from two populations in Japan were found with different haplotypes. Genetic diversity of L. fortunei is lowest in Taiwan ($H = 4$, $h = 0.229$, $\pi = 0.003$), middle in Argentina ($H = 5$, $h = 0.438$, $\pi = 0.002$), and highest in Japan ($H = 13$, $h = 0.899$, $\pi = 0.010$). All populations are under expansion inferred from mismatch analysis. We suggest that populations of *L. fortunei* in Taiwan were derived from a single-introduction event and transported by human activity into other drainages. Population in Argentina was also generated from a single-introduction event. Populations in Japan were established through at least two introduction events.

Determinants of Species Diversity and Genetic Diversity in a Community of Tropical Freshwater Molluscs

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The neutral theory of biodiversity has highlighted the similarity of the processes that govern variation in genetic diversity within species and species diversity in communities. Despite close parallels between these two levels of diversity they have been mainly studied separately. An increasing recognition of these similarities had grown up since 30 years and suggests that parallel processes could generate a positive correlation between species and genetic diversity. For example, in a fragmented habitat, variation in habitat structure (size, resource level, and connectivity of habitat patches), and in habitat dynamics (perturbation rate) can influence both kinds of diversity the same way, and generate a positive correlation between the two. This idea has been yet poorly tested.

Tropical freshwater snails are a good system to perform this test because habitat patches such as ponds or small rivers have variable size, connectivity, and degree of instability (frequency of dry episodes). The molluscan freshwater metacommunity of Guadeloupe (Lesser Antilles) inhabits a network of temporary to stable ponds more or less connected to each other. 31 species of Pulmonates and Prosobranchs have been described in that system, including many invasive species. We used microsatellite markers in three native species with contrasted mating systems, *Physa marmorata* (selfing), *Drepanotrema surinamense* (Selfing) and *Drepanotrema depressissimum* (Outcrossing) to evaluate genetic diversity in a broad range of sites (from 24 to 40 sites). We also used long term field surveys (ten years) to characterize species diversity and ecological features in the same sites. We thus could identify some important ecological variables affecting genetic diversity within species and species richness, and providing important cues to predict when a species-genetic diversity correlation might arise or not.

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Introduction to the Symposium on Speciation: Insights from Insular Environments to Global Patterns

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Darwin's famous and often cited "*mystery of the mysteries*" – i.e. the origin and, as a consequence, multiplication of species, still remains at the forefront of current evolutionary biology studies, as speciation and radiation ultimately results in the biological diversity in general.

Geographic distribution and spatial isolation play the crucial role in allopatric speciation *sensu* E. Mayr, which is still considered if not universially active at least being an important mechanism in many cases. However, over the last two decades other, additional as well as alternative, explanations became increasingly evident to account for how new species come into being. Among the most prominent factors discussed, particularly in the context of many species radiations, is adaptive divergence in concert with specialization, suggesting that ecology is an engine in speciation.

Today, with an increasing armamentarium of molecular genetic techniques for exploring the genetic structure of populations and species, the mystery has become many and the solutions multiplied as we uncover further complexities.

I will briefly outline in the introduction to this symposium the historical avenues and the three main empirical aproaches, based on phylogenetic pattern (or comparative methods), on fossils, and on microevolutionary studies. Building on evidence from land, freshwater and the marine realm, this symposium aims at bringing together various approaches, and will hopefully allow to evaluate some of the most conspicious current battlegrounds in speciation studies and the answers we are already able to give to Darwin's mystery.

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Effect of Geography, Tectonics, Ecology and Glacio-eustatic Processes on Speciation of Marine, Intertidal Gastropods

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The benthic, shallow-sea is defined as the region bordered on the one hand by the shoreline and on the other by a thermocline that separates warmer, shallower water from a more homogeneous, cooler deep-sea. Most marine adaptive radiations have occurred in this region, with more than 90% of marine animals occurring in shallow, benthic seas, much of it associated with tropical waters and coral reefs. Of all the shallow-water regions, the tropical Indo-West Pacific (IWP) harbours the greatest biodiversity in terms of numbers of species. Thus, the factors affecting speciation in shallow-sea are of vital importance if we are to understand how present-day levels of biodiversity arose. Four interrelated factors, ecology, geography, tectonics and sea level changes, play pivotal roles in the evolution of shallow-sea organisms within the IWP. Large-scale geographic boundaries such as the East Pacific Barrier, tectonic events such as the collision of continents and ecological limits such as thermal tolerances define generic and subgeneric distributions. The geography of habitat within a biogeographic zone, for instance, two dimensional island arrays or one dimensional coastlines, affects hydrological conditions and combined with dispersal abilities may affect the mode and rate of speciation. Sea level changes as a result of glaciation events and tectonic events have been important for speciation in some taxon groups, but in others isolation has been of insufficient duration for the formation of species and instead has left evidence at the level of population genetics. In this talk, I discuss patterns observed in turbinid gastropods.

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Host Races or Ecomorphs? Testing Host-mediated Speciation in Two Marine Commensal Bivalve Species

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Host-mediated speciation is one of the explicit models of ecological speciation. For symbiotic organisms, the survival and reproduction of the symbionts are highly associated with host species; host switching alone can potentially cause assortative mating and eventually lead to reproductive isolation. A large number of galeommatoidean bivalves form intimate commensal relationships with marine invertebrate hosts. Some commensal clams have the ability to form associations with multiple (often very different) host species, thereby providing potential opportunities to test mechanisms of host-mediated speciation. I hypothesized that species occupying different host species might form latent host races, characterized by host-specific genetic structuring and morphological traits, both of which are preconditions for host-mediated speciation. Two commensal clam species from the west coast of US were selected to test this hypothesis. *Neaeromya rugifera* has two strikingly different host species: the blue mud shrimp *Upogebia pugettensis* and polychaete sea mouse *Aphrodita* species. Similarly, *Mysella pedroana* occurs on both the sand crab *Blepharipoda occidentalis* and the hermit crab *Isocheles pilosus*. For each clam species, individuals from different hosts were collected and subjected to morphometric analyses of shell shape in order to detect host specific morphological traits. Samples were also genotyped using a mitochondrial Cytochrome Oxydase I gene (mtCOI) fragment. Haplotype networks were constructed to analyze population level genetic structures. Preliminary results showed that for both *N. rugifera* and *M. pedroana*, individuals possess host-specific morphological traits: populations from different hosts differ significantly in shell morphology. However, based on mitochondrial makers, neither species showed distinct genetic structuring, either based on host species or geographic distribution, indicating the existence of gene flow among populations that occupy different hosts. My preliminary conclusion is that the host-specific morphologies the clams exhibit may reflect ecophenotypic plasticity rather than the existence of host races, but this needs to be corroborated with additional genetic data.

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Origin of the Inverse Latitudinal Diversity Gradient among Southern Chilean Mollusks: Testing Hypotheses Using the Neogene Fossil Record

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Mollusks along the Pacific Coast of South America provide one of the main exceptions from the latitudinal diversity gradient of decreasing species numbers towards the poles. From 42°S southward, coincident with the onset of the mosaic coastline of the southern Chilean fiordlands, species numbers apparently show a two-to-threefold increase compared to the central Chilean coast. Here we use the Neogene fossil record of central and southern Chile to test hypotheses on the origin of this unusual pattern. Contrary to previous suggestions, we neither found evidence for a build-up of biodiversity since the Eocene, nor for the northward spread of Antarctic taxa into southern mid-latitudes. Rather, our data suggest that the mosaic coastline south of 42°S was colonized after the retreat of the glaciers from their marine termini since the later Pleistocene, by taxa that were already present along the Chilean coast. The majority of the most species-rich genera in this area are shallow-water hardground inhabitants, suggesting a rapid adaptive radiation of these taxa. Furthermore, during the Neogene mollusks in central and southern Chile followed the out-of-the-tropics pattern of expansion rather than having an Antarctic origin.

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Punctuated Equilibrium Reviewed: The Gastropods Point of View

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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 was the result of observations in the fossil record that phylogenetic lines comprise long periods of stasis, i.e., lack of morphological changes, which are punctuated by rapid speciation events. In this respect, PEE is frequently seen as a contrast to phyletic gradualism, but it also triggered the debate on general pattern and process of speciation remarkably.

Since its proposal, PEE has been debated intensively and the search of examples continues. Recent re-examination of the iconic Plio-Pleistocene Turkana Basin molluscs casts doubt about their supporting the theory because the rapid bursts of so-called punctuated evolutionary changes were shown to represent artefacts resulting from multiple migration events. This example shows that sampling problems may bias our perception of the tempo of evolutionary changes and perhaps some would argue that PEE is hardly falsifiable because several aspects are hard to control.

Our paper aims to discuss intralacustrine gastropod shell evolution of classical extant and fossil lakes: Lake Ohrid (Recent, Macedonia), Turkana Basin (Plio-Pleistocene, E' Africa), Vienna Basin (Late Miocene, Austria) and Steinheim Basin (Middle Miocene, S' Germany). Based on our studies on these sites and on literature data, we will examine the applicability of the PEE concept. We will show 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.

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Documentation of Punctuated Equilibrium Punctuations in the Morphology of *Bellamya* Gastropods from Lake Malawi via Quantitative Genetic Models

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Punctuated equilibrium theory claims that phenotypic evolution is concentrated in punctuations separated by long-lasting morphological stasis. Punctuations are hard to study because they occur faster than is observable in the fossil record, but generally too slow for study on biological timescales. Here we study such an evolutionary punctuation in four endemic *Bellamya* gastropod species derived from a common ancestor that is preserved in early to middle Holocene, radiocarbon-dated lacustrine deposits in the Malawi Basin. Morphometric comparison of extant and fossil morphs with semi-landmark analysis and traditional measurements documents a 3.1-5.4 times morphospace expansion since the middle Holocene. We combine modeling of evolutionary divergence and calculation of evolutionary rates of phenotypic change to show that morphological divergence could have completed within 25 to 500 years for each species, resulting in rates of morphological change within or above the genetic drift range but slower or equal to those commonly observed in selection experiments. We also illustrate that geographic isolation in separate drainage basins allowed cladogenesis and morphological conservatism in riverine taxa, which may result in the recognition of pseudo-stationary lineages, while speciation in lacustrine environments led to increased disparity by morphological adaptation following greater ecological opportunity.

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Biodiversity and Evolution in Ancient Lakes: Lessons from Molluscs

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The few ancient lakes in the world are famous for being evolutionary theatres, often displaying an extraordinarily high degree of mollusc diversity and endemism. Insights into endemic biodiversity, origin of biota, rates of evolutionary change, modes of speciation, recognition of species, as well as conservation and invasion biology have been derived from studies on ancient lake molluscs.

Based on phylogenetical, phylogeographical, and biodiversity case studies from several actual and potential ancient lakes, we address the above topics using various gastropod and bivalve taxa including both species poor groups as well as large radiations. Biodiversity within lake is often unequally distributed. Spatial and temporal levels of endemism, however, appear to be more complex than previously believed. Eco-insularity, for example, can act on different levels: on specific sites within the lake, on the level of the lake proper, on the level of adjacent water bodies, and on the level of the whole watershed. As for the temporal distribution of biodiversity, according to new fossil data, faunal compositions can be stable for hundred thousands of years. Environmental fluctuations can rapidly cause major extinctions. Few surviving lineages subsequently may give rise to rapid diversification events.

Our studies, however, indicate that in many cased a large share of endemic species has derived from intralacustrine speciation. True relic lineages are generally rare. We found both (often young) species flocks and species scatters. Speciation happens mostly in parapatry and allopatry, the role of ecology in this context is ill-understood.

Worldwide ancient lakes increasingly experience numerous anthropogenic impacts. Facing a dramatic decline and loss of mollusc diversity in many lakes is only one side of the coin. The simultaneous trends of losing and discovering mollusc diversity should trigger increased research efforts on the remarkable malacofaunas of those unique aquatic ecosystems, both on large and small temporal and spatial scales.

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Gastropod Evolution in Lake Malawi (Africa): Lessons from Endemic *Bellamya* and *Lanistes* Species

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Changes in habitat stability may significantly shape evolutionary patterns and processes in ancient lakes. Here we use a hierarchical combination of molecular phylogenetic and coalescent approaches to investigate the evolutionary histories of the endemic species of the gastropod genera *Bellamya* (Viviparidae) and *Lanistes* (Ampullariidae) in the African rift-lake Malawi. By integrating our findings with reported palaeontological and palaeolimnological data, we demonstrate that all but one evolutionary lineage of both the Pliocene *Bellamya* and *Lanistes* faunas in Lake Malawi became extinct. Based on trait-specific molecular clock analyses, we found that the accumulation of the extant molecular diversity in each taxon did not start in the Pliocene but at least 1 million years later in the Pleistocene from single lineages. Coalescent analyses indicate that the modern radiations underwent both a sudden demographic and a spatial expansion after a genetic bottleneck. We argue that a re-flooding of the lake after severe Pleistocene low stands offers a straightforward explanation for these concordant patterns and may have triggered speciation processes in the modern endemic radiations in Lake Malawi.

In contrast to previous reports, all specimens of the genera *Lanistes* and *Bellamya* found in the Malawi Rift are endemic and form monophyletic and – in a rift-wide phylogenetic context – highly distinct groups. Shell similarities to other species of these genera appear to be cases of parallel evolution or plesiomorphy. This 'rift-endemism' stands in contrast to reports from other lakes where endemism is restricted to the lake proper.

Future studies will show whether these concordant evolutionary patterns can also be found in other endemic taxa of Lake Malawi. Thus, our study is a plea for more detailed analyses of the invertebrate faunas of this famous rift-lake in order to shed more light on the timing as well as on general forces driving the evolution of Malawi's endemic taxa.

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Freshwater Biogeography at the Roof of the World - Lessons from *Radix* spp. (Gastropoda: Hygrophila: Lymnaeidae)

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The Tibetan Plateau is the highest and largest plateau on earth. It is located in central Asia and bounded at its south side by the Himalayas. Many major rivers of South and East Asia have their origin either on the Tibetan Plateau or in the Himalayas, while on the Tibetan Plateau itself many lakes are located. Based on biogeographical data of terrestrial organisms, the Tibetan Plateau is assigned to the Palearctic region with the Himalayan mountain ridge being the sharp southern border to the Oriental region. In freshwater biogeography, the biogeographic boundaries, however, were often drawn along watersheds.

In this study, we use the lymnaeid freshwater gastropod genus *Radix* as a model taxon for studying freshwater biogeography. *Radix* spp. are widely distributed on the Tibetan Plateau as well as on the southern side of the Himalayas.

Specimens of *Radix* spp. from the Tibetan Plateau and the Himalayas as well as from numerous other locations in Eurasia were investigated genetically by sequencing the two mitochondrial genes COI and LSU rDNA. The results show, that six major clades of *Radix* are distributed around the Himalayas. The *Radix* faunas north and south of the Himalayan mountain ridge, however, are phylogeographically distinct. Whereas the Tibetan Plateau is inhabited by two distinct *Radix* lineages, four clades were found at the southern slopes of the Himalayas.

The distribution patterns found in *Radix* spp. are more similar to those found in terrestrial taxa rather than those found in freshwater fishes from the region. This indicates that watersheds may play only a minor role for dispersal of *Radix* spp. at the "roof of the world". Instead land- and airborn vectors like birds might be more significant.

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Camaenid Land Snails in North-western Australia: A Model Case for the Study of Speciation and Radiation

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Camaenidae arguably are Australia's most diverse land snail group encompassing 454 currently recognised species. A survey of coastal regions of the Kimberley, a 430,000 km^2 sub-humid region in tropical north-western Australia, has led to the identification of 170 camaenid species through analyses of key morphological characters and mitochondrial sequences from 300 samples. While at least 120 of these species represent new discoveries, the present study almost quadruples the number of known species in the study area. Extrapolating this increase to the scale of NW Australia prompts estimates that arrive at a magnitude of 600 to 800 camaenid species, a figure that was earlier proposed for the whole continent.

This study seeks to understand the mechanisms that produced and maintained the high levels of diversity and endemism of land snails in the Kimberley. Most camaenid snails are usually confined to specific habitats, such as rainforest patches, vine thickets and woodlands, occupying very restricted ranges. The phylogeographic patterns imply that speciation was essentially driven by allopatric separation while consistent levels of genetic differentiation suggest that species have diversified more or less simultaneously. The fragmentation of formerly widespread rainforests, caused by more arid climatic conditions since the Miocene, has been identified as probable trigger of the camaenid radiation by mediating isolation and parallel patterns of allopatric differentiation. Unable to travel the distances between isolated rainforest patches, new species evolved within each patch. With the same evolutionary processes occurring within each of these patches in a number of land locked species, the end result has been a suite of species assemblages that are unique to each single forest patch.

Thus, the NW Australian Camaenidae are a prime example for the significance of climate change induced habitat fragmentation and ecological niche conservatism as drivers of a so-called non-adaptive radiation, which is a process capable of producing taxonomically and ecologically diverse species flocks over relatively short periods of time.

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Chirality in Speciation

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Speciation in snails has occasionally been accompanied by a shift in coiling direction (= SCD). It is also known that premating isolation may exist between 'conspecific' mirror-image snails. Furthermore it has been demonstrated in a computer simulation experiment that single-gene speciation on the basis of SCD is possible. It remains uncertain however, to what extent mutations in the enigmatic chirality gene have ever triggered speciation. Dextral chirality in most gastropods has been emphasized by many authors, but usually without any reference to the underlying data. The percentage of dextral species that has been indicated in the literature varies from 'over 99%' to simply 'most'. Species numbers are hardly ever mentioned.

The number of SCD related speciation events is even more obscure. The currently available data on gastropod phylogeny lack sufficient detail to enable conclusions for snails in general. To provide more insight we counted the number of both dextral and sinistral species in four terrestrial molluscan faunas, using data from recently published monographs. As a next step, the number of SCD related speciation events was reconstructed for each geographic region. Additionally we evaluated the minimum number of SCD events in the speciose pulmonate family Clausiliidae, using data for both fossil and recent taxa. According to the fossil record, this family originated in the Cretaceous. Our data shed a new light on the infrequent occurrence of SCD events in speciation.

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Left-handed Snails and Right-handed Snakes: Anti-predator Adaptation Drives Single-gene Speciation

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A gene for left-right reversal could generate a new snail species, because dextral and sinistral snails have difficulty in mating. However, theories predict that this speciation process should be suppressed by the severe mating disadvantage of reversal. I show that the single-gene speciation completes in response to specialized snake predation of dextral majority. Sinistrals survive snake predation superiorly. Speciation rate of sinistral snails by reversal has been accelerated in sympatry with the snakes, especially in snails that could gain stronger anti-snake defense and reproductive isolation from dextrals by sinistrality. This study demonstrates positive selection for pleiotropic effects of a gene on survival and premating isolation as a definitive mechanism. Speciation by natural selection may initially require genetically simpler changes of phenotype than previously expected.

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Spatial Distribution of Phylogenetic Diversity in Camaenid Land Snails of Eastern Australia

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A species-complete molecular phylogeny combined with fine-scale distribution data can provide a geographical picture of biodiversity, highlighting the contributions of diversification, accumulation and retention. I have done this for the camaenid land snails of eastern Australia using a 327 taxa phylogeny and 10,000 point distribution dataset, giving a fairly continuous map at 50km scale across 30º of latitude from Cape York to Victoria. Major rainforest regions, such as the Wet Tropics, are areas of accumulation and retention of historical diversity, with most recent local diversification occurring in areas peripheral to these domains and adjacent to major ecogeographical boundaries.

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A Molecular Phylogeny of the Land Snail Family Clausiliidae

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With more than 1300 species, Clausiliidae is one of the most speciose families of land snails. The family contributes to land snail diversity on a global scale, having a distribution with three main centres of diversity: 1) western Eurasia (6 subfamilies), 2) South-East Asia (2 subfamilies) and 3) South America plus two of the Greater Antilles (1 subfamily, Neniinae). No Clausiliidae, neither extant nor fossil, have been described from North America and from Australia. The family Clausiliidae is first known from the Upper Cretaceous of Europe. Presumably the family spread from Europe into South-East Asia and South America before the start of the Cenozoic. Despite a wealth of conchological and anatomical studies, the major phylogenetic relationships within the family have remained elusive, and the distinction between its nine subfamilies is based on combinations of non-unique morphological characters.

Here we present the first study of phylogenetic relationships within the family Clausiliidae as a whole, using an independent, molecular dataset. We obtained partial 28S rRNA, histone H3 and histone H4 DNA-sequences of 67 clausiliid species, representing all subfamilies, and 24 out of 26 tribes. Molecular phylogenetic analyses divide the family into seven highly supported basal clades, which are more or less geographically confined. The most remarkable difference with previous hypotheses is the evidence for a deep phylogenetic split between the Greater Antillean and the South American genera classified as separate tribes within the subfamily Neniinae. These two ‘tribes’ were retrieved as two of the basal clades within the family, and are most probably not sister groups. These results suggest that clausiliids crossed the (opening) Atlantic Ocean twice during their evolution.

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Testing the Limits in a Troubled Island: Intraspecific Variability of the Endemic *Napaeus pruninus* (Gould, 1846) (Stylommatophora: Enidae) from São Miguel, Azores

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In his “Histoire Naturelle des Açores”, Morelet (1860: 179, pl. IV) referred at length and profusely illustrated the variability in shell morphology of the enid *Napaeus pruninus*, which he considered the sole species of the thick-shelled enids of the Azores. Martins (Açoreana, 1989: 41-54), using characters of the reproductive organs, recognized *N. tremulans* (Mousson, 1858) from Santa Maria, restricted *N. pruninus* to São Miguel and elevated to specific level Morelet´s variety *alabastrinus*, from Terceira. A preliminary molecular analysis (COI) has confirmed the identity of these three species.

The anatomical variability of *N. pruninus* is here re-assessed and spermatophore morphology investigated. The key anatomical feature in species distinction is the length and shape of the epiphalus; it is typically long and coiled in *N. tremulans*, short and straight in *N. alabastrinus*; their spermatophores are correspondingly elaborated. Whereas *N. tremulans* and *N. alabastrinus* are quite homogeneous anatomically and their spermatophores vary little, there is considerable variation in *N. pruninus*, ranging from the typical short and straight *alabastrinus*-type to the long and heavily coiled *tremulans*-type, the former restricted to the western third of the island and the latter to the south center; an intermediate situation is found throughout the eastern third of São Miguel.

Studies on *Leptaxis* and *Oxychilus (Drouetia)* have revealed that molecular and anatomical variability reflect the volcanic sequence of the formation of the island, where two proto-islands are thought to have existed during half a million years before their unification 40 thousand years ago. Although more complex, the patterns observed in the variability of *N. pruninus* confirm in general the observations on other taxa; however, the morphological relationships with the other two species of *Napaeus*, from different islands, suggest curious biogeographical affinities, not readily explained by the assumption of the existence of only one species in São Miguel, as the molecular data seem to support. That being the case, the species specificity of spermatophore morphology is clearly put in question by our findings.

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Back to Africa and Out Again: the Evolutionary and Biogeographic History of the Land Snail Genus *Theba*

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Among oceanic islands the Canary Islands offer exceptional opportunities to study speciation and colonization because of their considerable habitat diversity, well documented geological history, and proximity to continents. Based on a combined COI+ITS1 data set for 148 specimens, we studied the diversification of the land snail genus *Theba* on the Canary Islands and adjacent African and European continental areas. Phylogenetic analyses resulted in the recognition of 18 genetically distinct clades including at least three new species. Divergence time estimates suggested an origin of *Theba* on the Canarian archipelago and an initial radiation on the three easternmost islands during the Late Oligocene/Early Miocene. The re-colonization of NW Africa occurred once during the Middle Miocene and led to a remarkable continental radiation. One clade expanded south to Mauretania. A second clade dispersed towards the North and eventually conquered Spain, possibly several times. A single species, *T. p. pisana*, has colonized the entire Mediterranean area as well as the Atlantic coasts of Western Europe and has been introduced to other continents, where it is regarded as pest.

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Phylogeographic Patterns of Mitochondrial and AFLP Markers across the Range of an Endemic Land Snail Species on Crete

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A non-adaptive radiation triggered by sexual selection resulted in ten endemic land snail species of the genus *Xerocrassa* on Crete. We investigated phylogeographic patterns inferred from mitochondrial COI sequences and AFLP markers within the most widespread and highly diverse endemic species *Xerocrassa mesostena* to understand the processes at the beginning of speciation. The AFLP data revealed a distinct phylogeographic subdivision of the range of *Xerocrassa mesostena* that corresponds at least partly with current barriers. Within the geographically coherent clusters the genetic variation is structured partly by isolation by distance. The variation in the mitochondrial data is also dominated by a subdivision in geographically coherent clusters. However, the distribution of the mitochondrial haplotype groups corresponds only partly with that of the clusters delimited with the multilocus data. In same cases phylogeographic breaks in the mitochondrial data differ only slightly from the geographic boundaries of the AFLP based clusters. This pattern can be explained by limited dispersal across barriers. However, there are also phylogeographic breaks in the mitochondrial data that do not correspond with patterns in the multilocus data. We corroborate the hypothesis that some of these boundaries represent random phylogenetic breaks by excluding alternative possibilities. Mitochondrial DNA can provide a first insight in the phylogeographic structure of a species. However, the comparison of the phylogeographic patterns inferred from mitochondrial COI sequences and the AFLP markers in *Xerocrassa mesostena* support suggestions that phylogeographic patterns found with single locus markers, especially mitochondrial DNA, might result in a misleading picture of the phylogeographic structure of a species and should be supplemented by data from multiple independent loci.

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Geomalacus and *Letourneuxia*. Are We Talking about the Same Thing (Pulmonata: Arionidae)?

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The terrestrial slug genus *Geomalacus* was described by Allman in 1843, and currently comprises four species, three endemic to the Iberian Peninsula (*G. anguiformis*, *G. oliveirae*, *G. malagensis*) and one also present in southwestern Ireland (*G. maculosus*). More than two decades later, in 1866, Bourguignat described the genus *Letourneuxia* for specimens from Tangier (Morocco). Since then, it has been debated whether or not these two genera should be kept separate. In order resolve this issue, we determined nucleotide sequences of fragments of the nuclear 18S rDNA and of the mitochondrial COI genes of topotypic specimens of *Letourneuxia numidica*. These data were then used to conduct a phylogenetic analysis of *Geomalacus* and *Letourneuxia*, with *Arion* sp. as outgroup. The 18S rDNA data yielded a species specifc pattern at three nucleotides by which four taxa were consistently separated: *G. maculosus*, *G. oliveirae*, *G. anguiformis* and jointly *G. malagensis* + *Letourneuxia*. The COI based phylogeny confirmed a well-supported sister-group relationship between *G. malagensis* and *Letourneuxia*, embedded within a strongly supported *Geomalacus* clade. This hence provides convincing evidence that a generic separation of *Geomalacus* and *Letourneuxia* cannot be maintained. Moreover, the COI data further suggest: (1) a sister-group relationship between *G. anguiformis* and *G. oliveirae*, (2) deep phylogenetic splits in all species except *G. malagenis*, and (3) a possible paraphyletic branchin pattern in *G. oliveirae*. The taxonomic and evolutionary implications of these results will be further explored and discussed.

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The *Bivalve Assembling-the-Tree-of-Life* Project (BivAToL)

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Bivalves are a diverse and familiar group of mollusks with an old and well-preserved fossil record, important ecological roles in marine and freshwater ecosystems, and economic roles including fisheries, the ornament industry, and health sciences. With some 20,000 living species they are the second largest class of living mollusks, which in turn constitute the second largest animal phylum and the largest in the marine realm. Despite the ubiquitousness of bivalves, past efforts to study and understand their evolution have been insufficiently coordinated and little consensus has been reached. As part of the U.S. National Science Foundation's Assembling the Tree of Life Program, a multi-national, multi-institutional effort is underway to assemble the bivalve tree of life. For this, we are undertaking a fresh look at bivalve anatomy (with special focus on gill and stomach anatomy, shell ultrastructure, and sperm morphology) and study selected molecular markers for the same species investigated morphologically to be able to understand bivalve evolution in an integrated fashion. In addition to the "hard science" efforts, the project's outreach activities engage various audiences in the project's results and in evolutionary science as a whole. This introductory presentation sets the stage for a series of individual presentation on morphological and molecular components of the BivAToL effort. [This project is supported by NSF grant DEB-0732854/0732903/0732860].

A First-tier BivAToL Analysis: Multiple Genes and Morphology

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As part of the U.S. National Science Foundation's Assembling the Tree of Life Program, a multi-national, multi-institutional effort is underway to assemble the bivalve tree of life or BivAToL. For this, we are undertaking a fresh look at bivalve anatomy (with special focus on gill and stomach anatomy, shell ultrastructure, and sperm morphology) and studying selected molecular markers for the same species investigated morphologically to be able to understand bivalve evolution in an integrated fashion. Here we will present preliminary results of a "first-tier" analysis where a number of species were selected to maximize body plan disparity and phylogenetic diversity across bivalves. The data sets include mitochondrial and nuclear ribosomal and protein-encoding genes, some never used before for studying bivalve systematics, and a novel morphological data matrix. The data are analyzed using an array of techniques based on two-step and single-step phylogenetic methods and the most commonly employed optimality criteria. [This project is supported by NSF grant DEB-0732854/0732903/0732860].

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Crystal World: Diversity of Bivalve Calcification

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It is well known that bivalves, along with other molluscs, construct their shells using crystals of calcium carbonate (either in the form of aragonite or calcite) grown within an organic matrix and that these crystals may be arranged in a variety of different microstructures (for example, argonitic nacre and crossed-lamellar structures and foliated and prismatic calcite). Different microstructures generally occur in discrete layers and different taxa are observed to use different combinations of numbers of layers and microstructural types to build their shells. It is evident that the details of shell microstructures are of considerable phylogenetic and adaptive significance.

Bivalve shell microstructures have been studied for over 150 years, but improved technology (e.g. better SEM resolution, crystallographic techniques such as EDSD) now permit a fresh look at already recognised microstructures and a search for novel characters which may be used in subsequent phylogenetic analyses. Of particular interest to us have been the development of characters associated with the often ignored periostracum, in particular features of intra and extra periostracal calcification in a variety of taxa; the identification of different or unusual mineral phases (for example growth of calcium and iron phosphates on the external surfaces of shells) and the recognition and differentiation of ordered microstructural fabrics previously recognised as 'homogeneous'. Re-examination of microstructures previously considered as homologous, such as calcite prisms in pteriomorph taxa, reveal details that have shown that they are in fact structurally different.

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The Bivalve Mantle – a Preliminary Report

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The mantle margin of bivalves is a multi-tasking organ consisting of several folds, which are homologized according to their relative position to the periostracum groove: The outer fold(s) secrete(s) the mineralized shell layers. The first inner fold(s) mainly bear(s) various sensory elements of all kinds, including eyes of various form and structure. Finally the innermost fold is responsible for water currents by means of ciliation or various fusion events. In order to check the various structures for phylogenetic significance and to infer functional traits we have so far checked 26 species of 20 families by means of light- or electron microscopy (SEM and TEM).

The results show major deviations of a general schema of the bivalve mantle margin and high variability of the various structures in the groups investigated. Phylogenetic significance of characters focuses mainly on the traditional superfamily level of bivalve evolution, where several clades can be supported by synapomorphic characteristics. On the other hand the functional significance of the various structures is not clear in all cases. Whereas in most cases the functions of shell and periostracum secretion as well as of mechano-, chemo- and photoreceptors can be clearly inferred from structural peculiarities, in particular various glandular organs occurring along the inner folds remain as enigmatic structures.

The current study is part of the BivAtol project and should provide another dataset for a combined analysis of phenotypic and genotypic characters in order to infer the still debatable phylogeny of the Bivalvia.

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Bivalve Top Hats – Descriptive, Ontogenetic and Evolutionary Perspectives

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Bivalve early ontogenetic shells bear numerous characters useful for taxonomic, heterochronic and evolutionary inferences. This contribution presents some of the characters and introduces a shell typology modified from a previous proposal. Both typologies emphasise shell morphological diversity rather than developmental connotations. However, the new proposal now separates protobranch morphotypes (Shell Type 1) from autobranch types (Shell Types 2 and 3) and includes unionids (Shell Type 4). Many larval shell characters are either continuous with or displaced towards the post-larva evidencing the fact that ontogeny is a continuum. Therefore, the proposal stresses the need to integrate nepioconch features for distinctions and for a better understanding of shell ontogeny and evolution. Differentiation of Shell Types 1 to 4 is based on the presence/absence of a prodissoconch 2 stage and type of hinge dentition (Type 1 vs. Types 2-4), primary respectively secondary absence of a prodissoconch 2 stage (Type 1 vs. some Type 2 subtypes), fusion of various shell stages (some Type 3 subtypes), absence/presence of circumferential shell margin denticles or hooks, and tubulation (Types 1-3 vs. Type 4). Further subdivisions within each group are based on landscape profile, micro- and macrosculptures, and prodissoconch 1 / 2 length ratios (only within Type 2). Due to the secondary absence of a prodissoconch 2 and/or similar landscape features, some autobranchs converge on protobranch Type 1. Although the principal objective is the development of an efficient descriptive tool, present observations reveal a number of homology problems which leads to an alternative hypothesis on the origin of a prodissoconch 2 stage. The typology may also provide for a more accurate means to predict reproductive modes than the prevalent three-partite division into planktotrophic, lecithotrophic and direct modes. However, this hypothesis still requires ample testing by field and laboratory observations.

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Know Guts, Know Glory: New Insights into the Evolution of the Bivalve Stomach

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The bivalve stomach is arguably the most complex organ in this class of mollusks. Principally, the stomach is an extensively ciliated and cuticulated sac equipped with a chitinous gastric shield against which the crystalline style revolves. Its walls contain areas of ridges and folds, and have openings to the dorsal hood, different outpockets (pouches or caeca), and the ducts of digestive of digestive diverticula. The esophagus enters the stomach at its anterior end, whereas the (often co-joined) intestine and the style sac leave the stomach at the posterior or ventral side. Despite the relative uniformity of the stomach's ground plan in Bivalvia, there is a great variation in the morphology, and relative development and position of many stomach characters across the class.

Despite the fact that there is a vast amount of information on the bivalve stomach anatomy scattered in the malacological literature, its utility for large-scale comparative studies is hampered by the lack of a consistent terminology and a standardized perspective on illustrating the features of the stomach's interior. In the context of a class-wide phylogenetic study (NSF-AToL Bivalve Tree of Life Project 0732854), we reassessed the taxonomic utility of traditional and newly defined stomach characters based on original anatomical studies and in light of recent molecular and morphological phylogenetic analyses. The new findings will be discussed against the historical background of the bivalve stomach research and contrasted with the generally accepted classification of stomach types proposed by R.D. Purchon.

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Up to the Gills: A New Look at an Old Bivalve Character System

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Within the Bivalvia several morphological character systems, including the shell, mantle, stomach structure, gills and labial palps have long been investigated and detailed descriptions of the gross anatomy of these character systems have been done over decades. But more recent investigations on these characters systems, using modern approaches, are often restricted to specific taxa and increasingly focus on bivalve species of economic interest or significant environmental impact.

Here we show the preliminary results of a comparative morphological approach regarding the gill and labial palp character system of the Bivalvia. Fourteen orders within the Bivalvia have been investigated using anatomical and electron microscopical techniques. We will present a preliminary revision of several existing gill and labial palp characters, introduce new characters and discuss the value of these morphological characters in relation to the classification and phylogeny of the Bivalvia. Within our comparative approach we will focus exemplarily on the Protobranchia and the association of ctenidia and labial palps. [Supported by NSF AToL DEB-0732854].

Molecular Systematics and Molecular Evolution within the Bivalvia

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Molecular evolutionary processes often affect our ability to reconstruct evolutionary relationships, especially when attempting to resolve ancient divergence events. We explore molecular evolution within a robust sample of bivalves using both mitochondrial and nuclear DNA markers to calibrate rates of molecular evolution and to determine whether molecular evolutionary processes such as rate variation and base compositional variation have biased phylogenetic hypotheses. The bivalves are an appropriate group in which to study rates of molecular evolution given their excellent fossil record. In addition, independent data on relationships provided by gross morphology, anatomy, and ultrastructure provide an independent check of hypotheses based on molecular data. [This project is supported by NSF grant DEB- 0732903].

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A Family Level Phylogeny of the Protobranch Bivalves

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Protobranch bivalves are deposit-feeders that reach their zenith of diversity in the deep sea. They are of evolutionary interest due to their early Cambrian or possibly Precambrian origins and an array of unique traits that unite them as a group. Morphological diversification within the Protobranchia has been conservative relative to the rest of the Bivalvia and has given rise to over 600 extant species divided among 13 families. The objective of this study was to assemble the first molecular phylogenetic survey of the Protobranchia and test family-level designations where possible. DNA was extracted from fresh-collected material and partial regions of several mitochondrial and nuclear genes were amplified by PCR. These products were directly sequenced and analyzed phylogenetically along with sequence data available on GenBank. High levels of divergence among taxa resulted in inconsistent clustering of taxa across genes, obscuring family boundaries. The best resolution perhaps was achieved with the nuclear gene histone H3 and the mitochondrial gene cytochrome oxidase *c* subunit I. Possible explanations for the patterns observed are discussed along with directions to be taken in continued investigations.

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On the Bloody Bivalves: Resolving Familial Relationships within Archiheterodonta (Bivalvia: Heterodonta)

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The subclass Heterodonta (Mollusca: Bivalvia) encompasses the majority of extant bivalve diversity and is presently considered a derived group of the modern bivalves (Giribet, 2008). Heterodonta is subdivided into two major groups, the hyperdiverse Euheterodonta and Archiheterodonta. The cladistic validity of, and phylogenetic relationships within, Archiheterodonta are poorly understood. We assessed the phylogeny of archiheterodont bivalves using a multilocus dataset comprised of molecular sequence data from four loci (18S rRNA, 28S rRNA, cytochrome *c* oxidase subunit I, and histone H3). We recover strong support for the monophyly of Archiheterodonta. Relationships amongst constituent Archiheterodont families are evaluated in the context of morphological character evolution and the archiheterodont fossil record.

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Molecular Phylogeny of Lucinidae - Classification, Diversification History and Habitat Occupation Patterns

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A new molecular phylogeny of the chemosymbiotic bivalve family Lucinidae is presented that will form the basis for a new classification and act as a framework to examine adaptations to the symbiosis and diversification patterns. Using sequences from 18S, 28S rRNA and cytochrome B genes, 105 taxa were analysed representing 87 species classified into 47 genera. Samples were collected from a wide range of habitats including mangroves, seagrass beds, shallow sands, offshore muds and hydrocarbon seeps at water depths ranging from the intertidal to over 2000 m. A chronogram, derived from the combined gene tree, was calibrated using 10 lucinid fossils. The trees show five well-supported clades and two single branches of *Fimbria fimbriata* and *Monitilora ramsayi*. A new classification of Lucinidae is proposed with seven subfamilial divisions; three new subfamilies are introduced and Codakiinae, usually treated as a synonym of Lucininae, is revived to include the *Lucinoma*, *Codakia* and *Ctena* subclades, while membership of the Lucininae and Myrteinae is considerably revised compared to the commonly used 'Treatise" classification of Chavan (1969). Fimbriinae is now regarded as a subfamily within Lucinidae. The status of Milthinae is presently equivocal pending further analysis and Divaricellinae is recognized as polyphyletic and therefore abandoned, with species and genera now grouped in various places within the Lucininae. The diversification and fossil history of the subfamilies is examined in relation to the chronogram, with a Mesozoic origin for the major clades and extensive radiations in the Cenozoic. We also use the trees to examine habitat occupation patterns of Lucinidae. Deeper water lucinids mainly belong to a new subfamily, the *Lucinoma* clade of the Codakiinae and Myrteinae, with *Lucinoma* species most frequently associated with hydrocarbon seeps. Species occurring in seagrass habitats derive largely from the 'pegophysemine' group, Codakiinae and Lucininae and species from mangrove habitats from the 'pegophysemines' and Lucininae.

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Application of Modern Geometric Morphometrics to Quantify Shell Shape and Detect Convergence Using Scallops (Bivalvia: Pectinidae) as a Model

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Convergence is a fascinating biological phenomenon, where similar environmental factors direct strong selection forces to produce similar phenotypic responses in organisms. Vertebrates like *Anolis* lizards and stickleback fish are classic examples of convergent evolution. However, convergent evolution has been examined to a much lesser extent in invertebrate groups. Scallops are a great invertebrate model to study convergence form and function due to repetitive evolution of many phenotypic traits. For example, long-distance swimming has independently evolved at least four times in the Pectinidae and these species possess shells that are qualitatively similar in overall shape. If the four lineages have experienced similar selective regimes, such as strong biomechanical requirements for effective swimming, we would expect a similar phenotypic response among lineages. We tested the hypothesis that the shell shape exhibited by long-distance swimming species is similar as a result of convergent evolution. Using landmark-based geometric morphometrics of three-dimensional scans, we quantified shell shapes of seven scallop species representing three of six major behavior categories. We found that the shell shapes of two long-distance swimming lineages occupied the same region of morphospace and were not significantly different from one another. These data support the convergent evolution hypothesis. Furthermore, the disparity or degree of morphological variation among these species is small when compared to other groups, indicating that shell shape of long-distance swimming species is under stronger selection than other behavioral categories.

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Cyanobacterial Symbiosis in the Periostracum of Astartidae (Mollusca: Bivalvia)

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The periostracum is the waterproof outermost layer of bivalve shells, composed by proteins, mucopolysaccharides and lipids. It protects the shell from acid dissolution and functions also as a matrix for the deposition of calcium carbonate crystals.

The astartids have a very characteristic periostracum, with a pitted outer layer in the genus *Astarte*, from cold waters, as well as in the small *Digitaria digitaria* from warmer coastal waters. During a study of the formation of the periostracum in *Digitaria*, the presence of prokaryotic organisms has been observed inside the pits of the periostracum in all the specimens analysed. The periostracum of *Astarte* spp., from the North Sea and Eastern Canada Banks, also presents these microorganisms in the periostracal pits.

These prokaryotic organisms have been recognized as Pleurocapsalean cyanobacteria, from the presence of baeocytes and from binary fission in many different planes, producing aggregates which are diverse in size and form.

Symbioses of invertebrates with bacteria have hitherto been grouped into four categories: a) bacteria capable of bioluminescence; b) bacteria for digestion of substrates, such as wood; c) chemoautotrophic bacteria capable to use sulphide or methane as an energy source; d) bacteria in hosts from oxygenated environment, with undefined functions (e.g. the symbiosis with sponges) but possibly as supplementary food.

The presence of cyanobacteria on the periostracum of astartids represents then a new type of symbiosis, not related *a priori* with either food sulphide- or methane-rich environments, nor bioluminescence, but possibly related to the reinforcement of the biomineralization process or the reduction of either the effect of the cold (and acid) sea water (*Astarte* spp.) or the shell erosion (*Digitaria digitaria*).This may be an ancient symbiosis, considering the early divergence of the family Astartidae, which belongs to the Archiheterodonta, recently recognized as sister-group to all other Heterodonta.

Advances and Challenges in Reconstructing Anomalodesmatan Phylogeny

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Anomalodesmatans comprise an ancient and ecologically diverse group of marine bivalves, but are nonetheless inconspicuous in most extant shallow water communities. For various reasons, which include their present scarcity and a bewildering array of disparate morphologies, anomalodesmatans have always proved difficult to interpret, and their systematics lagged behind those of most other major bivalve taxa. In recent years, morphological and molecular studies of the group have produced incongruent results, casting doubts over the monophyletic status of component superfamilies and precluding the recognition of putative synapomorphies for clades recovered in molecular investigations.

In the present investigation, cladistic analysis of a novel matrix of morphological characters, the largest compiled for anomalodesmatans to date, suggests that enhanced taxonomic sampling and more rigorous character analyses are paramount in solving conflicts among the distinct datasets. Among traditionally recognized superfamilies, Pholadomyoidea, Clavagelloidea and Septibranchia were found to be monophyletic groups. Taxa commonly referred to Pandoroidea and Thracioidea were recovered as part of two new clades, which are also supported by recent molecular studies. A sister group relationship between Parilimyidae and the septibranch families, commonly advocated in authoritative treatments of the Anomalodesmata, was rejected by the present analysis. Interpreted in the light of the fossil record, our reconstructed phylogenetic relationships favour the iterative evolution of shallow infaunal and epifaunal anomalodesmatans from deep-burrowing ancestors. [Supported by: Gates Cambridge Scholarships, ORSAS, Emmanuel College].

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First Records of a Diverse Fauna of Vesicomyidae (Bivalvia) in the European Tertiary

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The Vesicomyidae include highly specialized bivalves that live in reducing environments all over the World Ocean. The confirmed fossil history of these bivalves actually is traced back to the Late Middle Eocene and is based on records from along the continental margins of the Pacific and from the Caribbean basin in the Western Atlantic. Apart from single records of unidentified vesicomyid species from Italian Miocene seeps other members of that family have not been recorded from the European Tertiary so far.

Here the first report of a diverse fauna of Vesicomyidae in European Tertiary deposits is given. The family is represented by at least two well recognizable yet undescribed species of the genera *Vesicomya* s.s. and *Pliocardia*. A third genus described from the Mediterranean Miocene already in the 19th century but attributed to the family Glossidae is recognized here as a valid genus of the Vesicomyidae. The systematic relationships as well as the biogeographic implications of these new records are discussed.

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Needles and Pins: Extraordinary Crystalline Periostracal Calcification in Venerid Bivalves

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Periostracal calcification is being increasingly recognised amongst bivalves but that seen in Veneridae is the most spectacular. Scanning electron microscopy of the periostracum of 50 species of venerid bivalves reveals that periostracal calcification in the form of aragonitic needles and shorter pins is widespread within the family. Together with organic and sediment coatings that are found in some species, these needles form an intergral part of the functional shell. Visible as a white 'crust' on the outside of shells, long, slender needles (up to 400 µm long and 1 µm wide) without adherent material are seen in species of *Tivela*, *Lioconcha* and *Gomphina.* Other venerids including *Pitar* species, *Mysia undata* and *Compsomyax subdiaphana* have short pins, capped with a fibrous organic matrix and significant coatings of sediment. *Callocardia hungerfordi* and *Clementia papyracea* have very thick sediment coatings underlain by short pins, while *Gafrarium* and *Circe* species have short pins with a thin, robust organic coating and little particulate material. Finally, there are species, including *Venus verrucosa*, *Chione elevata* and *Mercenaria mercenaria*, where minute, <1 µm long pins also underpin a thin organic coating. Details of formation were studied in *Tivela lamyi* and *Lioconcha ornata* where the needles are elongate, hexagonal crystals of aragonite enveloped by an organic sheath. These grow at their proximal ends from within the periostracum, connected to the outer mantle epithelium via narrow channels. Growth of needles ceases following the onset of shell calcification. The distribution of the periostracal structures is examined in relation to a published molecular phylogeny for Veneridae that recognizes two major clades within the family. Larger needles and pins are confined to the clade that includes subfamilies Pitarinae, Gouldinae, Meretricinae and Petricolinae, while sub-micron sized pins are found only in the Venerinae and Chioninae of the second clade. Calcified periostracal structures appear absent in Tapetinae and Dosiniinae. Possible functions of the needles and pins are briefly discussed. Routine cleaning of venerid shells is discouraged.

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Evolution of Life Orientations in the Tellinoidea Based on Molecular Phylogeny.

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Infaunal bivalves adopt particular orientations in substrata, which are termed 'life orientation' or 'life position'. Some species of the Tellinoidea incline the commissure plane from vertical, although most bivalves orient it nearly vertically. Such characteristic life orientations are considered to be useful for horizontal migration to feed on sediment in various places, because the species involved are deposit feeders. However, the life orientations of various species in the Tellinoidea show wide variety, with some species adopting vertical orientation and others orienting the commissure plane diagonally or horizontally. In this study, we examined the evolutionary process behind the various life orientations and origin of these distinct characters in the Tellinoidea based on molecular phylogeny.

Life orientations of more than 60 species in the five Tellinoid families Tellinidae, Semelidae, Psammobiidae, Solecurtidae and Donacidae were observed, and total 2000 bps of 28SrRNA and 16SrRNA were analyzed. The life positions of almost all species could be classified as horizontal with left side down (HL), diagonal with left side down (DL), vertical (V) or horizontal with right side down (HR). The analysis revealed that the Tellinoidea consists of four major phylogenetic groups: the Donacidae, Psammobiidae+Solecurtidae, Tellinidae+Semelidae and the *Tellinella* group, which has until now been regarded as typical Tellinidae.

HL is adopted by all groups except for the Donacidae and all four types of life orientations are adopted in the Tellinidae+Semelidae. The origins of HL in the Tellinoidea remain obscure because of the unclear phylogenetic relationship between the four groups. Two hypotheses can be stated: the first is that this orientation evolved independently in the three groups, and the second is that it evolved in their common ancestor species. Whichever hypothesis is adopted, however, it is indicated that V, DL and HR in the Tellinidae+Semelidae are evolved from the HL position and acquired derivatively.

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The Mitogenomes of Pearl Oyster *Pinctada maxima* and *P. margaritifera*: High Genome Plasticity at Intra-genus Level and Mitogenomic Phylogenetic Analysis of the Bivalvia

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In most metazoan phyla, mitogenomes are conserved in length and content, with gene arrangement staying stable. However, extraordinary variations have been found in mitogenome gene content and arrangement among mollusks, particularly in bivalves. Analysis of the available bivalve mitogenomes indicates that the content and arrangement of mitogenomes are relatively conserved within genus in most groups. This study presents the first evidence of high mitogenome plasticity of bivalves at intra-genus level through analysis of mitogenomes of *Pinctada maxima* and *P. margaritifera*. Apparent differences in mitogenome organization were observed: 1) the sizes of two mitogenomes are distinct from each other, with 16, 994 bp for *P. maxima* and 15, 679 bp for *P. margaritifera*; 2) the two mitogenomes have different tRNA gene sets, with 24 (2 for *trnM*, *trnS*, *trnL*, *trnQ*, and 1 for other tRNAs) and 23 (2 for *trnM*, *trnL*, *trnR*, and 1 for other tRNAs) for *P. maxima* and *P. margaritifera* respectively; 3) the genomes show distinct gene arrangement patterns, due to the translocations among ten tRNAs, two protein-coding genes and one gene block (*trnC-cob-trnF-nad4L-nad4*). Phylogenetic analyses using complete mitgoenomic sequences have been widely used in different metazoan groups, but not well performed in bivalves' lineage. We perform a primary inference of bivalve phylogenetic relationship employing all available mitogenomes (30 species) and examine effects of high genomic rearrangement and usage of different outgroups on phylogenetic reconstruction. Results show that: 1) No topological difference has been observed among species for the same order using different outgroup, but different outgroup used could affect the positions of three marine mussels; 2) two pearl oysters are inferred to be more closely related with oysters (family Ostreidae), but not be grouped together with the Pectinidae; 3) though high genomic rearrangement in bivalve's lineage, no apparent effects have been observed in phylogenetic reconstruction using mtDNA sequences.

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Phylogenetic Reconstruction and Comparative Mitogenomic Analysis of Oysters from *Crassostrea*, *Ostrea* and *Saccostrea* (Bivalvia: Ostreidae)

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Oysters are widespread and species-rich group of bivalves, with many of economical importance worldwide. Mitogenomes offer a broad range of characters for studies of phylogenetic relationships and genome in animal taxa. While mitogenomes are conserved in length, content and gene arrangement in most metazoan phyla, high level mitogenomic variation have been found among mollusks, particularly in bivalves. In this study, comparative mitogenomic analyses were performed for 14 oyster species (among which twelve species were sequenced by our group) from genus *Crassostrea* (8), *Saccostrea* (3) and *Ostrea* (3), with the goal of characterizing the degree of variability of mitogenome organization among species and inferring their phylogenetic relationships. A high level variation in gene content and order are detected among species from different genera, characterized by extensive translocations of genes and genome size differences. Phylogenetic analyses based on a variety of mtDNA sequence data sets were carried out, and the results show that *Saccostrea* and *Ostrea* were inferred as sister group, and *C. hongkongensis* is robustly inferred to be a sister species of *C. ariakensis,* with this two species clade being sister to another clade containing *C. sikamea*, *C. angulata* and *C. gigas*. The newly-sequenced *Crassostrea* sp. is well grouped as sister species with *C. iredalei*. However, the results of pairwise comparison of complete mtDNA sequences indicate that genetic distance between *Crassostrea* sp. and *C. iredalei* is greater than those between *C. hongkongensis* and *C. ariakensis*, and between *C. angulata* and *C. gigas*, providing new evidence for our previous finding that *Crassostrea* sp. is a new species. Based on phylogenetic analysis, we hypothesized that duplication of the *rrnS* gene should be a common feature of Asian oysters, and this event may have taken place after the separation of *Crassostrea* between Asia and America.

The Different Strategy of Muscle and Neuronal Development in Larvae of the Mussel *Mytilus trossulus* and the Oyster *Crassostrea gigas*

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To compare the organization of bivalve muscular and nervous systems in evolution perspective, we have performed an analysis of myo- and neurogenesis throughout the complete larval cycle of the mussel *Mytilus trossulus* and the oyster *Crassostrea gigas.* An indirect immunofluorescence with specific antibodies (Abs) against the muscle proteins together with phalloidin and with Abs against the neuronal markers, FMRFamide (FMRFa), and serotonin (5-HT), has been combined with laser confocal microscopy and 3D reconstruction.

We have detected a well-organized muscle system in bivalve larvae. Main muscle structure in the mussel trochophores is a prototroch muscle ring, transforming into three pairs of velar striated retractors responsible for velum contractility. Oyster trochophores possess two paired muscle cells in the anterior hemisphere that form striated retractors whereas paired mesoderm bands in the vegetal region give raise a body wall muscle in the oyster veliger. The organization of muscle fibers allows us to suggest a similar function of early muscle structures of both species.

The cells of apical organ give rise neuronal elements at the trochophore stage. Neurogenesis starts at the apical extreme with the appearance of 5-HT-ergic cells surrounded by FMRFa-ergic cells in the mussel larvae. Oyster larvae possess the apical, pedal 5-HT-ergic cells and 5-HT peripheral innervations. FMRFa-ergic cells have appeared in pretrochal region in Mytilus and in pre- and postrochal regions in Crassostrea. In both bivalves early FMRFa-ergic neurons marking the scaffold of the adult nervous system are transient.

Thus, we have revealed both conservative and diversified features of neuro- and myogenesis in closely related species of bivalves. This developmental strategy can be regarded as a basis for evolutional diversity of neuronal and muscular systems in bivalve mollusks. [The study was supported by the FEB RAS (grants 09-I-P22-04 and 10-III-B-06-015), RFBR (grants 09-04-98529-p_vostok_a and 09-04-01326-a, 10-04-00330-a)].

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Bivalve Mollusks Biogeography in the Sea of Japan

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The Japan/East Sea – a marginal, deep basin enclosed by an island arc which separates it from the Pacific Ocean. Biogeographically, the sea belongs to two regions (geographical zones/subzones): boreal (=temperate) and subtropical. The number of bivalve species inhabiting the Sea of Japan is still unknown and might be at the level of 300-500 based on indirect estimates. We undertook a project on compilation of the first catalogue of bivalves along the continental coast of the Sea of Japan (from Pusan in the south to Tatarsky Strait in the north) which is in progress.

The boundary between boreal and subtropical parts of the sea was roughly set by previous workers between East Korean Bay and around Sado Island based on the fact that in these points subtropical species of bivalve mollusks begin to prevail over boreal ones. However, it seems that northern boundary of the subtropical subregion may lie further north, at around southern Hokkaido as many warm-water species penetrate to the north along the island coast of the sea due to influence of warm Tsushima Current. There is a pronounced asymmetrical pattern in the distribution and degree of penetration of warm-water mollusks to the north along the continental and island coasts of the sea. Another interesting feature of the bivalve molluscan biogeography in the Sea of Japan is a presence of so-called embaymental faunas characterized by presence of extra-zonal tropical species and relate to the complex Holocene history of the basin and current system. A combination of such factors as the considerable indentation of the coast (ria type of bays with shallow-water semi-enclosed areas in their tops) and penetration of the warm Tsushima waters to the northwestern Sea of Japan which intensified the effect of local warming had resulted in the formation of subtropical-type molluscan fauna in this boreal region. Zonal-geographical structure of the embaymental faunas is different in bays of the Sea of Japan and reflects not only modern temperature regime, but also late Quaternary climatic changes.

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The Systematic Status of *Physa natricina* Taylor 1988, an Endangered Freshwater Snail

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One of the most taxonomically difficult families of North American freshwater pulmonate snails (Hygrophila) is the almost ubiquitous Physidae. In North America these are the most common of the freshwater snails, being found in nearly every body of standing fresh water, and in the flowing portions of some streams. Many physid species have been named, mostly on shell characters, even though there is generally a paucity of easily defined consistent morphological shell variability on which to base species distinctions. Within the family, the only species that has been officially listed as endangered and threatened is *Physa* (*Haitia*) *natricina* Taylor 1988, living specimens of which seem to be limited to the Snake River in southern Idaho. However, this special protective status has been challenged by the claim that *Physa natricina* is none other than the common invasive snail, *Physa acuta* Draparnaud 1805. Previously we studied the conchology of *Physa natricina* in conjunction with a DNA analysis. We have now added to this study our anatomical observations on *Physa natricina*, as well as additional DNA analyses. For anatomical comparison of *Physa natricina* to *Physa acuta*, we used Taylor's original description of *Physa natricina*, buttressed by our anatomical study of that species, and Paraense and Pointier's study of topotype specimens of *Physa acuta*. Our anatomical results confirm our previous conclusion that the two physid species are specifically distinct. Our study also illustrates the editorial problem of getting adequate reviews for poorly researched papers that challenge previous research or concepts.

The Investigation of Element Levels in Pond Snail *(Lymnea stagnalis* L. Gastropoda, Pulmonata) from Lake Büyük Akgöl (Adapazarı), Turkey

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Specimens of pond snail, (*Lymnea stagnalis* L. Gastropoda, Pulmonata), lake water and sediment samples were collected in the summer-autumn of 2009 and winter-spring of 2010 from lake Büyük Akgöl (Adapazarı) in Türkiye. Whole soft tissues, shells, lake water and sediment samples were analyzed by ICP-OES (using microwave digestion techniques) for the measurement of following elements: Al, Ca, Fe, K, Mg, Na, P, S, Si, Zn, Ag, B, Cd, Cr, Cu, Mn, Ni, Pb and Se. The mean concentration of elements in the lake water and sediment compared with water and sediment quality criteria. For all the elements value of both soft tissue and shell of *L. stagnalis* were higher than element concentrations in the lake water and sediment. Mg, Na, P, S, Si, B and Mn showed the highest levels in soft tissues of *L. stagnalis* after Ca. In addition, the concentration of some toxic metals such as Al, Cr, Cd, Pb showed linear decreasing tendency with the increase in body weight. Our results have shown that *L. stagnalis* can accumulate elements and accumulation behavior was dependent on the amount of elements in the lake water and sediment and this indicated that ingestion may be main route to the uptake of these elements.

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Taxonomic Position and Phylogenetic Relationships of the Lymnaeid Genus *Aenigmomphiscola* Kruglov et Starobogatov, 1981 (Gastropoda: Pulmonata: Lymnaeidae)

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The lymnaeid genus *Aenigmomphiscola* includes 3 species endemic to the former USSR area (Russia and Kazakhstan). Though this genus demonstrates a quite unusual among Lymnaeidae structure of the copulative apparatus, its taxonomic position and phylogenetic affinities are still not clear and sometimes it is considered even as a probable synonym of the genus *Omphiscola* (Falkner et al., 2001). From a morphological viewpoint, Kruglov & Starobogatov (1981) regarded *Aenigmomphiscola* as a separate genus within the family non-allied to *Omphiscola* and originated from representatives of the (sub-)genus *Stagnicola*. Our aim was to clarify its taxonomic status by means of molecular genetic analyses. Sequences of 2 nuclear (ITS-2, 18S rDNA) and 2 mitochondrial (CytB, COI) genes were obtained from *Aenigmomphiscola* snails collected in Moscow Region and Altay (Siberia). A series of European and Siberian lymnaeid species, including *Omphiscola glabra*, were used for molecular analyses. In addition, structure of radula in representatives of *Aenigmomphiscola* and *Omphiscola* was studied. All trees generated on the basis of different genes and different algorythms of phylogeny reconstruction (maximum parsimony, maximum likelyhood and neighbour-joining methods) uniformly show that *Aenigmomphiscola* constitutes a separate clade that is sister to *Omphiscola*. The genetic distance between these clades is approximately comparable with those between another closely allied (sub-) genera of Lymnaeidae. Thus, *Aenigmomphiscola* differs from the other examined species of Lymnaeidae on the level of a genus. It is unlikely that any species of *Stagnicola* was an ancestor of *Aenigmomphiscola* though remote phylogenetic affinity between these genera is revealed. In spite of high level of conchological similarity between *Aenigmomphiscola* and *Omphiscola* and their close phylogenetic affinity, these taxa should not be synonymized. *Aenigmomphiscola* is characterized by some advanced traits in its copulative organ structure as well as differences in the radular structure and the prostate morphology.

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The Prevalence of *Angiostrongylus cantonensis* in the Main Hawaiian Islands

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Recently, there has been an outbreak of eosinophilic meningitis, a treatable but incurable disease, on the island of Hawaii attributed to a nematode parasite, *Angiostrongylus cantonensis*. The definitive hosts of *A. cantonensis* are rats and the intermediate hosts are gastropods. However, it can infect a wide range of accidental hosts, including humans. Although this disease in humans is commonly associated with accidental ingestion of the snails and slugs, it is unclear exactly which species and how many are vectors. Therefore, it is imperative to gain more knowledge of this parasite's vectors and prevalence throughout the Hawaiian Islands, which will permit better detection, monitoring and possible eradication. Ten of the most abundant species of introduced snails and slugs collected during surveys (2004-2009) throughout the main Hawaiian Islands are potential vectors of the parasite and are being screened for the presence of *A. cantonensis* using a PCR based approach with *Angiostrongylus*-specific primers. To corroborate our genetic results, tissue digestions using Pepsin-HCl are also being done to release nematode larvae for morphological verification. Specimens from five species (n=194) have been screened from the islands of Kauai, Maui, Oahu and Hawaii, and 4 of the 5 species tested positive for the parasite. All five of these species had previously been recorded in the literature as intermediate hosts of *A. cantonensis*. The majority of the specimens that tested positive for *A. cantonensis* are from windward areas of the island, which may reflect the wetter conditions normally found in these areas that may support greater populations of snails and slugs. However, additional sampling is needed to verify this pattern. Future work will extend the study to all main islands and to additional snail and slug species to obtain a comprehensive picture of the distribution of *A. cantonensis* and its intermediate hosts in Hawaii.

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Evolution at a Snails Pace-evolution and Phylogeny of Eupulmonata

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With more than 25,000 recent species Pulmonata have invaded mainly limnic and terrestrial habitats resulting in an enormous radiation of this group yielding many different life forms and adaptations. Phylogenetic relationships within Pulmonata (Gastropoda, Heterobranchia) are still unsettled, although based on morphological studies the monophyly of Pulmonata is widely accepted. However, some molecular systematic studies have lately revealed paraphyly of pulmonate gastropods and interrelationships are inconsistent.

Eupulmonata constitute the most speciose taxon within Pulmonata and interrelationships of its subgroups are likewise inconsistent and have been much neglected in phylogenetic studies in the past. We were interested in these relationships as a basis for further studies to gain insights into the evolution of this group.

The current investigation is based on a molecular multi-locus phylogenetic analysis, comprising 50 species including 34 eupulmonates which were sequenced for the nuclear 18S-rDNA, 28S-rDNA and the mitochondrial cytochrome c oxidase subunit I region (COI). Bayesian inference- and Maximum Likelihood analysis reveal the Eupulmonata monophyletic. In order to get information about the evolutionary age of these snails we performed a molecular clock analysis with BEAST v1.5.4 based on constraints through fossil data taken from the literature. We will discuss our dated phylogeny in the light of the evolution of Eupulmonata especially with regards to the transition from marine to terrestrial habitats.

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Molecular Phylogeny of the Stylommatophoran Land Snails and Slugs

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DNA sequence data has revolutionised our understanding of the evolutionary relationships among the stylommatophoran land snails and slugs. Yet, the stylommatophoran tree is still not fully resolved and in particular, relationships at the base of the tree remain uncertain. We present an extended phylogenetic analysis of the Stylommatophora including many new taxa and utilising a greatly extended length of DNA. We have expanded our analyses of the rRNA cluster to now include the full length of the large subunit ribosomal RNA gene. We have also utilised the actin and histone 3 genes in phylogenetic reconstructions. Our analyses provide improved support for the major divisions in the stylommatophoran tree but do little to improve resolution in areas where relationships are currently uncertain.

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The Impact of Certain Chemicals on Behavior of *Arion lusitanicus* Slugs in Laboratory Conditions

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Arion lusitanicus is a serious pest of crops in Europe. This slug species originates from the Iberian Peninsula and the first time was observed in Poland in the 1990s. In recent years, very rapid expansion of this species has been observed. Originally occurring only in the south-eastern Poland, it now may be present all over the country.

The research was conducted under laboratory conditions in a climatic chamber at a temperature of 16°C and 12h day length. In translucent plastic containers with 10 cm layer of soil two slugs were placed. The surface of the containers was divided into four parts: on the first the shelter for slugs was placed, on the other soil sprayed with tested active substances (except control), on the third four discs of cabbage soaked in active substances and the last part was clean soil. The tested active substances were: metaldehyde + N-acetyl-L-cysteine (1%), copper sulfate (1%) abamectin (0.2%) methiocarb (1%) and metaldehyde (1%). Each container was also equipped with an infrared camera connected to video recorder. Over the next 48 hours behavior of slugs in each container was recorded. Records obtained in this way were viewed and the time of each type of behavior at any hour of the day was noted. The results were statistically analyzed using the Student t test with significance level at $\alpha = 0.05$. The residence time in the shelter and slug movement and immobility time significantly differed among the active substances and control. While most of the time the slugs spent in the shelter after the application of metaldehyde and abamectin, the greatest physical activity was observed in control conditions. Significant differences were also observed during feeding time, which was considerably longer in control slugs than in containers with copper sulphate and metaldehyde.

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Effect of Feeding Mixture and Substrate on Growth and Survival of *Arion lusitanicus*

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At the Lab of Pharmaceutical Technology (Ghent University), a breeding culture of *Arion lusitanicus* has been established for many years, since this species is used as a test organism in an alternative mucosal irritation test (Slug Mucosal Irritation (SMI) assay). To obtain reproducible results in the SMI assay, a feeding experiment was set up for 2 purposes: (1) to investigate how the ideal body weight (BW: 3 - 6 g) can be reached in the short term and (2) to have slugs with an ideal BW in the longer term.

Five feeding mixtures (A - E) were compiled and two types of substrate were tested: soil ('S') and cotton cloth ('C'). Juvenile slugs, hatched in the lab were separated from the stock. Sixty slugs were randomly assigned to each of the 10 condition (AC, AS, BC, BS, CC, CS, DC, DS, EC and CS).

In the first months, slugs on soil gained more weight, with combination AS having the highest portions of slugs (30%) with sufficient BW. After 6 months, for mixtures B, C, and D the portion of slugs that reached the optimal BW was bigger for the boxes on cotton cloth, while for A and E these portions were bigger for the slugs on soil. Portions of overweight slugs increased in all treatments, with soil having the highest amount for every mixture. After one year, mortality reached levels > 50 % in all treatments on soil. For the slugs on cotton cloth, survival was generally > 80%. Treatments DC and CC had the highest portions of usable slugs (33% and 27% respectively), while for slugs on soil highest portions were seen in food mixtures B and C (20% and 18% respectively). We were able to influence growth and survival of *Arion lusitanicus* slugs on short and long term.

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Ecohydrological and Other Habitat Requirements of the Wetland Snail *Vertigo moulinsiana*

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The marsh snail *Vertigo moulinsiana* is listed on Annexe II of the European Union's Habitats Directive and this requires EU member states to establish a series of protected sites known as Special Areas of Conservation (SAC) to conserve the species. Where human activities may adversely affect the species, there is an obligation to undertake an 'Appropriate Assessment' to assess the impacts. The Habitats Directive requires member states to adopt a precautionary approach, so unless zero impacts can be demonstrated, there is a presumption that the proposed harmful activity may not proceed.

Water abstraction from rivers and aquifers has the potential to lower water tables and therefore to affect wetland habitats that support *V. moulinsiana*. This paper will describe some of the hydroecological studies that were undertaken to inform the Appropriate Assessment that was undertaken to establish the likely impacts of abstraction from the catchments of the Rivers Kennet and Lambourn in southern England. The studies were undertaken between 2003-2005 and involved the installation of hydrological monitoring apparatus and detailed studies on the distribution and abundance of the snail in fixed plots and along transects on the eight component sites of the Kennet and Lambourn Floodplain SAC.

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Co-occurrence Patterns of the *Vertigo* Species in Hungary in Association with Their Habitat Preferences

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Vertigo is a genus of tiny pulmonate land snails occurring mainly in wet areas of the Holarctic region. In Europe several species are protected and are the subject of many different studies. In Hungary seven species are present: *V. alpestris*, *V. angustior*, *V. antivertigo*, *V. moulinsiana*, *V. pygmaea*, *V. pusilla*, *V. substriata*. We worked with almost all of the available Hungarian collection data (almost 2000 distribution data from more than 1200 localities), and we enforced a null-model approach, using ensemble and pairwise metrics, to detect non-random associations of pairs of species. We found significant departure from randomness which is attributed to certain species pairs. *V. alpestris* and *V. moulinsiana* co-occur with four, *V. antivertigo* and *V. substriata* with five, and *V. angustior*, *V. pusilla* and *V. pygmaea* with six other *Vertigo* species. Those findings are concordant with data suggesting that in Hungary *V. moulinsiana* and *V. alpestris* have the narrowest ecological niche. The typical habitat of *V. moulinsiana* is wetlands dominated by large sedges, and *V. alpestris* seems to be only rock-dwelling species inside the country. *V. alpestris* and *V. pusilla* are separated from the other species according to their habitat. The habitat preference is most similar in three species, namely *V. pygmaea*, *V. angustior* and *V. antivertigo*, which seem to co-occur very frequently. *V. alpestris* and *V. substriata* are the rarest species, and are recommended for protection actions.

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The Distribution of the Invasive Predatory Snail *Oxychilus alliarius* (Miller, 1822) among the Hawaiian Islands

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The Pacific islands have had more recorded mollusc extinctions than anywhere else in the world. The invasive predatory snail *Oxychilus alliarius* (Miller, 1822) was first recorded in the Hawaiian Islands in 1937 and is currently present on the six main islands. *Oxychilius alliarius* is distributed over a wide elevational range (400 – 2100 m) and preferentially preys on snails of less than 3 mm in maximum dimension, but will also attack and consume larger snails. Even so, much of the malacological research in the Hawaiian Islands has largely ignored *O. alliarius* and its potential threat to the sensitive Hawaiian native snail biodiversity. It has been estimated that 90% of the more than 750 native Hawaiian snail species are now extinct; the main reasons for extinction being habitat destruction and predation by invasive species. Many Hawaiian native snail species survive only as relictual populations in high elevation refugia (> 500 m). During 2004 – 2010, R.H. Cowie and his students completed 200+ snail and slug surveys across the six largest Hawaiian Islands. Analysis of distributional data from the surveys shows that the abundance of *O. alliarius* in the Hawaiian Islands is positively correlated with increased elevation, and that the abundance of native Hawaiian snail species is negatively correlated with *O. alliarius* abundance. The possibility that *O. alliarius* will spread to other Pacific islands with rich endemic snail faunas, makes understanding the distribution and effects of this invasive snail essential to preserving native biodiversity.

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Conservation of Fiji's Unique Land Snail Fauna: Is It an Achievable Goal?

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The land snail fauna of the Fiji Islands is rich and highly diverse, consisting of at least 242 species that cover 28 families and 70 genera. Of these 242 species, 49 are native (indigenous) and 167 are endemic. Exactly how many of these endemic species are threatened or in need of some form of conservation action is debatable however, what is certain is that without increased effort towards strengthening information supply to local communities and government departments, a significant amount of this unique fauna will soon be lost. Although the Fijian Government accepts responsibility for these unique natural resources it currently has limited human resource capacity to collate the large amount of previously collected information on Fiji's land snail species and their distribution, let alone investigate current occurrence. Such baseline data is critical if we wish to monitor or manage potential endemic or native species loss. To date there is little information available locally that allows identification of even the most common snail families or genera however, with recent support from the South Pacific Regional Herbarium and Conservation International two small projects are now underway at the University of the South Pacific to encourage completion of the large task of documenting the native and endemic species present in Fiji and providing locally relevant information and tools to stakeholders. Some realistic conservation priorities will need to be set on available data and once identification problems are overcome we can move forward in partnership with local stakeholders to determine exactly where and how human-related development and invasive species are most severely impacting on Fiji's globally significant land snail resources. All projects in progress include the direct involvement of village community members and the training and mentoring of local USP students.

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Searching High and Low: Alien Snails and Slugs in the Horticultural Industry of Hawaii

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Globally, alien snails and slugs threaten the health of numerous ecosystems and result in major losses to agricultural crops. The horticultural trade has been widely associated with many unintended introductions of alien snails and slugs, particularly so in Hawaii. During 2004-2010, we surveyed nurseries, botanical gardens, and other similar facilities on the six largest Hawaiian Islands for snails and slugs. We recorded 40 terrestrial species, of which all but four were alien, five were new records for the Hawaiian Islands, and 24 were new island records. There are now 39 established non-native terrestrial snail and slug species recorded in the Hawaiian Islands. There was a significant difference in snail assemblages in nurseries among islands and among sites at high (> 500 m) and low (< 500 m) elevations. There was no significant difference in species richness among islands. However, this result may not reflect the actual pattern of species richness among islands because of small sample sizes on Maui and Oahu at low and high elevations, respectively. Many of the snail and slug species found pose public health concerns and impact the marketing and trade of horticultural products, both within the islands and overseas, sometimes resulting in considerable economic loss. Additionally the establishment of alien snails and slugs in the Hawaiian Islands may impact the health of native ecosystems by killing native plant seedlings, modifying native snail habitats, and through competition and predation. A clearer understanding of the non-native species being transported into and out of the islands will provide the basis for better quarantine and control measures.

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Biodiversity in Freshwater Snails of Turkey: Distribution, Endemism, and Conservational Problems

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From Turkey, 118 species and 15 subspecies of freshwater snails have been documented so far. Of these, 85 species and 15 subspecies belong to Prosobranchia, while 34 taxa belong to Basommatophora. Lakes Region, located in southwestern Turkey, is an area of endemism for freshwater mollusks in Turkey. A total of 40 prosobranch species and subspecies from Prosobranchia have been recorded in the region. Of these, 27 are endemic to Anatolia (as compared to 46 in total), 25 strictly being endemic to the region. The family Hydrobiidae (Prosobranchia), most diverse family of Anatolian freshwater snails, shows remarkable diversity centered in this region, also. With newly described Basommatophoran taxa from southern Anatolia, it is known understood that area histories are parallel to species histories for the freshwater snails of Turkey, which marks biogeographical importance of the fauna.

Under global climatic changes and due to present and future problems caused by increasing population across the Eastern Mediterranean basin including Turkey, freshwater snails are under great extinction risk. Depending on the studies on distribution and populations of native taxa, an assessment for the fauna of western Anatolia was made.

In this study, an account of present knowledge on distributions, endemism, and ecology of extant freshwater snail fauna of Turkey is given, also extinctions and vulnerability of the surviving taxa to extinction were discussed.

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Freshwater and Terrestrial Molluscs in Brazil: Current Status of Knowledge and Conservation

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Brazil, a country with continental dimensions, is recognized as one of the most megadiverse countries, harboring diversity of biomes and species richness. However our current knowledge about our biota is still scarce and heterogeneous, focused on few groups, especially when talking about invertebrates, including here the hidden invertebrates as parasites. The necessity of recognition of Brazilian biodiversity is pressed by the increasing threats, specially considering environmental alterations as urban development, deforestation to soy and crop plantation, forest fragmentation, building of hydroelectric plants and also invasion by exotic species. A summary of the threat level and conservation status of limnic and terrestrial molluscs, resulting from several private and governmental initiatives are here presented. Of the 26 Brazilian states and more the Federal District, only seven states (Pará, Minas Gerais, Espirito Santo, Rio de Janeiro, São Paulo, Paraná and Rio Grande do Sul) possess lists of threatened fauna, but only four include the molluscs in the lists. Considering the existing lists, only in Rio de Janeiro we have the indication of flagship species and umbrella species. The more recent national list includes 11 species of terrestrial gastropods and 27 of limnic molluscs, totalizing 6.06% of the fauna listed as threatened. The geographic distribution of the listed species and the comparison of these lists with that of the IUCN will be presented.

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Young but Promising: The Study of Tropical Land Snail Communities

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Although malacologists have been collecting land snails in the tropics for centuries, ecological studies have only begun to appear in the past few decades, much later than community ecology on temperate land snails on other tropical invertebrates, despite the fact that land snails offer advantages for community ecologists that many other groups lack, such as manageable numbers of species, high beta-diversities, and easy and unbiased sampling. In this lecture, I will present a review of the work done sofar, focusing on the following issues:

Sampling strategies. By the collecting of empty shells from the forest floor, communities can be sampled in an unbiased fashion. However, methodological issues such as cross-study standardization, completeness on calcareous vs. non-calcareous soils, and the advantages and disadvantages of time-averaging need more attention.

Habitat and biogeographical differences in community composition. Although data for many tropical regions are still scant, interesting differences in community structure are beginning to show, having to do with, among other things, proportions of carnivorous species and proportions of non-pulmonate species.

Macroecological patterns. I will advocate the use of tropical forest snail community data for use in studies of macroecological patterns, including latitudinal richness gradients, altitudinal richness gradients, and species abundance distributions.

Conservation. Even though mollusks are among the best-represented groups in the IUCN Red List, conservation biological work on tropical land snail communities is still in its infancy. I will highlight the role that students of tropical land snails could play in garnering support for the conservation of tropical communities.

Species Richness, Community Composition and Elevational Distribution of Land Snails on the Pico do Papagaio Trail, Ilha Grande, Rio de Janeiro State, Southeastern Brazil

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This study assessed the composition, diversity and altitudinal variation of land-snail communities along the Pico do Papagaio trail, Ilha Grande, Brazil. Sampling was carried out at five sites at ca. 100m altitudinal intervals. At each site we sampled suitable microhabitats for a total of 3.5 person hours, and collected leaf litter from ten 25x75cm plots, from which shells and live snails were subsequently extracted. Land snails collected in the field were identified to morphospecies-level; 34% of species correspond to known/decribed species. In total, 464 individuals, representing 32 species and 13 families were recorded. Extrapolation by EstimateS 8.0 showed that local richness (per site) ranged from 29-35 species. Micromolluscs (< 5mm) accounted for 44% (14) of species and 72% (334) of specimens. The families Diplommatinidae, Systrophiidae and Subulinidae together composed over 75% of all the terrestrial gastropods collected. Species richness ranged from 8-22 species per site, and snail abundance from 21-261 individuals. Species richness and snail abundance were highest at 200m asl, and 56% of all the specimens collected were from this site. Simpson's diversity index was higher in the sites at 400m and 500m asl. *Happiella* spp. and *Miradiscops* spp. were present at all altitudes, whereas *Beckianum beckianum*, Systrophiid species and *Alcadia* spp. were found only at 100m asl. *Neocyclotus prominulus* and *Habroconus semenlini* were collected from 200 to 400m asl. *Lamellaxis gracilis* was collected at 400m and 500m asl. *Alcadia* sp., *Rhinus* sp. B, *Simpulopsis* sp. B and Veronicellid sp. A were each represented by a single specimen. Simple regression analysis showed that there was no significant relationship between altitude and each of the following: Simpson's diversity index, Shannon's diversity index, snail abundance and species richness. This study represents a pioneering effort in the study of the elevational distribution of land snails in the Atlantic Forest of Brazilian Southwest.

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Land-snail Diversity Patterns from Taita Hills Forests, Kenya: Implication of Forest Fragmentation on Snail Biodiversity Conservation

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Taita Hills of South eastern Kenya is one of the most important biodiversity conservation centers in Kenya. The forests which form the north-most extension of the Eastern Arc Mountains and the only geological formation of such ecosystem in Kenya is a critical center of endemism and hotspot for many rare species in the country. Despite the forests biodiversity conservation, they are threatened by anthropogenic influences. The forest which was once a continuous forest block has slowly been fragmented to current 12 forests ranging from about 200ha to some just about 1 ha. From biodiversity conservation perspective the worry is that the impact of the forests fragmentation on many taxa remained to be described particularly the less mobile taxa like land-snail which are more vulnerable compared to highly mobile taxa. In view of the emerging biodiversity conservation challenge associated with these forests fragmentation, this study was carried to describe the forests land-snail diversity patterns and the associated impact of forest fragmentation on land-snails biodiversity. The study was implemented using standardized direct search and litter sample methods. A total of 3003 individuals belonging to 49 species were recorded from the entire study. The greatest diversity was reported from the largest forests fragments whereas the least diversity was recorded from the smallest fragments. Several species were only recorded in one forest. Interesting though the greatest populations of the endangered *Gulella taitensis* species were reported from the smallest forest fragments. A simple linear regression demonstrated a positive relationship between the forest size and number of recorded species. This study suggest Taita hills forest ecosystem as a land-snail biodiversity hotspot. However, the biodiversity appear potentially threatened by forest fragmentation. Increased conservation of these forests to safeguard destruction of land-snails biodiversity particularly the endangered species is recommended.

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Land Snail Community Structure in the Rainforest Region of Southern Nigeria

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Unprecedented rates of forest destruction and exploitation is leading to the on-going process of biodiversity loss and species extinction. In many places, tropical rainforests are converted to other forms of land uses that may be of conservational value to land molluscs. We study the effect of rainforest destruction or conversion on land molluscs species richness and community structure using fixed-time search and litter sieving techniques in standard plots of 400 m^2. Four different land use systems were studied: primary forests, secondary forests (young- and old-growth), agroforestry and plantation agriculture (cocoa, oil palm and rubber). Species richness decreased from primary forests and agroforestry systems to secondary forest and plantation agriculture. Species richness changed from being dominated by the carnivorous Streptaxidae in primary forest to detrivorous Subulinidae in rubber plantation. Our results show that the land snail community structure can be described by the Streptaxidae:Subulinidae ratio depending on the nature of the forest and level of disturbance. The Streptaxidae:Subulinidae ratio approximate 2:1 in primary forest, cocoa agroforest and limestone forest while secondary forests have a ratio of 1:1 and rubber plantation 1:2. Forest destruction and conversion to plantations led to local extinction of some land molluscan families: Alliyidae, Cerastidae, Cyclophoridae, Euconulidae and Veronicellidae. In order to conserve land snail biodiversity in the region, traditional agroforestry should be encouraged while the conservation of primary forest and near-primary forest fragment should be given much higher priority. We also advocate for the protection of limestone hills in the region because of its rich malacofauna.

Community Ecology of South Asian Land Snails, an Overview

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Over recent decades there has been increasing interest in exploring the diversity and composition of tropical forest land-snail communities. Studies of the South Asian land-snail fauna, particularly on Sri Lankan land snails, have contributed and continue to contribute significantly to our understanding of tropical land-snail community ecology. South Asian forest snail communities are often highly species-rich and taxonomically broad based. In Sri Lanka rainforest communities tend to be dominated by highly-localized restricted-range species. Studies to date suggest that the vast majority of South Asian land snails are entirely or largely restricted to natural forest, and that some restricted-range species have been surprisingly resilient to forest fragmentation and degradation over the last two centuries. Community ecological studies of much of the South Asian region (with the exception of Sri Lanka) are in their infancy; data on the species composition of the major natural forest snail faunas are needed, along with an in-depth understanding of the distributional limits of species. Future studies across the region would also benefit from integrating phylogenetic and ecological approaches, for example to explore the role of evolutionary vs. ecological forces in structuring land-snail assemblages.

A Review of Ecological Studies on Patterns and Processes of Distribution of Land Snails of the Western Ghats, India

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The Western Ghats is one of the 34 biodiversity hotspots with rich in flora and fauna. Amazing diversity and endemism is exhibited in few groups such as land snails with nearly 80% are endemic to this hotspot. The compiled works from past and present surveys have shown that the Western Ghats has 270 species described and another 20 awaiting description. Here we present the review of our work community ecology of land snails in the Western Ghats. The diversity at regional scale decreases from south to north. The diversity is also highest at mid- altitudinal range. At local scale, the diversity and endemism is highest in evergreen forest and least in plantations. Evergreen forest has harbors high density of micro snails (<5mm) compared to other habitat types. Home gardens have relatively high density of introduced and pest land snail species.

Community composition was assessed using beta diversity and PCA. There is a high species turnover both at regional scale as well as at the local habitat scale. This is evidenced by the fact that, at regional scale there is complete change in species composition from south to north. At the habitat level, the human modified habitats such as plantations and home gardens have distinct faunal composition compared to surrounding natural habitats. PCA analysis was performed for the species distribution data and for 18 environmental variables to assess the similarity among the different land-use types. The results show that there are two distinct clusters, one of areca plantations and other one of acacia, *haadi* (managed forests) and evergreen forest. It is evident that, on the positive side, the evergreen forest forms a slightly distinct cluster from *haadi* and acacia. A few habitat and environmental variables have significant contribution in limiting snail distribution. Some of the most important ones are soil pH, calcium and magnesium, electric conductivity, temperature and organic carbon. Nestedness analysis showed that there is a distinct nested pattern indicating that the land snail fauna in different land uses is a subset of undisturbed evergreen forest. Our studies in different parts of the Western Ghats consistently showed that the land snails in this region occur in very low density when compared to South-east Asia, where one can find snails in very high density. As in case of birds, the Western Ghats have very impoverished land snail fauna.

Biodiversity of Terrestrial Molluscs from North Maharashtra India

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Ecological diversity and systematic of molluscan species from North Maharashtra was studied during 2005-2006. Study area comprises 16 different sampling stations in about 300 sq km zone of North Maharashtra, India. A total of 380 individuals belonging to 16 different species were collected from 16 collection spots in 10 localities distributed along five districts of North Maharashtra . Seven families from 03 orders represent 16 species. A maximum of six species represented from Ariophantidae family, 03 from Cyclophoridae, 02 from Succinidae and Camaenidae and 01 from each of the Achatinidae, Subulinidae and Veronicellidae. North Maharashtra is allied zone of western Ghats. Changes in species composition and abundance are related to natural site variations (UD) as well as human impacts (MD). The Shannon 's diversity index shows maximum diversity index with 16 numbers of species is 1.60 in undisturbed area (UD) and 1.40 in moderately distributed area (MD). Need for biodiversity conservation is emphasized. These terrestrial molluscs are quite common in rocky areas among satpuda, mountain belts, and evergreen forests and in orchards. They prefer moist soil rich in organic carbon.

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Sampling Forest Snail Faunas: Some Problems and What We Can Do about Them

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Site inventories of snail faunas from forests are frequently incomplete, and this has proved to be a particular problem in tropical forests away from limestone, where densities are low and snail habits cryptic. Some of the problems arising from this will be illustrated with examples from the tropics and elsewhere, and the basic statistics explored. While there are a variety of statistical methods of estimating the number of omissions, and of compensating for these when comparing faunas, I will concentrate on how we might design our sampling to answer our questions with a minimum of error, and on the limitations errors place on our interpretation of results. In particular, I will contrast the study of richness with the details of changes in composition in relation to geography or environmental factors.

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The Determinants of Land Snail Diversity along a Tropical Altitudinal Gradient: Insularity, Geometry, and Niches

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We investigated the patterns of species richness in land snails and slugs along a tropical altitudinal gradient and whether these patterns correlate with area, altitude, geographic constraints, and productivity. We did so both at the scale at which land snail population processes take place and at the larger scale of altitudinal zones. Study was done in Mount Kinabalu (4,096 m) and the adjacent Mount Tambuyukon (2,588 m) in Kinabalu Park, Sabah, Malaysian Borneo. We used an effort-controlled sampling protocol to determine land snail and slug species richness in 142 0.04 ha plots at altitudes ranging from 570 m to 4,096 m. Extents of altitudinal ranges were determined by interpolation, where appropriate extended on the lower end with data from lowlands outside of the study area. We used regression analysis to study the relationships between species density and richness on the one hand and altitude and area on the other. This was done for point data as well as for data combined into 300-m altitudinal intervals. Species density (based on the individual samples) showed a decline with altitude. Altitudinal range length profiles revealed that range lengths are reduced at greater altitudes and that a Rapoport effect is absent. Diversity showed a mild mid-domain effect on Kinabalu, but not on Tambuyukon. When the data were combined into 300-m altitudinal intervals, richness correlated more strongly with altitude than with area. Ecomorphospace was seen to shrink with increasing altitude. The altitudinal species richness patterns show the combined effects of (a) reduced niche diversity at altitudes with lower productivity and (b) historical events in which upward migration of lowland species as well as speciation of highland endemics took place.

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Macro Land Snail Biodiversity across Habitat Degradation Gradients in Mount Makiling, Philippines

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The Philippines supports land snail faunas with high endemism. However their populations have declined drastically due to habitat destruction and modification. Thus, more baseline research on how land snail communities are affected by habitat degradation is urgent and important to generate information for effective conservation of these biological resources. The diversity and relative abundance of macro land snails were determined along habitat degradation gradients (Puting Lupa slope-undisturbed; UPLB Forestry slope-moderately disturbed and Makban slope-disturbed) of Mount Makiling. For each area, six 400m^2 quadrats were randomly set covering 18 sampling sites. Environmental variables influencing snail communities were determined, followed by extensive two-hour hand-searching for live snails and empty shells. A total of 890 macro land snails, representing 5 families and 17 species were sampled. Of these, 69.76% (621) were pulmonates while 30.24% (269) were prosobranchs. Land snails were significantly more abundant in moderately disturbed areas (101 ± 41.66) followed by those in undisturbed (33 ± 18.96) and disturbed (15 ± 9.79). Species richness was higher in the moderately disturbed and undisturbed sites (8 and 7, respectively) than in disturbed areas (2). Abundance and richness of pulmonate snails did not vary significantly between undisturbed and moderately disturbed sites. In contrast, prosobranchs had significantly higher abundance and species richness in the moderately disturbed areas. Canonical correspondence analysis showed significantly that the dominant limiting factors for land snail community composition were degree of habitat degradation, soil calcium, temperature and canopy cover. Endemic snail species were more associated with undisturbed and moderately disturbed forests. However, it appears that introduced species (i.e., *Achatina fulica* and *Bradybaena similaris*) are beginning to establish their populations in sites that are exposed to anthropogenic disturbance.

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Aquaculture of Gastropod Molluscs with Potential for the Aquarium Industry

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Investigations on the reproductive biology, life cycle and feeding habits have been undertaken to assess the potential of *Pomacea bridgesii* (algae eater) and *Anentome helena* (predator) as cultured species in aquarium conditions and plague controllers.

The study methodology comprised three main branches: life cycle studies (embryonic and larval development studies), species culture conditions optimization experiments and plague controllers efficiency studies. Ongoing research experiments, accomplishments and difficulties up to date will be presented.

Due to their versatile and resistant behavior, moderately amphibian nature, fast growth rate, short embryonic development, highly hatching development form and easy access, low cost diet, are among the characteristics that makes *Pomacea bridgesii* highly suitable for intensive culture regarding aquarium trade.

Anentome helena although not an intensive breeder, is an easy, low maintenance specie and very efficient as fresh water snails plague controller. This hability was tested with some of the most common fresh water aquarium invasive snails such as *Physia* sp. but particularly with *Pomacea canaliculata*, which in the last 20 years turned into a serious pest in Asia where they keep massively destroying taro and rice fields, by feeding on them. In late July 2009 an incipient invasion by *Pomacea canaliculata* was detected in the Ebro Delta, on the Mediterranean shore of Spain. By early September the spread of this applesnail was tremendous, with huge economic losses to rice cultivation, expanding the problem dimension in a global scale.

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Potential for Cockle Aquaculture in New Zealand

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The intertidal cockle *Austrovenus stutchburyi,* also known as tuangi or littleneck clam is endemic to New Zealand, where it commonly occurs in sheltered sandflats and estuaries. Over the past 30 years cockle populations have declined and shellfish health has been compromised possibly through human induced activities including industrial contaminants, urban development, land run off and increased sedimentation, as well as increased nutrient levels and reduced salinities. In some areas of New Zealand cockles are locally abundant and commercial harvesting occurs year round at Whangarei, Golden and Tasman Bays, Blueskin Bay and Otago harbour. This fishery is managed by strict quotas, with the limit being set at 3,214 metric tonnes for the 2009/2010 fishing year. It is not known if the current catch limits allow for sustainable yields. Recreational fishing occurs in other areas with the daily limit being 150 cockles/person/day. In some areas this limit is not sustainable. Customary Fishing Regulations and bed closures for cockles within Maori Marine Reserves are designed to encourage sustainable fisheries.

Our research shows that cockle populations differ both within and between locations and recent research suggests that this is often site specific and correlated with sediment properties, salinity and contamination levels. We present results from small- and large-scale enhancement experiments in the Canterbury region using transplanted individuals. These have had variable success and suggest that there are specific requirements for establishment, including, sediment contaminant levels, site stability and nutrient availability. The paper also discusses other aquaculture techniques including spat production and experimental manipulations of established populations which could be used to enhance the aquaculture potential of this species.

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Current Status of Commercial Farming of Thai Abalone, *Haliotis asinina* Linnaeus, 1758

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Abalones are well known as commercially important marine gastropods. They are widely distributed along rocky shores ranged from temperate to tropical zones of both northern and southern hemispheres. It should be pointed out that temperate abalone species are usually larger in their maximum sizes than that of the tropical ones. Three species of tropical abalone are native to Thai waters i.e. *Haliotis asinina, H. ovina,* and *H. varia*. More than 2 decades that artificial breeding of the first two species has been achieved. Of these two species, *H. asinina* has been first selected as a candidate species for commercial production, due to its high growth rate, ease of spawning, and high percentage of edible part. In addition, aquaculture production of this species is also necessary to replace a drastic decline in production from wild catch. Generally, commercial farming of abalone can be divided into three consecutive phases i.e. hatchery, nursery, and grow out. In this paper, current practices on various aspects of commercial aquaculture in this native species i.e. broodstock conditioning, spawning induction, seed production, nursery, and grow out techniques are presented together with encountered problems. Finally, further investigations to solve those problems are also suggested.

Rearing Juveniles of the Freshwater Pearl Mussel *Hyriopsis* (*Hyriopsis*) *bialatus* in a Natural Habitat vs. a Recirculating Aquaculture System

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Glochidia of the freshwater pearl mussel *Hyriopsis* (*Hyriopsis*) *bialatus* were cultured in an artificial medium consisting of M199, fish plasma (*Cyprinus carpio*), and antibiotics/antimycotic at a ratio of 2:1:0.5 (v/v). They were reared at a density of 2,000 glochidia per dish (10 ml of artificial medium) under sterile conditions until they transformed into juveniles. The culture dishes were incubated at 23 ± 2 °C with a constant supply of 5% CO_2. The duration of glochidia development until the juvenile stage was 8 days. After transformation, early juvenile mussels were reared in a closed recirculating aquaculture system. The system was composed of a particulate filter cabinet, a macrophyte (*Limnophila heterophylla*) filter cabinet, a biological filter cabinet, a water resting cabinet, and plastic culture units (24.5×40×14 cm). Mussels were fed twice a day on a 1:1 mixture of *Chlorella* sp. and *Kirchneriella incurvata* until 90 days. The survival rate of juveniles was 37.2%. The average length of these juveniles increased from 0.21 ± 0.01 mm to 4.18 ± 0.41 mm, and the average height from 0.24 ± 0.01 mm to 2.04 ± 0.14 mm. The surviving 90-day-old juveniles were then reared in two different locations, both within the natural habitat and the recirculating system, until 170 days. In the natural habitat, 50 juveniles were transferred to each of three culture units (each 20×12×72 cm). All four vertical sides of the culture units were lined with nylon net. The lower part contained 400 g of sand. The culture units were then hung 50 cm below the water surface in the natural habitat. Additionally, 50 juveniles were placed in a closed recirculating water system similar to that used for the previous stage. It was found that juveniles reared in the natural habitat had greater rates of growth than those in the recirculating system, with (respectively): lengths of juveniles of 25.97 ± 4.02 vs. 4.49 ± 1.63; heights of 18.39 ± 3.24 vs. 2.16 ± 0.54; and widths of 3.28 ± 0.57 vs. 0.89 ± 0.41mm. The survival rate in both locations approached 100%.

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Comparison of Gonadal Development of Blood Cockle (*Anadaragranosa*) in East Coast Sumatera, Indonesia and Pulau Pinang, Malaysia Using Condition Index

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The gonad development of *Anadaragranosa*found in East Coast Sumatera (Indonesia) and Pulau Pinang (Malaysia) using condition index (CI) was compared. Sampling was collected July 2009 until March 2010. Two sites were selected in east coast Sumatera, namely Banda Aceh and Lhokseumawe and one site in Pulau Pinang. The highest condition index in Banda Aceh sampling site was observed in June (10.74 ± 5.71 g/mL) whereas the lowest was observed in October (8.27 ± 3.03 g/mL). In Lhokseumawe sampling site, the highest CI was observed in October (13.97 ± 3.49 g/mL) and the lowest showed in January (6.76 ± 1.13 g/mL). The fluctuated in CI was shown in Pulau Pinang sampling site which the highest CI in the Pulau Pinang cockle population was observed in March (15.74 ± 2.95 g/mL) and the lowest in November (9.50 ± 2.15 g/mL). The blood cockle population in Lhokseumawe and Banda Aceh seemed to reach the highest condition index earlier compared to Pulau Pinang. These two populations eventually spawned earlier and showed the lowest condition index earlier compared to Pulau Pinang. The different rate of Condition Index was influenced by the environmental parameters.

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Spawning of Seven Species of Giant Clams in Sabah, Malaysia

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Giant clams are bivalve molluscs of the family Tridacnidae with eight living species from only two genera, *Tridacna* and *Hippopus*, commonly found in shallow clear waters in the Indo-Pacific region. Brood stocks for seven species of giant clams were collected from Sabah's coastal water for *ex situ* spawning at Marine Ecology Research Centre, Malaysia, as part of the centre conservation programme to restock the clams to the surrounding reef. The species involved were *Tridacna gigas, Tridacna derasa, Tridacna squamosa, Tridacna maxima, Tridacna crocea, Hippopus hippopus and Hippopus porcelanus*. Clams with matured gonad were induced to spawn by intragonadal injection of serotonin solution. All seven species were successfully spawned between May 2009 and April 2010. The larvae were fed with a mixture of *Isochrysis galbana* and *Chaetoceros calcitrans*, with increasing concentrations as the larvae grew bigger. Most tridacnid larvae from the seven species showed signs for settlement after 7-8 days. *Tridacna squamosa* and *Hippopus* sp. can be easily spawned while *Tridacna gigas* and *Tridacna derasa* spawned the least number of times and mostly confined between the month of April and June. The larval developments of all the seven species were quite similar and will be discussed in this paper.

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Induced Spawning and Larval Development of *Placuna ephippium* Philipsson, 1788 (Bivalvia: Placunidae)

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Unlike the well studied *Placuna placenta*, the reproduction and larval development of *Placuna ephippium* received relatively little attention. The aim of this research was to determine the induced spawning method and to investigate the growth and larval development of *Placuna ephippium*. *Placuna phippium* broodstocks were collected from a seagrass bed in Pulai River Estuary, Johor. After acclimatization, 12 adult specimens were induced by thermal shock with 19°C and 28°C cycle. The female specimen started to spawn after the first heat-cold cycle followed by 5 female and 4 male specimens. Gametes were collected in separate aquaria and a small amount of sperm was used for fertilization. Trochophore larvae were recorded 280 minutes after fertilization and D-hinged larvae were observed after 20 hours. Larvae were fed with *Isochrysis galbana*. The growth of the planktonic larvae was observed daily and measured every alternate day. Early umbo stage was observed on day-2 and a distinctive skewed-shaped larva shell was seen on day-3. Larvae remained planktonic for 9 days and started metamorphosed from the 10th day onwards. Although 20% of the larvae survived to metamorphosis stage, only 1 juvenile survived after settlement. More experiment need to be carried out to investigate the suitable environment and settlement substrate for this muddy bottom bivalve species.

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Broodstock and Egg Quality in *Donax trunculus* During Spawning Period in Algarve, South Portugal

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Wedge shell *Donax trunculus* is an economically important resource along the Algarve coast (south Portugal). Defining quality criteria based on biochemical indicators (protein, lipids and glycogen) of the wedge shell adults is of utmost importance to predict quality of the eggs and their viability. It is important to stress that during the endotrophic phase the larvae rely solely on their vitelline reserves to develop.

The aim of this study was to relate the broodstock condition, eggs quality and hatching rate. To accomplish this, samples of around 500 individuals were collected fortnightly during the spawning season (March to early August 2009) from Lota beach (Algarve). Thirty individuals were use to determine their condition (Walne-Mann index), ten for determining the biochemical composition, separately for males and females, and the remainder specimens were kept in an open circuit to induce spawning. Part of eggs obtained were stored for biochemical analysis whereas others were incubated until they reach veliger D-larvae. After 24 hours hatching rate was calculated.

Preliminary results showed that the condition index (CI) although decreasing during the spawning season presented two peaks, that may indicate a recovery of the glycogen reserves used in the gametogenic process. Although these two parameters do not correlate, glycogen oscillates during the spawning season, which may indicate a storage consumption pattern. Lipids of the broodstock (between 56,0–129,1μg mg^{-1}) decreased during the season due to gametes expulsion. Proteins were the predominant constituent (between 135,1–374,1 μg mg^{-1}) nevertheless they did not contribute significantly to gametogenesis, since this parameter was inversely correlated with total lipids of veliger D-larvae. The positive correlation found between veligers D-larvae total lipids and condition index may indicate that CI is an important criteria in the evaluation of the broodstock quality.

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Validation of the Commercial Cultured Black Scar Oyster Species Name, *Crassostrea bilineata* Rather Than *Crassostrea lugubris* and *Crassostrea iredalei* in Indo-Pacific Region

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Black scar oyster is different from white scar oyster, *Crassostrea belcheri* in having black scar or purple adductor muscle scar, kidney shape, oblong shape, flat right valves, and rather foliaceous shells. The species name, *C. iredalei* was recently used for commercial cultured oysters in Thailand and SE Asia, instead of the previously used synonym *C. lugubris*. The junior synonym to this species is *O. lugubris*

The specific name *Ostrea lugubris* was given a fossil species from Cretaceous and Tertiary periods from East and Red river, Canadian, New Mexico, Santa Fe' road. The species named *Ostrea lugubris* was recorded from North America. The specific name *Lopha lugubris* was used as fossil recorded in the middle and upper Turonian period from Southern Corolado, New Mexico and Texas. *O. lugubris* and *L. lugubris* are fossils recorded from United States and should not be valid for living species in tropical SE Asia and Indo-Pacific. This fossil species must be different taxon than *C. iredalei.*

The valid name of *Crasosstrea iredalei* becomes *Crassostrea bilineata*. The reasons: The oyster that was illustrated as *Ostrea parasitica indiae orientalis* was named as *Ostrea edulis* var. δ This oyster was named as *bilineata* by Roding. But Dillwyn named this oyster as *orientalis*, and Kuster, figure was a copy of Chemnitz. Hanley and Hidago were obeyed Dillwyn's name *orientalis*. Lamarck named *cristata* var. [b]. Sowerby did not show the figure because of no specimens to correspondence to *orientalis*. Anyhow there were all based on the Chemnitz's very rough figure and descriptions. Lamy stated that *bilineata* should be applied to this oyster, because according to the International code of Zoological Nomenclature, Roding's *bilineata* becomes valid name.

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Successful Survival of the Metamorphosis of *Pecten maximus* Cultured in Through Flow

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In majority of marine mollusc species, hatching results in an intermediate stage, usually called a larva, growing until a stage referred to as "competence". Competence could be defined as the capacity of a developing individual to initiate settlement and complete morphogenetic transformations associated with metamorphosis. In many cases, settlement and metamorphosis requires reception of environmental cues, like chemical, physical and biological inducers to facilitate habitat selection. In larval culture and artificial conditions of hatchery, generally lesser than 50 % of competent larvae is normally settled and metamorphosed in viable post-larvae. In this experiment, we have been interested to increase settlement and metamorphosis success of scallop, *Pecten maximum*, by the modification of hydrodynamic conditions. Competent larvae were collected on 150 µm mesh and allowed to settle on mesh screens in circular sieves in a down-welling flow-through system continuously supplied with seawater and algae. Larval quality has been estimated by lipids characteristics of larvae (lipid class and fatty acids profiles). Sleeves with 60 larvae cm-2 have been submitted to different flow rate conditions and hydrodynamic conditions estimated by screening with an ADV microvelocimeter. Results showed significant increase of settlement and metamorphosis with increase of flow rate until 2.4 ml min-1.

Effects of L-DOPA and Epinephrine on Larvae Settlement of Tropical Oyster, *Crassostrea iredalei* (Faustino, 1932)

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Neuroactive compound with different level of concentrations and exposure time was one of the factors to induce the settlement of bivalve larvae. Larval settlements of the tropical oyster *Crassostrea iredalei* were investigated by exposing the eyed-spot larvae to L-3, 4-dihydroxyphenylalanine (L-DOPA) and epinephrine (EPI) at five different concentrations (10^{-3}, 10^{-4}, 10^{-5}, 10^{-6} and 10^{-7}M). The optimum yield of cemented spat was induced by using 10^{-6}M EPI for both exposure time (1 and 24 hours), which is approximately 60%. Larvae exposed to all concentrations of L-DOPA yielded lower percentage of cemented spat (<50%). In this study, EPI had effectively induced the cemented spat compared to L-DOPA. The results showed significant differences between the control and the treatment groups which would provide useful information ad technique of seed production in hatchery.

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Detachment of Scallop *Pecten maximus* Post-larvae from Different Diet Treatments in Relation to Flow Velocity in Benthic Biological Flumes

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Several studies investigated the effects of flow velocity on the attachment strength of Mytilidae, but at our knowledge this information is limited for Pectinidae. Thus, this experiment was carried out in a benthic biological flume (HYCOBENTHOS) to determine the effect of u_* (shear velocity) and the attachment period on the percentage of detachment of *Pecten maximus* post-larvae of different sizes reared and supplied with two experimental diet. PTC (*Pavlova lutheri* (P), *Isochrysis galbana* (T), *Chaetoceros calcitrans* (C)) served as a reference diet, commonly used in bivalve hatcheries and nurseries, and the second PTCR was the standard diet (PTC) with an addition of *Rhodomonas salina* (R) microalgae. Our results indicated that the detachment of post-larvae fed with PTCR showed significant interaction between length, attachment period and u_*. For PTC fed post-larvae, the u_* factor has a significant effect on the percentage of detachment of post-larvae without any interaction with other factors. For both diets, post-larvae previously attached during 12 h had lower levels of detachment comparatively to those attached during 30 min. The exposure of juveniles in currents of various flume velocities showed a higher percentage of detachment for post-larvae reared with PTCR diet. This result could be related with differences in biochemical composition of the diets and have been discussed.

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Morphological Changes During Transformation of the Glochidia Larva of Freshwater Pearl Mussel, *Hyriopsis (Hyriopsis) bialatus* Cultured in Artificial Media

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The morphological development and the sequences of organogenesis from glochidium to the early juvenile stage of the freshwater pearl mussel, *Hyriopsis bialatus,* were observed. Mature glochidia of *H. bialatus* were cultured in an artificial medium consisting of M199, fish plasma (*Cyprinus carpio*), and antibiotics/antimycotic at a ratio of 2:1:0.5 (v/v). Larval samples were collected every two days during glochidia development and were subjected to histological processing. Three types of cell masses developed during this period: the ventral plate (the foot rudiment), lateral pits (the gill rudiment), and the oral plate or endodermic sac (the origin of the digestive tract). The ventral plate gave rise to two foot lobes which fused into one lobe. The gills were developed from the lateral pits next to the ventral plate, forming a pair of gill buds that became elongated and turned into gill bars. The digestive tract began with mouth formation by invagination of the oral plate (or endodermic sac) and formation of a tube underneath the growing foot. Several controversial aspects of organogenesis have been inferred, e.g. *de novo* formation of the anterior and posterior juvenile adductor, the fate of the mushroom body structure, and foot lobe formation from two separate precursor lobes. A mushroom body protruded into the mantle cavity and remained there throughout the transformation period.

POSTER PRESENTATION

Comparison of Various Factors Influencing Juvenile Survivability of Freshwater Pearl Mussel, *Margaritifera laevis* in Two Rivers in Japan

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One group of freshwater bivalve, Margaritiferidae, is a family that is particularly endangered and is devised for conservation measure in many countries. Life history of Unionoida including Margaritiferidae is very unique and their larvae known as glochidia are parasitic to fish. Thus host fishes and Margaritiferid mussels are deeply related. The major objective of the present study was to clarify the mechanism and causes of extinction of *Margaritifera laevis*.

The lack of juveniles has been often investigated in many mussel populations in Japan and it indicates decrease of the mussels. For clarifying the mechanism and causes of the lack of juveniles, I compared two contrasting populations, i.e. the population in the Chitose River, consists of adult and juvenile mussels, and the population in Abira River, consists of only adult mussels over 16 years. These mussels in both rivers utilized masu salmon (*Oncorhynchus masou masou*) as host fish. Although the population in the Abira River had sufficient reproductive potential, survival rate in the early life stage was very lower. Low survival rate was caused by some problems, i.e. no overlap of distribution between mussels and host fish in almost research stations leading to reduce the chance of parasitism to host, lower temperature which extended the duration of parasitic stage exposing attached glochidia to immune attack by host fish, and inappropriate water quality bringing on higher mortality of small mussels. Consequently, many adverse effects, which were closely related to host fish, led to the lack of juveniles. To avoid the reduction in population size of *M. laevis*, we must restore appreciate habitats for mussels in the early life stage as soon as possible.

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Exploring the Unexplored: the High-mountain Endemic Pea-clam (Bivalvia: Sphaeriidae: *Pisidium* spp.) Fauna of East Africa

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The East African freshwater fauna of mountain ranges is assumed to be species rich, yet largely unexplored. Recent studies highlighted the vulnerability of freshwater habitats in these mountain ranges to global climate change. The study of molluscs might potentially allow for valuable insights into the interplay of environmental variation and evolutionary change.

Pea-clams (Sphaeriidae, genus *Pisidium*) are worldwide distributed freshwater bivalves with high passive dispersal capacities, which might contribute to their often extremely large distribution ranges (though a number of endemic species have also been described). In Africa, a total of approximately 20 species occur with 6 of them having a wide distribution. Approximately half a dozen palae- or holarctic species are restricted to Northern Africa. Two lake endemics (Tanganyika and Victoria) are known. Another 6 or more species are endemic to rivers and streams, of which at least 4 are restricted to mountain ranges, namely the Ruwenzories, Mt. Kenya, Kilimandjaro or Mt Elgon. Most species had been described decades ago and no recent study has ever attempted to relocate these species. Additionally, no phylogenetic information exists for African species.

Extensive recent field surveys in East Africa have revealed (primarily topotypic) material from high mountain ranges. This new material was supplemented with material from other African sites and collectively analysed with world-wide data from previous studies. The analyses of both shell morphological variation and mitochondrial LSU rDNA sequences suggest the existence of more species than previously assumed, particularly in the Aberdares Range and Mt. Kenya region in Kenya. Phylogenetic data are discussed in the context of past and expected future environmental changes in tropical Africa.

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The New Stage of Invasion - the Quagga Mussel *Dreissena rostriformis bugensis* (Andrusov, 1897) Conquers Central Europe

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Originally distributed in a restricted area in the Dniepr-Bug Liman (Black Sea), the invasive quagga mussel *Dreissena rostriformis bugensis* (Andrusov, 1897) has conquered large areas in North America and Eastern Europe within a few decades. Following the invasion of its congener, the zebra mussel *Dreissena polymorpha* (Pallas, 1771), the quagga mussel often replaces the former species within a few years. In Western Europe, the quagga mussel was first recorded in the Dutch Rhine Delta (2006) and in the rivers Main and Rhine in Germany (2007). Until now, no attempt has been made to follow the invasion systematically along the main waterways of central/western Europe. Two of the main inland invasion corridors for Ponto-Caspian species to central/western Europe converge at the River Rhine: 1) the southern corridor (Danube → Main-Danube Canal (MDC)→ Rhine), and 2) the central corridor (Dniepr → Vistula → Oder → Elbe → Mittellandkanal (MLC) → Dortmund-Ems Canal (DEC) → Rhine).

Given the rapid spreading throughout central/western Europe, questions of concern are whether the distribution of the quagga mussel is still scattered or already continuous and which invasion corridors are utilized.

Between 2007 and 2009, a series of field trips was conducted, covering the southern corridor and German parts of the central corridor. Whereas the quagga mussel was found to be absent in the central corridor except for the westernmost parts (where it occurred in mainly low abundances), it could be recorded throughout the southern corridor, often in high abundances (up to 100%). These preliminary results suggest a first colonization through the southern corridor. The direction of invasion, however, remains unclear. Therefore future studies should utilize genetic analyses in order to test for the direction of invasion and for the possibility of multiple introductions.

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The Investigation of Element Levels in *Unio* sp. Inhabiting Porsuk Dam Lake, Turkey

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This study which was carried out between summer and winter 2009 aimed to determined macro and micro element levels in water and sediment of Porsuk Dam Lake (Eskişehir/Turkey) and mussel (*Unio* sp.) inhabiting Porsuk Dam Lake. The water, sediment and different parts of mussel samples were analyzed for element (cadmium, chromium, copper, mercury, nickel, lead, antimony, zinc, silver, aluminum, boron, barium, iron, manganese, potassium, sulfur, magnesium, calcium, sodium, phosphor selenium, silicon) contents. The analyses of elements were performed with inductively coupled plasma-optic emission spectroscopy (ICP-OES) by using microwave digestion techniques. The mean concentration of elements in water compared with water quality criteria. The results showed that Cd, Cr, Cu, Pb, Zn, Ag, Al, B, Fe, Mn, S, Na and P concentrations were found to be higher water quality criteria. Also, element levels in sediment compared with sediment quality criteria. According to the results, Pb, Zn and Mn levels in sediment were found higher than the criteria. The results for mussel obtain from Porsuk Dam Lake; indicate that the element namely calcium (%18.46) is very dense in mussel shell. All of the other elements in the soft tissue of the mussels were found to be higher than the shells. Particularly, Cd, Cr, Ni, Pb and Ag concentration of toxic elements were determined 8.266, 1.233, 3.466, 12.533 and 1.566 mg kg^{-1} dry weight, respectively. Hg was not detected in water, sediment and mussel samples. Amount orders of elements in interior of mussels were determined Na>Fe>Mn>Zn>Cu>B (micro nutrient); S>Ca>P>K>Mg (macro nutrient).

The West-Carpathian Tufa Fens–A 15-Thousand-Year-Old History

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Calcareous fens provide suitable sediments with good conditions for macrofossil and pollen preservation. However, only a few palaoecological studies have dealt with these sediments. We analyzed sediments of 47 well-preserved calcareous fens to study their age and development using a radiocarbon dating and analyses of pollen, plant macrofossils and molluscs. The age of studied sites varied from 13,810 yrs BP (ca 14,930 calibrated) to 250 uncal. yrs BP. We found regionally clustered distribution of sites with the Late-Glacial and Early-Holocene age. Six sites in the Inner Western Carpathians were dated back to the Late-Glacial and Early-Holocene (13,810-9,200 uncal. yrs BP). In contrast, site situated in the Outer part of the region were younger than 3600 uncal. yrs BP, except two sites (5745 and 7950 uncal. yrs BP). These differences in historical development fit well to the distributional pattern of species with presumably relictual distribution in the study region (e.g. snail *Vertigo geyeri* and *Pupilla alpicola*, and plants *Triglochin maritimum* and *Primula farinosa*). All these species inhabit open sites, which perfectly matches with the obtained results based on fossil material from bottom layers. All those six old sites in the Inner part stared as open fens or semi-open fen woodlands and have supported the occurrence of heliophilous species. In contrast, all older sites in the Outer part started as woody fens and were deforested by humans during recent centuries (mostly only 700 years ago). Originally open fens in this area developed due to human impact to the landscape, such as tree cutting and burning, which has increased erosion and decreased forest cover. Due to geomorphologic characteristics of flysh bedrock, many new open spring fens arose in the Outer Western Carpathians after this deforestation.

Glochidia Tooth Morphology of the Freshwater Mussel *Westralunio carteri* (Iredale, 1934) of South-West, Western Australia

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Freshwater mussels (Unionoida) are a very old group of bivalve molluscs found in rivers, lakes and other wetlands on all continents but Antarctica, which includes 854 species in two superfamilies (Unionoidea and Etherioidea) that are distinguished by larval forms. Larvae of Unionoids (Hyriidae, Margaritiferidae and Unionidae) are glochidia, distinct from the lasidia or haustoria of etherioids (Etheriidae, Iridinidae, Mycetopodidae). Unionoids are dioecious and reproduce sexually. Males release sperm into the water, which are then drawn into gills (ctenidia), of the females, where the eggs are fertilized within modified brood chambers (marsupia). The embryos then develop to become mature glochidia, and are brooded in the marsupia. They then attach to a suitable host, generally a fish, on the gills or body surface (often the fins or mouth) where they are encapsulated by epithelial tissue and, as obligate parasites, begin a metamorphosis and emerge as juvenile mussels. The host-glochidia relationship is an obligatory stage in the life cycle of mussels, and also provides a means of dispersal. Glochidial attachment is facilitated by specialized structures on the ventral margin of shells, known as larval teeth, which vary in morphology, but are generally hooked. In Australia, freshwater mussels are represented by 18 species (eight genera) of Hyriidae. Glochidia tooth morphology of Australian Hyriidae has been described for several species and implicated as a useful taxonomic tool to distinguish species. In this poster, we present the first images (Scanning Electron Microscopy) of *Westralunio carteri* Iredale, 1934 larval teeth, which appear to be unique and may have taxonomic value.

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The Chinese Giant Mussel *Anodonta woodiana* in a Natural Water Body in Northern Poland

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The Chinese giant mussel A*nodonta woodiana* has been introduced in Europe in the 1960's with fish imported from China. The species requires relatively high temperatures, and in Poland occurs almost exclusively in heated waters, such as lakes and canals receiving heated water from power stations. In October 2009 we found the Chinese giant mussel in Northern Poland, in an area directly adjacent to the Slowinski National Park. It is one of the most northerly sites of this species recorded in Europe to date. The water body inhabited by the mussel is an abandoned and spontaneously naturalized fish pond, with a natural thermal regime. The mussel has been introduced most probably with stocked fish. Locally the population reaches high densities. The shells of many individuals show 10 or more annual rings. The mean shell length is 182 mm (n=20), max = 260 mm. The sample we measured was biased towards large individuals, but their abundance indicates that it is a stable population inhabiting the pond since many years. The questions to be answered are: Are there any more populations of this species in natural water bodies in the region? Is the population we found exceptional in its physiology and thermal tolerance? Does the pond have a special and favorable thermal regime? Or maybe there is nothing special about the pond nor mussel population, and we are witnessing the beginning of colonization of natural water bodies by the Chinese giant mussel in Northern Europe?

First Data on Glochidial Shell Morphology of *Amuranodonta kijaensis* (Anodontinae) and *Nodularia schrencki* (Nodulariinae) from the Amur River Basin, Russian Far East

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Larval shells (glochidia) of any *Amuranodonta* Moskvicheva, 1973 species were not investigated before our study. Endangered anodontine bivalves *Amuranodonta kijaensis* Moskvicheva, 1973 is included in 2 regional Red Books (for Khabarovsky Territory and Amurskya Province) so any data on biology and reproduction of this species is very important. As to Amur's naiad mussels from the genus *Nodularia* Conrad, 1853 only glochidia of *N. amurensis* (Mousson, 1887) were studied before our research.

Mature glochidia of *Amuranodonta kijaensis* were collected in 2006-2007 (the middle of May, the end of September) around Khingansky Natural Reserve from 2 lakes of the Middle Amur R. basin. Mussels with mature larva of *Nodularia schrencki* (Westerlund, 1897) were collected in 2006-2008 (the end of May, the end of July) from 3 points of the Middle Amur. Preserved in 75% ethanol glochidia are cleaned by removal of its soft parts in 5% KOH. Cleaned glochidia were investigated by light and scanning electron microscopy.

Investigated glochidia subtriangular, elongated longitudinally (length is always more than height), with large styliform hooks. Larval thread presents in both investigated species. Glochidium of *A. kijaensis* slightly asymmetric, valve length 333.4 to 380.0 µm, height 333.1 to 365.0 µm, ligament 240.0 to 290.0 µm. Hook (137.8–140.0 µm) is 27–41% of the valve height, covered by at least 16 microstylets. Pores of the inner valve surface are 1.56–3.4 µm in diameter. Glochidium of *N. schrencki* also slightly asymmetric, valve length 155.0 to 165.0 µm, height 137.5 to 162.5 µm, ligament 125.0 to 137.5 µm. Hook (40 to 47.5 µm) is 28–33% of the valve height, covered by about 45 microstylets. Larval thread is 1.6 µm in diameter. [Work was supported by the Russian Foundation for Basic Research (grant No. 09-04-98583 "Mollusks of the Amur")].

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Comparative Mitogenomics of Dreissenidae and Unionidae

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The gene content of metazoan mitochondrial genomes is relatively stable. They usually contain 13 genes encoding components of the respiratory chain and the set of RNA genes needed for their translation: two rRNAs and 22 tRNAs. The exceptions comprising missing or duplicated genes are rare. Despite this stability the detailed organisation of mitogenome is very variable: there are big differences in mitochondrial gene orders among animals. Notoriously, bivalves are considered to be particularly polymorphic with regard to mtDNA organisation, often being contrasted with other, less polymorphic groups like vertebrates. However, while there are hundreds of complete mtDNA vertebrate sequences available, the much older bivalves are an order of magnitude less represented. Further complication comes from the peculiar mtDNA inheritance operating in some bivalves. Strictly uniparental (maternal) inheritance of mitochondrial DNA (mtDNA) is a rule in animal kingdom. However, in some species of marine (Mytilidae, Veneridae, Donacidae, Solenidae) and freshwater (Unionidae, Margaritiferidae, Hyriidae) bivalves different mode of mtDNA inheritance has been discovered. It is called doubly uniparental inheritance (DUI). Under DUI there exist two mitochondrial lineages: females pass their (F) mtDNA to all their offspring whereas males pass different (M) mtDNA to their sons only. All males are heteroplasmic, although the M genome is restricted to their gonads; somatic tissues are dominated by the F genome. In Unionidae the divergence between the M and F genomes is extreme and approaches 50%. Here we present, for the first time, the mitochondrial genomes of zebra mussel (*Dreissena polymorpha*) and two Unionidean species: *Unio crassus* and *Anodonta/Sinanodonta woodiana*. Both M and F mitogenomes of the unionids present the typical organisation known from American Ambleminae, while the gene order found in zebra mussel in novel and unique. Possible evolutionary scenarios leading to these gene orders are discussed.

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Subfossil Molluscs from Crab Fossil Site, Quaternary Peat Deposit in Chantaburi Province, Southeastern Thailand

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The crab fossil site at Chantaburi Province is based on Quaternary peat-clay deposit at Na Yai Arm District, Chantaburi Province, southeastern Thailand. The site consists mainly of sentinel crab *Macrophthalmus latreillei* yielded at 4 m layer depth at 10 m MSL elevation, 6 km far from sea coast and aging ca. 5000 years BP. This site also deposit several molluscan subfossil, at least 20 species from 13 family yielded. Seven gastropod families with 7 species found: Naticidae, *Natica* sp.; Strombidae, *Strombus canarium*; Cypraeidae, *Cypraea arabica;* Turritellidae, *Teritella terebra;* Cerithiidae, *Clypeomorus coralium*; Melongenidae, *Pugilina* sp. and Conidae, *Conus betulinus*. Six families of bivalves occurred, including Ostreidae, *Crassostrea* cf. *gigas, C. belcheri, C. falskali*; Arcidae, *Anadara granosa, A. transversa*, *A. nodifera;* Veneridae, *Mercenaria* sp. *Paphia undulate, Placamen isabellinum, Meretrix* sp.; Tellinidae, *Tellina* sp.; Corbiclidae, *Polymesoda* sp. and Pholadidae, *Barnea dilatata*. Bloody cockle *Anadara granosa* of family Arcidae is the most common subfossil occurred and cerithid snail is common a species of the gastropod fossil. Most of the fossil specimens are deposit at the local exhibition museum on the site.

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Up or Down? Limpet Orientation on Steeply Sloped Surfaces

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Variation in the distribution of animals across the landscape can occur at a variety of scales within and between habitats. At a smaller scale animals can either be positioned randomly or can be orientated in regards to variables. Differences in orientation can, for many animals, directly affect their reproductive success and may have implications for survivorship, and these effects may have down-stream ecological consequences. Organisms may orientate themselves in a specific way in response to environmental conditions and habitat properties, or instead they consistently orientate in a specific direction. The aim of this project was to investigate patterns of orientation during low tide in the intertidal, marine limpet *Cellana tramoserica* on steeply sloped, rocky surfaces (> 60° to the vertical). We also examined whether individual limpets consistently orientate in the same direction or if orientation is dependent upon their orientation the previous low tide. Limpet orientation was measured at intertidal sites in Cape Banks Scientific Reserve, Sydney. There was found to be a downward bias in orientation. Both mensurative and manipulative experiments measuring limpet orientation over different days found that individual limpets do not consistently orientate in the same direction and that their orientation is independent of their orientation the previous low tide. A second part of the study investigated the model that a downwards orientation leads to a reduction in desiccation stress. These findings have implications for understanding how limpets are distributed and with downstream consequences.

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Phylogeography and Geometric Morphometrics in Different Species of *Nacella* from the Magellan Strait, Southern South America

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The origin and diversification of *Nacella* is closely related to major oceanographic and climatic changes during the middle Miocene in the Southern Ocean. Divergence time estimation indicate a recent diversification of the genus in Southern South America. For this Region there have been described at least seven species based on morphology. At least four of them (*N. magellanica*, *N. deaurata*, *N. flammea* and *N. mytilina*) seems to represent real taxonomic units while *N. chiloensis*, *N. venosa*, *N. delicatissima* and *N. fuegiensis* could constitute only ecotypes or subspecies.

We examined phylogeographic patterns and demographic histories in seven morphospecies of *Nacella* using 671 bp of the mtDNA gene Cytochrome Oxidase Subunit 1 (COI). We include in the analyses at least 25 individuals of each species extracted from two localities (Punta Santa Ana, Magellan Strait and Puerto Montt) and we estimated genetic diversity indices and the degree of differentiation among them. We also performed Geometric Morphometric analyses of the shells.

Elliptic Fourier analyses detected significant differences among *Nacella* species with the exception of the comparisons between *N. deaurata-N.fuegiensis*, *N. chiloensis-N. venosa*, *N. chiloensis-N. magellanica*, and *N. venosa-N. magellanica*. Genetic analyses detected high levels of global similarities among the analyzed species while genetic diversity indices showed interspecific variations. N_{ST} and G_{ST} comparisions detected significant differences with the exception of *N. deaurata-N. fuegiensis N. chiloensis-N. venosa*, *N. chiloensis-N. magellanica*, and *N. venosa-N. magellanica* comparisons. Morphological and genetic results indicate that *N. fuegiensis, N. chiloensis* and *N. venosa* should be considered as synonims of *N. deaurata* and *N. magellanica*.

The median joining network resulted in a star-like shape with very short genealogy. The L-shaped pairwise distributions and the significant negative values of the Tajima and Fu indices suggest that *Nacella* experienced a very recent demographic expansion in the Magellan Province. [Thesis projects INACH B_01_07 and CONICYT 24090009 (C.G), projects INACH 02-02 y 13-05 (E.P), IDEAWILD. Ecology and Biodiversity Institute (IEB) ICM-P05-002 y PFB-023-CONICYT].

Diversity, Morphology and Geographic Distribution of Neotropical "Ancylidae" in the State of Rio de Janeiro, Brazil

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The Neotropical freshwater pateliform snails are commonly assigned to the family Ancylidae *sensu latum*, encompassing seven genera with at least 13 valid species and seven with doubtful identification. In order to contribute to systematic and biogeographical studies on these snails in the Rio de Janeiro state, a survey based on literature, scientific collections and field works was done. The species were identified by shell and soft parts morphology and the occurrences were plotted on a georeferenced map. As results we show that at least six species occur in the six different Mesorregions of the Rio de Janeiro state: *Burnupia* sp., *Ferrissia* sp., *Gundlachia ticaga* (Marcus and Marcus, 1962), *Gundlachia* sp., *Hebetancylus moricandi* (d`Orbigny, 1837) and *Uncancylus concentricus* (d`Orbigny, 1837). *Burnupia* sp. differs from *B. ingae* (Lanzer, 1990), described to South Brazil, in teleoconch and protoconch morphology and pattern of muscle scars. It was found only in three Mesorregions. *Ferrissia* sp. is widespread in Rio de Janeiro, differing from *F. gentilis* described to South Brazil. *Gundlachia ticaga* is the most widespread and abundant species in all studied Mesorregions. It shows great shell morphological variation and mantle pigmentation, perhaps as responses to the wide range of microhabitats it inhabit. *Gundlachia* sp. differs from *G. ticaga* on shell morphology, apical microsculpture and muscles scars. It was found at almost all Mesorregions, except North. *Hebetancylus moricandi* and *Uncancylus concentricus* have a restricted distribution. The first one occurs only at Mesorregion North and probably was introduced by fish farming as it was registered only to this kind of habitat, until now. The second one was cited only to small ponds on a continental island southeastern Rio de Janeiro. It could be introduced by avian transport as this occurrence is apart from the range area of the species.

Linking Genetic and Morphometric Variation: Shell Shape Analysis of Limpets of the *Cellana strigilis* Subspecies in the New Zealand Subantarctic Islands

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Before the era of modern genetics, most taxonomy was based on phenotypic variability, such that species were described according to their morphological or anatomical attributes. However, it has long been recognised that morphological and anatomical traits are non-neutral markers that may lead to incorrect estimation of biodiversity. With the advent and application of DNA sequencing and barcoding to questions of taxonomy, many species have been found to be cryptic, and many others previously classified as different have been reclassified as one.

Gastropods are known for their morphological plasticity and species classification often has to be updated. This work focuses on the *Cellana strigilis* limpet complex endemic to the New Zealand subantarctic islands. Classified into six subspecies based on morphological characters, two recent genetic studies have revealed that the complex is in fact made of two lineages, with strong genetic differentiation between them. Our aim is to compare this newly described genetic relationship with the shell characteristics of each nominal *Cellana strigilis* subspecies. For this, we use a morphological assessment of the length, width, height, dry mass and thickness of the shells and an Elliptical Fourier Analysis of digitised outlines of the shells. Our results suggest a significant difference in shell shape between the two lineages and also among different islands within each lineage.

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Phylogenetic Affinities and Biogeographic Origins of Three Endemic Limpets from the Kermadec Islands (New Zealand, SW Pacific)

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The Kermadec Islands are an isolated chain of volcanic islands in the southwest Pacific Ocean (SWP), approximately 1000 km northeast of New Zealand. As one of the few subtropical island groups of the SWP, they are of considerable biogeographic interest and conservation importance. A large proportion of the coastal marine molluscan fauna is endemic, and it is likely that dispersal of shallow-water marine organisms to the Kermadecs from other locations is rare due to their isolated position, a minimum of 750 km distant from other landmasses. The present-day endemic species may have arisen through colonization by immigrants followed by allopatric speciation, or alternatively as surviving relicts of previously more widespread species. Oceanic circulation patterns in the SWP suggest several possible sources of immigrants to the Kermadec Islands, including eastward flowing subtropical watermasses, warm temperate watermasses from northeastern New Zealand, and south to southwest-flowing tropical water. This study investigates the phylogenetic affinities and possible origins of three limpet species endemic to the Kermadec Islands. The giant Kermadec limpet *Scutellastra kermadecensis* has a fossil record dating to the early Pleistocene and may be a relict of a more widespread species that also occurred around New Zealand during the Oligocene. The patellid *Cellana craticulata* and the pulmonate *Siphonaria raoulensis* are thought to be more recent immigrants but their origins are unknown; both genera have other species found in New Zealand and the subtropical and tropical SWP. Mitochondrial DNA sequence data and phylogenetic analyses are used to investigate the relationships of these Kermadec-endemic limpets to their congeners elsewhere. Possible origins of the Kermadec species are evaluated in light of the phylogenetic relationships and estimated times of divergence from their closest relatives.

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Doubly Uniparental Inheritance of Mitochondrial DNA in *Neotrigonia margaritacea* (Bivalvia: Palaeoheterodonta)

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Several families of bivalves have been reported to contain two mitochondrial DNA types, phenomenon known as Doubly Uniparental Inheritance (DUI). Here we identify the presence of DUI in *Neotrigonia margaritacea*, using mitochondrial DNA from Cytochrome *C* Oxidase I and 16S ribosomal DNA genes. Male and female mitotypes, were identified in a single male specimen. Low divergences between the male and female mitotypes indicated either a recent acquisition of DUI in *Neotrigonia*, or a recent masculinization event. We analysed the data in a phylogenetic framework for Palaeoheterodonta. The *Neotrigonia* female COI mitotype forms the sister group to female COI unionid mitotypes, suggesting that no masculinization events have occurred in unionids since their divergence from *Neotrigonia*. The placement of the *Neotrigonia* clade as sister to female unionid mitotypes, and the low sequence divergence with *Neotrigonia,* suggests a recent masculinization event in *Neotrigonia*. On the other hand, analysis of 16S showed male and female mitotypes of *Neotrigonia* forming reciprocally monophyletic clades. That clade was then sister to a clade of reciprocally monophyletic male and female unionid mitotypes, suggesting an origin of DUI that preceded the divergence of Paleoheterodonta. When this new information was mapped onto a phylogeny of all bivalves, parsimony transformations indicate that DUI is the ancestral state for all Bivalvia.

DNA Barcoding – Evaluation of a 16S rDNA-Marker for Pectinidae

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Pectinidae, with more than 300 species worldwide, are a morphologically diverse group of bivalves. Still a lot of species cannot satisfactorily be distinguished by mere morphological characters, as for example within the species complexes of *Pseudamussium* and *Flexopecten*. In European waters 26 described pectinid species occur although many of them are morphologically ambiguous and therefore need taxonomic revision.

The DNA barcoding is a method to gather and compare DNA sequences, DNA Barcodes, of species for species identification. Therefore a universal sequence for a species group, the barcode, is chosen, for animals generally cytochrome oxidase subunit I (COI). The mitochondrial genome holds the best features for species identification via sequence analyses, however the COI sequence of many bivalves is difficult to obtain. Thus, we decided to establish another mitochondrial gene, namely the 16S rRNA gene as a DNA Barcode.

With the DNA barcoding approach we tested the possibility to distinguish even morphologically similar pectinid species by a partial sequence of the 16S rRNA gene, with a length of approximately 550 bp. We also investigated the effect of increased taxon sampling on the grouping of specimens of different populations in clusters of the same species. Therefore we sampled 14 species from 10 different localities in the Mediterranean Sea and Northeastern Atlantic as well as one species from the Northwestern Pacific, off Japan. We isolated DNA from the adductor muscle of each specimen, amplified the partial 16S rRNA gene and compared the sequences via neighbor joining to infer the genetic distances between the species.

Comparative Morphology of Labial Palps within the Protobranchia

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The labial palps of Bivalvia are generally prominent structures beside the mouth and are assumed to have three major functions, as sensory organs, as some kind of mouthparts interacting with the environment (especially the palp appendages of protobranchs) and in sorting of food particles provided by the gills and the palp appendages. In association with gills the labial palps have provided one of the major morphological character systems for classification and morphological phylogenetic analyses of the Bivalvia. Here we present a comparative study on the labial palps of the Protobranchia using anatomical and electron microscope techniques. We will discuss old and new characters with a focus on the similarities and differences between the Nuculoidea, Nuculanoida and Solemyoida. [Supported by NSF AToL DEB-0732854].

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Functional Morphology of Mytilidae (Bivalvia) Byssus in Relation to Their Habitation

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The bivalve mollusks *Mytilus trossulus* Gould, 1850, *Mytilus coruscus* Gould, 1961, *Crenomytilus grayanus* (Dunker, 1853) and *Modiolus modiolus* (Linnaeus, 1758) are biofouling mytilid species that attach to a substrate by means of their byssi to avoid dislodgement by hydrodynamic forces. Differences in the structure of byssus underlie the variety of morpho-physiological adaptations of the species to the life in different biotopes. The morphology of byssus and of foot glands, as well as the ability of the mollusks to attach repeatedly to various substrates (glass, boulders, sand, concrete, wood, and iron) at various water temperatures (20, 10, 0°C) was studied. Interspecific differences in the structure of groove surface and of foot glands were established. In accordance with byssus mechanical properties, the byssal threads of the mollusks vary in the length, thickness and the size of the adhesive discs. All the species have a common strategy of attachment to a substrate, however the rate of the production and the amount of threads are species-specific. The water temperature decrease from 20 to 0°C slowed down the byssal thread production rate. The mussels exhibited selectivity to anthropogenic, soft and hard substrates. *M. trossulus* attached to all the substrate types on the first day of observations. *M. coruscus* and *C. grayanus,* unlike *M. modiolus,* successfully attached to hard substrates. *M. modiolus* and *C. grayanus* have adapted to colonize closed coastal areas protected from waves, whereas *M. coruscus* and *M. trossulus* have confirmed to inhabit areas with active hydrodynamical conditions. The mytilid species provide the excellent example of morphological byssus changes reflecting ultimate stage of the evolution of this group of mollusks. The information concerning byssus morphology, thread formation and detachment may lead to developing certain technique to control biofouling mussels. [The study was supported by the grants FEB RAS (10-III-B-06-114, 09-III-A-06-210) and RFBR (10-04-00427-a, 10-04-10134-к)].

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Fiji's Introduced Land Snails: Agricultural and Human Health Risks

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Fiji's land snail fauna is rich and diverse with over 242 species present of which 70% are endemic to the archipelago. However, at least 18 of these 242 species are introduced aliens with some level of associated agricultural or human health "risk". Preliminary estimates of the relative risks have recently been made and basic information to allow easier identification of the species involved is being collated. We are hopeful that the availability of this information, in local languages, will increase detection of problematic species and strengthened management of invasive snail species particularly lowering the chances of associated biodiversity loss, related human health incidents and the unintentional spread of high-risk alien snails to non-infected islands. Fiji is fortunate to currently be free of well documented high-risk land snails such as the giant African snail *Lissachatina* [*Achatina*] *fulica* Bowdich, 1822 and the rosy wolf snail *Euglandina rosea* (Férussac, 1821) that have successfully invaded neighboring island countries and territories. Our project is designed to provide direct introduced land snail and slug identification assistance to local government units, such as agriculture, quarantine, forestry and environment as well as other local stakeholders, and in turn provide a solid platform on which to build a stronger understanding of how introduced land snail and slug species may be impacting on trade, agricultural production and human and livestock health in the Fiji Islands.

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Ecobiodiversity of Terrestrial Pulmonates from Satpuda Mountains with Special Reference to Their Use as Medicine among Tribal Peoples

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Biodiversity spectrum of terrestrial pulmonates has been studied from rural area of Satpuda Mountains . The present work has been carried out during the period of January 2004 to November 2005 from the tribal village area in and around Satpuda Mountains. The distribution and evaluation of terrestrial pulmonates was evaluated by field survey of Taloda and Dhadgaon tahesil of Nandurbar district, India. Collection of seventeen terrestrial snails was carried out from thirteen different locations. These seventeen pulmonates represent six families from two orders of class gastropoda. Three species represents from veronicellidae, four species from succineidae, two from Enidae and one from Subulinidae. Ariophantidae represents six species while glessulidae represents only one species.

Terrestrial snails and slugs in satpuda mountain area have been used by tribal peoples for various purposes. *Ariophanta* species are used as food for hen and ducks. Snails are also used as bait for fish catch. The medicinal use of some pulmonates in various types of preparations are valuable as a cure of many types of pains, injuries, gastric abnormalities, swellings, burn and also as a tonic for children. Some preparations were made with salt and local medicinal plants. These preparations are also used in pregnancy. Cattles and domestic animals are also treated with these preparations.

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The Land Snail Community of Vila Dois Rios, Ilha Grande, Angra dos Reis, Rio de Janeiro, Brazil Reflects the Environment Conservation

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The aim of this study was to compare the community composition of land snails in three different sites in Vila Dois Rios (VDR), to build indexes based on the proportion of synanthropic species of molluscs occurring in each site, useful as a tool to indicate environmental change. The sampling sites were: 1) urban area (UA) where human influence is pronounced and continued to nowadays; 2) VDR's mountain slope at 350m asl (VDR 350), where human influence ceased in 1975; 3) VDR's mountain slope at 450m asl (VDR 450), where there were no marked human influence. At each area we used ten plots (25x75cm), to randomly collect the litter. After, shells and live animals where carefully searched and identified to the least taxonomic possible level. In UA all species were synanthropic. The Subulinidae was the most abundant (91%), especially *Beckianum beckianum* (Pfeiffer, 1846) (67%). The Systrophiidae was the most abundant in VDR 350 (61%) and also in VDR 450 (53%). There was a decrease in the Subulinidae proportion from UA to VDR 350 and total disappearance in VDR 450. We concluded that the composition of terrestrial molluscs responds to environmental gradients. From these data, we suggest the use of the proportion of synanthropic mollusc species as an index to the diagnosis of Atlantic Forest environments as follows: environments with large human influence will have 90-100% of synanthropic species; environments that are recovering for at least 35 years will have 50-60% of synanthropic species; and a forest that is recovering for at least 50 years with no human influence will have 0-10% of synanthropic species. The aim of this work was to establish a rapid method of low impact and low cost to classify or evaluate the stage of conservation of forest fragments in the Atlantic Forest.

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First Record of *Neopetraeus* Martens, 1885 from Brazil (Mollusca: Gastropoda: Pulmonata: Bulimulinae)

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The genus *Neopetraeus* Martens, 1885 was described as a subgenus *Otostomus* Beck, 1837. Later Pilsbry (1898, 1901-1902) presented the generic diagnosis based on the teleoconch and protoconch, drawing attention to the peculiarity of the radula. Thiele (1931) and Zilch (1960) presented generic characteristics of the shell, jaw and radula, citing the type species and referring to geological and geographical distributions. The morphology of the shell and soft parts of *Neopetraeus* was presented by Breure (1979), who reported its geographical distribution as well as its ecological data. The studies mentioned above had been done in accordance with the conchological characterization presented by these authors, whose works reported the distribution of species solely in Peru. In this work, the material collected and studied consists of shells and specimens from localities of Bahia and Minas Gerais, in rocky outcrop and caves in deciduous forest seasonal areas. The conchological study showed: shell elongated oval, rather rigid, light brown, whitish spiral bands under crenulated ascending suture, axially striated; acuminate apex. Aperture vertical, ovate, broadly expanded; outer lip circular, elongated, oblique in upper region, basal lip circular, margin collumelar with strong callus, margin parietal with slight callus. Protoconch with extremely fine, incomplete, axial striae. The slight chitinous jaw has narrow 16 row plates and the radula unicuspid, arched teeth, central tooth not distinct from the lateral ones. Palial, digestive and reproductive systems of Brazilian species were studied, characterized and compared respectively with specimens of *Neopetraeus* proceeding from Peruvian localities.

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Past and Present of Records of Cephalopod Fauna in Thai Waters with Species Checklist

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Thai waters comprise two tropical zones, Gulf of Thailand, Southwest Pacific Ocean and Andaman Sea, East Indian Ocean. Although the cephalopod fauna from Thai waters was firstly recorded in 1928 but the first taxonomic study covering both zones was in 1974, 48 years later, reporting 5 families, 10 genera and 22 species. At present, 22 families, 36 genera and 81 species are recorded by various authors. One idiosepiid and one sepiolid squids, and three octopods are new to science. Five taxa are considered to be complex species due to difference in morphology and life histories from the literature. The present checklist is the third revision since 1995.

Land Snail Shell Degradation in Temperate Forest

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Much is known about ecology and population dynamics of land snails, but almost nothing about land snail shell persistence and degradation. How long can shells persist in various forest conditions? What are the factors affecting shell degradation? And, can be empty shells used in statistical analyses for ecological and population biology purposes?

We observed shell degradation of nine common Central European snails in six basic types of temperate forests (alder car, beech wood, cultivated spruce forest, oak-hornbeam forest, peat bog pine forest and ravine forest) and identified main degradation agents. Some of the most important abiotic factors affecting shell degradation are soil and leaf litter pH and soil moisture. Biotic factors, affecting shell durability, were also recorded: shells are infested by various kinds of fungi and bacteria, wild boards destroy shells by trampling and biting.

The shell degradation is influenced also by shell characters, mainly by the size of the shell. Small shells (under 6 mm) disappear in much shorter time than robust shells (bigger than 6 mm). First of them disappear within six months after burial (in the most acid locality with soil pH around 3,5). Microstructural and periostracal characters probably influence the shell degradation too.

Shell degradation is complex process, which involves three kinds of factors (biotic, abiotic and shell's own) and is hard to determine. Hence we recommend not to use empty shells for ecological statistical purposes, and to make all statistical analyses only on living specimens.

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New Data on Deep-Water Baikal Malacofauna Inhabiting Hydrothermal Vent and Oil Seep

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Lake Baikal, unlike other world ancient lake, is a unique locality inhabited by deepwater fauna registered below 1300m. In 2009, study of Baikal deepwater fauna by a submersible “Mir” showed that the oil seep located 860-920 m deep near Gorevoy Cliff (north-east of the central lake basin) were inhabited by both “dwarfs” and “giant” gastropods. The “drawfs” *Prolikhiancylus frolikhae* (Acroloxidae) and *Choanomphalus bathybius* (Planorbidae) were found on hard bitumen substratum. “Giants” *B. fragilis* (Hydrobioidea) were found on soft sediment between oil seeps. Aggregations of limpets *P. frolikhae* were found on the pebbles patchy covering bacterial mats of deepwater hydrothermal area in Frolokha Bay (east of the northern lake basin). Two pebbles occasionally taken from this place were almost totally covered with the snails and their egg masses. In each egg mass the number of embryos varied from 1 to 3, and their development was synchronous. Snails of different ages were presented on every pebble. Value of ratio stable isotope carbon and nitrogen of tissue of *P. frolikhae* displayed an insignificant intra-species variation: from –11.2 to –9.9‰ for $\delta^{15}N$ and from –70.1 to –75.0‰ for $\delta^{13}C$. The organic matter of the bottom sediment between clearings of the pebbles had $\delta^{15}N$ –1.5‰ and $\delta^{13}C$ –47.7‰. Anomalously low $\delta^{13}C$ and $\delta^{15}N$ values provide the evidence of methanotroph bacteria are one of the main food component for *P. frolikhae*. [This work is a part the Integration Project N 27 under the financial support of the RAS Presidium (Project N 20.9) and RFBR, Project N 09-04-00781].

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Complex Evolution in the Neotropics: Understanding Caribbean Marine Biogeography Using *Bulla occidentalis* as a Model Species

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This is a new project undertaken within the framework of a master programme recently started by the first author. The marine biogeography of the Caribbean region is highly complex and, though extensively studied, the patterns and processes behind its present diversity are still not completely understood. For example, Malaquias and Reid (2009) detected a large degree of genetic differentiation within the marine gastropod species *Bulla occidentalis* collected from several localities in the Caribbean region and Brazil. The authors found four relatively distant clades, which they regarded as evolutionary significant units that roughly corresponded to separate geographic localities. However, the geographical sampling and number of specimens studied by the authors hampered any sound explanation for the observed pattern.

The main goals of this project are: 1) to uncover the historical reasons for the present phylogeographic pattern of *B. occidentalis*, and 2) to shed light on the evolutionary patterns and processes of marine life in the Great Caribbean Region (GCR).

Whether the phylogenetic break in *B. occidentalis* is due to ecological segregation, transient allopatry, or whether past or present dispersal barriers are affecting gene flow between populations of *B. occidentalis* is not known. Possible and likely explanations are numerous. The GCR has gone through large changes in recent geological history as a consequence of the formation of the Panamanian isthmus (approximately 12-3 Mya). Changes in circulation patterns, climate, water temperature, salinity and sea level periodically led to heavy extinction and to severing of population connectivity with opportunities for speciation.

To address the questions posed by our two main goals an expanded sample set from throughout the tropical western Atlantic (e.g. Florida, Bermuda, Cuba, Yucatan, Venezuela, Guadeloupe, Panama and Brazil) will be analysed by a combination of different methods. Knowledge about phylogenetic relationships and population genetics inferred from molecular data (mitochondrial COI and nuclear 28S rRNA genes) will be combined with ecological, palaeontological, oceanographic and historical geologic data. Novel phylogeographic models implemented in MrBayes and Beast software packages will be used for phylogenetic inference and to test phylogeographic hypotheses. Population genetic statistics will be explored with Arlequin and DnaSP while TCS will be used to generate haplotype networks and Migrate to test for levels of gene flow. This combination of methods will hopefully lead to a full understanding of the processes behind the observed phylogenetic break in *B. occidentalis* as well as contribute to a better knowledge of the complex marine biogeography and evolution in the GCR.

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An Approach to the Biogeography of the Mollusks (Gastropods and Bivalves) from the Bellingshausen Sea and Adjacent Areas (Antarctica) Starting from Data of Bentart 2003/2006 Cruises

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The Bellingshausen Sea is located at the west side of the Antarctic Peninsula, but constitutes an area of difficult access and navigation. The previous biogeographic situation placed this sea outside of the other known Antarctic regions since the scarce number of species that have been recorded. The Spanish Cruises BENTART 2003/2006 were focused on the study of the Antarctic benthos from the South Shetland Island to the Bellingshausen Sea and Peter I Island, and constitutes a good opportunity for the biogeographic study of the molluscs (Gastropoda and Bivalvia) from this area. A database was performed with the BENTART Cruises records and SOMBASE data (available on internet). The records were taxonomically adjusted and confined in several pre-defined biogeographic regions (Antarctic and sub-Antarctic). Number of taxa (species to family) and estimation of endemic species were calculated. Biogeographic assemblages were surveyed by means of the Bray-Curtis (presence-absence) similarity index. The South Shetland Islands and the Western Antarctic Peninsula were represented by ~12% and ~14% of total species recorded in the Southern Ocean and adjacent areas, respectively. The Bellingshausen Sea and the Peter I Island were more poorly represented (< 9%). The endemic species constituted very low percentages. The similarities between areas showed that the South Shetland Islands and the Western Antarctic Peninsula formed part of a complex assemblage with several high Antarctic zones, but the Bellingshausen Sea and Peter I Island formed an independent cluster that only was grouped with other zones at higher taxonomic levels. Future studies that consider an improved taxonomical adjust may be elucidate more clearly the biogeographic situation of these areas.

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3D Reconstruction of a Gastropod "Worm": *Rhodope* sp. from Southern Australia (Heterobranchia: Euthyneura)

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The turbellarian-like, radula-lacking *Rhodope veranii* Kölliker, 1847 has been a mystery to systematists since its discovery in the Mediterranean. Since then, a few more minute rhodopid species have been found in coastal waters of other oceans and characterized mainly by differences in pigmentation and the form of subepidermal spicules. Together with the even more elongate worm-like *Helminthope* Salvini-Plawen, 1991, the Rhodopemorpha were usually regarded as Euthyneura incertae sedis with potential affinites to (dorid) nudibranchs or other shell-less groups such as the Gymnomorpha or Acochlidia. Within the framework of exploring the phylogenetic origin of the enigmatic Rhodopemorpha by molecular systematics, an undescribed *Rhodope* species has been found in temperate waters of Edithburgh, Southern Australia. All major organ systems have been reconstructed three-dimensionally from series of semithin sections using the software Amira. Microanatomy confirms the loss of the foot, mantle cavity, gill, heart, radula and cephalic tentacles, and shows considerable reduction of the digestive system and kidney. Structural details of the highly concentrated central nervous system, the genital system and the position of spicules are given. The evolution of this mosaic of strongly reduced and apparently complex or even unique features is discussed.

Phylogenetic Status of the Aeolid Genus *Babakina* (Opisthobranchia: Nudibranchia): a Molecular Approach

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The genus *Babakina* was erected in 1973 for *B. festiva* from California. Since then, just three additional species have been described (*B. caprinsulensis*, *B. anadoni* and *B. indopacifica*). The genus has been included in the facelinid aeolids, subfamily Babakininae. However, recent phylogenetic analysis based on morphological data supports not only the monophyly of this genus but also the inclusion in its own family. In this contribution, the first molecular phylogenetic analysis of the genus is presented, based on partial sequences of mitochondrial (COI and 16S) and nuclear (H3) genes. Bayesian phylogenetic hypothesis based on the combined data set of the three genes, supports the monophyly of *Babakina* (PP = 0.99), but not the monophyly of Facelinidae. Interspecific relationships among the *Babakina* spp. are not well resolved, although the amphiatlantic status of *B. anadoni* is supported (PP = 0.96). Moreover, the majority of our analyses do not recover neither the monophyly of the genus *Flabellin*a nor the family Flabellinidae. Furthermore, evidence suggests the inclusion of the aeolid genera *Piseinotecus*, *Calmella* and *Cratena* in a clade together with several *Flabellina* species. Finally, some phylogenetic considerations on the family Aeolididae and the facelinid genus *Pruvotfolia* are provided.

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The Opisthobranchs of Bermuda

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Islands and seamounts are very important to understand the overall biogeography of the Atlantic Ocean, since they can act as stepping-stones or staging posts for species. However, their role in marine dispersal and speciation in the North Atlantic is not yet fully understood and additional data is required from these places. Bermuda is the last truly offshore archipelago in the western Atlantic that can act as a source of larvae across the dispersal routes towards Europe and Africa, and is therefore of fundamental importance to understand patterns of dispersal, colonization, and speciation of temperate and tropical marine organisms in the Atlantic Ocean. A two-weeks campaign was carried out in Bermuda in June 2009 to collect opisthobranchs with two main aims: (1) to improve the overall knowledge of this molluscs in the archipelago and (2) to collect new material for molecular phylogenetic analyses and biogeographic inference. One hundred and forty-two species of opisthobranchs mollucs are referred to Bermuda, but 45 of them are pelagic forms. This fauna is dominated by species with Caribbean affinities. During our campaign 34 benthic species were collected; 11 species are new records for Bermuda and 3 of them are new to Science. Moreover, material of a previously recorded and undescribed *Okenia* was also collected. Three additional unrecorded species were identified from the photographic database of the Bermuda Aquarium and Museum of Zoology. This raises the total number of species of opisthobranchs known in Bermuda to 153.

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From Tropical Waters to Northern Seas: Biogeography and Taxonomic Revision of the *Microhedyle* Species Complex in Europe

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The worm-shaped, tiny gastropods of the genus *Microhedyle* (Acochlidia: Heterobranchia) are common and frequently encountered members of the mesopsammic communities in the Mediterranean and adjacent seas. In contrast to their local abundance, there is a lack in knowledge concerning diversity and taxonomic validity of the different described *Microhedyle* species as well as their distribution and biogeography in European Waters. For the present study we sampled the type localities of all described European *Microhedyle* species and several intermediate localities of European/ African coasts from the North Sea, Atlantic, Mediterranean, Black Sea and Red Sea to evaluate the distribution range of the different species. We performed histological semithin sectioning and 3D reconstruction of the anatomy as well as SEM examination of the radula to redescribe the key species *Microhedyle glandulifera* (Kowalevsky, 1901), which, combined with comparative anatomy and molecular analysis, constitutes the basis for the taxonomic revision of this species complex. Detailed re-examination revealed several characteristics especially in the central nervous system and digestive system that are valuable for the separation of species. Based on the mitochondrial COI-sequences of representatives of the *Microhedyle* species complex at species and population level a haplotype network was generated. This network and additional phylogenetic analyses are used to discuss the biogeography of this group of mesopsammic gastropods, with potentially low dispersal ability.

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The Alder and Hancock Collection of Nudibranchs at the Natural History Museum, London

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The Mollusca Section of the Natural History Museum (NHM), London has a large number of nudibranchs collected by Joshua Alder and Albany Hancock. The collection has great historical significance as it contains type material described in various publications as well as material mentioned in their Monograph of British Nudibranchiate Mollusca vol. 1 (1845-1855) and vol. 2 (1910). This poster illustrates how we plan to make the information associated with this material available to the wider scientific community, in part due to the NHM's adoption of KE EMu, developed by KE Software, as the NHM's primary collections management system. The aim is to bring together all of the information relating to the specimens in order to provide a detailed picture of the collection as a whole. The finished product will be available on the NHM website and will contain detailed specimen-level data including type status and photographs of each specimen. In addition to this, we will also include bibliographical information including scans of publications relating to the collection and detailed biographical records which will bring together all of the different kinds of media relating to individuals involved with the collection, such as photographs, handwriting samples or archival notes. The finished product will be useful to anyone interested in the collection whether from a historical or scientific point of view and will help to preserve the specimens themselves as detailed pictures may reduce the need for direct handling.

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"Himitsu Namekuji" – the Secret Slug(s): 3D-Reconstruction of Aitengidae

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The amphibious sea slug *Aiteng ater* Swennen and Buatip, 2009 was recently described from Thailand - a mysterious species with a worm-like body shape lacking any cephalic tentacles or body processes. Anatomically it shows an unusual mix of sacoglossan and acochlidian characters, however, the systematic affinities remain open.

In the present study a paratype of *Aiteng ater* is re-examined and compared with an undescribed, equally tiny and vermiform Aitengidae species - the "secret slug" - from Japan. Of the latter, all major organ systems were 3-dimensionally reconstructed from serial histological sections using AMIRA software. The secret slug resembles acochlidians by possessing calcareous spicules, a prepharyngeal nerve ring, and a uniseriate radula with an ascending and descending limb lacking a sacoglossan-like ascus. The prominent rhachidian tooth, which is used to pierce insect eggs and pupae in *Aiteng ater* and the well-developed, laterally situated eyes resemble the situation found in *Strubellia*, a member of the limnic acochlidian family Acochlidiidae, which feed on gastropod eggs. A relationship of Aitengidae with Acochlidiidae also is indicated by recent molecular analyses. This would, however, imply that Aitengidae have lost the most characteristic acochlidian apomorphy, the subdivision of the body into a head-foot complex and a free, elongated visceral hump. Also, the absence of cephalic tentacles gives the Aitengidae an appearance very different to other marine or limnic Acochlidia.

The Order Cephalaspidea (Mollusca: Gastropoda) in Norway: Systematic Revision of Species with a Molecular Phylogenetic Analysis

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Cephalaspid gastropods are a diverse worldwide group of Opisthobranchs characterised by evolutionary trends that lead to shell reduction, internalisation, or loss. One of the earliest to mention Cephalaspids in Norway was Danielsen (1859) listing 16 species followed by several others such as Sars (1870) and Friele and Grieg (1901). The most recent survey of Norwegian species was conducted by Brattegard and Holthe (2001) naming 30 species in 12 genera. Most importantly, Lemche (1948) made a revision of cephalaspid species. However he includes only drawings of the shells, none of the reproductive systems or any photographs.

Cephalaspid taxonomy is very complex and prone to changes since species have been mostly described based on shells alone and those can be very similar particularly between species of the same genus, leading to high taxonomic uncertainty.

This is a new project undertaken on the framework of a master degree programme. The main aim is to revise the systematics of the Norwegian cephalaspids, establishing the valid species and their synonyms, while providing characters to discriminate between species.

Shells, external morphology, and anatomical characters (e.g. jaws, radula, gizzard plates, and male reproductive system) will be studied through fine dissection work and scanning electron microscopy, and compared with type material. Species will be barcoded using the mitochondrial COI gene and molecular phylogenetic hypotheses inferred to help delimiting species. Here we present an overview of the project and preliminary results obtained for the genus *Philine*.

The Phylogeny of Nembrothinae: an Increasingly Intricate Story

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Traditionally, the subfamily Nembrothinae has been comprised by the genera *Nembrotha*, *Roboastra* and *Tambja*. However, although recent molecular phylogenetic analyses recover Nembrothinae as monophyletic, only the monophyly of the genus *Nembrotha* was supported, since the allocation of *Tambja tentaculata* Pola, Cervera and Gosliner, 2005 prevented to recover the genus *Roboastra* in all the analyses. This led to transfer this last species to *Roboastra*, which would be characterized by having grooved and well developed oral tentacles as its single synapomorphy. Recent field trips in different regions of the world have provided material of some undescribed nembrothid species, as well as new additional material of other known but not previously available species for molecular studies. Partial mitochondrial sequences (COI and 16S) for these 12 additional species are added to the previous phylogeny. The phylogenetic hypothesis presented in this contribution based on combined molecular data and represented by Bayesian inference confirm the monophyly of Nembrothinae and the genus *Nembrotha*. The monophyly of the *Roboastra* + *Tambja* clade is strongly supported (97%). *T. zulu* inserts within the clade composed by all *Roboastra* spp. A detailed observation of the new specimens as well as good pictures of these specimens alive shows that *T. zulu* has grooved and well developed oral tentacles. Thus, *Tambja zulu* should be transfer to *Roboastra*. Remaining *Tambja* spp are arranged in five clades, but the relationships among them and with the *Roboastra* + *T. zulu* clade have not a strong support. Thus, on the basis of our results, even if none synapomorphy can be identified for the *Roboastra* + *Tambja* clade, it is suggested that all the species included in this clade are considered as *Roboastra*, since is the oldest name. We consider that this additional information is significantly relevant to re-assess the phylogenetic relationships of Nembrothinae.

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The Distribution of Nudibranchs (Gastropoda: Opisthobranchia) on the Coral Reefs of Pemanggil Island, Johor, Malaysia

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The taxonomy and diversity of nudibranchs from 15 locations at Pemanggil Island, Johor were investigated. From this study, it is summarized that the nudibranchs in Pulau Pemanggil compromised of 9 families consisting of 17 genera and 33 species of nudibranchs. The most dominant species during the survey was *Phyllidiella pustulosa* which was found at all the study locations except in the intertidal area of Teluk Pa' Kaleh. Among the rare species were *Ceratosoma* sp.*, Ceratosoma trilobatum, Chromodoris coi, Hypselodoris centunculus, Risbecia tryoni, Dicscodoris boholiensis, Notodoris gardineri* and *Roboastra gracilis.* The percentages of 25% of nudibranchs in Pulau Pemanggil were found on sponge. Data also showed that Teluk Assam Jawa has the highest number of species that was 16 species.

The Sea Slugs from the Gulf of Thailand and Andaman Sea

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The diversity of sea slugs along the coral reefs from the eastern coast of the Gulf of Thailand, Losin Rock and Andaman Sea were reported. The fifty-nine sites from both the Gulf of Thailand and Andaman Sea had been carried out during 2006 – 2010. The field surveys were conducted by SCUBA diving on daytime randomly throughout the reefs together with the other organisms. 51 species of sea slugs were recorded and had been classified in 5 orders 19 families 34 genera as follow: Order Sacoglossa (4 species), Order Anaspidea (1 species), Order Cephalaspidea (1 species), Order Notaspidea (1 species), Order Nudibranchia (44 species). The most widely diversity of sea slugs in the Gulf of Thailand were as follow: Losin Rock (8 species) in Pattani Province, Noi Bay Kood Island, Ngam Island, Loayanok Island (7 species) in Trat Province, respectively. In Andaman Sea, the greatest diversity of sea slugs were 6 species each at Paed Island, Koaw Island in Similan Islands and Talotopo Bay, Adang-Rawi Islands. The great distribution of sea slug species were *Jorunna funebris* (Dorididae) and *Phyllidiella pustulosa* (Phyllidiidae) which distributed in 18 sites, *Pteraeolidia ianthina* (Facelinidae) and *Phyllidia elegans* (Phyllidiidae) distributed in 13 sites and *Phyllidiella nigra* (Phyllidiidae) distributed in 12 sites. There were 14 species occurred only in the Gulf and 10 species only in Andaman Sea. 7 species are the new records of Thailand: *Thuridilla vatae* (Risbec, 1928) (Placobranchidae), *Asteronotus cespitosus* (van Hasselt, 1824) (Discodorididae), *Phyllidia picta* (Pruvot-Fol, 1957), *Phyllidiella granulata* Brunckhorst, 1993 (Phyllidiidae), *Hypselodoris obscura* (Stimpson, 1855) (Chromodorididae), *Janolus* sp. (Proctonotidae) and *Cerberilla* sp. (Aeolidiidae).

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A Preliminary Study on the Cytotoxic Activity of the Edible Sea Hare *Dolabella auricularia* in Fiji

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The sea hare *Dolabella auricularia* and it egg masses are eaten in a number of countries in the Pacific Islands although they can contain poisonous and cytotoxic compounds. In Fiji, some parts of the digestive gland of the animals are initially removed before it is cooked and eaten. Egg masses on the other hand, are eaten raw after marinating with lemon. Several biologically active metabolites have been isolated from *Dolabella auricularia,* including the highly toxic and biologically active dolastatin family of cylic peptides. The current preliminary study evaluates the toxicity level of the secondary metabolites present in the local animals and investigates the anatomical distribution of biologically active compounds particularly in its digestive glands and the exterior, which includes the skin and mantle.

Three extracts of *Dolabella auricularia* were subjected to a bioscreening study to detect cytotoxic activity by the brine shrimp lethality bioassay. The extracts studied were: (1) metabolites from the digestive glands (internal organs), (2) metabolites from the whole organism, and (3) metabolites from the skin and mantle (external organs) of the animal. Extracts (1), (2) and (3) were shown to be toxic to brine shrimps with lethality levels found at <100 ppm, 480 ppm and 2000 ppm respectively. Although further works needs to be completed, our preliminary results show that the metabolites extracted from the digestive organs were significantly more toxic than those obtained from the skin and mantle of the animal. This result is not surprising as many researchers have shown that sea hares are a rich source of bioactive substances believed to be of dietary origin.

In Fiji, where this sea hare is sold at the local market, the high lethality levels found for the digestive glands suggest that it is crucial that the digestive gland of the animal be removed before the animal is consumed. Although low lethality levels are found from the extracts of the skin and mantle, further research is needed to ascertain whether the sea hares as sold and consumed locally have acceptable toxicity levels.

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Diversity and Systematics of Tropical West Pacific Shallow-Water Shell-Bearing Cephalaspidean Gastropods

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Cephalaspids are a major group of opisthobranch gastropods with an estimated 840 species worldwide. Taxonomic uncertainty is common among the majority of shell-bearing cephalaspids, where shells remain in most cases the only source of systematic characters, and anatomical data when available tend to be limited to few characters. Moreover, molecular data now offer enormous potential to discriminate among cryptic species.

The tropical West Pacific is the region in the world of highest marine biological diversity and this has also been documented for molluscs and is likely the case in cephalaspidean gastropods too.

The major global reviews that included western Pacific cephalaspidean species in a broad sense are still the classical molluscan monographs by Sowerby (1843-78), Adams (1850), Watson (1886), Pilsbry (1895-96), Bergh (1900), and Schepman (1993). Recently, Valdés (2008) published a milestone work on the systematics of western Pacific deep-water cephalaspids in which the author gave for the vast majority of species a combination of shell and anatomical characters.

This project aims to provide new insights into the systematic of this poorly known group by providing new data on the morphology and anatomy of species. The study of shells will be complemented by fine anatomical dissection work and SEM analysis. Moreover, DNA molecular sequences from three genetic markers (the mitochondrial COI and nuclear 18S rRNA and 28S rRNA genes) will be used to generate phylogenetic trees to help delimiting species.

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Systematics, Phylogeny and Biogeography of the Family Aglajidae (Gastropoda: Cephalaspidea)

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Aglajidae is a family of marine radulaless cephalaspideans (except *Odontoglaja guamensis*) occurring worldwide in tropical and temperate habitats, inhabiting coral reefs, rocky shores, and soft bottoms. Systematic work has been based mostly on the description of the external morphology; anatomical data and knowledge on the internal shells are only known for a minority of species. Description of species based on juvenile forms and chromatic variations have been common and this lead to a confusing taxonomy with high numbers of synonym names. *Navanax aenigmaticus* is a good example of this, with over 13 nominal names available. In this new project, the systematics of aglajid species will be revised and hypotheses on their evolutionary history inferred. Characters of the external morphology and new anatomical data obtained through fine dissections and scanning electron microscopy will be combined with DNA sequence data of the mitochondrial COI, 12SrRNA, and 16SrRNA genes and nuclear 28SrRNA and Histone-3 genes. These will be used to discriminate between species and generate species-level phylogenies to hypothesize on the origin, diversification patterns, and biogeography of the Aglajidae. Here, we present a description of the project and a summary of the present knowledge on the diversity and phylogeny of the Aglajidae. This project is funded through a doctoral grant to the first author by the Consejo Nacional de Ciencia y Tecnologia (CONACYT-Mexico), fellowship BAZS/188890/2010.

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The Hemocyanin of *Laevipilina hyaline* (Monoplacophora)

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We have cloned and sequenced the first partial cDNA of *Laevipilina hyaline* hemocyanin (LhH). The deduced amino acid sequence of the polypeptide chain strongly resembles the primary structure of gastropod, caudofoveate and chiton hemocyanins (Hc) as that of the hemocyanin of *Nucula nucleus* (Protobranchia) all possessing a C-terminal functional unit h (FU-h). This FU is lacking in cephalopod hemocyanins. Thus, we assume that 20 subunits form a cylindrical native hemocyanin of ca. 8 MDa as observed in Gastropoda or Protobranchia. On the basis of multiple sequence alignments we calculated phylogenetic trees and a molecular clock. These data show a strong relationship of Polypacophora and Monoplacophora whereby a sistergroup relation of Cephalopoda and Monoplacophora also cannot be excluded. The molecular clock data suggests 490 mya as the first appearance date of Monoplacophora. Further analyses of the hemocyanin gene structure of *L. hyaline* are instantly in progress, and will provide further substantial hints to elucidate the true origin of Monoplacophora and their sistergroup.

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Pallial Oviduct Structure of Three Species of the Genus *Semiculcospira* (Mollusca: Gastropoda: Pleuroceridae) from China

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The ovoviviparous freshwater mollusks of the genus *Semisulcospira* (subfamily Cerithioidea) are widely distributed in the water-bodies of the East Asia. The cerithioideans are well known as prosobranchs having very similar shell morphology. That is why identification of representatives of the group is very difficult and needs anatomical data. Literature data on *Semisulcospira* reproductive anatomy is known only for *S. libertina* from Japan (Nakano, Nishiwaki, 1989). In our research we examined three *Semisulcospira* from China, as a result two of them it was shown were not *Semisulcospira.*

To study the morphology of *Semisulcospira* pallial oviduct we used histological methods. Mantle cavity of ethanol fixed specimens was dissected, stained by hematoxylin and eosin and examined under light microscope.

Pallial oviduct of *S. gredleri* is presented by lateral and medial laminae with inter-lamellar cavity between them, which is opened into mantle cavity and closed only proximally. Lateral lamina possess brood pouch with embryos. Medial lamina consists of seminal receptacle and semen-accepting pallial pocket both covered with connective tissue. In proximal part of lateral lamina there is small pararenal gland with the same size as seminal receptacle.

Pallial oviduct of *S. perigrinorum* is formed by medial lamina only. Lateral lamina is weakly developed and presented by small groove lined with mucous cells. On the base of that facts *S. perigrinorum* need to be transferred to the genus *Brotia* of the family Pachychilidae. Lateral lamina of *S. textoria* pallial oviduct includes pararenal, nidamental and albumen glands instead of brood pouch, so that pallial oviduct is typical for egg-laying Pleuroceridae. Based on that and other morphological characters we regard *S. textoria* need to be transferred to the genus *Hua* of the family Pleuroceridae. [The work was partly supported by the Russian Foundation for Basic Research (grant No. 09-04-98583)].

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Patterns of Genetic Diversity in European Spring Snails and the Role of Pleistocene Refugia in Generating Biodiversity Hotspots

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The current study aims at increasing our understanding of patterns of biodiversity in highly isolated and stenoec freshwater gastropods in particular and of European freshwater diversity in general. Based on genetic data from 717 *Bythinella* specimens sampled at 194 sites, we aim to identify areas of elevated diversity and to determine the role of Pleistocene refugia in generating these biodiversity hotspots.

As the delimitation of *Bythinella* species is still under discussion, we used haplotypes as operational units in all performed analyses. This usage of genetic data instead of purely taxonomic information has proven to be very useful for detecting biodiversity hotspots in *Bythinella* spp.

Mean pairwise genetic distances between *Bythinella* populations within 1°x1° geographical grid cells sampled in Europe were calculated to identify areas of elevated genetic diversity. Several biodiversity hotspots of the spring snail genus *Bythinella* were identified: Massif Central/Pyrenees, the Eastern Alps, the Western Alps/Northern Apennines, and the Eastern and Western Carpathians.

Some of the regions recognized coincide with biodiversity hotspots found in other freshwater taxa, others appear to be new. Thus spring organisms may reflect a unique evolutionary history that is distinct from lentic and lotic taxa. Furthermore, hotspots are not necessarily identical with Pleistocene refugia. It is suggested that refugia per se are not responsible for high levels of biodiversity.

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Progenetic Dwarf Males of Deep-sea Wood-boring Bivalve *Xylophaga* (Myoida: Xylophagaidae)

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Deep-sea wood-boring bivalves of the genus *Xylophaga* in the family Xylophagaidae are known to harbor tiny individuals on the shell surface or soft body. These individuals have been widely believed to be 'brooded juveniles' since the 1960s. In this study, we first to verify the 'brooded juvenile' hypothesis by examining *Xylophaga supplicata* which distributes in the West and South Pacific with serial sectioning and scanning electron microscopy observations.

The tiny individual of *X. supplicata* is proved to have 1) larval features in the soft parts in a plantigrade stage; 2) mature spermatozoa in testa at the anterior portion of visceral mass; 3) a large visceral volume due to the development of testa that prevents crawling locomotion and complete valve closure; 4) both prodissoconchs typical of planktotrophic development and internal dissoconch such as ligament shelf and thickened valve margin; and 5) a large resilium indicative of the completion of metamorphosis. These features clearly demonstrate that the tiny individuals are progenetic dwarf males and reject the 'brooded juvenile' hypothesis previously interpreted. Furthermore, our examinations on sexual differentiation upon host individuals in boring mode of life suggest that *X. supplicata* first grows up as a male (protandry) when it starts to bore into the wood and the sex change into female occurs when the dwarf male(s) settles on the host after a temporal hermaphroditic stage.

If that previously recorded 'brooded' juveniles in 18 species of *Xylophaga* other than *X. supplicata* are all dwarf males, 42.4 % of them bear dwarf males in bottoms deeper than 1,000 meters. Hosting the dwarf males in *Xylophaga* is therefore thought to be an adaptive strategy to live in the deep-sea woody substrata of ephemeral and sporadic presence, as is the case in the bone-eating annelid *Osedax*.

Phylogeography of the East-Alpine Members of the Landsnail Species *Orcula dolium* (Gastropoda: Pulmonata: Orculidae)

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Orcula dolium has the widest distribution among the species of the genus *Orcula* and inhabits the calcareous parts of the Alps and the Northern Carpathians. Since it had been described in 1801 by Draparnaud, various authors added a minimum of 23 further subspecies. Most of these subspecies represent local forms that inhabit only small, partly isolated regions and differ from the nominate subspecies in their shell shape and the expression of their aperture's folds. Besides the common *O. dolium dolium*, six subspecies have been described from the Eastern Alps. Two of them, *O. dolium edita* and *O. dolium raxae*, are restricted to different elevations of high mountain areas. According to the literature, the nominate subspecies is sporadically found in the same habitats as the high alpine forms, but no intermediate morphs have been detected. This observation raises the question if these taxa represent distinct species. To determine whether these taxa are differentiated genetically and to reveal their relationships, snails were collected from sites covering the main part of the East Alpine distribution range of the species. Two mitochondrial genes (COI and 16S rRNA) as well as the nuclear histone H3-H4-spacer region were sequenced and genetic distances calculated.

In the trees based on mitochondrial data several highly distinct clades were found, which are mostly not congruent with the described taxa. In particular, the high Alpine subspecies do not represent distinct lineages. In the H3-H4-spacer region almost no variation was found within the *O. dolium* group and the tree does not reflect the mitochondrial haplogroups.

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Spatial Modelling of Faunal Turnover of Gastropod Composition Reveals Vertical and Horizontal Zones within the Watershed of Ancient Lake Ohrid

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Biodiversity arises from evolutionary processes, constraints of environmental factors and biota interactions. Unfortunately, there is no single measure to cover all aspects of biodiversity. In general, ecosystem diversity is estimated by a combination of α-diversity (i.e. species richness at one location), β-diversity (i.e. rate of change in species distribution along environmental gradients), and γ-diversity (i.e. the total number of species of the ecosystem). The border of an ecosystem, however, may be diffuse, making spatial analyses challenging. Here, ancient lakes, such as Lake Ohrid in the Balkans, may constitute excellent model systems for spatial studies due to their high degree of eco-insularity.

Extensive field studies in the Ohrid watershed yielded representatives of 68 gastropod species with 50 of them being endemic (= 73.5 %). Moreover, α-diversity distribution appears to be heterogeneous.

In order to model major habitat entities, we here study gastropod species turnover utilizing a special case of β-diversity, i.e. the rate of species change along horizontal and vertical gradients.

Major results of this study are: 1) few variables can explain gastropod assemblage similarities; 2) these explanatory factors reflect the impact of large scale effects such as type of water body or water depth and small scale effects such as minor environmental gradients within a particular depth zone; and 3) compared to deeper parts of Lake Ohrid, the uppermost layer shows a more heterogeneous distribution of species turnover.

In conclusion, partly distinct vertical and horizontal zones within the Ohrid watershed could be inferred by combining measures of α- and β-biodiversity. These zones are governed by a combination of large and small scale effects and are characterized by similar gastropod assemblages, species richness, geological and hydrological settings. Transitions among zones are depicted by high species turnover rates.

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Phylogeographic Pattern of *Assiminea taiwanensis* (Habe, 1942) Indicating the Possibility of Human-Mediated Transportation

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Phylogeography deals with the relationship between spatial distribution and genealogical lineages within species level. However, our understanding of phylogeographic pattern is biased because of most researches were focused on vertebrates, studies focused on invertebrates were less than 25%. Land snail is suitable for phylogeographic research due to its low mobility and high genetic diversity. Many widely distributed land snails in Taiwan showed deep divergence among geographical regions based on molecular data. *Assiminea taiwanensis* (Habe, 1942), an amphibian snail, is widely distributed throughout Taiwan nowadays. However, earlier records showed that *A. taiwanensis* were restricted in the northern Taiwan. Here, I propose two predictions to test the distributional pattern of this species: (1) if *A. taiwanensis* is naturally distributed throughout Taiwan, regional differentiation among populations will be observed; (2) if *A. taiwanensis* is native in northern Taiwan and dispersed by human activities into other regions, highest genetic diversity will be observed in the northern region, while other regions are supposed to show lower diversity. Partial sequence of mitochondrial cytochrome c subunit I were sequenced from 131 individuals belonging to 26 populations throughout Taiwan. Totally 6 haplotypes were identified from 24 polymorphic sites and all haplotypes occurred in northern Taiwan. The distributions of haplotypes are mosaic and no regional endemic haplotype is found. Totally haplotype and genetic diversity is high ($h = 0.741$, $\pi= 0.01151$). The analysis of SAMOVA shows all populations should be divided into 3 groups, but some geographically distant populations are grouped together suggesting the possibility of human-mediated transportation. Increasing sample size and sequence length is needed in future work. Ecological niche modeling will be used to predict snail distribution nowadays and during Last Glacial Maximum. Multiple-hypothesis of dispersal route will be analyzed via MIGRATE-N software to figure out the most possible dispersal scenario.

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Cryptic Phylogeographical Structure in a Southern Australia Bivalve Species: *Lasaea australis*

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Three major temperate coastal marine bioregions/provinces are recognized in Southern Australia: Peronian (southeast), Flindersian (southwest) and Maugean (southern Victoria and Tasmania). The original zonations were established based on species distribution patterns at the community level. Recent phylogeographic studies of Southern Australian marine invertebrates have recovered cryptic genetic structuring that in some cases conforms to these provincial boundaries, but not so in other cases. *Lasaea australis* is arguably the most common bivalve on Southern Australian rocky shores and occurs in all three biogeographic provinces. Initial analysis indicates that *L. australis* exhibits high levels of among-population genetic differentiation and might represent a cryptic species complex. Samples from 6 locations along the coast of Southern Australia were collected and included in phylogenetic analyses of mitochondrial (16S) and nuclear (ITS2) DNA sequences. Individuals from different populations are morphologically indistinguishable. But analysis based on 16S rDNA revealed three well supported clades within *L. australis*, corresponding to the three biogeographic provinces. Nuclear marker ITS2 had relatively lower phylogenetic resolution, but yielded a different phylogeographical pattern. This discrepancy concerned the Eyre Peninsula population. Mitochondrially, it placed in the western Flindersian clade but the nuclear marker identified it as part of the southern Maugean clade. The combined initial results suggest that *L. australis* have gone through multiple isolation and secondary contact events and that while cytoplasmic marker structuring adheres to marine province expectations, the nuclear marker does not.

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A Molecular Phylogeny of the Pheasant Shell Genera (Mollusca: Gastropoda: Phasianellidae) Based on Mitochondrial and Nuclear Sequence Data

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A molecular phylogeny based on sequence data from mitochondrial (COI and 16S rRNA) and nuclear (18S rRNA and 28S rRNA) DNA is presented for the family Phasianellidae, including representative species from four genera *Tricolia s.l., Eulithidium*, *Phasianella* and *Gabrielona*.

The molecular data suggest that, with the exception of *Tricolia s.l.*, each of these genera represents a distinct lineage and this is also supported by morphological characters of the shell, operculum, radula and external anatomy. In contrast *Tricolia s.l.* is paraphyletic and is clearly an artificial assemblage of no phylogenetic significance. The southern Australian and Indo-West Pacific species traditionally referred to *Tricolia* do not cluster with the European and African species (= *Tricolia s.s.).* Instead, the genus *Phasianella* emerges as the sister taxon to *Tricolia s.s.* Morphological differences in the shell, radula and external anatomy are also evident between these lineages of *Tricolia s.l.* Strong support was obtained for the grouping of the southern African *Tricolia* species together with the type species (the European *T. pullus*). Within the southern African group the molecular data identify two further clades for which there are also corresponding differences in radula form. The Indo-Pacific taxon *Hiloa* is clearly distinct and should not be considered a component of *Tricolia*. Its position within the family Phasianellidae, like that of *Gabrielona* is unresolved. The New World tricolliine taxa all evidently belong to the genus *Eulithidium*. This is well characterised morphologically and emerges as the most basally divergent lineage within the Phasianellidae in our molecular phylogeny. Using 28S rRNA data, this split was tentatively dated at ca 98 mya. corresponding with the formation of the Atlantic Ocean.

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Comparative Phylogeography of Two (Micro-) Sympatric *Carychium* Species in Europe (Gastropoda: Pulmonata: Ellobioidea)

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Ellobioidea of the genus *Carychium* are minute, microphagial terrestrial Pulmonata which can be found in moist habitats such as leaf litter and the littoral of small streams. In Europe mainly two sibling species *C. minimum* and *C. tridentatum* can be found, which show very similar pretensions for their niches. Inhabiting the same microenvironment and having similar ecological niches could lead to the hypothesis of a shared population history. We tested this assumption in a comparative approach focusing on the phylogeography of these two species. Using and combining geographical and population genetic data has established the relatively young and dynamic field of phylogeography. This field of research gives new insights into the ancestry of populations, routes of recolonisation and refugial areas e. g. during glacial periods.

For our study we sampled more than 25 populations of *C. minimum* and more than 30 populations of *C. tridentatum* throughout their range in Central Europe. We sequenced partial cytochrome c oxidase subunit 1(CO1) from up to ten individuals per population and inferred the phylogeographic history of both taxa by constructing haplotype networks, analysis of molecular variability (AMOVA), as well as modeling climatic niches. Our analyses clearly show that the two species reacted differently to the European glacials. We will discuss refugial areas and recolonisation routes in light of postglacial paleogeoraphy of Central Europe. This study highlights the individuality of species behaviour and genetic response to changing climatic conditions.

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The Intra- and Interspecific Variation of Slugs in Genus *Arion* in the Context of Genetic Studies

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The genus *Arion* in the family Arionidae and subfamily Arioninae was divided into five subgenera: *Arion*, *Carinarion*, *Kobeltia*, *Mesarion* and *Microarion*. This genus includes several slug species occurring in Europe, where some of them are widely discussed and still pose unresolved taxonomic problems. The genus *Arion* also includes a few species considered as pests in plant crops, whose monitoring requires precise species determination at different stages of their development. The present study attempts to identify molecular taxonomic marker by which all the species of the genus *Arion* could be determined. A comparative analysis of the nucleotide within the nuclear and mitochondrial DNA (16S rRNA and cox1) on the basis of own research and data obtained from GenBank for different species of slugs of the genus *Arion* was conducted. Mitochondrial genes are suitable for taxonomic identification much better than nuclear DNA (18S, ITS1, 5.8 S ITS2, 28S). In the case of the species *A. lusitanicus* a surprisingly large intraspecific variation due to a Spanish population was observed, which strongly suggests the presence of a distinct species in that site.

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Comparative External Morphometry of Pharaoh Cuttlefish, *Sepia pharaonis* Ehrenberg, 1831 from Two Waters of Peninsular Thailand

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Morphometry of 37 external characters of pharaoh cuttlefish *Sepia pharaonis* Ehrenberg, 1831 from the Gulf of Thailand and the Andaman Sea, Peninsular Thailand, were compared. The total of 216 specimens were collected, 51 from the Gulf of Thailand and 165 from the Andaman Sea. Twelve characters of combined sex were significantly different, particularly numbers and diameter of enlarge suckers on the tentacular clubs. In the male cuttlefish, 9 of those 12 characters were significantly different. Only 2 characters of number of enlarge suckers on club were different in the female. Male and female cuttlefish of combined two waters were different in 7 characters, particularly of the arm length. The male and female cuttlefish from Andaman Sea were significantly different in 6 of those 7 characters. In contrast, the male and female cuttlefish from the Gulf of Thailand were different in 6 characters, but, particularly, of number and diameter of the enlarge suckers on tentacular clubs. The difference in patterns of sexual difference and the difference in males indicate the variation between populations from the two waters of Peninsular Thailand.

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Phylogeography and Population Genetics of the Freshwater Pearl Mussel (*Margaritifera margaritifera*) in Finland

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The freshwater pearl mussel (*Margaritifera margaritifera* L.) is one of the most endangered freshwater mussels in the world. Freshwater pearl mussel populations are declining in Europe. Their decline is the result of increasing human activity and habitat loss. In Finland, at the start of the last century, there were 200 freshwater pearl mussel rivers, and at the end of the century there were only 70 rivers. This study investigated the genetic structure and variability of 18 freshwater pearl mussel populations originating from Finland, Russia, Ireland and Spain using mitochondrial cytochrome oxidase subunit I sequences. Results show a high degree of differentiation of Finnish pearl mussel populations and thus emphasize how important it is to maintain these populations in future. The COI gene also indicates the existence of two evolutionary lineages: from Ireland, one extending northwards and the other extending southwards.

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Taurus Mountains: An Area of Endemism for Land Snails

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Terrestrial malacofauna of Mediterranean Region is notably diverse with a high level of endemism. Taurus mountains, extending across the region, present a wide range of habitats with extensive altitudinal variation. As a result of Miocene palaeogeography and dispersal events, a combination of continental and Aegean migrants with mesic Mediterranean relicts was formed. Boreal and xerophilic groups are not represented well.

At the present, apart from semiendemic subfamily Mesolimacinae (Agriolimacidae) and the genus *Gollumia* (Pristilomatidae), Taurus mountains is a speciation center/area of endemism for the genera *Turcozonites* (Zonitidae), *Sprattia*, *Pamphylica*, *Phyrgica* (Clausiliidae), and *Isaurica* (Helicidae). Although the malacofaunistic surveys are still incomplete, 4 different groups of endemic land snail taxa based on the distributions types are noticed: stenoendemics, common endemics (some oddly absent from central part), dispersist neoendemics, and relict populations of northern/southern elements. Due to repeated colonizations, it is difficult to define biotic elements. This may apply also to Eastern Aegean islands and Antitaurus chain extending to Levant.

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Taxonomic Investigation of the Genus *Platyrhaphe* from Thailand (Prosobranchia: Cyclophoridae)

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Platyrhaphe Möllendorff, 1890 is a distinctive genus readily distinguished from other cyclophorids such as *Cyclophorus* and *Pterocyclus*. Previously reported from southern peninsular Thailand, we have discovered *Platyrhaphe* in surveys recently carried out in northeast Thailand. Using the shell, radula and characters of the genitalia and by comparison with reference material of the closely related species *P. lowi* Morgan, 1887 and *P. leucaeme* Möllendorff, 1901 we were able to confirm that the newly collected samples are new species. In addition, karyotype investigations were carried out on an unidentified species. The karyotypic data has been recorded as $n = 14$, $2n = 28$, FN = 56, 7m + 5sm + 2st and the ZZ-ZW sex system is also reported, which is similar to that of many cyclophorid groups.

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Taxonomic Research on Non-Marine Molluscs of India: History and Current Scenario

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Research on non-marine mollusc in India is mainly concerned with taxonomy till mid 20th century. Most of the taxonomic research is done by British naturalists and very little contribution from Indian Malacologists such as Prashad, Hora and Rao. The database on the bibliography of non-marine mollusc on India was analysed to assess the patterns of publication on the subject, date and group, has shown that the maximum research paper was on the taxonomy. This is mostly contributed by early researchers/naturalists. Since independence the number of publications dealing with taxonomy has reduced drastically, but one can see increase in the biology and to a lesser extent ecology and conservation. Much of the taxonomic work post independence was confined to preparing checklist of states or a protected area. There only handful of new species described in the last 60 years. I have also analysed the data on Indian representation in previous three World Congress of Malacology. Data shows that a very negligible amount, accounting for less than 5% of the paper submitted/presented in last three congresses was from India. Similarly, the analysis was done for the papers appearing in three poplar mollusc journal- Journal of Molluscan Studies, Molluscan Research and Malacologia shows similar patterns. This decreased pattern in taxonomic studies in recent years could be mainly attributed to lack of funding for taxonomic research in India, tougher Federal Act that restrict exchange of materials, non availability of type specimens in the host country and finally lack of interest in taxonomic studies as there are more lucrative job option for current generation.

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Variation in Antiviral Activity in Abalone *Haliotis laevigata* Contributed by Genetic and Environmental Factors

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Severe mortality of abalone due to Abalone Viral Ganglioneuritis (AVG) has been reported in south-east Australia and is caused by a herpes-like virus, similar to that reported from Taiwan. In all reported outbreaks on farms and in the wild, a small proportion of the populations survive, indicating some individuals may have relatively strong antiviral defense. We have optimized the plaque assay using herpes simplex virus 1 (HSV-1) in mammalian Vero cells for screening antiviral activity in the hemolymph and lipid extracts of greenlip abalone *Haliotis laevigata*. Significant antiviral activity has been found in haemolymph plasma (5 %, v/v) and the lipid extract of digestive gland of adult abalone (500 μg ml^{-1}). Substantial variability in antiviral activity was observed among farmed abalone of the same family line and wild abalone collected from the same geographic location. Overall, greater activity was observed in wild greenlip abalone compared to farmed greenlip abalone. Future research will investigate the specificity of antiviral activity in abalone haemolymph against a range of fish herpes viruses and other fish viruses. Abalone with relatively high antiviral activity against these viruses will be tested for resistance against AVG, to address the question of whether antiviral activity can be used to select AVG virus-resistant abalone populations.

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Effect of the Sediment Remotion on the Metabolic and Grow Rates of *Tapes semidecussata*

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The collection of bivalve molluscs on the beaches is a very important activity in Galicia (NW Spain). The extraction is made by hand and it is recommended during this activity to stir the sediment. The present work analyses the effect of the sediment remotion on different physicochemical aspects (compactness and Eh), as well as growth and metabolic rate of *Tapes semidecussata*. Two tanks with 15 cm of sediment were put in a chamber with light and temperature controlled. Each tank was divided equally in six parts. Four treatments (three parts for each treatment) were made: remotion each 3, 7 and 14 days and control (no remotion). 30 individuals of *T. semidecussata* of 12,5 cm (± 0,2) were collocated at each partition, and were kept with a semiopen water circulation at 17 ºC during 14 months. Significant differences were observed for the physicochemical variables, with higher compactness on the control and 14 days remotion period. No significant differences were observed between the treatments stirred every 3 and 7 days. The growth was significantly higher on the controls, and no significant differences were observed between the treatments. The metabolic rate was significantly higher on the controls compared with the stirred treatments. This results shows that a more intense remotion of the sediment not increase the metabolic and growth rate of *T. semidecussata*.

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Embryonic and Post-Hatching Development of Marbled Octopus, *Amphioctopus aegina* (Gray, 1849) (Cephalopoda: Octopodidae)

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The development of the marbled octopus, *Amphioctopus aegina* (Gray, 1849) embryos of brooded females reared in the laboratory is studied. The egg capsule is a single type, small with approximately 3.2 mm in length, white colour, grape-shape. Each capsule is equipped with a stalk which attach to the festoon, forming a string. The embryos undergo two reversions during development, in stages IX and XIX. Chromatophores which firstly appear on ventral head besides the naked funnel are specific. The embryonic phase is approximately 18-19 d (385 hrs) at 30°C. The course of embryogenesis is similar to other octopus species with small eggs and small planktonic hatchlings. The planktonic hatchling of *A. aegina* is 2.7 mm in the average mantle length with approximately 50% arm length index. The settlement to benthic mode of life is 20-25 days after hatching.

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The Comparative Growth and Survival of Juveniles Tropical Oysters (*Crassostrea belcheri* Sowerby) at Different Growout Sites in the West Coast of Peninsular Malaysia

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The juvenile hatchery-produced tropical oysters, *Crassostrea belcheri*, were cultured at different selected locations around the coastal areas of Peninsular Malaysia. Four locations were selected for the growout trials. The selection of the growout sites were based on the accessibility of the sites and salinity (ranging between 17-30ppt). The sites selected were Pulau Betong (Pulau Pinang), Kuala Gula (Perak), Telaga Nenas (Perak) and Muar (Johor). The method applied in this project was floating raft system. A total of 10,000 oyster juveniles of 1.5cm to 2cm were transferred to each growout sites, where a total of 500 oyster juveniles were placed in each tray. A total of 100 oysters from each tray were measured the shell length. Three trays were used for the shell length measurements. The number of oysters per tray was recorded to determine the survival. Dead oyster shells were removed monthly. At the end of 9 months, the results showed that the best survival rate was observed in Pulau Betong (Pulau Pinang) (82%), followed by the site at Muar, Johor (75%) and Kuala Gula, Perak (65%). The growout site at Telaga Nenas (Perak) showed the lowest survival rate. The results showed that the highest growth was observed in the oysters cultured at Pulau Betong (Pulau Pinang) (reached shell length of 8.3±0.8cm after 8 months in the site), followed by the oysters cultured at Kuala Gula, Perak (reached shell length of 6.5±0.6cm after 8 months in the site). The growout site at Telaga Nenas showed the lowest growth rate. Discussion will be focused on the site suitability for commercial oyster culture in the west coast of Peninsular Malaysia.

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Impact and Control of Polychaete Infestation in Hatchery-Reared Oyster Seed Production

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Polychaete cause problems for hatchery-reared oyster seed production. The sedimentary tube-forming polychaete and sabellid polychaete were found present during the nursing period under hatchery conditions. The sedimentary tube-forming polychaete infest juvenile oysters by forming an elaborate tube from the grinding oyster shell with the juvenile oyster attachment. In such polychaete infestation, many juvenile oysters died after tube formation. The sabellid polychaete attaches itself to the shell of juvenile oyster, resulting in valve movement and the death of most juvenile oysters within 2 days. The sedimentary tube-forming polychaete can be controlled by maintaining hygienic conditions by means of washing the juvenile oysters with freshwater and exposure to air at daily intervals. The sabellid polychaete can be completely controlled by immersing the juvenile oysters in freshwater for 2 min at daily intervals.

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The Effect of Different Salinities on the Depuration Efficiency of Blood Cockles, *Anadara granosa*

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The effect of different salinities on the depuration efficiency of blood cockle, *Anadara granosa* L., was studied in the laboratory. The salinities used were 5, 10, 15, 20, 25 and 30ppt. A total of 50 cockles were placed in a tray, with a total of 15 trays being used in the set-up for each salinity. The trays were designed to facilitate the water flow. They were placed in a fibreglass tank. A flow rate of 100L/min would give 1 exchange of water per hour for the system. Sterilisation of the water was obtained by an Sanitron-UV sterilizer. The sterilizer contained a UV lamp of 110 W and was capable of sterilising at the rate of100-150 L/min. For bacterial determination, 20 cockles were sampled at intervals of 0, 24, 48, 60 and 72 hours. Total coliform, faecal coliform and total plate counts were done, according to recommended procedures for shellfish. The numbers of initial total and faecal coliform bacteria in cockles were 40,000 and 9,600 MPN per 100 g meat respectively. The total coliform bacteria count was reduced to acceptable levels of 99.52-99.78 % reduction after 24 hours and 99.94-99.98% reduction at 48 hours at both 25 and 30ppt. In addition, at salinities of 25-30ppt, the corresponding number of faecal coliform bacteria was reduced to 99.90-99.92 % at 24 hours and 99.95-99.97% at 48 hours, a reduction, which is far below the acceptable levels of 230 MPN/100 g meat. The reduction of total coliform and faecal coliform of cockles at salinities below 15ppt was significantly lower than at salinities 25 and 30ppt. Mass mortality of cockles was observed at salinities 5 and 10ppt after 24 hours in the depuration system.

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Effects of Body Size on Courtship Role, Mating Frequency and Sperm Transfer in the Land Snail *Succinea putris*

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Sex role preferences in simultaneous hermaphrodites may vary with individual condition and partner quality across consecutive matings. Theoretical and empirical studies highlighted an individual's body size and the relation of that with body size of the partner as potential factors that influence the preferred sexual role. Here, we studied effects of body size of focals and partners on (1) mating frequency and mating interval, (2) courtship role, and (3) number of sperm donated in successive copulations in the land snail *Succinea putris* where 'active' individuals mount the shell of their 'passive' partner before penises are intromitted reciprocally. We found body size-dependent differences in mating behaviour between small and large individuals; (1) smaller individuals of mating pairs more likely adopted the active role, (2) small individuals seemed to prefer inseminating larger partners, (3) a positive relation between body size and sperm number donated was found, (4) large individuals adjusted sperm number to their partner's body size, and (5) the smallest number of sperm was donated by large focals to small partners. In addition, (1) we found a positive correlation between the number of sperm donated and mating interval, and (2) sperm number donated decreased in later copulations indicating that the number of previous matings may affect male resources allocation. Our results support the view of models addressed to explain sex role preferences, gender conflicts and solutions to gender conflicts which predict that the preferred sexual role is variable within a species (e.g. size-dependent sex allocation models and the gender ratio hypothesis).

Reproductive Cycle of *Oxychilus (Drouetia) minor* (Pulmonata: Zonitidae) Over an Altitudinal Gradient

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Land snails represent an important component of the endemic fauna of the Azores and their reproductive cycles are relevant to the understanding of the evolutionary phenomena that lead to their speciation. Studies on *Oxychilus atlanticus* (Pulmonata: Zonitidae) have revealed that the maturation of the reproductive system has a strong correlation with size of the shell. This study is an attempt to correlate the maturation cycle of the *Oxychilus (Drouetia) minor,* an endemic species from Pico Island, with the growth of the animal and the abiotic factors. Specimens were collected from two stations with different altitudes and microhabitats: Furnas de Stº António, 5 m and Cabeço da Bola, 1044 m.

The spermatozoa are available throughout the year; independently of the phase of sperm maturation; however, in Furnas de Stº António the spermatozoa reach their maximum volumetric density in September and in Cabeço da Bola the maximum occurs in July. In Furnas de Stº António, the mature oocytes reach their highest volumetric density in September, when photophase and soil temperature reach approximately the maximum value. Between September and November mature oocytes decrease following photophase and temperature. In Cabeço da Bola, the mature oocytes reach their highest percentage between May and July. These results are in accordance with the growth of the animal and with temperature and pH of the soil. In September the percentage of mature oocytes is very low, contrary to what was expected when the abiotic factors are considered, what could suggest that a new generation was sampled.

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Microsatellite DNA for Population Genetic and Parentage Analysis of Banana Slugs (Pulmonata: Arionidae: *Ariolimax*)

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Based on genital morphology and mtDNA sequence data, banana slugs (Genus *Ariolimax*) are currently interpreted as a group of six species level taxa, viz *Ariolimax columbianus*, *A. buttoni*, *A. stramineus*, *A. californicus*, *A. dolichophallus* and *A. brachyphallus*. However, phylogenetic analysis of mtDNA sequences (COI, CytB and 16S rDNA) show that the latter three species are so closely related that the mtDNA sequences cannot consistently separate them. Nevertheless, mating behaviour in the three species is different and sexual selection has been suggested to be the driving force for this apparently rapid speciation. Hence studying the eventual role of sexual selection in this alleged rapid species divergence, requires genetic markers that evolve faster than mtDNA. Therefore we characterized 19 microsatellite DNA loci for A. californicus and tested their cross-species amplification in the other five *Ariolimax* species. Five of these loci were monoallelic, yet the 14 remaining loci were polymorphic (2-19 alleles) and amplified consistently in the six species. A first comparison between the species suggested that *A. brachyphallus* is far less variable than the other species, though this needs to be confirmed by a more comprehensive sampling. A preliminary parentage analysis based on four microsatellite DNA loci in potential interspecific crosses of *A. californicus* x *A. dolichophallus*, showed that none of these crosses produced hybrid broods, but that at least *A. californicus* reveals multiple paternity under natural conditions. These preliminary data suggest that the microsatellite DNA loci will be a very useful tool to investigate the role of sexual selection in the speciation and population genetic structuring of *Ariolimax* species.

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Morphological and Population Genetic Structuring in the Land Snail *Rumina decollata* (Pulmonata: Stylommatophora): Montpellier Revisited 30 Years Later

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The hermaphroditic terrestrial snail *Rumina decollata* is capable of both self-fertilization and cross-fertilization, and shows a high degree of body color and shell shape variation. Two color morphs of *R. decollata* have been previously described in the Montpellier region (southern France): a “dark” morph and a “light” morph. Both corresponded with two homozygous multilocus genotypes that consistently differed at 13 out of 26 allozyme loci. These observations suggest that in the Montpellier region *R. decollata* reproduces by sustained selfing. Yet, this amount of morphological and allozymic differentiation also imitates a taxonomic differentiation at the species level. Moreover, the light morph increased in frequency from 1973 to 1979 because it has a higher fecundity than the dark morph.

In order to re-assess the population structure and taxonomic interpretation of *R. decollata*, nine polymorphic microsatellite markers were developed. Cross-species amplification of these microsatellite loci was tested in the sister taxon *R. saharica.* The microsatellite markers were then applied, in combination with allozyme data, to new samples from the Montpellier region with the aim to (1) compare current morphological and population genetic composition and structure with the situation in 1973-1979, and (2) explore the taxonomic implications of sustained selfing in *R. decollata*. [This work is supported by the FNRS (Belgium) that conceded a FRIA PhD grant to V. Prévot].

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Embryonic Phase and Hatchling Size in Atlantic Bobtail Squid *Sepiola atlantica* (Cephalopoda: Sepiolidae)

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Cephalopods have a complex life history, and the early life stages are of interest, either as components of the life history of a given species, or models for generalized ontogenetic patterns and processes. The aim of this work is to know the time of embryonic development in different temperatures, and if the egg size is a determinant of the hatchling size in *Sepiola atlantica*. A total of twelve spawns in aquaria and 721 hatchlings from these spawns were examined. Each egg clutch was divided in three groups and exposed each on different temperatures (13±0.4 ºC, 18±0.3 ºC and natural variation (NV) 16.4±1.1 ºC). We obtained at all temperatures viable hatchlings. The percentages of successful hatching were 98.5 up to 100% of the amount of spawned eggs for each female. Much as in other coleoid cephalopods, in *S. atlantica* the temperature determines the time length of embryonic development, and the obtained data were very similar to other known sepiolid species. Thus, at 13 ºC developmental duration was 61.8±3.8 days, at 18 ºC it was 22.6±1.7 days, and for NV it was 40.1±4.8 days. The mean egg volume was 75.9±31.6 mm^3, the hatchling's mantle length (ML) was 1.5±0.3, and total length was 3.2±0.5. The time length of embryonic development and hatchling ML were not strictly related ($p>0.05$), on the other hand, the egg volume was positively related to hatchling ML ($p<0.001$). Our results provide new records on duration of embryogenesis and other information on reproductive patterns in this species. Some hatching and post-hatching behaviour are shown and discussed.

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Evolution of an Enigmatic Freshwater Limpet – the Genus *Protancylus* (Hygrophila: Planorbidae) Endemic to Ancient Lakes on Sulawesi, Indonesia

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Ancient lakes on the Indonesian Island of Sulawesi are recognized as evolutionary theatres with spectacular gastropod radiations. These lakes are also home to gastropod taxa exhibiting very special morphological or behavioral features. One such case is the lacustrine freshwater limpets of the genus *Protancylus* (Planorbidae) which live exclusively as epizoans on pachychilid gastropods on Sulawesi. *Protancylus* has a unique reproductive strategy involving brood care. We here aim at unraveling evolutionary and phylogeographical patterns of *Protancylus* spp. from the Malili lakes and Lake Poso using mitochondrial COI and LSU rDNA data.

The phylogenetic analysis revealed three major clades, of which one corresponds to *P. pileolus* from Lake Poso and the other two to *P. adhaerens* from the Malili lakes. There are two deeply divergent subclades within Lake Poso. Populations from lakes Towuti and Lontoa cluster together and collectively represent the sister clade to the closely related Lake Matano/Lake Mahalona populations. These patterns are supported by phylogeographical and gene-flow analyses which indicate strong gene flow between lakes Matano and Mahalona. Gene flow is much less pronounced between the latter lakes and Lake Towuti and negligible between Lake Poso and the Malili system. Molecular clock analyses place the initial divergence event of *Protancylus* spp. as well as the basal splits both within the Malili system and in Lake Poso in the Pliocene. Thus lineages and populations of *Protancylus* spp. are rather old in contrast to lacustrine species of *Tylomelania*.

Driving forces of speciation within the endemic *Protancylus* are discussed using ecological and behavioral data. At least three species evolved allopatrically. These species are characterized by low morphological variation and a specific life-history. A drift-based speciation mode is most likely. Further studies of this fascinating model system in freshwater gastropod evolution should focus on co-evolutionary patterns in the “substrate” pachychilid species.

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Molecular Characterization of *Arion ponsi*, an Endemic Slug of the Balearic Islands (Pulmonata: Arionidae)

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Arion ponsi Quintana Cardona, 2007, is an endemic terrestrial slug from the island of Menorca (Balearic Islands), where it formerly has been regarded as *Arion subfuscus*. Yet, subtle, though apparently consistent differences in the genital anatomy of *A. ponsi* underpin its specific separation from this latter species and its endemic relatives from the Iberian Peninsula, such as *A. molinae*, *A. lizarrustii*, and *A. iratii*. Still, corroboration of the taxonomic differentiation of *A. ponsi* is needed in view of the current confusion in the taxonomic interpretation of South European, and in particular Iberian, *A. subfuscus*-like taxa (i.e. the subgenus *Mesarion*). Moreover, the phylogenetic relationships of *A. ponsi* are still unclear. The current study therefore attempted to resolve both these issues by applying a DNA barcoding approach via a comparative nucleotide sequence analysis of mtDNA gene fragments (COI and 16S rDNA). These data show that *A. ponsi* is phylogenetically well-differentiated from any other *Arion* species. Yet, although the species tends to cluster with other Iberian endemic *Arion (Mesarion)* species, there is no consistent support for pinpointing its siter-group relationships. Further DNA data are hence needed to clarify the phylogenetic position of this species.

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Rediscovery of a Cryptic Snail Species: *Arion transsylvanus* (Pulmonata: Arionidae) from the Romanian Carpathians

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Cryptic species are abundant among invertebrates and are often hard to recognise. Molecular markers are an extremely useful tool to delineate cryptic taxa, although they should be applied with caution because different genes and techniques may yield different outcomes. We illustrate how cross-validation by molecular and morphological data can be applied to optimise taxonomic interpretations when cryptic species are involved. This is performed for the terrestrial slug *Arion subfuscus* species complex which represents a historical 'taxonomic garbage can'. Gonad morphology, allozymes and mtDNA data consistently showed that slugs from Romania and a location in Eastern Poland represent a strongly differentiated taxon within this complex. These slugs are therefore formally redescribed and assigned to *A. transsylvanus* Simroth, 1885; a forgotten nominal taxon from Transylvania. Diagnostic characters, including DNA sequences for the mitochondrial 16S rDNA are presented. Animals with the morphology of *A. brunneus* Lehmann, 1862, a nominal taxon which has also been reported from Romania, have the gonad type, allozyme alleles and 16S rDNA haplotypes of either *A. fuscus*, *A. subfuscus* or *A. transsylvanus*. Therefore, *A. brunneus* is regarded as a colour morph shared by several species and hence, *A. transsylvanus* is probably the only *A. subfuscus*-like species in the Romanian Carpathians.

Preliminary Molecular Systematics of the Genus *Napaeus* (Pulmonata: Enidae) in the Azores

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Frias Martins (1989, Açoreana 7:41-54) redescribed two Azorean species of the Macaronesian land snail genus *Napaeus*, viz. *N. pruninus* (São Miguel) and *N. tremulans* (Santa Maria) and elevated to species Morelet's (1860, Histoire Naturelle, 179) variety ζ *alabastrinus,* from Terceira. The three species differ in the colour and sculpture of the shell and in the shape of the epiphallus. Here, we used DNA sequence analysis of both mitochondrial (16S rDNA and COI) and nuclear (ITS-1) DNA to examine the specific status of the members of the '*N. pruninus*'-complex and to determine their phylogenetic relationships. We also included several other Azorean *Napaeus* taxa. ITS-1 showed no resolution. Yet, the results from both mitochondrial genes were congruent and showed that 1) the species from the '*N. pruninus*'-complex constitute a monophyletic group, 2) *N. pruninus* sensu stricto from São Miguel may be paraphyletic by inclusion of *N. tremulans* and *N. alabastrinus*, 3) *N. tremulans* and *N. alabastrinus* and all other *Napaeus* sp. included are monophyletic taxa with often substantial intraspecific sequence divergences of >3% (K2P distance), 4) the *Napaeus* species from neither São Miguel, nor Santa Maria form monophyletic groups and 5) the Azorean *Napaeus* show high degrees of interspecific sequence divergence (up to >12%).

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Conchological and Anatomical Differentiation in *Drouetia* Land Snails from São Miguel (Azores)

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Members of the Azorean land snail genus *Drouetia* show a large variation in shell size and variation in the reproductive system, namely the internal morphology of the penis. This is especially so in the taxa on the largest island (São Miguel) where, based on the shell and internal penis morphology, seven OTUs have been distinguished. We measured six shell and 21 genital characteristics in more than 400 individuals. Uni- and multivariate statistical techniques were used to examine the presumed conchological and anatomical differences among these OTUs. The results showed that there is a large variation in shell size with two OTUs ('*atlanticus*' and '*batalhanus*') having a significantly larger shell than the other OTUs of which '*parabritoi*' has a significantly smaller shell size than all other OTUs. Some of the OTUs also showed differences in their genitalia but these were sometimes subtle. Therefore, the OTUs are currently being characterized using DNA sequences to evaluate the morphological differences among the OTUs and to stabilize the taxonomy of *Drouetia*.

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Comparative Cytogenetics of the Genus *Geomalacus* (Pulmonata: Arionidae)

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Cytogenetic data are rarely used in the taxonomy and phylogenetics of terrestrial slugs. Yet, chromosome studies by Beeson [Nature 186 (1960): 257-258] have suggested that karyological data may be useful to distinguish (sub)genus level taxa in limacid and arionid slugs. Against this background we tested to what extent cytogenetic data allows to separate the subgenera *Geomalacus* and *Arrudia* within the arionid slug genus *Geomalacus*. To this end we established karyotypes of *Geomalacus maculosus*, *G. anguiformis*, *G. oliveirae*, and *G. malagensis*. These kayotypes were obtained by Giemsa-banding of air-drying technique chromosomes. They showed that all four species have the same haploid chromosome number of n=31. Hence, at least with respect to chromosome numbers the subgenera *Geomalacus* and *Arrudia* cannot be distinguished. Yet, the four species do show characteristic karyotypes as defined by numbers and morphologies of meta-, submeta- and telocentric chromosome pairs. Our results further contradict the general view that in stylommatophorans higher chromosome numbers is a derived character state.

Speciation Processes in Pyrgulinid Gastropods of Ancient Lake Ohrid (Macedonia/Albania)

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Ancient Lake Ohrid (Macedonia/Albania) has become a model system for speciation and radiation studies. There are distinct vertical zones within the lake presumably promoting either parapatric speciation along geographical/ecological gradients or even “micro-allopatric” speciation due to bathymetrical barriers. Examples include the largely continuous belt of *Chara*-algae in depths of some 3-20 m as well as the adjacent shell zone (20-35 m), both impeding migration of benthic invertebrates. Two potential cases of speciation events related to these zones are to be found within the gastropod subfamily Pyrgulinae. 1) The subspecies *Ginaia munda munda* (Sturany, 1894) and *G. m. sublitoralis* Radoman, 1978 and 2) the sister species *Macedopyrgula pavlovici* (Polinski, 1929) and *M. wagneri* (Polinski, 1929). In both cases, the former taxon is assumed to occur above/within the *Chara*-belt and the latter taxon below the *Chara*-belt.

Phylogenetic and phylogeographical analyses utilizing the mitochondrial cytochrome *c* oxidase subunit I gene were performed in order to study the genetic differentiation of the taxa. *Ginaia munda* ssp. showed a distinct genetic differentiation of the two depth forms. A differention in distinct genetic groups between the species of *Macedopyrgula* could not be found. However, some degree of genetic substructuring was observed.

These results are discussed in the context of underlying speciation processes. Due to the facts that the subspecies of *Ginaia munda* as well as the species of *Macedopyrgula* occur continuously in all depths of the littoral and sublittoral, and that the *Chara*-belt does not appear to be a distinct geographical barrier, allopatric speciation events appear to be unlikely. Instead parapatric speciation along a geographical and/or ecological gradient is assumed.

Population Density of the Topshell *Trochus niloticus* on Coral Communities of Khang Khao Island, Gulf of Thailand

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The topshell *Trochus niloticus* is a common gastropod on coral reefs in the Gulf of Thailand. It is harvested by local fishermen in many locations. The present study aimed to examine spatial and temporal variation of population density of *T. niloticus* on coral communities around Khang Khao Island, the inner part of the Gulf of Thailand. A belt transect method was applied at three study sites during March 2009 – March 2010. The highest population density was 0.89 individual/m^2 at study site on the east side of Khang Khao Island while the lowest one was 0.10 individual/m^2 at the study site on the north side of the island. There was no clear seasonal variation of population densities of *T. niloticus* during the study period. We highlight the importance of comprehensive studies on population ecology of *T. niloticus* in the Gulf of Thailand in order to develop a proper management plan of small-scale subsistence and artisanal fisheries of this topshell.

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Preliminary Phylogenetics of the Non-Achatinelline Achatinellidae

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The land snail family Achatinellidae contains five subfamilies, Achatinellinae, Auriculellinae, Pacficellinae, Tornatellininae and Tornatellidinae. The Achatinellinae and Auriculellinae are Hawaiian endemics, while the other three have Pacific wide distributions. The Achatinellinae, which includes the endangered Oahu tree snails (*Achatinella* spp.), have been extensively studied in recent decades, but the remaining subfamilies have not been revised or studied substantially since 1960. These four subfamilies include more than 100 nominal species of small (1 – 10 mm), often inconspicuously colored snails, which have garnered far less attention than the more colorful achatinelline tree snails. As such, much of the taxonomy and systematics of these highly diverse subfamilies remains confused. Specimens representing these four remaining subfamilies were collected during an ongoing snail and slug survey of the main Hawaiian Islands. Partial sequences of mitochondrial cytochrome *c* oxidase subunit I were obtained from 305 individuals from 20 locations throughout the six main Hawaiian Islands. Preliminary analyses provide robust support for the monophyly of all subfamilies and clear resolution at the species level within each subfamily. All islands harbor more than one species and there are no single island endemics. The wide distributions and the lack of isolation by distance pattern suggest high levels of dispersal among the Hawaiian Islands, contrasting with the Achatinellinae. Morphometric analysis and additional molecular markers are currently being developed and preliminary results indicate that these additional data will provide further resolution of the relationships among and within these four subfamilies.

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Powelliphanta in Peril: The Risky Translocation of an Endangered Snail to Make Way for Mining

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Almost all the members of a newly-discovered species of the New Zealand *Powelliphanta* land snail, over 6000 individuals, were removed from their habitat and placed in captivity to make way for an open-cast coal mine. At the time of capture, *Powelliphanta* had never before been kept in captivity successfully, no site suitable for their potential re-settlement had been identified, and the likelihood of their successful translocation back to the wild yet to be demonstrated. The project has been politically controversial and has received continuous national exposure in the media.

To date, approximately 4000 snails have been moved to 3 sites in the wild. To monitor the survival of these, a proportion have been tracked using harmonic radar. Approximately 2000 snails remain in long-term captivity as part of the conservation strategy.

Rehabilitation of the Nephrocoel Theory? The Example of *Mytilus*

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Coelomic cavities of metazoans – in the Mollusca represented by the pericardium – have been among the most debated organ systems concerning metazoan evolution. The nephrocoel theory was among the most important ones on ontogenetic and evolutionary origin of the coelom. First expressed by E. Ray Lankester in 1873, it was formulated in detail by Heinrich E. Ziegler in 1898. In essence the nephrocoel theory states that the coelomatic cavity ontogenetically (and by the recapitulation rule also evolutionary) is derived from enlarging end-bulbs of paired protonephridium-like excretory organs. This idea was dismissed vigorously by contemporaries of Ziegler and finally setback by the elaborate and most influential study of Edwin S. Goodrich in 1946 on nephridial organs.

In the mussel *Mytilus galloprovincialis*, the adult metanephridial system is formed during early juvenile development from paired lateral anlagen in posterior position. In an initial stage, there is a strongly ciliated excretory duct with a small, bulbous distal end. Large portions of the bulb wall contain (ciliated) podocytes, a cell type that marks ultrafiltration sites. During further development, the end-bulbs become substantially enlarged and transformed to the (paired, later on fused) pericardial cavity with subsequent formation of the heart components. Since we found similar conditions in another bivalve (*Lasaea adansonii*), a chiton (*Lepidochitona corrugata*) and a scaphopod (*Antalis entalis*), we forecast that this is the general way of coelomogenesis in the Mollusca. Hence, these findings perfectly match the predictions by Lankester and Ziegler. Although there are supportive indications of a similar formation mode in annelids and other invertebrate taxa (e.g. hemichordates), broader comparisons with conditions of other invertebrates, particularly lophotrochozoans are needed for a reconsideration of the nephrocoel theory in general.

Comparative Study of the Karyotypes and Electrophoretic Patterns of *Biomphalaria alexandrina* and *Bulinus truncatus* and the Ova of Their Corresponding Trematode Hosts

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The karyotype of *Biomphalaria alexandrina* and *Bulinus truncatus* were analyzed comparatively. The two species have the same diploid chromosome number, 2n=36. Chromosome analysis of *B. alexandrina* snails showed that the karyotype consists of 8 pairs metacentric, 8 pairs submetacentric and 2 pairs subtelocentric chromosomes. The typical karyotype for *B. truncatus*, was identified and classified into 4 groups; 10 pairs metacentric, 4 pairs submetacentric, 2 pairs telocentric and 2 pairs subtelocentric. Also, the electrophoretic analysis of tissue protein has been used to determine the relationships between ova of *Schistosoma mansoni* and *Schistosoma haematobium* and their snail hosts *B.alexandrina* and *B. truncatus*, respectively. Results of SDS-PAGE revealed that seven similar protein bands are found in ova of *S. mansoni* and its snail host *B. alexandrina* and five similar protein were recorded for the parasite *S. haematobium* and its snail host *B. truncatus*.

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The Department of Malacology at the Museum of Comparative Zoology (Harvard University)

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This year, 2010, marks the 150th anniversary of the opening of the Museum of Comparative Zoology (MCZ) at Harvard University. The enthusiastic oversight of past curators J.G. Anthony, W.J. Clench, R.D. Turner and K.J. Boss enabled the Department of Malacology at the MCZ to develop one the largest and biologically diverse collections in the world. Wooden drawers and cabinets have housed the collection since the late 1890s. By 1922 the cabinetry used and systematic arrangement of the collection was considered far more advanced than any other collection. The MCZ has recently initiated renovations that facilitate collections storage and conservation, collections-based research and teaching. In 2006, renovations began in the Department of Malacology and included the installation of new storage efficient collections cabinetry and shelving. Alphabetical reorganization sorted the specimens by family, genus and species. This cabinetry, shelving and specimen organization provides much needed space for collections growth and decompression, easier specimen retrievability and enhanced security. This poster provides a brief history and summary of recent and current activities within the Department of Malacology.

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Bivalves in Time and Space (BiTS): Developing Bivalves as a Preeminent Model for Macroevolutionary Studies

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Most evolutionary questions require an understanding of history, but analyses based exclusively on extant taxa require inferences whose uncertainties are poorly understood. With an excellent fossil record, bivalves are one of the few groups where methods can be confronted directly against historical data. This project aims to develop bivalves as a preeminent model for macroevolutionary studies. The project will address species-level evolution over time in Bivalvia. More importantly, we will test and develop generally applicable methods for comparative analysis of organisms. All studies will be conducted on two not-closely related clades, to estimate the generality of the results. This research will provide four primary contributions to evolutionary biology. (1) Estimate phylogenies for two clades (Cardiidae and the pitarine group in Veneridae) using a combination of multiple genes and morphological characters. (2) Integrate the extensive fossil records for the two clades by estimating combined-data phylogenies, adding extinct species to each extant combined-dataset. (3) Reconstruct temporal and geographic diversification patterns using the tree from (2) to assign all fossil occurrences to clades. The dense fossil sampling in the combined-data phylogenies will provide the framework for step (4), which will test the accuracy of three principal macroevolutionary methods: molecular clock dating, ancestral state reconstruction, and historical biogeographic reconstruction. We will cross-validate and rarefy the combined-data sets, subsampling fossils down to levels typical of macroevolutionary studies, to compare to the "known" dates/traits/ranges from the integration (2) and (3). Only the exceptional fossil record of bivalves makes it possible to treat the combined-data estimate of ancestral values as "known". The full integration of these three data sets with macroevolutionary diversification models and parallel tests of the three primary macroevolutionary methods will yield significant insights on the spatial and temporal dynamics of a major marine group, and establish bivalves as a key model system for macroevolution. [Supported by NSF award DEB-0919124/0918982/0919451].

Molecular Phylogenetics of Freshwater Snail Genus *Sermyla* in the Gulf of Thailand

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Freshwater gastropod, *Sermyla* sp. was the member of Subfamily Thiarinae; Family Thiaridae. They served as the intermediate hosts of human intestinal flukes like *Haplorchis pumilio*. Only one species of *Sermyla* in Thailand was observed by Brandt (1974). A revision of Thiarid snails in Thailand showed that there were several shell morphologies. Eight morphs of snails which were collected from six sampling sites: Klong Don Ko, Samut Sakhon Province (SrDK1 and SrDK2), Don Hoi Lot, Samut Songkram Province (SrDH), Bang Pu, Samut Prakarn Province (SrBP), Klong Pang Rad and Klong Hin Khao, Rayong Provicne (SrPR, SrHK1 and SrHK2) and Klong Sua Noi, Chachuengsao Province (SrSN). A comparative study of shell morphology and molecular data were analyzed. The conchology of SrDK2 was slightly different from the others in terms of size, rib and shoulder. Using Neighbor Joining Algorithm, Phylogenetic trees based on partial sequences of 12s ribosomal gene revealed that SrDK2 much closely related to *Thiara* sp.. This preliminary study inferred that the systematics among these taxa should be revised. [This work was supported by the Thailand Research Fund through the Royal Golden jubilee Ph.D. Program (Grant No. PHD/0195/2551) and Department of Biology, Faculty of Sciences, Silpakorn University, Thailand].

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Ancestral Patterns in Caenogastropods? Comparative Analysis of Larval Neurogenesis and Myogenesis in Limnic Cerithioidea

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Caenogastropods, comprising almost two thirds of all living gastropod species, play a pivotal role not only for our understanding of gastropod evolution, but also for assumptions on the origin of different life history strategies. In both cases, organogenesis is an important key for the essential identification of homologous structures. However, very few studies have been undertaken and attention has been paid mainly to more derived caenogastropods such as the Neogastropoda. Accordingly, we here document for the first time the development of the nervous system and the musculature in three more basal representatives within the Cerithioidea: *Thiara amarula*, *Melasma onca* and *Plotiopsis balonnensis*. These three closely related Australian Thiaridae exhibit distinct reproductive strategies, including different breeding modes. Our results are based on the application of fluorescence-coupled antibodies directed against the neurotransmitter serotonin, as well as F-actin labelling for muscles in conjunction with confocal laser scanning microscopy (cLSM). The first serotonergic signals appear in the developing central ganglia, and the peripheral neurons associated with the velum, foot and the visceral part of the veliger larva. As the caenogastropods are particularly notable for interspecific differences in the arrangement of serotonergic cells within the apical organ, we describe and compare this aspect in detail. At the onset of myogenesis the cephalopodial muscles form quite rapidly a complex network. In addition, the thiarids exhibit a shell attached larval retractor muscle and a paired accessory larval retractor muscle. The presence of these two retractor muscles represents most likely a plesiomorphic condition, as an accessory larval retractor is found as well in nudibranchs, patello- and vetigastropods, but not in the more derived caenogastropods that possess only one larval retractor. Our immunocytochemical data broaden the knowledge on neuro-and myogenesis and, thus, enable a better understanding of thiarid and gastropod development, in general.

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The Phylogenetic Position of Neritimorpha Based on the Mitochondrial Genome of *Nerita melanotragus* (Mollusca: Gastropoda)

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Relationships between the five major gastropod clades remain generally unclear, although there is currently broad agreement that Patellogastropoda is the sister group of all other extant Gastropoda and that Caenogastropoda and Heterobranchia are sister groups forming the Apogastropoda. Which of the Neritimorpha or Vetigastropoda is more closely related to the Apogastropoda is doubtful, although current evidence favours the former. Complete mitochondrial DNA sequences are available for four of the major gastropod groups but not for Neritimorpha, prompting this investigation of *Nerita melanotragus*.

The mitochondrial gene order in *Nerita* is apparently very nearly the plesiomorphic condition for Gastropoda. The only difference from the cephalopod *Octopus vulgaris* is a tRNA transposition that is also shared by Vetigastropoda and Caenogastropoda. There are no synapomorphic changes in gene order or transcription direction in any pair of Neritimorpha, Vetigastropoda and Caenogastropoda that would resolve their evolutionary relationships.

Analyses of the DNA of coding regions and rRNAs suggested that Neritimorpha belongs to a clade with Vetigastropoda and Patellogastropoda that is the sister group of Caenogastropoda. Excluding third codon positions, Neritimorpha was the sister group of Apogastropoda. This was the only analysis where the known extreme divergence of heterobranch sequences did not contradict this group.

Analyses of inferred protein sequences strongly supported monophyly of the clade comprising Vetigastropoda, Neritimorpha and Caenogastropoda, with the latter two strongly supported as sister groups.

Application of PCR-RFLP Analysis of mtDNA 16S rRNA Gene on Identification of *Conus* Species in Taiwan

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Conus is a kind of sea snails which have sting toxin(conotoxin) and diverse patterns. They anesthetize the preys through venom injecting by their harpoon-like radulae. Because of their specific characteristics, they can be alive in perilous environment over a long period of time. In spite of acute neurotoxicity, conotoxin still has the potency as a therapeutic medical agent on lenitive treatment. The purpose of this study is to authenticate Taiwan common *Conus* species. Three species of *Conus* were selected to identify species by using PCR technique with direct sequencing and the PCR-RFLP (polymerase chain reaction – restriction fragment length polymorphism) technology. The results showed that approximate 547 base pair fragment of the mitochondrial 16S rRNA gene was amplified from *Conus radiatus*, *C. australis* and *C. ochroleucus*. Furthermore, two restriction enzymes *Dra*I and *Ssp*I with specific cutting sites were chosen to obtain the digestion patterns from approximate 547 bp fragment and could distinguish these *Conus* species. The results indicated that PCR with direct sequencing and PCR-RFLP are easily and effectively tools for identification of *Conus* species.

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Ultrastructures of Germ Cells and the Accessory Cells During Spermatogenesis and Sperm Morphology in Male *Gomphina veneriformis* (Bivalvia: Veneridae)

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The morphology of the spermatozoon has a primitive type and is similar to those of other bivalves in that it contains a short midpiece with four mitochondria surrounding the centrioles. Accessory cells are observed to be connected to adjacent germ cells, they contain a large quantity of glycogen particles and lipid droplets in the cytoplasm. Therefore, it is assumed that they are involved in the supplying of the nutrients for germ cell development, while any phenomena associated with phagocytosis of undischarged, residual sperms by lysosomes in the cytoplasm of the accessory cells after spawning was not observed in this study. The morphologies of the sperm nucleus type and the acrosome shape of this species have a cylindrical and modified long cone shape, respectively. In particular, the axial filament appears in the lumen of the acrosome, and subacrosomal granular materials are observed in the subacrosomal space between the anterior nuclear fossa and the beginning part of axial filaments in the acrosome. As some characteristics of the acrosome structures, the peripheral parts of two basal rings show electron opaque part, while the apex part of the acrosome shows electron lucent part. These charateristics belong to the family Veneridae in the subclass Heterodonta, unlikely a characteristic of the subclass Pteriomorphia showing all part of the acrosome being composed of electron opaque part. Therefore, it is easy to distinguish the families or the subclasses by the acrosome structures. The number of mitochondria in the midpiece of the sperm of this species are four, as one of common characteristics appeared in most species in the family Veneridae.

Morphological and Molecular Systematics of the Pelagic Mubble-Rafting Caenogastropod Genus *Janthina*

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The caenogastropod family Janthinidae has achieved the transition from a benthic (sea floor) to neustonic (sea surface) habitat through unique and remarkable means; using specialized fast-setting mucus secreted by their foot, these remarkable snails trap air to build a bubble raft from which they hang upside-down. The family is grouped into the Epitonioidea with the benthic family Epitoniidae, based on a suite of putative synapomorphies, but this has not been tested with molecular characters. Molecular analysis of four species of *Janthina*, a taxonomically representative sub-sample of Epitoniidae, and exemplars of other ptenoglossan families and superfamilies (including Colgan's (2007) "GC group") using mt 16S+COI and nuclear 28S rDNA supports the monophyly of Epitonioidea. Molecular analysis of a global sampling of janthinids suggests that the most recent conchological taxonomy (Laursen, 1953) of the oviparous species is inadequate, at least for *Janthina prolongata*, and that his finding of cosmopolitan distributions for these janthinid lineages may therefore be erroneous. We present morphological data corroborating the four molecular clades of *Janthina* recovered: (*J. cf. prolongata* Pacific, (*J. cf. prolongata* Atlantic, (*J. janthina*, *J. exigua*))), using standard dissection, serial histological sections, and SEM of the radulae and protoconchs. Distinguishing species-level characters are present in the male and female reproductive systems, adult and larval shells, foot, salivary glands, gastric pouch, anterior intestine, and the proportions of the mantle cavity, kidney, and pericardium. Confirmation of the sister relationships of epitoniids and janthinids will now allow us to identify the synapomorphies underlying *Janthina's* bodacious ecological transition to a neustonic existence.

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Karyotypic Analysis of Two Veronicellid Slugs, *Laevicaulis alte* (Ferussac, 1821) and *Sarasinula plebeia* (Fischer, 1868)

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Analysis of karyotypes of certain species may assist in establishing phylogenetic relationships and understanding their evolution. Family Veronicellidae includes terrestrial slugs grouped together due to resemblances in anatomical and morphological characteristics only. Performing cytogenetic analysis on these slugs will confirm their positions under the family. The study aimed to subject two veronicellid slugs, *Laevicaulis alte* and *Sarasinula plebeia*, to karyotypic analysis to confirm their taxonomic positions within the family Veronicellidae. Thirty slugs from each species were collected and dissected, isolating their ovotestis. Squash technique was used, staining the chromosomes with aceto-orcein and viewing them under 55000x magnification. Results revealed that both *L. alte* and *S. plebeia* possess haploid (n) chromosome number of 17, falling within the range of the proposed chromosome number for Veronicellidae. Karyotypic analysis shows that the karyotype formula for the haploid chromosome number of *L. alte* is 4m+13sm while *S. plebeia* possesses the karyotype formula 4m+5sm+4a+4t. Results obtained can be used as reference for future studies when determining the karyotype evolution of veronicellids. The study performed was the first account on the description of the karyotype of *L. alte* and *S. plebeia*. This was also the first report on the haploid chromosome number of *S. plebeia*.

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Phyloproteomics: Species Identification of Freshwater Snails Genus *Melanoides* spp. from the East of Thailand Using Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry

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The suitability of a proteomic approach was explored to establish phylogenetic relationships among closely-related species. To evaluate matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) as a tool for rapid identification of 8 freshwater snails from Khao Kheow Open Zoo Reservoir, Chonburi Province (ME1), Ban Nong Pla Lai, Chonburi Province (ME2, ME3), Klong Hin Kow Canal, Rayong Province (ME4), Klong Pung Rad Canal, Rayong Province (ME5), Plew Waterfall Stream, Chanthaburi province (ME6), Sar-Keaw Pond, Sarkeaw Province (ME7), Khao Ee Toh waterfall, Prachinburi Province (ME8), proteins from foot of the snail were prepared and analyzed with Bruker Ultraflex III Maldi TOF/TOF MS. Spectra were reproducible from preparation to preparation and comprised approximately 200 peaks primarily representing proteins with masses up to 1000-100000 Da. Based on the cluster analysis of the MALDI-TOF spectra obtained, a dendrogram was generated by using the Clinprotool 2.2 software. MALDI-TOF MS analysis of proteins from foot of freshwater snails revealed a group of unique, characteristic, and reproducible spectral markers in the mass range of 6000-16 000 Da. The freshwater snail ME1, ME4, ME5, ME7 and ME8 were closely related to each other and were readily distinguishable from others including ME2, ME3, and ME6. These results suggest that MALDI-TOF MS offers a rapid, sensitive, low cost and reliable approach for performing phyloproteomics i.e., identification of snails in Thailand based on similarities within protein biomarker databases. [This work was supported by the Thailand Research Fund through the Royal Golden Jubilee Ph. D. Program (Grant No. PHD/0225/2550) and Department of Biology, Faculty of Science, Silpakorn University, Thailand].

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Survey of Nematodes, with Emphasis on *Angiostrongylus cantonensis* (Chen), from Global Populations of the Giant African Snail, *Achatina fulica* Bowdich, and Other Snails

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Achatina fulica serves as an intermediate host for the rat lung worm, *Angiostrongylus cantonensis*, which is a major concern from a human health perspective as it causes the food-borne disease eosinophilic meningioencephalitis (EME) or angiostrongyliasis. This study surveyed the presence of 3rd stage juvenile *Angiostrongylus contensis* from 10 global populations of *Achatina fulica* as well 2 populations of African *Achatina* sp. and 1 Philippine population of Laevicaulis alte using the 5' end of the rRNA gene as a molecular barcode for identification. *Angiostrongylus cantonensis* was detected in *A. fulica* populations in the Philippines and Tahiti and in the *Laevicaulis alte* population in the Philippines. This is the first confirmed report of *A. cantonensis* in *Achatina fulica* in Tahiti. Other worms found in these gastropods included 12 strongyloid species and 3 ascarid species that probably used the snails as intermediate hosts and 5 rhabditid species that probably used the snails as definitive hosts. One panagrolaimid nematode species each from Ogasawara and the Philippines most likely used *A. fulica* and *L. alte*, respectively, as accidental hosts.

Testing the Monophyly of Rissooidea

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The Rissooidea is one of the largest and most diverse molluscan superfamilies, with 22 recognized Recent families and includes marine, freshwater and terrestrial members. Recently published molecular analyses of caenogastropod relationships, including only a few rissooideans, have indicated that the group may be at least diphyletic. Within the marine members of the superfamily, only the relationships within Rissoidae have been phylogenetically examined, based on morphology, but there have been several molecular analyses encompassing components of the diverse freshwater members of the group, which comprise at least nine families. However, to date no comprehensive molecular and morphological phylogenetic analyses of most of the members of the superfamily have been carried out, and the relationships of rissooidean taxa with the assumed related superfamily Cingulopsoidea are also unresolved. Our research encompasses several species belonging to most of the families of Rissooidea and Cingulopsoidea based mainly on material collected from Australia, the Mediterranean Sea and New Zealand, and supplemented by material obtained from other parts of the world. Our aim is to generate combined phylogenetic analyses and test the congruence of commonly adopted morphological characters with molecular data. The phylogeny produced will be used to modify the classification of these groups where necessary. Preliminary phylogenetic hypotheses based on DNA sequences of 16S, 28S and 18S, obtained from a subset of taxa, are presented for the Rissooidea and the Rissoidae.

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Crystallographic Texture of Late Triassic Gastropod Nacre: Evidence of Long-Term Stability of the Mechanism Controlling Its Formation

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An analysis of the crystallographic texture of nacre (mother-of-pearl) in the Late Triassic gastropod *Wortheniella coralliophila* is presented. The primary aim of this study is to test the time stability of the crystallographic texture pattern of gastropod nacre over an extremely long time span. Our results show that the crystallographic axes of individual aragonite platelets in the Late Triassic *Wortheniella coralliophila* have an identical arrangement to those in living vetigastropods. The same microstructure as well as the crystallographic texture of nacre in Recent and Late Triassic gastropods implies the same biological mechanisms for its formation. Our study suggests that the proteins controlling the shape and orientation of individual nacreous platelets in living gastropods have not changed since the Late Triassic. The molecular mechanisms driving the origin and the development of gastropod nacre are thus extremely old and have remained unchanged for at least 220 million years.

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Smeagolidae of Japan – A Marine Pulmonate Family Newly Discovered from the Northern Hemisphere

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The genus *Smeagol* Climo, 1980 is bizarre, blind and white slugs discovered from the intertidal zone of a rocky shore in South Island, New Zealand. In his description of the type species *S. manneringi*, Climo attributed it to the new family Smeagolidae in the new order Smeagolida belonging to the subclass Gymnomorpha. Later Tillier (1984) regarded the Gymnomorpha as a polyphyletic taxon and synonymized the Smeagolidae with the Otinidae which was believed to be closely related to the Onchidiidae and Ellobiidae of the order Archaeopulmonata. Tillier and Ponder (1992) added four new species of *Smeagol* from southeastern Australia and New Zealand and revived the Smeagolidae as a distinct family from the Otinidae. However, because of their extremely strange morphology, the systematic position of *Smeagol* still remains uncertain and is known as one of highly important taxa for the phylogenetic studies of primitive pulmonates.

Recently, one of us (HF) found smeagolids in three localities of Japan: 1) Kitagishima Island, off Kasaoka, Okayama Prefecture; 2) Hienhama Beach, Amami Island, Kagoshima Prefecture; 3) Ishima Island, off Anan, Tokushima Prefecture. These are the first records of the Smeagolidae outside New Zealand and Australia. They were all found in the middle intertidal zone (about 1 m deep when high tide) on rocky shores. Japanese species are similar to *Smeagol* in external and radular morphology. However, they are extremely small (about 2 mm in body length) and the penis is less developed. Thus they are distinguishable from the species of the Southern Hemisphere.

Tillier and Ponder assumed that smeagolids may be Gondwanan judged from the previously known distribution records. However, it is doubtful because we found that their members are also distributed in Japan.

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Predation on Hardest Molluscan Eggs by Confamilial Snails (Neritidae) and Its Potential Significance in Egg-laying Site Selection

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Neritid snails (Gastropoda: Neritimorpha) protect their eggs in a hard capsule, of tough conchiolin, reinforced by mineral particles derived from the faeces and stored in a special sac near the anus and oviduct opening. Here we illustrate predation on this arguably hardest molluscan egg capsule for the first time; neritids of the freshwater to brackish-water genera *Clithon* and *Vittina*, generally classified as herbivores, feed facultatively on the eggs of various confamilial species. In aquaria, the egg capsules were frequently attacked by all species of *Clithon* and *Vittina* investigated, but by none of two other freshwater neritid genera, *Neritina* and *Septaria*. Our preliminary molecular phylogeny of Neritidae suggests somewhat ambiguously that *Clithon* and *Vittina* form a terminal clade in the family and that the egg-feeding behaviour may have evolved only once as a synapomorphy.

Each predatory snail spent a long time (4.9 min on average) creating a hole in the capsule wall by repeated radular rasping. Once it broke through the wall, it sucked up all eggs inside by the pumping action of the buccal cavity (3.3 min). Almost all consumed capsules retained a part of the lid with a broken edge; they can therefore easily be distinguished from hatched capsules, where the lid is lifted off when the young escape. Intensive predation pressure by these common inhabitants in Indo-West Pacific coastal streams may have given rise to the remarkable egg-laying behaviour of *Neritina* on the shells of other living snails. *Neritina* species deposited clusters of egg capsules more frequently on the living shell than on other substrates, and that the predation rate was significantly lower on this moving ‘nursery.’ Predation rate was even lower on the small capsules of *Clithon* and *Vittina* themselves, which were deposited one by one in the depressions on the rough surfaces of stones.

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Epibiosis on *Jujubinus striatus* in an Eelgrass Bed in Southern Spain

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Seagrass beds represent an important habitat for some invertebrates, including molluscs and sessile animals such as epibionts. In eelgrass beds the availability of hard substrate for settlement of epibionts is restricted to some parts of the plant (shoots), pebbles, bioclasts and shelled invertebrates such as the gastropods. We have quantified the epibiosis on dominant gastropods of an eelgrass bed in southern Spain, with special emphasis on the top dominant *Jujubinus striatus*.

Epibiosis is common on most species but displaying a different composition of epibiont taxa and degree of colonization that may be related to shell features and to behaviour. For example, epibiosis was low (< 25%) on species with smooth shells (*Smaragdia viridis*, *Calliostoma planatum*) and also on species that bury in the sediment (*N. pygmaeus*, *N. reticulatus*). On the other hand, epibiosis on *J. striatus* (living in the leaf canopy and with a striated shell) affects 90 % of its population, to the point of covering the entire shell of adult individuals. Epibiosis in small size individuals of *J. striatus* varies with seasons along the year, with a maximum settlement in summer months. A relationship between growth of the gastropod and number of epibionts and colonized area has been obtained. In adult individuals, there may be massive growths of epibionts which can outweigh the supporting individuals, thus affecting negatively their viability.

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A Molecular Phylogenetic Analysis of Amphiboloidea (Gastropoda: Heterobranchia)

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The Amphiboloidea are a small (~13 named species) but exceptional group of intertidal mangrove- and mudflat-dwelling snails which were recently revised to include several new taxa based on anatomy. Their unusual combination of anatomical and ecological characters, such as the presence of an operculum and pneumostome, bizarre reproductive anatomy, and intertidal estuarine lifestyle, suggests that they may represent a lineage which diverged early in the evolution of pulmonate gastropods. Some recent molecular analyses of Heterobranchia have suggested that they belong at the base of Pulmonata in a clade with Glacidorboidea and possibly Pyramidelloidea. The internal relationships of Amphiboloidea have not yet been tested using molecular data. In this first molecular phylogeny of the Amphiboloidea, COI and 16S mtDNA sequences from all but one of the known species of Amphiboloidea, plus several unnamed taxa, and 28S rDNA sequences from a subset of taxa, strongly supported the monophyly of the superfamily and its position at the stem of, or possibly outside, Pulmonata. A Bayesian phylogenetic analysis of Amphiboloidea using BEAST software revealed ancient genetic differentiation between lineages, especially the peculiar monotypic family Maningrididae (*Maningrida arnhemensis*), which is basal to the remaining amphiboloids. The inclusion of specimens from multiple Southeast Asian locations across the distribution of *Salinator burmana* showed that this name has been applied to several undescribed taxa belonging to two genera.

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Characteristics of Bathyal Gastropod Fauna off the Pacific Coast of Northern Japan

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The Molluscan fauna off the Pacific coast of northern Japan has been fairly well surveyed since the beginning of the 20th century, both in connection with the prosperous deep-sea shark fishery and via cruises by research vessels such as the USFC *Albatross* and R/V *Soyo-Maru*. Nevertheless the general picture of the gastropod fauna in this area remains unclear. This is due to a lack of knowledge of the smaller species and the insufficiency of material with sufficient depth and position data to elucidate the range of intraspecific variation, even in common species.

The present study is a detailed taxonomical investigation based on specimens collected by means of otter trawls or dredges in an area from off the Shimokita Peninsula (40°N) to off Joban (36.5°N) within a depth range of 200 to 1500 m, during the years 2005 to 2008. Considerable variation was found in many taxa, but at the same time some confusingly similar species were separated. In total, ca. 1800 lots of specimens were classified into 177 species representing 38 families; 117 were identified to species level (at least tentatively), whereas 60 (34%) were not identifiable with any species previously known in the northern hemisphere. With regard to the species assemblages, boreal components comprise 52% of the total identified to species level, and temperate components 11%. Excluding the undetermined (and mostly undescribed) species, the remaining 37% are considered endemic to this area, although most of them have closely related counterparts in boreal waters. This suggests a predominantly boreal origin for this fauna. A clear biogeographical border is present around Sagami Bay, and this may be related to the bottom topography.

What Is the Impact of Invasive Plants on Land Snail Assemblages in the Alluvial Ecosystems?

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Invasive plants are recognized as a major threat to the biodiversity over the world. It is generally known that invasive plant species can modify soil properties such as nutrient content and can directly influence the composition of the original vegetation. However, it is very little known about their impact on invertebrate soil fauna communities in terms of density and diversity. We investigated the impact of five exotic invasive plant species, *Fallopia sachalinensis*, *Fallopia japonica*, *Fallopia bohemica*, *Impatiens glandulifera* and *Helianthus tuberosus*, on land snail assemblages in the alluvial ecosystems in the Czech Republic. The main project objective was a comparison of the snail assemblages of the natural alluvial ecosystems and invaded river floodplains within the area of the Labe River lower course tributaries. One of these tributaries was Ohře River in the western Bohemia. There were 47 invaded and non-invaded sites researched and the resulting data are presented.

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Tissue- and Species-Specific Accumulation of Trace Metals in Two Land Snails (Gastropoda: Pulmonata)

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We examined the tissue distribution of six trace metals (Ag, Cd, Cr, Cu, Ni and Zn) in two land snails (*Cepaea nemoralis* and *Succinea putris*) at four polluted and four reference plots by means of ICP-AES. Animals from polluted plots had elevated levels of Ag, Cd and Zn in their tissues. At the polluted plots the metal concentrations in the tissues of both species may be: (1) different among polluted plots, (2) tissue-specific (with for most metals highest levels in the digestive gland and lowest levels in the albumen gland; but with high levels of Cu in the foot), and (3) species-specific (higher levels of Ag, Cr, Cu and Ni in the foot in *C. nemoralis*). Therefore, it will remain difficult to provide general explanations for the observed patterns of metal accumulation. Moreover, it means that the definition of bioavailability of metals should not only incorporate dietary and behavioural factors that govern pollutant uptake, but also that it has to be species-specific.

Diversity of Central European Urban Land Snails

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Effect of urban habitats on species composition and diversity of land snails was assessed in 32 large cities of 10 countries in Central Europe. In each city, species composition of all land snails was recorded in seven 1-ha plots. Each plot represented one urban habitat with different disturbance regime: city square, boulevard, residential area with compact building pattern, residential area with open building pattern, park, early-successional and mid-successional site. For each plot we collected temperature and precipitation data. A total of 87 snails were recorded. Both habitat types and climate had significant effects on species composition with no shared variation between these two predictors. Habitat types explained higher proportion of the total variance in snail assemblages (8.2%, respectively) than climate (6.3%). Main differences in species composition of land snails were between strongly urbanized plots with high proportion of annual plants situated in city centers and early-successional and mid-successional sites. Comparatively small differences were found between species compositions of parks and both types of residential areas. The number of species of snails was lowest in the city squares, followed by boulevards and early-successional sites and boulevards, residential areas and parks, and reaching the highest values in the mid-successional sites. High beta diversity of snail assemblages was observed among habitat types, with city squares and early-successional sites being most variable among cities and residential areas being least variable.

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Living Monoplacophorans: Morphological Conservativeness or Recent Diversification?

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Until the discovery of the first living specimens in 1950's, Monoplacophora was thought to be a long extinct group of Cambrio-Devonian ages (540-375 Mya). Most extant species are still exceedingly rare and represented only by empty shells or a few live-caught animals from the deep sea. This rarity has rendered our knowledge insufficient for a rigorous ingroup classification. The extant monoplacophorans have generally been classified into eight genera based on slight and inconsistent differences in shell shape and sculpture, radular morphology and external anatomy. Morphological conservativeness over a long span of time in a 'living fossil' lineage may theoretically result in distant but closely resembling taxa, and this idea apparently led some authors to recognise as many as six families and three superfamilies for only a few dozens of living monoplacophoran species. However, no genetic or fossil data has been available to date regarding diversification among the living monoplacophorans.

In October 2009 a single specimen of a new monoplacophoran species was found alive on a siltstone dredged from 816-841 m deep off Mie, Japan, as the first record of the class from the western Pacific. The cancellated, small-sized shell (3.15 mm) indicates its position in either *Veleropilina* or *Rokopella*. Other morphological details of the specimen, however, blur the distinction of the two genera and *Rokopella* is considered to be a junior synonym of *Veleropilina*. Approximately 6-kb DNA fragments from the new *Veleropilina* are intriguingly similar to the homologous sequences of *Laevipilina*, the only other monoplacophoran group so far available for genetic studies. Our phylogenetic analyses estimated that the divergence of *Veleropilina* and *Laevipilina* dates back only to late Cretaceous or early Cenozoic, despite their prominent morphological differences. These findings suggest that the Recent Monoplacophora have radiated fairly recently from a small, cryptic lineage with ordinary rates of morphological evolution.

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Invasive Veronicellid Slugs in the Main Hawaiian Islands

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The Veronicellidae include some of the most damaging and widespread slugs in Hawaii. These invasive slugs have become major domestic, agricultural, and environmental pests. The first record of a veronicellid in Hawaii was in 1900. However, the different veronicellid species are difficult to distinguish and correctly identify, and the focus of this study was to resolve this problem, which has led to considerable confusion as to the actual species present in Hawaii. According to historical collection data (Bishop Museum) and literature reports, and more recent surveys, three species have been recorded: *Laevicaulis alte*, *Sarasinula plebeia*, and *Veronicella cubensis*. I have re-examined these collections using three approaches. External morphology can distinguish the black slug, *L. alte* from the other two, but it was not possible to distinguish *S. plebeia* and *V. cubensis* reliably by external morphology. Adult specimens of these two species were therefore dissected and distinguished on the basis of key reproductive structures. Juveniles, however, could not be distinguished by dissection, so a DNA sequencing approach involving the 16S mitochondrial marker was used and proved reliable for distinguishing individuals with undeveloped reproductive structures. Using a combination of these three approaches, I am now able to confidently identify these veronicellid species. A number of specimens labeled as *S. plebeia* in the Bishop Museum and more recent collections were sequenced and shown to be *L. alte* or *V. cubensis*. It is possible that the brown slug, *S. plebeia*, may never have been in Hawaii or that it was but was not able to establish.

Dart Shooting and Mucus Effects on Reproductive Organ of Dart Recipients in a Species of Bradybaenid Land Snails

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Dart shooting is one of the impressive mating behaviors of hermaphroditic molluscs. The roles of dart shooting have been examined in many studies using helicid land snails. Those studies have revealed that darts are applied with mucus from mucus glands and transfer it to dart recipients and that the substances from mucus glands lead temporary structural change of the reproductive organ of dart recipients. In addition, dart shooting increases the paternity of dart shooters as dart recipients lay more eggs using the sperms of them. However, effects of mucus have tested only in a few species of helicid snails. In many species of stylommatophoran land snails, including Helicidae, bursa tract diverticulum (BTD) where a spermatophore of mating partner is transferred exists in reproductive organ and the known case of structural change induced by mucus is on BTD and its surrounding parts. However, not all species that bear darts and mucus glands have BTD in their reproductive organs. Although the phylogenetic relationship between BTD-bearing and mucus-bearing traits is not clear, to know how mucus has evolved in land snails, it is essential to examine the effects of mucus in BTD-lacking species. We examined mucus effects in bradybaenid snails that lack BTD and discuss mucus evolution.

Shell and Radula Morphology of Freshwater Snails Genus *Melanoides* in the East of Thailand

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Shell and radula morphology of freshwater snail genus *Melanoides* were studied for species identification. Eight groups of snail were collected from the East of Thailand. Ten snail samples were examined by sampling in every each groups. A total of 80 snails were differentiated by size and characteristic of shell and radula. The shell morphology was studied by Conchology, and the radula meristic characters was examined and counted using light microscope and scanning electron microscope. The cusps regardless of the size, were counted from ME1, ME2, ME3, ME4, ME5, ME6, ME7 and ME8 snails. The lateral cusps of the central teeth were 3:1:3 (50%) or 4:1:4 (50%), 2:1:2 (100%), 2:1:2 (50%) or 3:1:2 (50%), 2:1:3 (100%), 2:1:3 (15%) or 3:1:3 (15%) or 3:1:4 (20%) or 5:1:4 (50%), 3:1:3 (100%), 2:1:2 (100%) and 3:1:3 (100%), respectively. The number of cusps on the central tooth was species-specific; they were distinct regular sized lateral cusps in snails from Nong Pla Lai, Chonburi Province (ME2), Klong Hin Kow Canal, Rayong Province (ME4), Sar Keaw Pond, Sarkeaw Province (ME6), Plew Waterfall Stream, Chanthaburi province (ME7) and Chanthaburi River, Chanthaburi province (ME8). The statistical analyses included principal component and stepwise discriminant analyses using SPSS 11.5 for Windows. Principal component analysis was used to verify the existence of taxa, whereas stepwise discriminant analysis was used to maximize the separation of taxa. For discriminant analyses were performed both with and without the characteristic of radula. The percentage correct classification was higher when the including radula. The snails ME2, ME3 and ME8 were correctly classified. Whereas, there was some overlap of ME1, ME4, ME5, ME6 and ME7. [This work was supported by the Thailand Research Fund through the Royal Golden Jubilee Ph. D. Program (Grant No. PHD/0225/2550) and Department of Biology, Faculty of Science, Silpakorn University, Thailand].

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A Comparison of Anatomical Data Collected by Computer Tomography (micro-CT) and Histological Sections on Small, Skeneimorph Vetigastropoda

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Anatomical and morphological data are crucial to shed some light onto the polyphyletic assemblage of skeneimorph vetigastropods. Until now histological semi-thin sectioning of plastic embedded material was the only way to get these data sets. Recent methodological progress allows us to get computer tomographic (CT) data sets with high resolution in micro scale. In this study a specimen of *Protolira valvatoides* Warén and Bouchet, 1993 (diameter soft parts approx. 1.8 mm) was investigated by CT-scan (thickness 1.5 µm). Anatomy and 3D reconstructions are compared with the data of *Munditiella ammonoceras* Adams, 1863 (diameter soft parts approx. 1.4 mm) serially sectioned with a histo-jumbo diamond knife. 3D-reconstructions of the data sets were performed using the software AMRIA, to compare the anatomical information of both methods. The manual histological section and the virtual CT sections were also compared to their morphological significance. CT-data are very helpful to get perfectly aligned section series without destroying critical point dried soft parts. Also it is a good method to investigate problematic specimens, e.g. those containing stones in the mantle cavity or the intestine, which cannot be sectioned with diamond knifes. The resolution of the CT-scans does not reach the same quality as a good histological section series photographed with digital camera setup. Especially small details like tiny nerves or histological details are missing. CT-scans are really helpful getting a first, fast overview of the general anatomy, but they cannot replace semi-thin sectioning concerning the microanatomy of these small gastropods.

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Emergence of the American Blood-Fluke Snail *Biomphalaria tenagophila* in Europe and Monitoring of Introduced Freshwater Snails in Hungary

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Tropical snails belonging to the genus *Biomphalaria* are known as intermediate hosts of *Schistosoma mansoni* trematodes in Africa and America. Though some *Biomphalaria* species had been introduced to certain tropical and subtropical areas outside their historical range, it has been assumed that there is no risk of their emergence in the temperate zone because of the snails' ecological needs. Here we report a stable population of South American *B. tenagophila* in Europe established in the Carpathian Mountains, where winter temperature regularly drops below zero. This provides evidence that schistosome intermediate hosts may be able to survive in the temperate zone and calls attention to the dangers of inadvertent introduction of these hazardous species into new territories.

In 2005 and 2006, malacological collections took place in a hypothermal spring near Răbăgani, Romania close to Hungarian border. We collected hundreds of shells and living planorbid snails. Based on shell morphology and anatomical examination we identified snails tentatively as *B. tenagophila*. Considering the extreme variability of the morphological characters in this genus we carried out a molecular biological study to confirm this result. DNA was extracted and amplificated the partial 16S ribosomal RNA gene. Sequencing revealed 99.74% similarity to *B. tenagophila* (Brazil) sequences deposited in GenBank. A haplotype network showed one base difference to the Brazil and two bases to Congo and Paraguay isolates, respectively. These data unambiguously proved the occurrence of *B. tenagophila* in Romania. Since the snail has been present in this brook for at least 4 years this species has not only been introduced, but also established in Răbăgani.

Because of the hazard of introducing *Biomphalaria* snails a survey was launched to reveal their presence in Hungary. Till now *Biomphalaria* species haven't been detected in Hungary, although the close related *Planorbella* (*Helisoma*) snails are frequent in some springs.

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Radula and Operculum Anatomy of *Theodoxus* Montfort, 1810

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Theodoxus, belong to gastropod family Neritidae, common in the freshwaters around Antalya and adjacent provinces was investigated anatomically because of striking complexity in their shell morphology. Scanning electron micrographs of radula and operculum of the samples were studied. Radula showed characteristic teeth formula of rhipidoglossate, but differred structurally. Opercular anatomy showed significant differences in their peg and ridge formations. *T. altenai*, *T. anatolicus*, *T. heldreichi* and *T. fluviatilis* were discriminated in the area. It, however, was revealed that some of the diagnostic characters of *Thedoxus* spp. need to be revised.

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Cause of Bimodal Distribution in the Shape of a Terrestrial Gastropod

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The distribution of a phenotypic state is often discontinuous and dispersed. An example of such a distribution can be found in the shell shapes of terrestrial gastropods, which exhibit a bimodal distribution whereby species possess either a tall shell or a flat shell. Here we propose a simple model to test the hypothesis that the bimodal distribution relates to the optimum shape for shell balance on the substrates. This model calculates the theoretical shell balance by moment and obtains empirical distribution of shell shape by compiling published data and performing a new analysis. The solution of the model supports one part of the hypothesis, showing that a low-spired shell is the best balanced and is better suited for locomotion on horizontal surface. Additionally, the model shows that both high- and low-spired shells are well balanced and suited on vertical surfaces. The shell with a spire index (shell height divided by diameter) of 1.4 is the least well balanced as a whole. Thus, spire index is expected to show a bimodal distribution with a valley at 1.4. This expectation was supported by empirical distribution of a spire index, suggesting that the bimodality of shell shape in terrestrial gastropods is related to shell balance.

The model also showed the optimum shell swelling and the optimum angle of elevation of the coiling axis as follows: (1) low-spired gastropods should have pointed shapes as cone and large angles (90°), (2) high-spired gastropods should have rounded shapes as column and small angles (0°). We measured swellings and angles of terrestrial gastropods to test these predictions.

Studies on Giant Clams (Family Tridacnidae) in the Northern Territory, Australia

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Giant clams (family Tridacnidae) are a conspicuous and iconic element of coral reefs throughout the Indo-Pacific. Despite international protection from illegal trade and harvest, wild stocks of giant clams continue to rapidly diminish across the region to the point of local extinction; a situation potentially exacerbated by both climate change and anthropogenic pollution. Although populations of giant clams are stable within Australian and its Territorial waters there has been a relative paucity of research outside of the Great Barrier Reef beyond surveys of abundance. Seven species of giant clam are recorded from the northwestern Western Australian and tropical eastern Australian coasts but, oddly, the rocky and coral reefs of the Northern Territory coast appear to support only a single species, *Tridacna squamosa* (fluted giant clam). This research is the first to investigate the abundance, distribution, phylogenetic and population diversity of giant clams within the coastal reefs of the Northern Territory. From transects surveyed by a remotely operated video camera, estimates will be made of abundance, spatial distribution, size, and habitat preference. Non-lethal biopsies of randomly selected specimens will be sequenced for multiple genes (16s, 18s and COI) and microsatellites. Preliminary results suggest that there is only a single species (*T. squamosa*), with little variation within the 16s gene either within or between populations. Populations of giant clams around offshore islands may be relatively pristine, compared to mainland coastal reefs, and may have densities orders of magnitude greater than populations in similar habitats in the Indo-Pacific.

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A Simple PCR Method for the Identification of the Wedge Shell *Donax trunculus*

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The wedge shell *Donax trunculus* is an important bivalve commercial species in Portugal which can be easily confused with another three morphologically similar species (*D. semistriatus, D. vittatus* and *D. variegatus*) that have a lower market price. This may lead to situations of species mislabelling either unintentionally or deliberately when made available to retail sale. This scenario becomes even worst when only the edible part is sold as a processed product.

To overcome this problem, European Union introduced the Council Regulation EC 104/2000, stating that fishery product may not be offered for retail sale unless appropriate marking and labelling indicates commercial designation of the species, the production method and the catch area. Thus, the setting up by independent laboratories of fast, reliable, reproducible and low cost techniques to identify bivalve species used as raw material is an important goal for both food safety and consumer rights protection.

In this study we present a simple PCR methodology for the accurate identification of *D. trunculus* based on the amplification of the nuclear marker 5S with a set of oligonucleotides. This methodology was already applied successfully in Ensis species. The PCR amplification results showed that it is possible to differentiate *D. trunculus* from the remaining *Donax* species, since fragments of *D. trunculus* were about 275-300bp while the other three species present fragments of higher molecular weight.

DNA extraction using CHELEX resin was compared with other technique (bivalve specific) in order to determine if there is any advantage in its application. The results showed that CHELEX is undoubtedly faster, simple (less intermediary steps), cheaper and is as reliable as bivalve specific method, allowing to obtain DNA from a tissue sample in only half an hour.

Biogeographic Distribution of Gastropod Associated Mangrove from Thailand

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Molluscs, particular gastropods are one of the most dominant invertebrate groups in the mangrove community of the World. The main objective of this study is to examine the basis biogeographical distribution of mangrove gastropods in Thailand that on the basis of literatures since 1974 and personal data. Thai mangrove has been divided into four zones; At Center, Eastern and Southern the Gulf of Thailand and Andaman Sea. Seventy-one species belonging to sixteen families were recorded that the number of species from family Neritidae (13 species) is highest, following Littorinidae (10 species) and Ellobidea (9 species) respectively. Andaman Sea shows the highest number, forty-five species while with lower species numbers were recorded at the Centre, twenty- eight species. *Ellobium aurisjudae, Cassidula aurisfelis, C. multiplicata* (Ellobiidae), *Littoraria melanostoma, Littoraria pallescens, L. strigata* (Littorinidae), *Neritina violacea* (Neritidae), *Cerithidea cingulata* (Potamididae) and *Assiminea brevicula* (Assimineidae) are commonly found in Thai mangrove habitat. The similarity analysis based on present and absent shows that some possible geographic linked between mangrove region in the East and South Gulf of Thailand.

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Freshwater Molluscs Introduced in Belgium in the Last Two Decades

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Invasions of freshwater molluscs have become a major concern due to the increase of transoceanic transport and the expanding inland waterways. Therefore, we present distributional data on four invasive freshwater molluscs introduced in Belgian inland waters in the last two decades. The invasive clams *Corbicula fluminea* and *C. fluminalis*, native species in Asia, but also known from the Lower Pleistocene in NW Europe, were reintroduced in Europe in the 1980s. The first Belgian record dates from 1992. The Unionacean bivalve *Sinanodonta woodiana*, also known as the Chinese mussel, is a native of S.E. Russia (Amur river), China and Cambodja. Its glochidia reached European waters in 1962 with imported fish. Both juvenile and adult specimens were found in Belgium in a fishpond in 1999.The quagga mussel *Dreissena rostriformis bugensis* originates from the Ponto-Caspian area. By 2006 it reached The Netherlands. In 2009 it was found in Belgium. We assume that the quagga mussel spread via the Main-Danube canal, as did so many other Ponto-Caspian invaders. The freshwater pulmonate gastropod (Planorbidae) *Menetus dilatatus* is native in the eastern part of the U.S.A. In 1998 it turned up in Belgium. Finally, the North American ancylid *Ferrissia fragilis* is a cryptic invader of European and East Asian freshwater ecosystems. We summarize the known records of this overlooked freshwater snail in Belgium.

Observing and quantifying the progress or decline of any species is a time consuming discipline. Unfortunately traditional taxonomy (based on phenotypes), a vital part in the process, is on the decline and in need of a popularity boost to attract young scientists.

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DNA Barcoding Indonesian Acanthopleurinae (Polyplacophora)

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The approximately 14 recognized species of Acanthopleurinae worldwide include conspicuous and large tropical shore chitons of the genera *Acanthopleura*, *Liolophura*, and *Squamopleura*. They are well studied for their impressive homing behavior, shell eyes (ocelli), radular biomineralization, and bioerosion activities, but have a relatively shallow fossil record, not recorded from before the Miocene. The accessibility of these chitons on the shores of Indonesia made them an excellent test case for new efforts to DNA barcode biodiversity, training and employing Indonesians with the objective of initiating a more complete assessment of biodiversity throughout the Coral Triangle. The latest monographic treatment including Acanthopleurinae was published in 2006 and reports only four members of this taxon in the vicinity of Indonesia: *Acanthopleura spinosa* (Bruguière 1792), *A. gemmata* (De Blainville 1825), *Squamopleura miles* (Carpenter in Plsbry 1893), and *S. curtisiana* (Smith, E. A. 1884). Here we apply current and accepted DNA barcoding methods to assess biodiversity in Acanthopleurinae throughout Indonesia, also employing available published or unpublished relevant sequences. Because Indonesian marine research has been historically underrepresented in the international scientific community until recent years, we hypothesized that we would discover new operational taxonomic units (OTUs), which could represent previously-undescribed species. If the Coral Triangle acts as a center of origin of chiton biodiversity, we hypothesized that the phylogenetic positions of the Indonesian chitons will be more derived than described species. Our combined analysis of mitochondrial COI and 16S rDNA gene portions for over 200 Acanthopleurinae from Indonesia has confirmed this expectation. Our preliminary analyses have identified as many as 11 OTUs, indicating that either cryptic species or strong phylogeographic structure are to be expected in this region of known high endemism. We conclude by making recommendations for future intertidal research in Indonesia and the Coral Triangle.

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Population Expansion and Color Polymorphism in *Umbonium costatum* on a Shallow Sandy Bottom Off Niigata, Japan Sea Coast

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Filter feeding molluscus are one of the major components in coastal sandy bottom ecosystems. These filter feeders are known to exhibit large population fluctuations, which prevent stability of local fisheries. We focused on a recent population expansion of a trochid gastropod species, *Umbonium costatum*, in order to understand the process of the population fluctuation. *U. costatum* is one of the major filter feeders of the study site at Niigata (139E, 38N), on the Japan Sea coast, and its geographic range extends from 30N to 45N. In the summer 2007, abundant juveniles of *U. costatum*, which showed polymorphic shell color types, were captured by dredge (50 cm span, 2 mm mesh diameter) surveys at 2 - 10 m depth points. Majority of the *U. costatum* shells were brown (80%) and black types (20%): only 1 - 2 % shells were white type. Proportion of the black type slightly decreased in the dead shell samples. Subsequent seasonal and yearly surveys showed that a cohort with a mode of 3.5 mm shell width in the summer 2007 disappeared by the next winter. In the summer 2008, a new cohort with 3 - 8 mm mode appeared more abundantly than the previous summer. Individuals of this cohort grew steadily and survived the next winter. In the summer 2009, the size frequency histogram showed two peaks: one represented the new recruits and the other the 2008 cohort. Dead shells with a hole (preyed on by naticid gastropods) increased in proportion in the summer 2009. These results suggest that the abundant recruitment and the success in over-wintering survival are the key factors for the population expansion, but the following increase of predation risk will lead to decline of the *U. costatum* population.

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Molecular Phylogeny of Japanese Species of the Assimineinae (Caenogastropoda: Assimineidae)

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Fukuda and Ponder (2003) divided 48 assimineid genera from the world into three "Groups" on the basis of the presence/absence of the cephalic tentacles and the basal cusps of the central radular teeth. Most of Japanese estuarine assimineids belong to Group 1 (Assimineinae). Four genera, *Rugapedia*, *Paludinella*, *Solenomphala*, and *Taiwanassiminea* were assigned to Group 2 (Ekadantinae), and *Paludinellassiminea* and *Ditropisena* to Group 3 (Omphalotropidinae).

More than 20 species of the Assimineinae are known from estuarine habitats of Japan. Some of them are locally abundant and important members of ecosystems in brackish waters. However, identification of these taxa based on external morphological characters is often difficult. About 60 % of them are undescribed, and 20 % do not have even available generic names. The relationships of species and genera still remain uncertain. Therefore, this is a major impediment for faunal surveys, ecological research and environmental assessments.

We revised Japanese assimineines by means of comparative anatomy and molecular phylogeny. The results showed that each of *Assiminea*, *Angustassiminea*, *Pseudomphala* and *Ovassiminea* was monophyletic and recongnizable as a distinct genus. *Ovassiminea* was the sister taxon of Australian *Cryptassiminea*. These five genera and four other undescribed genera formed a large clade which is regarded as the Assimineinae.

Taiwanassiminea and *Paludinella* in Group 2 were included in the Assimineinae. Thus, Group 2 is polyphyleticand the Assimineinae need to be redefined. *Assiminea* s. str. of Japan consists of 13 species, 9 of which are still undescribed. *Assiminea parasitologica* is closely related to *A. grayana* (type species of *Assiminea*; western Europe) and *A. violacea* (type of *Euassiminea*; China).

Cold Hardiness of the Invasive Freshwater Apple Snail *Pomacea canaliculata* Lamarck

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The apple snail *Pomacea canaliculata* (Caenogastropoda: Ampullariidae*)* was introduced into Japan and many countries in Southeast and East Asia in the early 1980s. This freshwater snail originally from South America, was initially introduced as a human food. However, commercial markets failed, and escaped snails invaded rice ecosystems, becoming a serious pest of rice in many countries.

The apple snails inhabiting temperate Japan showed seasonal adaptation to cold weather, with enhancement of cold hardiness before onset of winter. Gradually descending temperatures (cold acclimation) enhanced cold hardiness and limited water availability (dryness) also increased cold hardiness to a certain extent even at high temperature. Photoperiod did not affect cold hardiness. Physiologically, cold-tolerant snails show an increased concentration of glycerol in their bodies with decreasing glycogen concentration.

We compared cold hardiness among snails collected in Japan and tropical Philippines. Snails from the Philippines demonstrated the same response to cold temperature (enhancement of cold hardiness) which they had never experienced in the natural condition. Moreover, cold hardiness of Philippine snails both with and without cold acclimation was identical with that of the counterparts in Japanese snails, in spite that it had been over 30 years since the introductions of apple snails into both countries having different climates. Cold-tolerant snails with cold acclimation survived longer after exposure to desiccation than cold-intolerant snails. This linkage of tolerances against cold and desiccation stress might contribute to retain the response of tropical snails to cold temperature.

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Bacterial Symbionts in Marine Nudibranch Molluscs: Invention or Reality?

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The lipid composition of marine organisms can provide valuable physiological and ecological information. The fatty acids may serve as biological markers for elucidation of symbiotic association of the mollusks with bacteria and for determination of food sources. Tropical nudibranch molluscs *Dendrodoris nigra*, and *Risbecia tryoni* collected from waters of the Northwestern Pacific were investigated for lipids and fatty acids. A histological and ultrastructural research of the notum, mantle edge, digestive gland and gonads was performed. The fatty acid composition of *D. nigra* and *R. tryoni* differed greatly from that of other marine gastropods. They displayed large amounts of very long chain fatty acids known as demospongic acids characteristic of marine sponges, thus suggesting predation on sponges. Another unique feature concerned an abundance of various odd and branched fatty acids which could have originated from symbiotic bacteria. Ultrastructural observations of the tissues revealed symbiotic bacteria in the epithelial cells of the notum and mantle edge. These single bacterial cells located mainly in the apical part of the epithelial cells and between microvilli were gram negative. Their density, appearance and localization within the nudibranchs pointed to their functional relationships and active reproduction. A histological and ultrastructural examination of the digestive system and gonads revealed no bacteria. This suggests that bacteria do not play a digestive role in the nudibranchs. Nudibranch molluscs unprotected by a shell are protected by an effective chemical defense. Microbial association is able to produce secondary metabolites; therefore we suggest that these endosymbiotic bacteria are likely to provide the chemical defense of the nudibranch molluscs from pathogens and predators.

Social Control of Sex Change in Scallop *Patinopecten yessoensis*: Response to Population Composition

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Sex structure is very labile and specific for each population as it is a result of genetic, ontogenetic and biocenose effects on the mollusc population. This study using field observations on the sex ratios in the populations of the scallop *Patinopecten yessoensis* (Jay) showed that different age groups had highly variable sex ratios. Age-frequency analysis of scallop populations indicated that females became more prevalent as the age increased, with significantly more females occurring in the oldest age groups for all studied populations. The significantly greater age of females suggests a protandric sex reversal. This is not a case of strict protandry, as a small percentage of scallops first became female without any preceding male phase. It was revealed that in different populations the sex change was occurred at different scallop age. At populations that predominantly consisted of young (2–4-year-old) individuals the males prevailed over females in 2 year age group, the equal ratio was found in 3 year class, and in older age groups the females prevailed over males. Another pattern was observed in the populations mainly consisted of middle aged (5–6-year-old) individuals. Here, the equal sex ratio was respected to age about of 4–6 years. In the oldest populations (mainly 6–12-year-olds) the equal sex ratio was respected to age 8–9 years; the sex ratio was slanted towards the oldest groups, too. Plasticity in age at sex change suggests a socially controlled sex change.

Effects of Radioactive Environment on Forming of Abnormalities in Shells and Genital Structures in Pond Snail *Lymnaea stagnalis*

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Shells and soft tissues of pond snail *Lymnaea stagnalis* are used traditionally as a simple tool for detection of man-made radionuclides in environment. Radionuclides should be considered as agents for both chemical toxicity on organisms and irradiation dose. Surprisingly, their biological responses to radioactive contamination of environment are poorly documented. Nothing has been published about response of carbonate shell which can be considered as a depository of radionuclides coming to organisms from environment. Our aim was to find a link between radioactive contamination of environment and percentage of shell and genital organs abnormalities in *L. stagnalis*. In case of shell study, more than 8000 specimens from 88 sampling sites in Russia, Kazakhstan, Ukraine, Germany, USA and Canada were examined. Sampling sites can be subdivided into three groups: 1) "non-radioactive", 2) "non-radioactive" with high anthropogenic loads, 3) heavily contaminated by radionuclides after nuclear accidents. Eventual abnormalities of genital structures were investigated through dissection of 130 specimens coming from sites of groups 1 and 3 located in Russia. Six different types of shell abnormality were documented; only four of them were previously discussed in malacological literature. The percentage of abnormal shells did not exceed 3 % of all examined shells from both clean and polluted sites. The only exception was a single locality representing a radioactive environment nearby Chernobyl NPP (Ukraine) which revealed a high percentage (up to 50 %) of an unusual coarse seam produced by a growth interruption. Examination of genital characters revealed two types of praeputium abnormalities from both types of sampling sites. Thus, our results could not confirm the hypothesis that a radioactive environment could represent a major factor causing the observed abnormality in *L. stagnalis*.

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