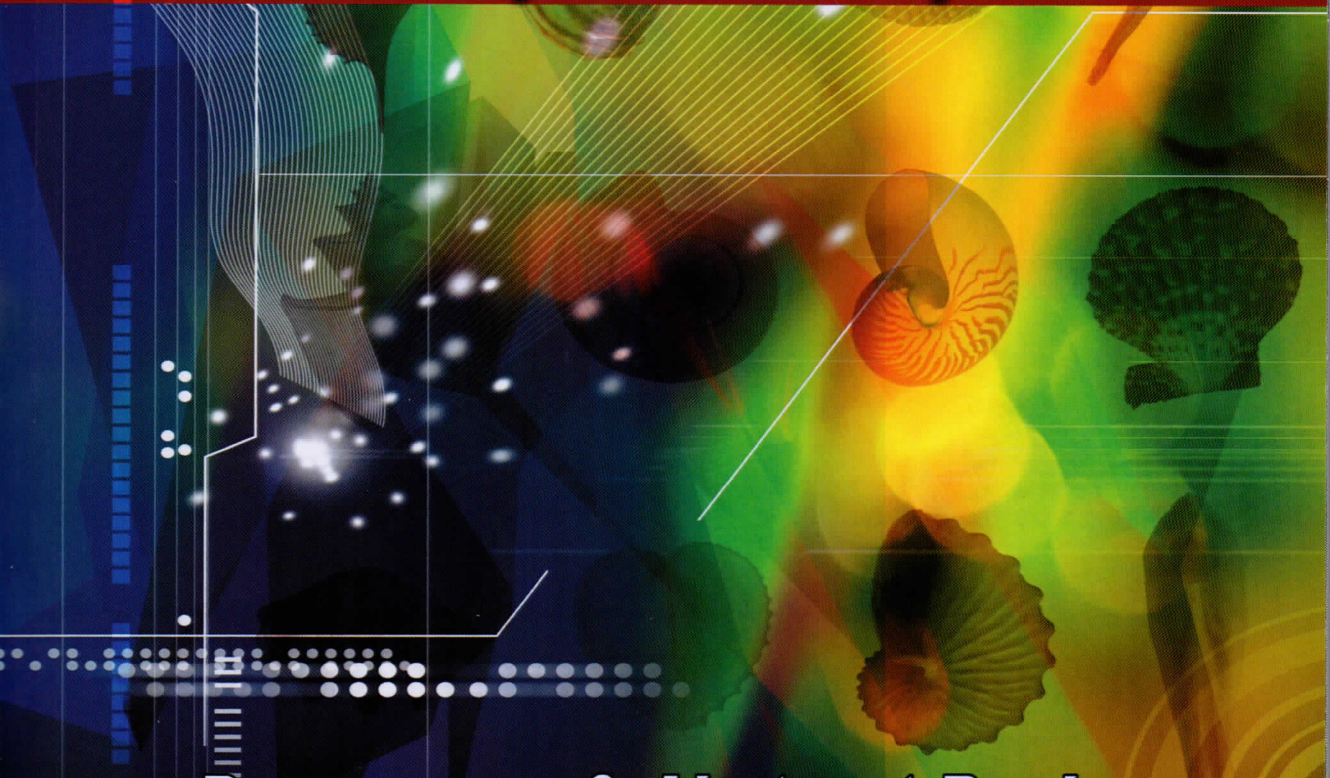
The 19th International Congress of
UNITAS MALACOLOGICA

World Congress of Malacology 2016

18 - 24 July 2016
Penang, Malaysia

Unity in Diversity



Programme & Abstract Book

UNITAS Malacologica
UM
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APEX
WCM 2016

The 19th International Congress of UNITAS MALACOLOGICA

WORLD CONGRESS OF MALACOLOGY 2016

18-24 JULY 2016
PENANG, MALAYSIA

Programme & Abstract Book

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MESSAGE FROM DEPUTY MINISTER OF MINISTRY OF SCIENCE, TECHNOLOGY AND INNOVATION (MOSTI), MALAYSIA

First and foremost, I would like to take this opportunity to congratulate Universiti Sains Malaysia (USM) and Unitas Malacologica on their initiatives and successful efforts in organising the World Congress of Malacology (WCM) 2016. I am very pleased that this congress has attracted researchers and academicians from near and far. I wish you a very warm welcome to Malaysia.

The field of Malacology in Malaysia mainly focuses on bivalve aquaculture and ecological research of mollusks diversity in Malaysia. In 2014, the capture and aquaculture of mollusks alone has contributed RM12.2 billion in wholesale value, which represents 16.6% of the total capture and aquaculture wholesale value to our economy. Apart from contributing to the National Gross Domestic Product (GDP), it is also a source of employment, foreign exchange and a source of protein supply in the country. The aquaculture industry plays a significant role to ensure Malaysia's food security and subsequently reduce the need for import into the country.

At the Ministry of Science, Technology and Innovation (MOSTI), we are tasked to transform Malaysia into a high economic growth country and a developed nation inclusive of socio-economic development. The need for research and development (R&D) towards building a nation with enhanced quality of life is only possible through the development and retention of first world talent base. I believe WCM 2016 will serve as an excellent platform that would holistically tackle knowledge gaps and share transboundary good-case practices.

MOSTI has successfully granted nineteen (19) funds for the purpose of research, development and innovation in the Malacological field in Malaysia for the past 10 years. The multidisciplinary fields funded comprised of biodiversity distribution of mollusks, the effect of the changing ocean and environment on mollusks, aquaculture development and agricultural crop management.

The Government of Malaysia aspires to strengthen the quadruple helix model collaboration between research institutions, industry, Government and the community. The World Congress of Malacology 2016 is a testament to this ideal. I sincerely hope that you will have a successful congregation in which there will be transboundary knowledge exchange for the betterment of this industry and to the community.

Mr heartiest congratulations once again, thank you.

Abu Bakar

YB DATUK DR. ABU BAKAR BIN MOHAMAD DIAH,
Deputy Minister
Ministry of Science, Technology And Innovation (MOSTI), Malaysia

MESSAGE FROM VICE-CHANCELLOR UNIVERSITI SAINS MALAYSIA (USM)

On behalf of Universiti Sains Malaysia, I warmly welcome all participants to the World Congress of Malacology (WCM) 2016 in Penang, Malaysia. This is the first time that WCM is held in Malaysia and I am proud that USM has the opportunity to host its maiden arrival on our shores. I am also very pleased that this congress has attracted researchers and academics from more than 40 countries.

At Universiti Sains Malaysia, we envision to transform higher education for a sustainable tomorrow. In order to stay relevant in any industry, everyone is expected to generate income and contribute in building the economy. However, this alone is not sufficient to guarantee total sustainable living. More is needed to ensure that the knowledge and business is made accessible and applicable to the community. Therefore, USM's life-long mission is to be *the* pioneering, transdisciplinary research-intensive university that empowers future talents and enable the bottom billions to transform their socio-economic well-being.

USM has led Malacological studies in Malaysia for the past thirty years. Our very own School of Biological Sciences has produced numerous publications on this very field. The University has been supportive of the need of these studies and has supported funding throughout the duration.

Through some of these researches, a pilot programme to assess the suitability of mollusks aquaculture to enhance incomes of local communities was launched with support by The Ministry of Higher Education under its Knowledge Transfer Partnership (KTP) programme. Through this KTP programme, the livelihood of the local communities has been improved. The success of this project has shown immense potential and the pilot model will be replicated in other communities.

My sincere hope for WCM 2016 is that the participants make good use of this platform to learn and share knowledge amongst each other for future collaborations on research that will benefit all walks of life. Let us go forth and not hold ourselves back in making this happen and may there be more WCMs to come in the future.

I would like to thank Associate Professor Dr. Aileen Tan Shau-Hwai and the congress committee for their hard work in realising this congress. I am confident that this event will be a great success and I wish all participants a pleasant stay in Penang.

PROFESSOR DATO' DR. OMAR OSMAN
Vice Chancellor
Universiti Sains Malaysia

WELCOME REMARKS BY THE PRESIDENT OF UNITAS MALACOLOGICA

Greetings and a very warm welcome to all.

It is our great pleasure and honour to welcome all of the delegates here today – to the World Congress of Malacology 2016, which is the 19th International Congress of UNITAS MALACOLOGICA. We are such a diverse group. There are altogether 280 delegates representing 41 countries from all of the continents of the world.

The UNITAS MALACOLOGICA Society with its 54 years of history has evolved into its present form since its inception in 1962. It has provided the world with an invaluable platform for the discussion and discourse on the world of mollusks.

The human race depends on mollusk for food and the mollusks industries have contributed more than 23 million tonnes with about USD 20.7 billion worth of revenue from aquaculture alone. This represents the culture and capture of numerous species of cockles, oysters squids, octopus and other shellfish. However landing tonnage for many of these species sees a downward trend over the years. Coastal degradation, pollution, habitat loss, over-exploitation of resources and disease has each contributed to this loss. In Malaysia whose cockle culture represents its main aquaculture fisheries, we see a drop of more than 84 % in the last ten years.

The latest threat to this group has come from the sea. Scientific evidence has pointed to the negative impacts of ocean acidification on the deep-sea pteropod mollusk of Antarctica – pointing to the negative impact of climate change and it ensuing effects on the marine ecosystem. This event and similar studies of analogous natural systems such as underwater thermal vent habitats has given us a window into the effect of a future high CO_2 world on carbonate-bearing organisms.

Perhaps then the needs are evident from this important group of scientists for the understanding, protection and sustainable use of mollusks in a rapidly evolving world.

- Clearly we see the increased need of a multi-disciplinary approach to look at the issues affecting mollusks.
- A need for the accelerated deployment of new tools and approaches to handle the threats to mollusks at both the local and large scale.
- And a continued push for the mentoring and training of young scientists required - to understand the mollusks and bridge gaps in the traditional disciplines.

The Tropical Marine Mollusks Programme (TMMP) is one such story that could be duplicated. This programme, which started in 1990, may illustrate a success story of this mentoring and long-term collaborative approach to the study of mollusks. This is especially so in the ever-important fields of ecology and taxonomy with its long learning curve but short in career options. I am happy to report that today we see the fruits of this labor of dedication as children of this group meet up at this conference. There are other success stories too and we hope such rich traditions will be continued.

This time the theme for the congress is "Unity in Diversity". This reflects on the diverse disciplines in the present fields and approaches in malacology. However, there is an ever growing need for cooperation amongst us to finding solutions and to understand issues about the mollusks.

The many papers that will be presented and the number from the many countries we see here today also reflects on this theme.

In this conference, I am also pleased to announce that one of the symposia will honour the late Professor Luitfried Von Salvini-Plawen for his contributions in the field of Mollusksan phylogeny and invertebrates in general.

I would like to take this opportunity to thank the local organizing committee for their tire-less work, the council and members of the UNITAS MALACOLOGICA Society for making this important congress possible and Universiti Sains Malaysia for her continued support.

On behalf of the organizing committee, we would like to thank all participants for your attendance and we hope this congress will be very fruitful in providing you with a valuable opportunity to share your knowledge and thoughts.

Lastly while you are here please take the opportunity to experience the local scene at this UNESCO World Heritage Site. May you have a wonderful and rewarding time in Penang.

Thank you so much.

ShauHwai Tan

ASSOC. PROFESSOR DR. AILEEN TAN SHAU HWAI

President of UNITAS MALACOLOGICA 2013-2016

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THE SCIENTIFIC SYMPOSIA

The World Congress of Malacology represents malacologists from across the globe that aims to share their knowledge and experience and discuss their research on this platform. Fifteen (15) thematic symposia define the framework for the 19th WCM 2016 – *Unity in Diversity* – to ensure delegates with a broad range of interests can participate in this meeting. The symposia are:

ECOLOGY OF MARINE MOLLUSCS

Juan Moreira Da Rocha Universidad Autónoma de Madrid, SPAIN.
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Jesús Souza Troncoso University of Vigo, SPAIN.
E-mail: troncoso@uvigo.es

Marine molluscs show a great diversity of feeding habits and life histories; they play a major role in marine habitats and trophic webs, through complex interactions with other taxa and the environment. Understanding the ecology of marine molluscs is paramount to disentangle the functioning of marine ecosystems and to provide the much-needed scientific knowledge to face the new challenges emerging in this changing world, such as the impact of global warming, urbanization, pollution and spread of exotic biota. Therefore, the objective of this symposium is to bring together contributions of experts and students from around the world in the wide field of marine ecology, focusing on molluscs and covering all habitats and environments, from the intertidal to the deep sea.

FREHSWATER BIVALVES OF THE WORLD: DIVERSITY, DISTRIBUTION, EVOLUTION & ECOLOGY

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Manuel Lopes-Lima CIIMAR, University of Porto, PORTUGAL.
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A total of 16 bivalve families are known to live and reproduce in fresh water. In recent years, freshwater bivalves have received increasing scientific attention due to their importance in ecosystem functioning, their endangered status, their unique reproductive traits and the effects of invasive species. This symposium will provide a global platform for sharing and discussing (1) advances in understanding global freshwater bivalve diversity, distribution and evolution; (2) new knowledge on the functions and value of freshwater bivalves to their ecosystems and people; (3) major and emerging threats to freshwater bivalve diversity and functionality in different regions and continents; (4) lessons learned through (un)successful efforts towards the protection and restoration of endangered populations and their habitats; and (5) advances in understanding the effects of invasive freshwater bivalve species and how to combat them.

"HOW TO QUANTIFY SHELL FORM?"

Liew Thor Seng Universiti Malaysia Sabah, MALAYSIA.
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Manuel Jimenez Tenorio Universidad de Cádiz, SPAIN.
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The Molluscan shell has been a popular example in morphological evolution studies because it is geometrically simple, yet diverse in form. Although generally considered an easily-measurable structure, the quantification of mollusca, especially gastropods, shell form is still a challenge because shells lack homologous structures and have a spiral form that is difficult to capture with linear measurements. The evolution of shell forms has been studied either by using empirical approaches that focus on the quantification of actual shell forms or by using theoretical approaches that focus on the simulation of shell ontogenetic processes and geometric forms. The symposium will involve both theoretical and empirical biologists, who use different methods to quantify shell form while answering similar research question. Emphasis will be on the possibility to synthesis between the two schools of shell morphologists and to the finding generalized ways to quantify shell forms.

INTEGRATING MOLECULES, MORPHOLOGY, BIOLOGY & BIOGEOGRAPHY IN 'OPISTHOBRANCH' RESEARCH

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The traditional "Opisthobranchia", marine sea slugs and bubble snails, are not a monophyletic group. However, the "Bye, bye Opisthobranchia?" is still left with a question mark. The taxa formerly included in "Opisthobranchia" share so many characteristics in where they occur, how they are collected, preserved and studied, in addition to the similarities (whether convergent or homologous) in morphology and biology that it is difficult to completely abandon the concept. Instead we need to reassess some of the traditionally shared characters in the light of new phylogenetic hypotheses. We hope that this symposium will bring together participants working on any of the traditional "opisthobranch" groups as well as the similar groups that have not yet found a stable home on the heterobranch tree.

INTEGRATIVE RESEARCH ON MOLLUSCAN PHYLOGENETICS: A TRIBUTE TO THE LATE PROFESSOR SALVINI-PLAWEN

Douglas J. Eernisse California State University Fullerton, USA.
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Gerhard Steiner University of Vienna, AUSTRIA.
E-mail: gerhard.steiner@univie.ac.at

As a pioneer in pursuing both deep-level questions of molluscan phylogeny and as a major contributor to the worldwide systematics of the worm-like Solenogastres and Caudofoveata, Professor von Luitfried von Salvini-Plawen (1939-2014) helped to directly or indirectly inspire a current generation of malacologists who are pursuing molluscan phylogenetic research. This symposium honors his many outstanding contributions as an active teacher and former Head of the Institute of Zoology at the University of Vienna, President of Unitas Malacologica from 1998 to 2001, and as a broad-thinking and collaborative researcher. It will feature diverse research on molluscan phylogeny with integrative themes, reflecting the current vibrant state of the field. There will be a special extended keynote address by Gerhard Haszprunar to begin the symposium. Professor Haszprunar will present an overview of Salvini-Plawen's career and will give his own special insight into the influence of the late researcher on modern molluscan phylogenetics. Both established and young symposium speakers from across the world will present overviews and specific details of their own integrative research programs. The phylogenetic scope will range from the investigation of ancient molluscan relationships and the implications for the reconstruction of molluscan ancestry to cases where phylogeny has been used to evaluate contemporary patterns and processes in specific molluscan lineages.

LIMESTONE BIODIVERSITY & CONSERVATION ISSUE

Tony Whitten Fauna & Flora International, UNITED KINGDOM.
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Limestone is used worldwide as a building and ornamental stone and as an essential ingredient of cement, and is essential to major infrastructure projects, from dam and bridge construction to road building and port development. It is one of the building blocks for development and economic growth, but its extraction risks harming species we barely understand. In tropical and temperate regions alike, limestone areas – externally and internally – are home to a diversity of bats, snails, orchids, fish, spiders and beetles found in no other habitats. Some species are so highly adapted to the conditions that they cannot survive outside caves. Limestone quarrying – the process of extracting the valuable rock from the ground – is one of the primary threats to biodiversity found only in limestone areas. Biodiversity in limestone areas is some of the most challenging to study due to the simple fact that it's tough to access. It's often the first to be overlooked by governments, companies and scientists and the last to be included in national or regional biodiversity surveys. An even bigger challenge is that many limestone species are confined to very small areas – in some cases a single hill or cave. For these species, a single extractive operation or quarry can lead to a global extinction. Conservation organizations are beginning to acknowledge the high extinction risks but cement companies tend to be locked into attitudes that are some decades behind those of other extractive industries. This session will explore the distribution of snails found in limestone areas, their habits, the threats and feasible mitigation actions.

MOLLUSCAN AQUACULTURE IN A CHANGING CLIMATE

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As human populations are projected to grow rapidly in the next 50 years, with > 60% of people found in Asia, the reliance on marine resources such as shellfish for food will increase. These resources are under threat from eutrophication, over-fishing, pollution and especially climate change. Of these threats, the projected increase in global warming and ocean acidification are of greatest concerns, and so understanding their impacts is a pressing issue for scientists and politicians. Of particular concern is the rate of this change, which is potentially beyond the capacity of shellfishes to adapt to or recover from. This is especially important in SE Asia, which is the centre for marine biodiversity, but also accounts for >90% of the world's shellfish production. Worryingly, this impact is intensified as (1) climate warming is occurring faster in SE Asia than in other parts of the world, and (2) our inability to predict the impacts of these stressors on marine life threatens shellfish survival and food security. As such, we are increasingly interested in how beneficial species and aquaculture practices associated with them will respond to changing environmental conditions, such as coastal warming and related heavy precipitation or hypoxia, and ocean acidification. The primary aim of this symposium is to form a multidisciplinary group involving scientists, seafood consumers and molluscan growers to revise edible mussel and oyster aquaculture practices through modern scientific approaches to suite for a rapidly changing climate.

MOLLUSCAN BIODIVERSITY & BIOGEOGRAPHY IN THE INDO-WEST PACIFIC

Benoit Dayrat The Pennsylvannia State University, USA.
E-mail: bdayrat@gmail.com

The tropical and subtropical Indo-West Pacific ranges from eastern Africa all the way to Hawaii and other western Pacific islands, and within the latitudes of 35 degrees North and South. It hosts the most highly diverse marine fauna in the world, with a peak of diversity in the Coral Triangle (Philippines, Borneo, and West Papua). However, there are still many large gaps in our knowledge of the marine biodiversity and biogeography of the Indo-West Pacific. Some of the most obvious issues are: 1) Many species are still unknown and remain to be discovered and described; 2) Many areas and habitats remain unexplored; 3) Many taxa need taxonomic revisions (lists of nominal species do not tell us much about the actual diversity); 4) Biogeographic boundaries and sub-regions with high rates of endemism are still debated; 5) Diversification processes can only be studied with very few taxa because of our lack of fine-scale, accurate data on species diversity and distribution. The symposium will provide a venue for researchers to present new discoveries and discuss challenging ideas.

MOLLUSKS IN CLIMATE CHANGE RESEARCH: NEW USES OF AN OLD GROUP

Maria Helena Fortunato Martins Hokkaido University, JAPAN.
E-mail: helenaf@mail.sci.hokudai.ac.jp

Abundant and conspicuous, mollusks have been important in marine environments since their appearance. As major calcareous organisms with a long fossil record, their shells provide an excellent archive of past climate events and oceanographic changes thus increasing our understanding of present day conditions. Their potential to provide long chronologies of oceanic conditions is being actively explored in order to obtain better predictions of future changes in marine ecosystems. This symposium aims to provide a venue to discuss mollusks as tools in climate research by presenting results and methods and use this opportunity to engage students towards new research areas in malacology.

MORPHOLOGY BASED SYSTEMATICS IN ACTION

Barna Páll-Gergely Shinshu University, JAPAN.

E-mail: pallgergely2@gmail.com

Morphology based revisions of systematics may nowadays be considered classic. Nonetheless, morphological taxonomy remains essential for the exploration of biodiversity and provides indispensable bases for all the disciplines of science. At the era of the on-going 6th mass extinction, morphological taxonomy has been becoming more important than ever. This symposium aims to enlighten the actions of morphology based revision and fauna study and their unique outcomes across all the molluscan groups.

PLANKTIC GASTROPOD

Deborah Wall-Palmer <Plymouth University, UNITED KINGDOM.

E-mail: deborah.wall-palmer@plymouth.ac.uk

Planktic gastropods are a fascinating, yet mysterious component of the ocean zooplankton. They are thought to be an important food source for many commercially fished species, and recent research has revealed that they are likely to be threatened by current and future global changes. However, the difficulty in keeping these gastropods under laboratory conditions means that we still don’t understand enough about their ecology and biology to appreciate their importance to the ocean food web and their sensitivity to a changing ocean environment. For this truly interdisciplinary field of research, there is now a rare opportunity to come together for a planktic gastropod symposium at the World Congress of Malacology in 2016. We invite talks on all aspects of planktic gastropod biology, ecology, biogeography, geochemistry and palaeontology.

PREDATORS OF MOLLUSCS

Asami Takahiro Shinshu University, JAPAN.

E-mail: asami99@shinshu-u.ac.jp

Coexistence of molluscs with their predators poses diverse arrays of puzzling questions on their ecology and evolution through predator-prey interactions. This symposium aims to synthesize the multidisciplinary outcome of recent studies on the natural history and biology of predators and parasitoids that specialize in exploiting molluscs as resources.

TROPICAL MARINE MOLLUSC PROGRAMME (TMMP): PAST & PRESENT

Jaruwat Nabhitabhata Prince of Songkhla, THAILAND.
E-mail: jaruwat.n5@gmail.com

The Tropical Marine Mollusc Programme (TMMP) was initiated in 1991 as an extension of a capacity-building programme comprising Thailand, India and Indonesia (from 1992). Over the following 10 years more countries were included, i.e. Vietnam, Cambodia, Malaysia and the Philippines, and the number of international resource persons also increased. Funding came from DANIDA, the Danish Development Assistance and the "founding father" was Prof. Jørgen Hylleberg from University of Aarhus, Denmark. Proceedings from annual congresses and workshops were published in Phuket Marine Biological Center Special Publications, and the number of articles steadily increased, as did the scientific quality. At this point, 15 years after the TMMP programme, we would like to bring together participants and resource persons to present research carried out in member countries as a result of TMMP networking, and possibly outline future perspectives. We also welcome contributions from persons not directly involved in the TMMP, but who have benefited in some way from research and network of the TMMP.

TSUNAMI & MARINE LIFE IN ASIA

Kenji Okoshi Toho University, JAPAN.
E-mail: kenji.okoshi@env.sci.toho-u.ac.jp
Suchana Apple Chavanich Chulalongkorn University, THAILAND.
E-mail: suchana.c@chula.ac.th

Major earthquakes with big tsunami have occurred along the Pacific coast of Japan and Indian Ocean in recent year. The tsunami caused severe damage to ecosystems including mudflats, rocky shores, mangroves, coral reefs and mollusk biodiversity. We have to clarify not only short-term effect, which may explain an initial recovery of intertidal and subtidal animals, but also a long-term effect, which may explain continuous changes in population with land subsidence. In this session, we would like to focus on the rapid impact of the earthquake for marine life and also on the long-term effect of the earthquake on mollusk population and biodiversity.

CONFERENCE VENUE

All sessions will be held in the conference rooms of Jen Hotel, Penang. The rooms are: Room 1 (PINANG BALLROOM), Room 2 (PANGKOR), Room 3 (LANGKAWI), and Room 4 (RAWA). The floor layout of the conference room is shown in Figure A below.

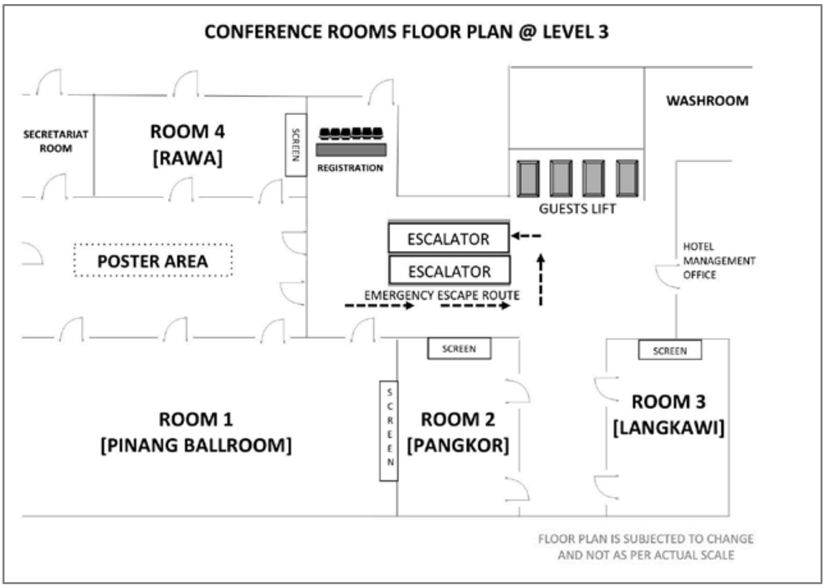

Figure A. The floor plan for all the conference rooms located at Level 3 in Hotel Jen, Penang.

GUIDELINES & USEFUL INFORMATION

Guidelines for ORAL Presentations: Oral presentations are organized in sessions scheduled in specific conference rooms, indicated in the programme together with the time of presentation of each contribution including discussion and change over. **Please note that the duration given to your oral presentation includes 5 minutes for questions and discussion** (e.g. a 20-minute slot should be 15 minutes of presentation + 5 minutes of Question & Answer session and change over). The oral presentations are organized centrally. Therefore, the authors are kindly asked to upload their presentations preferably **1 day before** the presentation. A staff person will be available at the registration booth to assist you.

Guidelines for POSTER Presentations:

Posters should be put up on the registration day or by 9:30am the day of your assigned session. Posters may be left up until 5:00 pm on Sunday, July 24. All poster boards will be numbered, indicating assigned poster spaces for each presenter. You will receive your specific assignment location during the registration or you may also refer to the detailed programme in this book. A staff person will be on hand to help you find your space in the exhibit hall. Thumbtacks will be provided for putting up your poster. Presenters are asked to be available at their posters during the entirety of the poster session to discuss their posters with interested viewers.

Some useful information:

- Morning and afternoon breaks will be served at the same level as the conference rooms. Lunch will be served in the hotel restaurants at Level 2.
- Welcoming dinner (Tues, July 19) will be held at 59Sixty, KOMTAR Tower, where you will be having a buffet dinner with 360° panoramic view of Penang. This dinner is sponsored by Universiti Sains Malaysia.
- Friday (July 22) is a free and easy day during which participants can discover the places of attractions or go for a food hunt in Penang. They can also opt for the tour package offered at the travel agency booth that will be put up during the conference.
- Farewell dinner (Sun, July 24) will be held at the St. Giles Wembley Hotel located directly opposite of the conference venue.

World Congress of Malacology 2016
Student Travel Grant Award Recipient

Travel grants were provided for selected participants. Successful grant recipients and the awarding institutions are listed below. These are:

UNITAS MALACOLOGICA

1. Anna Mikhlina
2. Bastian Brenzinger
3. Delianis Pringgenies
4. Deneb Ortigosa
5. Do Van Tu
6. Ellen Grace M. Funesto
7. Emanuel Redl
8. Fernando Aneiros
9. Fia L. H. Irsyad
10. Fitri Jatmika Purnama Sari
11. Franziska S. Bergmeier
12. Gloria L. Galan
13. Hatta Fauzia
14. Heidi C. Porquis
15. Irina Ekimova
16. Jennifer Austin
17. John Pfeiffer
18. Kara Layton
19. Khadija Boulaassafer
20. Lauren Sumner-Rooney
21. Lindsey Dougherty
22. Luis Chueca
23. Maria Rosario Martin
24. Marie Grace P. Faylona
25. Mark Phuong
26. Mary Cole
27. Matthew J. Nimbs
28. Mohd. Zacaery Khalik
29. Monisha Bharate
30. Nariman Asadi
31. Ng Ting Hui
32. Pedro Romero
33. Peter Kohnert
34. Phung Chee Chean
35. Sabrina Medrano
36. Samuel Alcaino Abarca

37. Sheeja Gireesh
38. Ravinesh Raveendran
39. Trevor Hewitt
40. Victoria Moris
41. Yumiko Osawa

Malacological Society of London

1. Auke-Florian Hiemstra
2. Katharina von Oheimb
3. Parm Viktor von Oheimb
4. Renee Rossini

Malacological Society of Japan

1. Hiroaki Fukumori
2. Kaito Asato
3. Masahiro Suzuki
4. Risho Motochin
5. Yuta Morii

Malacological Society of Australasia

1. Kara Layton

Sky Group of Companies

1. Geraldine Olive Chang Ju Lien

Lee Kum Kee

1. Cherrie Teh Chiew Peng

Turut Mekar Sdn. Bhd.

1. Nurul Hidayah Mohamad Ridwan

KEYNOTE SPEAKER I

Kathe R. Jensen
Zoological Museum
(Natural History Museum Denmark)
Universitetsparken 15,
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REVIEW OF THE SACOGLOSSA: NO LONGER OPISTHOBRANCHIA, NOT QUITE PULMONATA

The sap-sucking sea slugs, Sacoglossa, are famous for two things: The discovery of bivalved sea slugs in 1959 by Japanese scientists, and for harboring functional chloroplasts from their food algae. The latter has made several species model organisms for the study of photosymbiosis. Although the Sacoglossa has long been recognized as a monophyletic group, the relationship with other heterobranch groups remains disputed. Many molecular analyses have indicated a relationship with formerly pulmonate Siphonariidae, but there is no morphological support for this. Relationships of families and genera within the Sacoglossa are also still debated. Most studies agree that the non-shelled Plakobranchacea is a monophyletic group. The shelled Oxynoacea is also usually considered monophyletic, but whether the genus Cylindrobulla is included differs among studies. Other problems include an apparent paraphyly of the family Caliphyllidae, lack of proper, synapomorphy-based definitions of several genera of Limapontiidae, and relationships of monogeneric families Boselliidae and Costasiellidae. The present study will give a historical overview of the Sacoglossa, including palaeontological information and extinct species. A review of morphological characters will also be presented along with data on behaviour, feeding, reproduction, kleptoplasty and biogeography. Data from molecular and integrative studies will be summarized, and problematic issues, from species delimitation to affiliation with Siphonariidae and Panpulmonata, discussed.

KEYNOTE SPEAKER II

Fred E. Wells
Enzer Marine Environmental Consulting
PO Box 4176
Wembley WA 6014,
Australia
Enzer.Marine@iinet.net.au

INVASIVE MARINE SPECIES: A HIDDEN PROBLEM IN SOUTHEAST ASIA

In recent years, there has been a growing awareness of the problems posed by invasive marine species as they colonise and dominate new marine environments. Governments in various parts of the world have responded to the issue in different ways. Australia has been active in developing information to use in managing the invasive marine species issue, but it has been little recognised in Southeast Asia. There have been a number of records of marine invasives in Southeast Asia that suggest the issue is larger than is currently recognised and there is an urgent need for more information. The issues are discussed in detail using molluscan examples.

KEYNOTE SPEAKER III

Takahiro Asami
Faculty of Science
Division of Ecology and Evolution
Department of Biology
Shinshu University, Matsumoto 390-8621
Japan
asami99@shinshu-u.ac.jp

EVOLUTION OF REPRODUCTIVE BARRIERS IN SNAILS

Genetic diversity between populations can be efficiently retained in sympatry when they are reproductively isolated. This requires speciation by the evolution of reproductive barriers which biologically interfere gene flow. Eyes of gastropods are not useful for visual search for or distinction between potential mates. Without good vision, instead, their mate recognition could only rely on chemical or physical cues. This means that reproductive isolation without hybridization in sympatry requires the divergence of chemical or physical traits for mating through their histories in allopatry or sympatry. Immediate means for chemical recognition should be sex pheromones. Genital morphology may function as a barrier to physical recognition or copulation. Despite these biologically straightforward predictions, however, we know only little about how chemical or physical barriers isolate populations, especially in terrestrial gastropods. This is most probably because of difficulty in using land snails for necessary experiments. I will review what we know so far for the evolution and functions of chemical and physical traits as reproductive barriers and discuss what are challenging problems to resolve for understanding pulmonate speciation.

KEYNOTE SPEAKER IV

Tony Whitten
Regional Director, Asia-Pacific
Fauna & Flora International (FFI)
Jupiter House, Station Road
Cambridge CB1 2JD
United Kingdom
www.fauna-flora.org

LESSONS LEARNED FROM ENGAGING WITH CEMENT COMPANIES FOR SNAIL CONSERVATION: FAILURES AND SUCCESSES

Over the last 20 years I have been engaging with cement companies in the hope of getting acceptable compromises for the conservation of the micro-endemic snails on the limestone hills in SE Asia where limestone quarrying is known to have caused species extinctions. I examine the issues, the companies, the approaches, the results, and the lessons, and provide some recommendations to reduce disappointment and increase positive conservation outcomes.

OVERVIEW OF CONFERENCE PROGRAMME

OVERVIEW OF CONFERENCE PROGRAMME

MONDAY, JULY 18

1500 - 2000	Registration & Poster Setup

TUESDAY, JULY 19

0800 – 0900	Registration & Poster Setup			
0900 – 1030	Opening Ceremony (Ballroom, Hotel Jen)			
1030 – 1050	Morning Break			
	Room 1 BALLROOM	**Room 2 PANGKOR**	**Room 3 LANGKAWI**	**Room 4 RAWA**
1050 – 1210	**PC*/EMM**	**MBB**	**OR**	**MA**
1210 – 1340	Lunch			
1340 – 1500	**EMM**	**MBB**	**OR**	**MCC**
1520 – 1540	Afternoon Break			
1540 – 1700	**EMM**	**MBB**	**OR**	**TML**
1700 – 1830	Free & Easy			
1830 – 2200	Welcoming Dinner (59Sixty, KOMTAR Tower)- **Sponsored by Universiti Sains Malaysia, USM**			

WEDNESDAY, JULY 20

0930 – 1030	Keynote Session 1 (Ballroom, Hotel Jen)			
1030 – 1050	Morning Break			
	Room 1 BALLROOM	**Room 2 PANGKOR**	**Room 3 LANGKAWI**	**Room 4 RAWA**
1050 – 1210	**EMM**	**MBB**	**OR**	**FB**
1210 – 1340	Lunch			
1340 – 1500	**EMM**	**MBB**	**OR**	**FB**
1500 – 1520	Afternoon Break			
1520 – 1700	Poster Session (ODD number)			

THURSDAY, JULY 21

0930 – 1030	Keynote Session 2 (Ballroom, Hotel Jen)			
1030 – 1050	Morning Break			
	Room 1 BALLROOM	**Room 2 PANGKOR**	**Room 3 LANGKAWI**	**Room 4 RAWA**
1050 – 1230	**EMM**	**MBB**	**LSPS**	**FB**
1230 – 1340	Lunch			
1340 – 1520	**OS**	**MBB**	**LSPS**	**FB**
1520 – 1540	Afternoon Break			
1540 – 1700	Poster Session (EVEN number)			

FRIDAY, JULY 22

Free & Easy

SATURDAY, JULY 23

0930 – 1030	Keynote Session 3 (Ballroom, Hotel Jen)			
1030 – 1050	Morning Break			
	Room 1 **BALLROOM**	**Room 2** **PANGKOR**	**Room 3** **LANGKAWI**	**Room 4** **RAWA**
1050 – 1230	**OS**	**TMMP**	**LSPS**	**MBS**
1230 – 1340	Lunch			
1340 – 1520	**OS**	**TMMP**	**LSPS**	**MBS**
1520 – 1540	Afternoon Break			
1540 – 1700	**OS**	**TMMP**	**LSPS**	**HQSF**

SUNDAY, JULY 24

0930 – 1030	Keynote Session 4 (Ballroom, Hotel Jen)			
1030 – 1050	Morning Break			
	Room 1 **BALLROOM**	**Room 2** **PANGKOR**	**Room 3** **LANGKAWI**	**Room 4** **RAWA**
1050 – 1210	**OS**	**LB**	**LSPS**	**PM**
1210 – 1340	Lunch			
1340 – 1500	**OS**	**LB**	**LSPS**	**PG**
1500 – 1520	Afternoon Break			
1520 – 1700	UNITAS General Assembly (Ballroom, Jen Hotel)			
1700 – 1830	Free & Easy			
1830 – 2300	Farewell Dinner (St. Giles Wembley Hotel)			

LEGEND

EMM	Ecology of Marine Molluscs
FB	Freshwater Bivalves of the World: Diversity, Distribution, Evolution & Ecology
HQSF	How to Quantify Shell Form?
LB	Limestone Biodiversity & Conservation Issue
LSPS	Integrative Research on Molluscan Phylogenetics: A Tribute to Late Professor Salvini-Plawen
MA	Molluscan Aquaculture in A Changing Climate
MBB	Molluscan Biodiversity & Biogeography
MBS	Morphology Based Systematics in Action
MCC	Mollusks in Climate Change Research: New uses of an old group
OR	Integrating Molecules, Morphology, Biology & Biogeography in "Opisthobranch" Research
OS	Open Session
PG	Planktic Gastropod
PM	Predator of Molluscs
TML	Tsunami & Marine Life in Asia
TMMP	Tropical Marine Molluscs Programme (TMMP): Past & Present
***PC**	Press Conference

Sessions & Venues

ORAL PRESENTATIONS

TUESDAY, JULY 19

ROOM 1 (BALLROOM)

		Page
0800 – 0900	Registration & Poster Setup	
0900 – 1030	Opening Ceremony (Ballroom, Jen Hotel)	
1030 – 1050	Morning Break	
1050 – 1130	Press Conference (for VIP and press only)	
	Chairperson: Jesús Troncoso	
1130 – 1150	Intertidal gastropods and global warming along the Atlantic coast of the Iberian Peninsula **Marcos Rubal (EMM)**	1
1150 – 1210	“In desiccating environments snail aggregation is adaptive because it lowers water loss.” An analogy showing why this statement is very difficult to validate **Mark Davies (EMM)**	2
1210 – 1340	Lunch	
	Chairperson: Fernando Aneiros	
1340 – 1400	Carry-over effects of environmental stress: lessons learned from *Siphonaria australis*, an intertidal limpet with mixed development **Nicole Phillips (EMM)**	3
1400 – 1420	Distribution patterns of *Tridacna maxima* and its response to natural thermal-bleaching event **Ranjeet Bhagooli (EMM)**	4
1420 – 1440	The sclerochronology of the ancient giant clam, *Hippopus hippopus*, from the Balobok Rockshelter, Philippines **Marie Grace Pamela Faylona (EMM)**	5
1440 – 1500	The ecological importance of giant clams in coral reef ecosystems **Mei Lin Neo (EMM)**	6
1500 – 1520	Giant clams (Bivalvia: Cardiidae) as potential counteractors of algal blooms **Ambert Ang (EMM)**	7
1520 – 1540	Afternoon Break	
	Chairperson: Mark Davies	
1540 – 1600	A novel filtering mutulism between sponge host and its endosymbiotic bivalve *Vulsella vulsella* **Remi Tsubaki (EMM)**	8

TUESDAY, JULY 19

1600 – 1620	Mollusc diversity and dominance in Late Paleozoic and early Mesozoic marine environments **Alexander Nutzel (EMM)**	9
1620 – 1640	Fatty acid as markers to bridge an existing gap of bivalve food sources in the tropical lagoon of Setiu Wetland, Terengganu, South China Sea **Zainudin Bachok (EMM)**	10
1640 – 1700	Comparison of two years' oscillation and life span of *Cypraea moneta* L. 1758 (Gastropods: Cypraeidae) from Sepanjang Beach, Yogyakarta, Indonesia **Felicia Zahida (EMM)**	11
1700 – 1830	Free & Easy	
1830 – 2200	Welcoming Dinner (59Sixty, KOMTAR Tower)	

TUESDAY, JULY 19

ROOM 2 (PANGKOR)

		Page
0800 – 0900	Registration & Poster Setup	
0900 – 1030	Opening Ceremony (Ballroom, Jen Hotel)	
1030 – 1050	Morning Break	
	Chairperson: Benoit Dayrat	
1050 – 1110	Molluscan fauna of Lakshadweep Islands, India: diversity and conservation challenges **Ravinesh Raveendran (MBB)**	25
1110 – 1130	Diversity and distribution of sea slugs of the Lakshadweep Islands and west coast of India **Appukuttannair Bijukumar (MBB)**	26
1130 – 1150	Marine minishells and microshells (Mollusca: Gastropoda) in Thai waters **Sararat Tanamai (MBB)**	27
1150 – 1210	Short DNA species barcodes: a valuable, low-cost tool for studying gastropod taxonomy and biology **Rebecca Loh (MBB)**	28
1210 – 1340	Lunch	
	Chairperson: Lisa Kirkendale	
1340 – 1400	Gastropods in Bucas Grande Island, Surigao Del Norte **Gloria Galan (MBB)**	29
1400 – 1420	Abundance of pelecypods in Bucas Grande Island, Surigao Del Norte **Heidi Porquis (MBB)**	30
1420 – 1440	Mollusk diversity at aquaculture stations in different marine habitats in Iloilo and Guimaras, Philippines **Teodora Bagarinao (MBB)**	31
1440 – 1520	**FREE TIME**	
1520 – 1540	Afternoon Break	
	Chairperson: Gloria Galan	
1540 – 1600	Patellogastropoda in Japan and Asia: morphology, molecular phylogeny and systematic revision **Takenori Sasaki (MBB)**	32

TUESDAY, JULY 19

1600 – 1620	Population and reproductive biology of the deep-sea mussel from methane seeps offshore southwestern Taiwan **Li-Lian Liu (MBB)**	33
1620 – 1640	Abyssal and bathyal gastropod fauna of the Japan Trench **Kazunori Hasegawa (MBB)**	34
1640 – 1700	Impact of habitat, sediment depth, and sieve size on biodiversity of coral reef-associated molluscs from the northern Red Sea (Gulf of Aqaba) **Imelda Hausmann (MBB)**	35

1700 – 1830	Free & Easy
1830 – 2200	Welcoming Dinner (59Sixty, KOMTAR Tower)

TUESDAY, JULY 19

ROOM 3 (LANGKAWI)

		Page
0800 – 0900	Registration & Poster Setup	
0900 – 1030	Opening Ceremony (Ballroom, Jen Hotel)	
1030 – 1050	Morning Break	
	Chairperson: Kathe Jensen	
1050 – 1110	Session introduction **Kathe Jensen (OR)**	
1110 – 1130	Exploration of enigmatic ‘dorsal vessel systems’ in panpulmonate gastropods **Timea Neusser (OR)**	52
1130 – 1150	On the origin and biogeography of the sap-sucking sea slugs genus *Thuridilla* **Maria Martin-Hervas (OR)**	53
1150 – 1210	It loves me, it loves me not: Counting species of the "rose petal sea slug", *Polybranchia* (Mollusca: Gastropoda) with a molecular systematics approach **Sabrina Medrano (OR)**	54
1210 – 1340	Lunch	
	Chairperson: Lucas Cervera	
1340 – 1400	Monitoring of opisthobranch biodiversity in Indonesia – and its applied aspect **Heike Wägele (OR)**	55
1400 – 1420	Abundance, distribution and ecology of specialist sacoglossans from Palk Bay, India **Sheeja Gireesh (OR)**	56
1420 – 1440	Kleptoplasts-starch storage factories in solar-powered sacoglossan sea slugs? **Victoria Moris (OR)**	57
1440 – 1500	Major changes in aeolidida systematics: When five families become one **Leila Carmona (OR)**	58
1500 – 1520	**FREE TIME**	
1520 – 1540	Afternoon Break	

TUESDAY, JULY 19

	Chairperson: Heike Wägele	
1540 – 1600	Fine scale geographic diversification in the tropical western Atlantic: the phylogeography of *Bulla occidentalis* **Manuel Malaquias (OR)**	59
1600 – 1620	Diversity, systematics and trophic ecology of the tropical Indo-west Pacific genus *Phanerophthalmus* (Cephalaspidea, Haminoeidae) **Jennifer Austin (OR)**	60
1620 – 1640	The end of the cold loneliness: 3D comparison between *Doto antarctica* and a new sympatric species of *Doto* (Heterobranchia: Nudibranchia) **Juan Moles (OR)**	61
1640 – 1700	The origin of species: evidence on boreal *Dendronotus* (Gastropoda: Nudibranchia) speciation, by geographic radiation and adaptations to different feeding modes **Irina Ekimova (OR)**	62
1700 – 1830	Free & Easy	
1830 – 2200	Welcoming Dinner (59Sixty, KOMTAR Tower)	

TUESDAY, JULY 19

ROOM 4 (RAWA)

		Page
0800 – 0900	Registration & Poster Setup	
0900 – 1030	Opening Ceremony (Ballroom, Jen Hotel)	
1030 – 1050	Morning Break	
	Chairperson: Thiyagarajan Vengatesen	
1050 – 1110	Laboratory spawning and embryonic development in the false-limpet *Siphonaria pectinata* (Gastropoda: Pulmonata) from the Bizerte Channel (Tunisia) **Najoua Trigui El Menif (MA)**	70
1110 – 1130	Shell repurposing is an important consideration for the future sustainability of mollusc aquaculture **James Morris (MA)**	71
1130 – 1150	Metamorphic and proteomic responses of fast-growing and slow-growing larval cohorts of a Pacific oyster to ocean acidification and warming **Ginger Ko Wai Kuen (MA)**	72
1150 – 1210	Oyster aquaculture in a polluted and changing climate: problems and wayforward **Thiyagarajan V. (MA)**	73
1210 – 1340	Lunch	
	Chairperson: Helena Fortunato	
1340 – 1400	The shellfish beyond fish: integrating local ecological knowledge in the assessment of molluscan diversity and abundance changes **Ariadna Burgos (MCC)**	74
1400 – 1420	Upper temperature limits of mangrove snails: deviation from the general prediction of tropical ectotherm vulnerability to climate warming **Nursalwa Baharuddin (MCC)**	75
1420 – 1440	The impact of different temperatures conditions on behavior of *Arion vulgaris* Moquin Tandon 1855 from some European populations in laboratory conditions **Tomasz Kaluski (MCC)**	76
1440 – 1500	Global invasion patterns of non-marine molluscs under climate change scenarios **Aravind Neelavar Ananthram (MCC)**	77
1500 - 1520	Using mollusks as environmental archives **Helena Fortunato (MCC)**	78

TUESDAY, JULY 19

1520 – 1540	Afternoon Break	
	Chairperson: Kenji Okoshi & Suchana Chavanich	
1540 – 1600	Impacts of 2011 earthquake and tsunami on lagoon and subtidal macrozoobenthos communities **Waka Sato-Okoshi (TML)**	177
1600 – 1620	Short-term and long-term effects of the 2011 Great East Japan earthquake on intertidal mollusks **Kenji Okoshi (TML)**	178
1620 – 1640	Impacts of the 2011 Great East Japan earthquake and tsunamis on shell formation of the invasive naticid gastropod *Euspira fortunei* and commercially important bivalves **Masahiro Suzuki (TML)**	179
1640 – 1700	2004 tsunami in thailand: the impact and recovery of reef communities **Suchana Chavanich (TML)**	180
1700 – 1830	Free & Easy	
1830 – 2200	Welcoming Dinner (59Sixty, KOMTAR Tower)	

WEDNESDAY, JULY 20

ROOM 1 (BALLROOM)

		Page
0930 – 1030	**Keynote Session: Prof. Kathe Jensen** (Ballroom, Jen Hotel)	
1030 – 1050	Morning Break	
	Chairperson: Marcos Rubal	
1050 – 1110	Brooding in the Chilean oyster *Ostrea chilensis*: much more than just keeping the kids safe! **Victor Cubillos (EMM)**	12
1110 – 1130	Mollusc diversity associated to the ecosystem engineer *Lithophyllum byssoides* (Rhodophyta) across a latitudinal gradient **Juan Moreira Da Rocha (EMM)**	13
1130 – 1150	The eastern Pacific coast as a natural transect of the globe for understanding latitudinal diversity gradients and biogeographic structure of rocky shore gastropods **Phillip Fenberg (EMM)**	14
1150 – 1210	Thyasirid bivalves from ancient methane seeps **Krzysztof Hryniewicz (EMM)**	15
1210 – 1340	Lunch	
	Chairperson: Juan Moreira	
1340 – 1400	Diversity of molluscs (class Bivalvia and Gastropoda) in relation to habitat characteristics in tropical mangroves of Penang Island, Malaysia **Nor Syuhaidah Binti Mohammad Zee Hood (EMM)**	16
1400 – 1420	*Crepidula fornicata* (Linnaeus, 1758): from absent to dominant in Ría De Vigo (NW Iberian Peninsula) **Fernando Aneiros (EMM)**	17
1420 – 1440	Dynamics of corallivorous *Drupella* snails on coral reefs with diving-related tourism (Koh Tao, Gulf of Thailand) **Rahul Mehrotra (EMM)**	18
1440 – 1500	Does species-specific epiphyte, *Pseudocladophora*, negatively affect host *Turbo*? **Yumiko Osawa (EMM)**	19
1500 – 1520	Afternoon Break	
1520 – 1700	Poster Session (ODD number)	

WEDNESDAY, JULY 20

ROOM 2 (PANGKOR)

		Page
0930 – 1030	**Keynote Session: Prof. Kathe Jensen** (Ballroom, Jen Hotel)	
1030 – 1050	Morning Break	
	Chairperson: Teodora Bagarinao	
1050 – 1110	Species diversity and biogeography of amphidromous neritid gastropods in the Indo-West Pacific **Hiroaki Fukumori (MBB)**	36
1110 – 1130	A hotspot of mangrove biodiversity: Comparative biogeography of mangrove gastropods across the Indo-West Pacific **Tricia Goulding (MBB)**	37
1130 – 1150	Exploring patterns of diversity and speciation in Indo-Pacific *Chromodoris* with special insight into a biodiversity hotspot in western Australia **Kara Layton (MBB)**	38
1150 – 1210	Molecular systematics of the baler shells (Volutidae: *Melo*) supports putative hybrid zones **Nerida Wilson (MBB)**	39
1210 – 1340	Lunch	
	Chairperson: Tricia Goulding	
1340 – 1400	Phylogeography of the rock shell *Thais clavigera* (Mollusca): evidence for long-distance dispersal in the northwestern Pacific **Park Joong-Ki (MBB)**	40
1400 – 1420	Initial studies of the phylogeography of the mussel genus *Xenostrobus* **Don Colgan (MBB)**	41
1420 – 1440	Cardiid biogeography, phylogenetics and evolution **Lisa Kirkendale (MBB)**	42
1440 – 1500	**FREE TIME**	
1500 – 1520	Afternoon Break	
1520 – 1700	Poster Session (ODD number)	

WEDNESDAY, JULY 20

ROOM 3 (LANGKAWI)

		Page
0930 – 1030	**Keynote Session: Prof. Kathe Jensen** (Ballroom, Jen Hotel)	
1030 – 1050	Morning Break	
	<u>Chairperson: Manuel Malaquias</u>	
1050 – 1110	Deep sea mysteries: a molecular phylogeny of newly discovered nudibranchs in the genus *Halgerda*) from low light Philippine reefs **Terry Gosliner (OR)**	63
1110 – 1130	One slug, two slug, white slug, new slug: Diversity and systematics of the nudibranch genus *Gymnodoris* **Vanessa Knutson (OR)**	64
1130 – 1150	Development of sexual cannibalism in a simultaneous hermaphrodite, *Gymnodoris citrina* (Nudibranchia Doridacea) **Keita Kosoba (OR)**	65
1150 – 1210	A nudibranch removes allo-sperm and throws it away along with own thorny penis after copulation **Ayami Sekizawa (OR)**	66
1210 – 1340	Lunch	
	<u>Chairperson: Terry Gosliner</u>	
1340 – 1400	Novel hypotheses on heterobranch evolution from microanatomy and sequences **Bastian Brenzinger (OR)**	67
1400 – 1420	Relay race, the turn of the resurrected genus "*Felimida*" Ev. Marcus, 1971 (Heterobranchia: Chromodorididae), let's split it! **Deneb Ortigosa (OR)**	68
1420 – 1440	Evolution of dorid nudibranchs: A call for integration of molecular, morphological and developmental data **Alexander Martynov (OR)**	69
1440 – 1500	Summary of sessions	
1500 – 1520	Afternoon Break	
1520 – 1700	Poster Session (ODD number)	

WEDNESDAY, JULY 20

ROOM 4 (RAWA)

		Page
0930 – 1030	**Keynote Session: Prof. Kathe Jensen** (Ballroom, Jen Hotel)	
1030 – 1050	Morning Break	
	Chairperson: Manuel Lopes-Lima	
1050 – 1110	Factors driving changes in freshwater mussel (Bivalvia, Unionida) diversity and distribution in Peninsular Malaysia **Alexandra Zieritz (FB)**	82
1110 – 1130	Comparative phylogeography of freshwater mussels in mainland Southeast Asia **John Pfeiffer (FB)**	84
1130 – 1150	Freshwater mussels (Unionoida) of Vietnam: Diversity, distribution and conservation status **Do Van Tu (FB)**	85
1150 – 1210	A global bioregionalization based on freshwater bivalves **Torsten Hauffe (FB)**	86
1210 – 1340	Lunch	
	Chairperson: John Pfeiffer	
1340 – 1400	Freshwater bivalve diversity in Turkey **Ümit Kebapçı (FB)**	87
1400 – 1420	Model for the conservation assessments of the freshwater bivalves in Russia **Igor Popov (FB)**	88
1420 – 1440	Phylogeny of the most species rich freshwater bivalve family (Bivalvia: Unionida: Unionidae): Defining modern subfamilies and tribes **Arthur Bogan (FB)**	89
1440 – 1500	Phylogenomics of freshwater mussels (Bivalvia: Unionida) preliminary results and lessons learned **Manuel Lopes-Lima (FB)**	91
1500 – 1520	Afternoon Break	
1520 – 1700	Poster Session (ODD number)	

THURSDAY, JULY 21

ROOM 1 (BALLROOM)

		Page
0930 – 1030	**Keynote Session 2: Prof. Fred Wells** (Ballroom, Jen Hotel)	
1030 – 1050	Morning Break	
	Chairperson: Suzanne Williams	
1050 – 1110	Opisthobranch assemblage composition and seasonality in a Mediterranean littoral unconsolidated wave-disturbed community **Federico Betti (EMM)**	20
1110 – 1130	Solar-powered sea slugs – how sacoglossan slugs survive on sunlight **Elise Laetz (EMM)**	21
1130 – 1150	Molecular phylogeny and behavioral ecology of "*Lottia kogamogai*" species complex (Patellogastropoda, Lottiidae) in Japan **Ryo Nakayama (EMM)**	22
1150 – 1210	The identification of shell pigments and the genes involved in their synthesis in two species of the marine genus *Clanculus* **Suzanne Williams (EMM)**	23
1210 – 1230	Surviving development: Ecological changes of marine molluscs in Pulai River Estuary seagrass ecosystem, Johor, Malaysia **Nur Leena Wong (EMM)**	24
1230 – 1340	Lunch	
	Chairperson: Thierry Backeljau	
1340 – 1400	Incipient hybrid speciation of door snails in previously glaciated areas in the Caucasus **Bernhard Hausdorf (OS)**	102
1400 – 1420	The last glacial to Holocene history of *Helix pomatia* in central Europe **Ondřej Korábek (OS)**	103
1420 – 1440	Lymnaeid snails from geothermal springs across north Eurasia: Endemic species or ecotypes of widespread taxa? **Olga Aksenova (OS)**	104
1440 – 1500	Dealing with permanent impermanence: The ecology and physiology of endemic spring snails in Australia's desert springs **Renee Rossini (OS)**	105

THURSDAY, JULY 21

1500 – 1520	Temporal variability in heterobranch (Gastropoda: Heterobranchia) sea slug assemblages on three intertidal rocky reefs of the Solitary Islands Marine Park, New South Wales **Matthew Nimbs (OS)**	106
1520 – 1540	Afternoon Break	
1540 – 1700	Poster Session (EVEN number)	

THURSDAY, JULY 21

ROOM 2 (PANGKOR)

		Page
0930 – 1030	**Keynote Session 2: Prof. Fred Wells** (Ballroom, Jen Hotel)	
1030 – 1050	Morning Break	
	Chairperson: Benedikt Wiggering	
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Integrating Molecules, Morphology, Biology & Biogeography in "Opisthobranch" Research

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Abstracts

ORAL PRESENTATIONS

INTERTIDAL GASTROPODS AND GLOBAL WARMING ALONG THE ATLANTIC COAST OF THE IBERIAN PENINSULA

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Beginning in August 2011, we have been studying the distribution and abundance of several intertidal species of gastropods along the Atlantic coast of the Iberian Peninsula; this is been done to explore the effect of the global warming in these molluscs. A preliminary study showed that temperate-water gastropods did not show any substantial change on their distribution range or abundances along the studied latitudinal gradient when compared to previous data. On the other hand, cold-water boreal species like *Littorina littorea* (Linnaeus, 1758), *Littorina saxatilis* (Olivi, 1792) or *Nucella lapillus* (Linnaeus, 1758) showed significant contractions on their distribution while the sub-tropical false limpet *Siphonaria pectinata* (Linnaeus, 1758) showed a range extension northwards. Two years later (2013-14), an exhaustive survey of the same area confirmed the range shifts previously detected. Thus, the aforementioned boreal species showed a range contraction although a few isolated populations were found in areas where the species seemed to be absent previously. The role of these populations in the conservation of boreal species in a global warming scenario should be explored in the future. In the case of sub-tropical species the range expansion of *S. pectinata* was confirmed as well as for two other sub-tropical species (i.e. *Stramonita haemostoma* (Linnaeus, 1767) and *Phorcus sauciatus* (Koch, 1845)). We have also studied the effects of range extension on the populations of subtropical species. Thus, populations recently established out of their historical range showed, in general, lower densities but larger body sizes than populations within their historical range of distribution. Concerning to their intraspecific diversity, results did not show significant differences in the number and diversity of haplotypes of the mitochondrial COI between "historical" populations and those recently established out of their historical range. However, the number of unique haplotypes was always higher in historical populations.

Keywords: NE Atlantic, gastropods, intertidal, distribution range, population structure

"IN DESICCATING ENVIRONMENTS SNAIL AGGREGATION IS ADAPTIVE BECAUSE IT LOWERS WATER LOSS." AN ANALOGY SHOWING WHY THIS STATEMENT IS VERY DIFFICULT TO VALIDATE

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Molluscs (and other creatures) living in extreme environments are by definition at risk, typically from physical factors. In the high-shore, gastropods worldwide when exposed by the tide utilise a range of supposedly adaptive physiological and behavioural mechanisms to ameliorate harsh environmental effects, effects increasingly mediated by climate change. Perhaps the most obvious of these mechanisms, and perhaps the most cited, is the on-shore aggregation of snails to reduce desiccation stress. Though snails clearly do aggregate and do so increasingly in response to increased physical stress, demonstrating *in situ* the seemingly logical relationship between aggregations and lowered desiccation has proved elusive. By way of the analogy of drinking alcohol, an analogy many malacologists will be familiar with, we try to explain why this might be so. Attempts to determine the adaptive benefits of aggregation are commonly made by comparing water contents, or body fluid osmotic potentials, of aggregating and non-aggregating individuals. However, this method has two flaws: it diminishes the true relationship between aggregation and desiccation because though measurements are largely taken contemporaneously, at the time of measurement individuals will have experienced varying periods within aggregations; it also does not measure reduction in the rate of water loss, which is the benefit of aggregation. Measurement of this benefit is fraught with procedural difficulties, mostly in relation to disturbance: typically either behaviour is unnaturally restricted or compromised repeated measurements are needed. One answer to obtaining fine spatial and temporal resolution in measuring water loss *in situ* lies with biomimetics. These sensors, if carefully designed for their mimicry, can provide a useful approach to determining the true relationship between aggregation and desiccation stress, and thus reveal the adaptive benefit of aggregation behaviour.

Keywords: aggregation, desiccation, gastropod, shore, snail, water loss

CARRY-OVER EFFECTS OF ENVIRONMENTAL STRESS: LESSONS LEARNED FROM *SIPHONARIA AUSTRALIS*, AN INTERTIDAL LIMPET WITH MIXED DEVELOPMENT

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In a rapidly changing ocean, organisms will be faced with exposure to stressors at multiple times over the course of their lives, with early stages particularly vulnerable. For organisms with complex life cycles, experiences at one life stage can have carry-over effects on the performance of later life stages, such that sub-lethal effects may mediate later vulnerability to further stress. *Siphonaria australis* is a marine pulmonate limpet endemic to New Zealand's rocky intertidal coasts and has a mixed development life history (i.e. embryos develop in a benthic egg mass before hatching into planktonic larvae). Recent experiments using *S. australis* demonstrate that the responses of early life stages (i.e. embryos and larvae) to environmental stress are highly context dependent, and often the result of complex interactions between stress regimes experienced by both the parents and those of the offspring. For example, when both parents and their egg masses were subjected to stress regimes that include exposure to copper pollution, high UV and high temperature, the viability of embryos in the egg masses, hatching success and size at hatch of larvae from stressed egg masses were all lowest when parents had also been subjected to the most stressful conditions. Similarly, for planktonic larval stages survival and growth was dependent not only on whether they were directly subjected to stress (UV and temperature), but also on whether as embryos they had previously experienced stress in benthic egg masses, or whether their parents had. Taken together, these results demonstrate that the responses of early life stages to environmental stress can be heavily dependent on conditions that prevailed during earlier life stages or even during previous generations. Therefore focusing on immediate effects on a single life stage will underestimate cumulative and interactive effects of agents of global change.

Keywords: intertidal gastropods, global change, environmental stress, larvae, carry-over effects, egg mass

DISTRIBUTION PATTERNS OF *TRIDACNA MAXIMA* AND ITS RESPONSE TO NATURAL THERMAL-BLEACHING EVENT

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Ocean warming-induced mass mortalities of giant clams, living symbiotically with the dinoflagellate *Symbiodinium*, have been reported from the Pacific. However, little is known about giant clams bleaching in the Indian Ocean. This study investigated the spatio-temporal distribution of *Tridacna maxima* at three stations (near-coast, lagoon and reef flat) during the non-bleaching years 1999 and 2010, and the bleaching year 2016 at Belle Mare (BM), Mauritius. Triplicate 50mx10m belt transects surveys per station (n=3) were conducted in April and individuals were enumerated and classified into recruits (<50mm) and adults (51-100, 101-200 and 201-300mm.) A significant decrease in the mean density of both recruits and adults of *T. maxima* was observed during this study. The highest mean density of *T. maxima* recorded (per 500m^2) was at the reef flat in 1999 with 5.67 ± 0.58 as recruits, 4.00 ± 1.00 (51-100mm), 3.33 ± 1.15 (101-200mm) and 3.00 ± 1.0 (201-300mm) as adults. The maximum seawater temperatures at BM recorded were 29^{o}C in 1999 and 2010, and 32^{o}C in 2016. The high seawater temperature anomaly in 2016 resulted in severe coral bleaching and almost 90% of this occurred at the reef flat of BM. However, none of the *T. maxima* was observed to bleach. The effective quantum yield (Φ_{PSII}), often used as an indicator of photosynthetic functioning and coral bleaching conditions, and measured using a Diving-Pulse-Amplitude-Modulated fluorometer, was not significantly affected in the *Symbiodinium* of *T. maxima* while the Φ_{PSII} in the adjacent bleached corals was greatly reduced. This suggests that the *Symbiodinium* of *T. maxima* was thermally more tolerant than those of corals during the thermal anomaly at BM in 2016. Further studies on other factors linked to the decline of *T. maxima* at BM are required over the long term to thoroughly understand its population dynamics and the implications for conservation and management.

Keywords: bleaching, giant clam, *Tridacna maxima,* Mauritius, PAM, thermal anomaly

THE SCLEROCHRONOLOGY OF THE ANCIENT GIANT CLAM, *HIPPOPUS HIPPOPUS*, FROM THE BALOBOK ROCKSHELTER, PHILIPPINES

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The Balobok Rockshelter is one of the archaeological sites that produced significant findings and greatly contributed to the understanding of the Philippine prehistory, especially based on its shell deposit from prehistoric humans 9000 years ago. A sample of *Hippopus hippopus* belonging to the Early Occupational Phase (8760 +/- 130 BP) of the Balobok Rockshelter is one of the most commonly recovered bivalve from archaeological shell middens in the Philippines. This study presents the sclerochronology of ancient *H. hippopus*, i.e., the growth was examined via the study of the growth increment thickness changes in the inner shell layer. The specimen analyzed was approximately one year old and started to show distinct changes in its internal growth increment thickness in the last quarter of its life. The method presented can be used to provide information on shell age and to interpret environmental variations. Indeed, shell growth lines are well preserved that allows sclerochronology studies. However, larger (older) shells should be selected to obtain palaeoenvironmental information. On the whole, the study provides new insights into the biology, in terms of shell growth, of *H. hippopus*, which is crucial for paleoclimate reconstruction.

Keywords: giant clams, sclerochronology, palaeoenvironmental reconstruction

UNITAS MALACOLOGICA Grant Recipients

THE ECOLOGICAL IMPORTANCE OF GIANT CLAMS IN CORAL REEF ECOSYSTEMS

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Giant clams (*Hippopus* and *Tridacna* species) have long been associated with coral reefs, where they are thought to play various ecological roles. These roles, however, have not previously been quantified. Using data from the literature (n=481 publications) and our own studies we elucidate the ecological functions of giant clams. We show that giant clams are important providers of food and shelter, and function as reef builders and shapers. Giant clam tissues are an attractive food source to predators and scavengers, while opportunistic feeders exploit their discharges of live zooxanthellae, faeces and gametes. Their shells also provide additional surfaces for epibiont colonisation, and their mantle cavities serve as refuges for reef fishes, commensals, and parasites. Giant clams can enhance the topographic relief of seabed, serve as reservoirs of zooxanthellae, and also potentially counteract eutrophication via water filtering. Finally, dense populations of giant clams can produce large quantities of calcium carbonate shell material that is eventually incorporated into the reef framework. Unfortunately, giant clams around the world are facing pressures of overfishing and habitat loss, resulting to extirpations that are likely to have negative impacts on tropical coral reefs. A greater understanding of giant clams' contributions to coral reefs health will reinforce the case for their conservation.

Keywords: carbonate budgets, conservation, epibiota, eutrophication, *Hippopus*, *Tridacna*, zooxanthellae

GIANT CLAMS (BIVALVIA: CARDIIDAE) AS POTENTIAL COUNTERACTORS OF ALGAL BLOOMS

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Coastal eutrophication can lead to undesirable algal blooms, with negative impacts for a wide range of marine organisms and communities. One approach to counteracting algal proliferation is biological control. Due to their ability to filter microalgae from the water column, giant clams (Bivalvia: Cardiidae) are potential counteractors of algal blooms in coral reef ecosystems. To date, however, no research has quantified this important role. Our study investigated the clearance efficiency of juvenile *Tridacna maxima* when exposed to two species of microalgae monocultures (*Isochrysis* sp. and *Tetraselmis suecica*) at three levels of algal density: eutrophic density, feeding density and natural density. Test clams were maintained in mini Vortex Resuspension Tanks (mVoRTs) that were designed to keep particulates suspended in the water column. The clearance rates after 5 hours were calculated from algal densities (initial and final) enumerated using flow cytometry. The clams reached their maximum clearance capacity more rapidly when exposed to larger-sized microalgae species. Results indicate that *T. maxima* filter feed readily but are more effective in clearing microalgae during the earlier stage of an algal bloom where algal density has yet to reach eutrophic levels. Giant clams can potentially exert a significant top-down regulation on reef phytoplankton during pre-eutrophic conditions, but this effect is dependent on dense and healthy giant clam populations. Unfortunately, giant clam numbers are in decline from contemporary anthropogenic impacts, impeding the benefits of this biological control.

Keywords: eutrophication, biological control, giant clam, *Tridacna*, *Hippopus*, filter feeding, algal bloom

A NOVEL FILTERING MUTULISM BETWEEN SPONGE HOST AND ITS ENDOSYMBIOTIC BIVALVE *VULSELLA VULSELLA*

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Sponges, porous filter-feeding organisms consisting of vast canal systems, provide unique substrates for diverse symbiotic organisms. The *Spongia* (*Spongia*) sp. massive sponge is obligately inhabited by the host-specific endosymbiotic bivalve *Vulsella vulsella*, which benefits from this symbiosis by receiving protection from predators. However, whether the host sponge gains any benefit from this association is unclear. Considering that the bivalves exhale filtered water into the sponge body rather than the ambient environment, the sponge is hypothesized to utilize water exhaled by the bivalves to circulate water around its body more efficiently. I tested this hypothesis by observing the sponge aquiferous structure and comparing the pumping rates of sponges and bivalves. Observations of water currents and the sponge aquiferous structure revealed that the sponge had a unique canal system enabling it to inhale water exhaled from bivalves, indicating that the host sponge adapted morphologically to receive water from the bivalves. In addition, the volume of water circulating in the sponge body was dramatically increased by the water exhaled from bivalves. Therefore, this sponge-bivalve association can be regarded as a novel mutualism in which two filter-feeding symbionts promote mutual filtering rates. This symbiotic association should be called a "filtering mutualism".

Keywords: mutualism, sponge, suspension feeding, bivalves

MOLLUSC DIVERSITY AND DOMINANCE IN LATE PALEOZOIC AND EARLY MESOZOIC MARINE ENVIRONMENTS

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Molluscs, especially gastropods and bivalves, are commonly dominant in modern shallow marine environments both, according to species richness and relative abundance. By contrast, Palaeozoic marine faunas are much more characterized by other groups such as articulate brachiopods and crinoids. Mollusc dominance is therefore considered to be a relatively modern feature. However, analyses of Late Palaeozoic and early Mesozoic faunas based on bulk sampling and the use of relatively small mesh sizes (0.5 mm) shows that molluscs and especially gastropods were much more important during this period of time than previously assumed. Mollusc dominance has accelerated during the recovery phase from the end-Permian mass extinction and is very pronounced in samples from the Cassian Formation (Late Triassic, N Italy), which provides unique insights about an early Mesozoic tropical ecosystem. Low-grade lithification and diagenesis of the sediments of this formation facilitated the perseveration of small species representing especially gastropods. Gastropods are by far the most diverse group followed by bivalves. Strong mollusc dominance is a modern, advanced feature of the Cassian biota. Standardized quantitative sampling methods as well as statistical sample standardization were applied and results suggest that the diversity of the Cassian biota is probably in the magnitude of that of modern tropical shallow water biota. The keys to gastropod and bivalve diversification are probably possible planktotrophic larval development (the veliger larva) and motility as well as diet and habitat diversity.

Keywords: diversity, mollusc dominance, palaeozoic, mesozoic, ecology

FATTY ACID AS MARKERS TO BRIDGE AN EXISTING GAP OF BIVALVE FOOD SOURCES IN THE TROPICAL LAGOON OF SETIU WETLAND, TERENGGANU, SOUTH CHINA SEA

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The nature of the habitat and the available organic material influence bivalve diet. Suspension feeding bivalve usually rely on phytoplankton as a main food sources, however, a lot of other studies indicated that suspension-feeding bivalves had an ability to assimilate organic material sources from seaweed, seagrass and mangrove detritus. This study was conducted at Setiu Wetlend, Terengganu in order to compare the food sources of three different genera of suspension-feeding bivalves that inhabit different habitat, *Anadara* – benthic, semi-infaunal, seagrass bed; *Isognomon* – sessile, water column, and *Meritrix* – benthic, semi-infaunal, sandy bottom. The lipid content and fatty acid composition in the tissues of the animal were determine. Fatty acid that assigned to specific organic sources were analysed among bivalves to indicate their sources of food. The result found that three main categories of organic materials detected in the bivalves tissues, microalgae (phytoplankton, benthic diatom), bacteria and macroalgae-seagrass-mangrove. The composition of those materials in the studied bivalves was presented and discussed. Eventually, this finding might contributed to bridge an existing gap in the food webs of Setiu Wetland ecosystem.

Keywords: fatty acid marker, bivalve, food source, food web, Setiu Wetland

COMPARISON OF TWO YEARS' OSCILLATION AND LIFE SPAN OF *CYPRAEA MONETA* L. 1758 (GASTROPODS: CYPRAEIDAE) FROM SEPANJANG BEACH, YOGYAKARTA, INDONESIA

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The fact that shells of *Cypraea moneta* (money cowry) have been harvested for a long time by inhabitant along Southern Beach of Yogyakarta, Indonesia has been a reason beyond this research. This research aims to estimate oscillation and life span of *C. moneta*. This was done, in order to be able to give some recommendation to a decision maker about harvest regulation of shells. Sampling was done once a month for two years, every low tide, by hand picking for half an hour, randomly. Sample then measure for its shell length and tabulate in length frequency data. Data was analyzed by using Elefan I, the graph of Von Bertalanffy Growth Formula (VBGF) formed, and got growth parameter such as K, and analyzed descriptively. Results show that population's oscillation fluctuated and has only one peak at September. This two years result was quite unusual since this is a tropical species and expected to have two peak or bimodal. The growth's constant, K, was 0.35 (slow growth, less than 0.5). It means that *C. moneta* has a quite long time to reach its mature size. The life span of *C. moneta* at the year 2013 was about 7-9 years and at the year 2014 was more than 10 years. Another trial, using two years data at once, resulted in life span *C. moneta* of 7-9 years. This species should be treated carefully since it has a slow growth, susceptible and exploited extensively.

Keywords: *C. moneta*, susceptible, slow growth, and VBGF

BROODING IN THE CHILEAN OYSTER *OSTREA CHILENSIS*: MUCH MORE THAN JUST KEEPING THE KIDS SAFE!

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Brooding in gastropods and bivalves protects embryos from the external environment by retaining them inside the pallial cavity of the female, resulting in changes in the characteristics of the pallial fluid, including a reduction in oxygen content. Brooded embryos are usually immobile, but in some *Ostrea* species they move freely inside the pallial cavity in close association with the female gills for up to eight weeks. We used endoscopy to examine the circulation pattern of brooded embryos in the oyster *Ostrea chilensis* and measured the oxygen concentration in the pallial cavity. Embryos and veligers circulated in fixed pathways, including the dorsal and ventral food grooves (DFG, VFG) on the gill, which directed the progeny anteriorly. Embryos and veligers accumulated around the palps of the female and remained there until an active countercurrent moved them to the inhalant area of the pallial cavity. Both food grooves transported embryos, veligers and food-particles. Early embryos moved more rapidly than veligers within the DFG. A microcirculation of embryos was apparent on the gill lamella: when close to the VFG, most embryos lost contact with the gill surface and "fell" towards the DFG. Those that reached the DFG moved anteriorly, but others contacted the base of the lamella and again moved towards the VFG. The circulation pattern appears well suited for cleaning the progeny and directing them posteriorly, where there is more oxygen and food than in the palp region. The pallial fluid in the palp area became hypoxic when the female was brooding advanced veligers. This mechanism for actively circulating the progeny involves the feeding structures (gills and palps) and appears to be energetically costly for the brooding female. It also interferes with feeding by the female, which may explain the reduction in energy balance previously documented for brooding females of this species. (Fondecyt-Chile Grant1141052).

Keywords: brooding, oyster, embryos, veligers, circulation patterns

MOLLUSC DIVERSITY ASSOCIATED TO THE ECOSYSTEM ENGINEER *LITHOPHYLLUM BYSSOIDES* (RHODOPHYTA) ACROSS A LATITUDINAL GRADIENT

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Marine ecosystem engineers include corals, bivalves, tubeworms and macroalgae. Among the latter, the crustose calcareous macroalgae *Lithophyllum byssoides* (Lamarck) Foslie (Rhodophyta, Corallinaceae) is commonly found along the Atlantic and Mediterranean coast of the Iberian Peninsula. In the intertidal, this alga provides shelter for many small-sized invertebrates such as peracarid crustaceans, polychaetes and molluscs. However, few quantitative studies have been done to assess the diversity of associated invertebrates at large spatial scales (i.e. >10s kms). Therefore, we aim to describe the diversity and composition of the mollusc assemblage associated to *L. byssoides* along the Atlantic coast of the Iberian Peninsula at several spatial scales. Along this coast, comprising about 885 Km from northern Galicia to southern Portugal, several latitudinal environmental gradients may potentially shape intertidal assemblages (e.g. increased sea surface temperature southwards). Sampling was done during the spring tides of July and August 2011 following a hierarchical sampling design, considering four different spatial scales (from ms to 100s of kms). Five regions separated from each other by 100s of km were considered (i.e. A Mariña, Costa da Morte in NW Spain and North, Central and South Portugal). Within each region, three rocky shores separated by 10s of km and three sites within each shore, 10s of ms apart, were randomly selected. At each site, five replicate 100 cm^2 quadrats containing *L. byssoides* were sampled at midshore (2–2.5 m above low tide). Aggregates of *L. byssoides* were scraped and sieved through a 0.5-mm mesh, fixed in ethanol and then molluscs sorted and identified in the laboratory. Differences in number of species and abundance were tested by a 3-way nested ANOVA; a similar design was used for assemblage composition by means of PERMANOVA.

Keywords: NE Atlantic, intertidal, distribution, ecosystem engineer

THE EASTERN PACIFIC COAST AS A NATURAL TRANSECT OF THE GLOBE FOR UNDERSTANDING LATITUDINAL DIVERSITY GRADIENTS AND BIOGEOGRAPHIC STRUCTURE OF ROCKY SHORE GASTROPODS

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A casual glance of the globe reveals that the eastern Pacific (EP) coast spans uninterrupted across nearly the entire north-south length of the planet - from Tierra del Fuego to Alaska. The denizens of this natural transect of the globe are ideally suited for testing the underlying causes of basic, yet poorly understood concepts in macroevolution and macroecology. For example, the processes driving the latitudinal gradient of biodiversity (higher species richness towards tropical latitudes) are elusive despite its near ubiquity. Using EP rocky intertidal gastropods as a model group, we assess the shape of the latitudinal gradient of diversity and explore the macroevolutionary dynamics that may underlie its origination and maintenance. By comparing modern and fossil occurrences of genera, we show that origination rates are not different between regions, but extinction rates are lower in the tropics. Moreover, many taxa that do originate within temperate latitudes tend to migrate towards tropical latitudes over time. We refer to this macroevolutionary dynamic as the "Into the Tropical Museum Hypothesis". In addition, we gathered geographic range data from museum occurrences and the literature to assess the biogeographic structure of EP rocky shore gastropods and discuss the physical variables that likely underlie it. Our study reveals the oceanographic and habitat variables that likely drive biogeographic structure of modern day rocky shore gastropods along the eastern Pacific coast.

THYASIRID BIVALVES FROM ANCIENT METHANE SEEPS

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This work presents results of a systematic study on thyasirid bivalves from Cretaceous and Palaeogene methane seeps. The species indentified in this study belong to four known genera: *Conchocele* Gabb, 1866; *Cretaxinus* Hryniewicz, Little and Nakrem, 2014; *Maorithyas* Fleming, 1950 and *Thyasira* Lamarck, 1818. Thyasirid bivalves appear for the first time in earliest Cretaceous seep from Spitsbergen, Svalbard, which is the only occurrence of a unusual, large thyasirid genus *Cretaxinus*. Until the Late Cretaceous, the species of the genus *Thyasira* are an the only thyasirids found at some fossil seep deposits, although they were never common and never attain lenghts of more than few millimeters. The first mass occurrence of a large (30 mm and longer) thyasirid bivalves at seeps are the latest Cretaceous (Maastrichtian) Snow Hill and Seymour Island seeps from Antarctica, where *Conchocele townsendi* (White, 1890) dominates the seep assemblages for the first time in the evolutionary history of thyasirids. Similar mass occurence of *Conchocele* is also known from slightly younger (Paleocene) seep from Spitsbergen in the Arctic, which shows that the appearance of the genus had a bipolar aspect. With the appearance of *Conchocele*, thyasirids become more frequent element of seep communities, especially in cool and shallow water seep environments of the Northern Pacific area. We argue that until the Late Cretaceous most of the thyasirids were not symbiotic, which is testified by their infrequent occurrence at seeps and by their small average sizes. We also suggest that the appearance of symbiotic thyasirids in the Late Cretaceous may have been influenced by the overall low sulphide content at seeps of that time, which promoted infaunal chemosymbiotic invertebrates.

Keywords: thyasirids, methane seeps, chemosymbiosis, palaeoecology, evolution

DIVERSITY OF MOLLUSCS (CLASS BIVALVIA AND GASTROPODA) IN RELATION TO HABITAT CHARACTERISTICS IN TROPICAL MANGROVES OF PENANG ISLAND, MALAYSIA

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The structural complexity in mangroves supports a diverse array of macrofauna across various spatio-temporal scales. However, there is a lack of information on the current distribution of macrofauna specifically molluscs in the tropical mangroves of Malaysia. Penang Island is undergoing rapid urbanization, introducing potentially negative effects on the diversity of molluscs in mangroves. A diversity assessment on mollusc assemblages was conducted in mangrove forests around Penang Island across multiple spatio-temporal scales. Habitat characterisation involved recording the density of pneumatophores, detrital matter and organic matter biomass, and sediment particle size. To identify the effect of spatio-temporal scales on molluscs, multivariate analysis and univariate analysis were done. We have identified 15 genera of gastropods and 4 genera of bivalves, with gastropods representing 80% of 403 individuals m^{-2}. Spatio-temporal variation in mollusc abundance was significant (PERMANOVA $P<0.01$). There was significant variability between the low and high intertidal (PERMANOVA $P<0.01$), however this differed among sampling occasions. The red berry snail, *Assiminea* sp. represented 82.10 % of mollusc assemblage composition across all forests. There were significant differences in total mollusc abundance among sites (ANOVA $p<0.05$), with high abundance of individuals m^{-2} found in Gurney (826 ± 133) and Sg. Pinang (332 ± 118), when compared with low abundances found in Pulau Betong (50 ± 15). Organic matter and density of pneumatophores described the patterns of mollusc assemblage composition, however this relationship was weak ($\rho=0.237$, $P<0.01$). Although the correlation was weak, there is a possibility that fluctuations in physical structures and organic matter content could affect mollusc abundance. Organic matter could provide more food to molluscs, however increase in organic matter could cause hypoxia, thus resulting in mortality of less tolerant mollusc species. This could have an alarming consequence on molluscs, particularly as habitat simplification and modification are on the rise due to unsustainable human activities.

Keywords: tropical mangrove, mollusc, gastropod, bivalves

CREPIDULA FORNICATA (LINNAEUS, 1758): FROM ABSENT TO DOMINANT IN RÍA DE VIGO (NW IBERIAN PENINSULA)

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Ría de Vigo is a semi-enclosed bay surrounded by a heavily populated coastline and affected by different human activities. The gastropod *Crepidula fornicata* (Linnaeus, 1758), native from eastern North America, is a non-indigenous species in this area. It was first reported in Europe in the late 19th century, when it got stablished after being imported along with *Crassostrea virginica* (Gmelin, 1791) for culture. In Galician Rías (NW Iberian Peninsula), where Ría de Vigo is located, it was introduced in the late 1970's along with individuals of *Crassotrea gigas* (Thunberg, 1793) from France and Ireland. It was first cited there in 1983 by Rolán, who did not find the species in the non-estuarine zones of Ría de Vigo, but only in the estuarine zone of the bay. Subtidal epibenthic megafauna in the non-estuarine zones of Ría de Vigo (75 sites) was sampled in June 2014 using a bottom trawl. Among the 113 different taxa identified, *C. fornicata* was the most numerous considering all the samples and the dominant species in terms of both abundance and biomass in the inner part of the Ría. The species is known to prefer enclosed areas, less exposed than our area of study, what may explain why abundances are lower than in other bays along European coast. However, the conditions in the Main Channel of Ría de Vigo seem to have been suitable for the establishment of a large population of *C. fornicata*. The results suggest that benthic diversity has not been severely affected, but we lack enough data prior to the settlement of the species in order to confirm this. The commercially exploited bivalve *Aequipecten opercularis* (Linnaeus, 1758) is also abundant in the area. As both species are suspension-feeders, the spread of *C. fornicata* is likely to have affected the population of *A. opercularis*.

Keywords**:** *Crepidula fornicata*, alien species, North East Atlantic, epibenthos

UNITAS MALACOLOGICA Grant Recipients

DYNAMICS OF CORALLIVOROUS *DRUPELLA* SNAILS ON CORAL REEFS WITH DIVING-RELATED TOURISM (KOH TAO, GULF OF THAILAND)

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Diving-related tourism is known to contribute both directly and indirectly to reef degradation around the globe. However, of the known publications on reef threats at Koh Tao (Gulf of Thailand), only two mention the effects of coral predators despite their high abundance. The present study combines results of seven years (2008-2014) of reef surveys to evaluate the abundance and impact of corallivorous *Drupella* snails in the area. This study provides the first record of coral predator abundances and simultaneous outbreaks on Koh Tao's reefs, and is compared to other studies in order to evaluate how predation has influenced declines attributed to diving and other anthropogenic stresses. The findings suggest that the effect of these corallivores have contributed significantly to coral degradation over the last decade and indicate that future assessments of reef decline in areas impacted by heavy tourism also need to address the effect of coral predation.

Keywords: *Drupella* snails, corallivore, coral reef, SCUBA diving

DOES SPECIES-SPECIFIC EPIPHYTE, *PSEUDOCLADOPHORA*, NEGATIVELY AFFECT HOST *TURBO*?

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The shells of *Turbo* (*Lunella*) *coreensis* (Récluz, 1853), which are commonly infested by different epibionts, are often found to be physically damaged. Abrasion damages with the peristracum being abraded and the inner layers exposed, and perforation scars are the two most common types of damages observed. Based on a GLMM analysis, our study revealed the size of host shells and the coverage of an alga *Pseudocladophora* might be related to the appearance of abrasion damages. On the other hand, there was no significant correlation between the appearance of scar damages and red algal biomass density, size of host shells, and *Pseudocladophora* coverage. This suggests that the appearance of two types of damages may result from different factors.

Keywords: intertidal stony shore, species specificity, epibiosis, algal competition, algal-invertebrate interactions

UNITAS MALACOLOGICA Grant Recipients

OPISTHOBRANCH ASSEMBLAGE COMPOSITION AND SEASONALITY IN A MEDITERRANEAN LITTORAL UNCONSOLIDATED WAVE-DISTURBED COMMUNITY

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The habitat preferences of Mediterranean opisthobranchs are generally well known; however, some environments are poorly studied, because often considered few structured or poor in terms of biodiversity. The aim of the present work was to study the annual variations in species composition, seasonality and diet preferences of the opisthobranch assemblage living on the unconsolidated wave-disturbed environment of Noli Cape (North-western Ligurian Sea), from 7 m to 20 m depth. The assemblage, studied by means of 40 scuba diving surveys from January 2015 to March 2016, resulted to be particularly unique. Firstly, it appeared to be extremely rich in terms of biodiversity, with 39 recorded species on a total richness in the Ligurian Sea of about 140 species, in just 5.000 m^2. Six opisthobranchs new for the Ligurian Sea were recorded. Moreover, several species showed a strong seasonality: winter time appeared to be the most suitable season for the majority of them, when up to 12 species were recorded in each survey: 60,5% of the opisthobranchs showed cold affinity, even though the most common species were endemic. Most of them were surprisingly typical of hard bottoms communities, and despite the high species richness, the main feature characterizing the assemblage is the low presence of sponge-eaters (10,5%), while the majority of the species were cnidarian-eaters (28,9%), or omnivorous and true predators (23,7%); in total, 7 feeding groups were recognized. *Onchidoris neapolitana*, which feed on bryozoans, was abundant, and the oophagus *Favorinus branchialis*, usually extremely rare, appeared to be relatively common. Some usually common Mediterranean species were absent or very rare, because of the lack of their preys. In general, the Noli Cape opisthobranch assemblage resulted to be composed by species strongly selected by their feeding habits, independent of substrate and hydrodynamism effects, with the sea water temperature as a main selection force.

SOLAR-POWERED SEA SLUGS – HOW SACOGLOSSAN SLUGS SURVIVE ON SUNLIGHT

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Solar-powered sea slugs (Sacoglossa: Gastropoda) represent the only known animals capable of stealing chloroplasts from their algal food, retaining them for months while undergoing extended starvation periods. These stolen chloroplasts, termed kleptoplasts, are stored within their digestive gland tissues and can remain photosynthetically active for months after ingestion. Active carbon fixation could prolong a starving slug's life span, likely due to the photosynthates produced, although photosynthate accumulation and degradation have only recently been considered. The long-term plastid-retaining slug, *Elysia timida* and its sole food source, *Acetabularia acetabulum* were examined to determine whether or not the main photosynthate produced by *A. acetabulum,* starch, is produced by the stolen plastids. We present here for the first time, a significant increase in amylose concentration, within the slug's digestive gland cells during a starvation period, followed by a sharp decrease. This suggests that kleptoplasts function as both, a nutritive producer and storage device, holding onto the polysaccharides they produce for a certain time until they are finally available and used the starving slug. Despite now knowing that plastids may directly contribute to slug longevity during starvation due to the photosynthates produced, little is known about the number and longevity of the plastids themselves. Recent research has investigated this activity using Pulse Amplitude Modulated Fluorometry, a technique that measures the chlorophyll a autofluorescence originating from photosystem II, a qualitative assessment. Here, we present a detailed, quantitative look at chlorophyll degradation in sacoglossan tissues, examine chloroplast digestion in situ and explore the correlation between chlorophyll breakdown and the degradation of the kleptoplast itself. Chlorophyll a content was measured using confocal microscopy to detect the autofluorescence and compared to Acridine Orange stained lysosomes detailing an inverse relationship with a strong correlation between decreasing chlorophyll content and lysosome abundance. The relationship between chlorophyll a breakdown and the degradation of the plastid is currently being examined to determine if there is any correlation and/or causation.

MOLECULAR PHYLOGENY AND BEHAVIORAL ECOLOGY OF "*LOTTIA KOGAMOGAI*" SPECIES COMPLEX (PATELLOGASTROPODA, LOTTIIDAE) IN JAPAN

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"*Lottia kogamogai*" species complex is a group of small lottiid limpets distributed in Japan. It consists of four species, *Lottia kogamogai*, *L. tenuisculpta*, *L. lindbergi* and *L. luchuana*. These four species inhabit intertidal rocky shores, and these species have partly overlapping distributions in Japan mainland, Honshu. Although shell sculpture is considered as one of important diagnostic characters for identifying these species, it is often eroded in adult individuals and similar between the species in juveniles. To correctly identify and to reveal phylogenetic relationships of the "*Lottia kogamogai*" species complex, we first performed a molecular phylogenetic analysis based on COI, and H3. In addition, in terms of behavior, juveniles of some species are found on shells of trochids and muricidis snails, but the adaptive significance of this behavior is not elucidated. Then, to clarify their life history, we investigated the number of limpets on the snails for one year. Furthermore, to clarify the adaptive significance, we observed predator avoidance of limpets on the snails. The molecular phylogeny revealed that the species complex is divided into two clades; each consists of 2 and 3 subclades including two cryptic species. It also revealed that two species, *L. tenuisculpta* and *L. lindbergi*, live on snail shells. The field observation showed that the number of limpets on snails had two clear peaks in a year, each corresponding to the settlement season of each species. The laboratory experiment showed that limpets attaching to the snails had better survival against the predator (*Pilumnus vespertilio*). Therefore, this behavior contributes to predator avoidance. Further analyses on the phylogeny of the whole *Lottia* species, character mapping, another behavioral and ecological observations such as desiccation resistance will clarify the evolutionary history and adaptive significance of living on the snail.

Keywords: limpet, molecular phylogeny, phylogeography, life history, predator avoidance

THE IDENTIFICATION OF SHELL PIGMENTS AND THE GENES INVOLVED IN THEIR SYNTHESIS IN TWO SPECIES OF THE MARINE GENUS *CLANCULUS*

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The phylum Mollusca includes some of the most beautiful exemplars of biological pigmentation, with the vivid colours of sea shells particularly prized by collectors and scientists alike. Here, I will discuss results of work undertaken by an international team using modern chemical and multi-modal spectroscopic techniques to identify two porphyrin pigments and eumelanin in the shell of marine snails *Clanculus pharaonius* and *C margaritarius*. The same porphyrin pigments were also identified in coloured foot tissue of both species. We refer to the two differently coloured porphyrin pigments as trochopuniceus (pink-red) and trochoxouthos (yellow-brown) in order to distinguish between them. Trochopuniceus and trochoxouthos were not found in the shell of a third species of the same superfamily, *Calliostoma zizyphinum*, despite its superficially similar colouration, suggesting that this species has different shell pigments. These findings have important implications for the study of colour and pattern in molluscs specifically, but in other taxa more generally, since this study shows that homology of visible colour cannot be assumed without identification of pigments. I will also present transcriptomic and qPCR results by a second international team. These results confirm the presence of genes associated with the synthesis of all three pigments in all three species, but consistent with biochemical studies, comparison of relative expression rates suggest that trochopuniceus and trochoxouthos are synthesised *de novo* only in *Clanculus*.

Keywords: shell colour, pigment, mollusc, porphyrin, melanin, marine

SURVIVING DEVELOPMENT: ECOLOGICAL CHANGES OF MARINE MOLLUSCS IN PULAI RIVER ESTUARY SEAGRASS ECOSYSTEM, JOHOR, MALAYSIA

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A massive reclamation project has been ongoing around Merambong Shoal seagrass bed at Pulai River Estuary since 2014, with the vision of building a new city on the reclaimed land. While the project developer is committed in preserving the seagrass bed, ecological impacts are inevitable with the presence of the long-term environmental stressors. Several monitoring projects have been on-going since early 2015 to monitor and examine the ecological changes of the seagrass and benthic communities of the seagrass beds in this area. Changes in the benthic marine mollusc communities have been observed, along with the seagrass and seaweed temporal covers. Hydrological alterations caused by reclamation activities had instigated shifts in mollusc community composition by introducing mangrove species from the nearby coastal mangrove and mudflats. In this presentation, marine mollusc diversity in this seagrass ecosystem will be presented, and their survival, adaptability and future prospect in this changing environment will be discussed.

Keywords: reclamation, marine mollusc ecology, seagrass ecosystem

MOLLUSCAN FAUNA OF LAKSHADWEEP ISLANDS, INDIA: DIVERSITY AND CONSERVATION CHALLENGES

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The Union Territory of Lakshadweep, India with an area of 32 square kilometres comprises 27 islands, 3 reefs and 6 submerged sandbanks and represents the only atoll in the country. The recorded diversity of marine molluscs in the island ecosystem includes around 773 species. This study documented 469 species of molluscs from Agatti, Amini, Andrott, Bitra, Chetlat, Kadmat, Kalpeni, Kavaratti, Kiltan and Minicoy islands, including 21 molluscs classified under various schedules of the Indian Wildlife (Protection) Act. The recorded diversity includes 12 range extensions into the Western Indian Ocean (11 gastropods and 1 bivalve) and 73 new records (59 gastropods and 14 bivalves) from the Lakshadweep islands, including 24 species recorded for the first time from the Indian coast. Trochidae, Cerithiidae, Strombidae, Ranellidae, Cypraeidae and Conidae are the most abundant gastropods while Cardidae, Spondylidae, Pinnidae, Lucinidae and Tellinidae are the most diverse bivalve families on the Lakshadweep coast. The IUCN Red-listed clams *Tridacna maxima* and *Tridacna squamosa* are abundant at all the islands. *Octopus vulgaris* and *O. cyanea* are the most important molluscan food source for the islanders. The collection of cowries, cone shells and cephalopods has resulted in population declines of up to 50 percent at some of the islands. The major threats to the molluscan diversity identified during the study include climate change-driven coral bleaching, coral mining, and utilization of resources, pollution and unsustainable coastal zone development. This paper discusses sustainable management strategies for molluscan resources, with community involvement, in order to ensure the livelihoods of people who depend on these molluscan resources.

Keywords: Lakshadweep, Red list, conservation, cowry, octopus, management

UNITAS MALACOLOGICA Grant Recipients

DIVERSITY AND DISTRIBUTION OF SEA SLUGS OF THE LAKSHADWEEP ISLANDS AND WEST COAST OF INDIA

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Sea slugs, a heterogeneous group of marine gastropods, exhibit great variety in Indian coastal waters, though documentation of their diversity is far from complete. For this study, sea slugs were collected from the west coast and Lakshadweep island ecosystem of India. This study documents 98 species with the following representing new records for the region: *Atys semistriata, Colpodaspis thompsoni, Ascobulla ulla, Volvatella viridis, Thuridilla indopacifica, Pleurobranchaea maculata, Goniobranchus rufomaculatus, Noumea norba, Trapania euryeia, Cuthona ornata, Phestilla melanobrachia*, and *P. minor*. Aeolidiidae, Aplysidae, Chromodorididae, Dendrodoridae, Discodorididae, Haminoeidae, Plakobranchidae and Phyllidiidae were the most abundant families. The invasive *Thecacera pennigera* was recorded from southwest coast of India for the first time. *Dolabella auricularia* was the most abundant species in sea grass beds. *Phanerophthalmus smaragdinus, Plakobranchus ocellatus, Elysia ornata, E. rufescens, Dendrodoris nigra, Aplysia oculifera, Stylocheilus striatus, Berthellina citrina, Pleurobranchus peronii* and *Halgerda tessellata* were the most abundant species on intertidal rocky shores, while *Asteronotus cespitosus, Jorunna funebris, Phyllidia alyta, P. marindica, P. varicosa, Phyllidiella rosans, P. zeylanica* and *Embletonia gracilis* were common in lagoon ecosystems. The use of DNA barcoding for documentation of sea slug diversity is discussed, with suitable examples from the Indian coast. The pattern of biogeographic distribution of sea slugs in various habitats along the Lakshadweep archipelago and southwest coast of India and the challenges towards their conservation are also discussed.

Keywords: opisthobranch, molecular taxonomy, invasive species, biogeography

MARINE MINISHELLS AND MICROSHELLS (MOLLUSCA: GASTRPODA) IN THAI WATERS

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Thirty-eight families and 156 species of minishells and microshells of marine gastropods were recorded from sand sediments, which were collected from several locations in Thai waters. Distribution of 10 species and 110 species (6.41 % and 70.51%) are recorded only from the Gulf of Thailand and the Andaman Sea respectively and 36 species (23.08%) recorded from both zones. Except, *Finella pupoides* and *Scaliola bella*, all are new recorded in Thai Waters.

Keywords**:** minishells, microshells, Thai waters, diversity

SHORT DNA SPECIES BARODES: A VALUABLE, LOW-COST TOOL FOR STUDYING GASTROPOD TAXONOMY AND BIOLOGY

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Gastropods are a hyperdiverse molluscan class with many taxonomic challenges: It contains many cryptic species, many described species are difficult to identify by non-experts, the available identification tools generally do not cover eggs and juveniles and there are few taxonomists who can help with solving these taxonomic problems. DNA barcodes have gained some popularity in the past decade as tools that can help with overcoming these hurdles. However, adoption in Gastropoda has been slow due to high cost, high amplification failure rates, and uncertainty with regard to the barcodes' taxonomic accuracy. In this study, these issues are addressed through the use of a short 313 bp mitochondrial COI barcode in combination with low cost Next-Generation barcoding and by comparing species limits based on morphological and genetic tools. A large number of adult specimens (*n*~400) from two marine gastropod clades (Caenogastropoda and Cycloneritimorpha), and egg/juvenile (*n*~50) gastropod specimens were barcoded in this study. Following optimization, success rates of up to 91.9% were achieved for properly preserved specimens, at an estimated cost of ca 0.88 USD per specimen. Sequence clusters based on the short COI barcode exhibited a low level of incongruence with morphological species (2.5%) and revealed several taxa that are conceivably cryptic species, which had been overlooked based on morphology. Overall, short 313 bp NGS barcodes promise to be a valuable addition to the gastropod taxonomic toolbox, as they are reliable, cost-effective, and can be used for specimens from difficult taxa and life history stages that cannot be identified based on morphology.

Keywords: DNA barcoding, Next Generation Sequencing, Caenogastropoda, Cycloneritimorpha, Singapore

GASTROPODS IN BUCAS GRANDE ISLAND, SURIGAO DEL NORTE

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The study aimed to determine the species composition and abundance of gastropods on the eastern and western part of Bucas Grande Island, Surigao del Norte. Sampling was done in plots with and area of 50x100meters laid on each sampling site: sampling sites 1 and 2 (eastern) and sampling sites 3 and 4 (western). Collection of gastropods were done by handpicking. A total of 1, 285 individuals were observed and counted during the study which were distributed to 51 species, 31 genera, 23 families, and 8 orders. Among the 51 species, 11.76% were found in all sampling sites, 21.57% found only eastern sites (1 and 2), 49.02% found in western sites and 17.65% found in both eastern and western but not in all sampling sites. Gastropods found on the western sites (3 and 4) were more abundant (70.51%) compared to eastern sites (29.49%).

Keywords: gastropods, Bucas Grande Island, Surigao del Norte, abundance

ABUNDANCE OF PELECYPODS IN BUCAS GRANDE ISLAND, SURIGAO DEL NORTE

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The study aimed to determine the species composition and abundance of pelecypods in Bucas Grande Island and to determine the local status of each species. A sampling plot of 20 x 20 meters was established in four sampling sites: 1) Lungsod, 2) Puyangi, 3) Mabua and 4) Pamosaingan. Each of these was being divided into grids of 1 x 1 m subplots. Beach combing was then done within each plot for an effort of about 1 hr and 30 min. Sampling was done during the low tide. A total of 55 individuals were encountered in the four sampling sites, distributed to three orders, seven families and nine species. Species richness revealed that 36.36% (20 individuals) of the total population was found in SS_1 (Lungsod), followed by SS_4 (Pamosaingan) with 34.55% (19 individuals), then by SS_2 (Puyangi) with 16.36% (9 individuals) while SS_3 was observed to have the least number of species recorded with 12.73% or 7 individuals. Shannon Weiner index result showed a high level of diversity in study site 4 (H'=0.811) with eight species, followed by study site 2 (H'= 0.62), with five species, it is followed by study site 1 (H'= 0.605) which has also five species and study site 3 (H'= 0.587) with four species which has the lowest species diversity of bivalves. The results also revealed that only one (1) is common, three (3) were rare, and five (5) were assessed to as very rare.

Keywords: pelecypods, Bucas Grande Island, Surigao del Norte, abundance

MOLLUSK DIVERSITY AT AQUACULTURE STATIONS IN DIFFERENT MARINE HABITATS IN ILOILO AND GUIMARAS, PHILIPPINES

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Biodiversity should now be a mainstream issue in aquatic production systems. Species inventories were made at the research stations of the SEAFDEC Aquaculture Department for use in biodiversity monitoring. Tigbauan Main Station faces the deep open waters of the Panay Gulf and Sulu Sea and is flanked by densely populated fishing villages. Sampling at the sand-gravel intertidal and monitoring of the catch of various fishing gears showed at least 579 species including 228 species (67 families) of gastropods, bivalves, and cephalopods. Spawning aggregations of *Bursatella leachii* and *Aplysia* species occurred around March and thousands were stranded on the beach. Mass strandings of *Bulla* also occurred during the southwest monsoon. Igang Marine Station in southern Guimaras includes 40 ha of seagrass beds and sandflats around five rocky islets and two 6–12 m deep basins where broodstock and grow-out cages are moored. Some 786 species were collected or photographed at Igang, including 391 species (80 families) of gastropods, bivalves, polyplacophorans, and cephalopods. Several species of *Cypraea* and *Conus* were found among the seagrass, and *Nerita* and muricids on the rocks. The cage nets and platforms provided additional attachment surfaces for many filter-feeding invertebrates including *Hyotissa* and *Dendrostrea* species. Dumangas brackishwater Station has 16 ha of mangrove-derived ponds and a narrow mangrove greenbelt, flanked by fringe mangroves and an extensive mudflat at the northeastern end of Iloilo Strait. Some 312 species were collected at Dumangas including 112 species (32 families) of bivalves and gastropods. The snails *Cerithideopsilla* spp., *Batillaria* spp., and *Cerithium coralium* were very abundant in the ponds, and *Crassostrea* and *Placuna* species provided edible biomass. Brackishwater ponds serve as proxy for mangrove lagoons and harbor resident mollusks and gobies and the transient juveniles of migratory species. The three stations still have high biodiversity after 20–40 years of operation.

PATELLOGASTROPODA IN JAPAN AND ASIA: MORPHOLOGY, MOLECULR PHYLOGENY AND SYSTEMATIC REVISION

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Patellogastropod limpets represent one of the most common organisms in intertidal rocky shores throughout the world oceans. Since most intertidal species are easily obtainable, numerous scientific names have been proposed since the eighteenth century. Despite long-standing research in the past, the taxonomy of Patellogastropoda is still incomplete especially in Asia. Recently we have conducted a taxonomic revision of entire patellogastropods in Japan based on comparative morphology and molecular phylogeny. Our results suggest taxonomy of some groups such as *Nipponacmea* is well resolved, but far from completion in other genera/species groups. The most complicated problems are difficulties in detecting species boundaries in widely distributed species. Typical examples include *Scutellastra flexuosa* complex, *Patelloida saccharina* complex, and several species groups of *Lottia* and *Cellana*. We further need a revision covering wide areas of Asia to settle species taxonomy of these groups.

Keywords: limpets, taxonomy, anatomy, phylogeny

POPULATION AND REPRODUCTIVE BIOLOGY OF THE DEEP-SEA MUSSEL FROM METHANE SEEPS OFFSHORE SOUTHWESTERN TAIWAN

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The Formosa Ridge belongs to the gas hydrate-bearing area, which is located in the southwestern Taiwan. The deep-sea mussels inhabit around the areas and form cold seep ecosystem. In this study, the population, reproductive biology and heavy metal concentration of cold seep mussel *Bathymodiolus platifrons* were investigated. The samples were collected from 3 sites (39-2, 42-2 and 50-1) by the German research vessel *RV SONNE* from Formosa Ridge. The mussel *B. platifrons* had parasitic polychaete *Branchipolynoe pettibonae* and the infestation rate was 41.96%. The morphological characters of tissue wet weight, tissue dry weight, tissue condition index, shell volume and Gonad Somatic index were significantly larger at site 50-1 than those of others ($p < 0.05$). The male mussel was characterized with 7 reproductive stages, and the females had 6 stages. Thus the mussel may reproduce year round. Heavy metal concentrations of different tissues of the mussel were also determined and compared in this study.

Keywords: Formosa Ridge, cold seep, mussel, reproductive biology, polychaete, heavy metal

ABYSSAL AND BATHYAL GASTROPOD FAUNA OF THE JAPAN TRENCH

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The Japan Trench is located along northern Honshu, the main island of Japan. It corresponds to the subduction zone of the Pacific Plate and is connected to the Kurile-Kamchatka Trench to the north and the Izu-Ogasawara Trench to the south. Of the gastropods inhabiting the trench and its surrounding waters, those occurring on the continental slope in the bathyal zone at depths of 200 to 1500 m were summarized by Hasegawa (2009) as representing 177 species. However, those occurring in the abyssal and hadal zones (from 2000 to 8000 m) have been only sporadically examined, mainly in Russian papers, and so far comprise only 33 identified and ca. 60 unidentified species. In the present study, newly acquired material from more than 140 stations at depths of 150 to 7800 m and deposited in the National Museum of Nature and Science, Tsukuba, together with that collected by the R/V *Vityaz* and stored in the Institute of Oceanology, Russian Academy of Science, are examined in detail. As a result, the number of species occurring in the bathyal zone (down to the depth of 2000 m) is updated to 185, and 173 species in total are recorded from the abyssal to hadal zones (from 2000 to 7800 m). Only 37 species commonly occur in both the bathyal and abyssal/hadal zones, highlighting the significant difference in species composition between the two areas. In the abyssal/hadal zones, 109 taxa (67%) could not be identified as previously named species, at least from the northwestern Pacific. The extremely wide vertical distribution of certain species is exemplified by *Cylichna alba*, which was recorded from 150 m to 7500 m. Although several phenotypes were recognized at various depths, they cannot be separated objectively and more detailed study using molecular analysis will be necessary to clarify their precise taxonomic relationships.

Keywords: gastropoda, fauna, Japan Trench, bathyal, abyssal, hadal

IMPACT OF HABITAT, SEDIMENT DEPTH, AND SIEVE SIZE ON BIODIVERSITY OF CORAL REEF-ASSOCIATED MOLLUSCS FROM THE NORTHERN RED SEA (GULF OF AQABA)

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The biodiversity of marine benthic molluscs is influenced by a great variety of factors, each of them affecting diversity to a different degree. Such factors include the habitat and sediment depth containing the assemblage but also methodological decisions, such as the use of sieve size for sample preparation. To evaluate these influences on diversity and ecology of molluscan assemblages two sediment samples were taken from coral reef associated habitats in the Gulf of Aqaba (northern Red Sea). One of them was collected near a patch reef, the other in the vicinity of a *Millepora*-fringing reef. Both samples were separated according to sediment depth (upper 10 cm and lower 10 cm of the sediment column), respectively, and were sieved with mesh sizes of 2 cm, 2 mm, and 1 mm. Gastropods and bivalves were picked from all samples, identified to species level, and quantified. For statistical analyses only the sieve size fractions 2 cm – 2 mm and 2 – 1 mm were used, because the number of shells found in the fraction larger 2 cm was too small. The influence of habitat, sediment depth, and sieve size on biodiversity and ecological features, including taxonomic composition, species-abundance, and drilling frequencies, was evaluated. A total of 334 molluscan species was found in the samples. Species richness differed between both reef types and this was also found for sieve size fractions. However, sediment depths showed virtually no influence on species richness. Diversity indices showed only pronounced differences between sieve size fractions. Regarding taxonomic composition, species-abundances and drilling frequencies habitat type had the strongest influence, followed by sieve size. Again, sediment depth had almost no influence, which indicated that the uppermost 20 cm of the sediment column were homogenized by mixing processes.

Keywords: molluscs, Red Sea, coral reef, biodiversity, ecology

SPECIES DIVERSITY AND BIOGEOGRAPHY OF AMPHIDROMOUS NERITID GASTROPODS IN THE INDO-WEST PACIFIC

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Island biodiversity and endemism have been a major topic of debate in evolutionary ecology, biogeography and conservation. Freshwater streams on tropical and subtropical islands worldwide are, however, often dominated by amphidromous animals that have potential to disperse long distances to other islands: hatched larvae are swept downstream to the sea to feed on phytoplankton, settle at river mouths and then ascend for post-metamorphic growth and reproduction. We have studied the natural history of limnic snails and limpets in the family Neritidae as a model group for understanding the role and importance of amphydromy in freshwater ecosystems on coastal and oceanic islands. Re-classification of the Indo-western Pacific species based on shell morphology and mitochondrial COI sequences revealed that most amphidromous taxa have very small intraspecific variation throughout their wide-ranging distributions that often span several thousand kilometers. Indeed, the comparison of species compositions between two distant geographic regions demonstrates high faunistic homogeneity: 22 out of 39 Japanese species are also found in the ca. 6,000-km apart Solomon Islands and Vanuatu. Summary of the compiled locality data reveals that species richness peaks in the Coral Triangle and declines with increasing distance from this region, both latitudinally and longitudinally, again corresponding with the pattern for marine taxa. The Neritidae as well as many other amphidromous animal lineages with their origins in the tropics may have rapidly changed distribution ranges according to the fluctuating climate and shaped the present-day regional diversity almost entirely by dispersal but rarely by speciation through small-scale vicariance.

Keywords**:** amphidromy, freshwater streams, Neritidae, taxonomy, tropical islands

MALACOLOGICAL SOCIETY OF JAPAN Grant Recipients

A HOTSPOT OF MANGROVE BIODIVERSITY: COMPARATIVE BIOGEOGRAPHY OF MANGROVE GASTROPODS ACROSS THE INDO-WEST PACIFIC

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In the Indo-West Pacific, mangroves are heavily threatened but the biodiversity of most groups of invertebrates is still largely unknown. In the past five years, our lab has been undertaking extensive fieldwork across the Indo-West Pacific, particularly South-East Asia, to collect mangrove gastropods. Our dataset now includes DNA sequences from nearly 5,000 individual gastropods from 240 sites, representing more than 200 species. Substantial taxonomic effort is being dedicated for revising the taxonomy of many taxa of mangrove gastropods. So far, our lab has been focusing on the onchidiid slugs and ellobiid snails, which are the two most diverse groups of mangrove gastropods, and are both desperately in need of taxonomic revision. Our data set is used to address biogeographic questions of broader interest.

EXPLORING PATTERNS OF DIVERSITY AND SPECIATION IN INDO-PACIFIC *CHROMODORIS* WITH SPECIAL INSIGHT INTO A BIODIVERSITY HOTSPOT IN WESTERN AUSTRALIA

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Chromodoris is a group of closely related nudibranch species exhibiting aposematic colouration and planar spawning behavior, with many congenerics displaying striking morphological similarities. Prior work suggests this genus contains close to 35 members but many geographic areas and putative species in the Indo-Pacific remain unsampled and as such the true diversity of this group is unknown. Moreover, recent phylogenetic inquiry has uncovered short branch lengths and poor support within *Chromodoris*, suggesting additional work is needed to establish a well-resolved phylogeny. This work aims to address this deficit by employing two mitochondrial loci (COI, 16S) for phylogenetic reconstruction and species delimitation. Nearly 300 specimens from 25 morphospecies were sampled from multiple localities in the Indo-Pacific, with special emphasis on diversity in the poorly understood northwestern region of Western Australia. In turn we fill in significant sampling gaps in the Indian Ocean, which are often lacking for "Indo-Pacific" taxa. The number of unique genetic clusters recovered from phylogenetic analysis exceeds the number of previously described morphospecies, suggesting hidden diversity in this genus. This study ultimately advances our understanding of phylogenetic patterns in *Chromodoris* and further highlights an apparent rapid radiation. Future work will incorporate an exon-capture approach for resolving species-level relationships.

Keywords: Indo-Pacific, nudibranchs, marine, biodiversity, molecular, phylogeny

UNITAS MALACOLOGICA & MALACOLOGICAL SOCIETY OF AUSTRALASIA
Grant Recipients

MOLECULAR SYSTEMATICS OF THE BALER SHELLS (VOLUTIDAE: *MELO*) SUPPORTS PUTATIVE HYBRID ZONES

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Balers (*Melo* spp.) are the largest members of the marine caenogastropod family Volutidae and are limited to the Indo-West Pacific in distribution. The name derives from use of baler shells by some indigenous groups to remove water from canoes. In Australia, the animals were used as food, and the shells as water carriers, which were also fashioned into important ceremonial objects. Whole shells or pieces have been traded for hundreds of miles inland. *Melo* species are found on the coast of most of Australia, except NSW, eastern Victoria and Tasmania. The nominal species can show considerable overlap in the morphological characters used to differentiate them. We utilise DNA data to build a molecular phylogeny of the genus. We used mitochondrial Cytochrome Oxidase I (COI) and 16S genes, as well as nuclear ADP/ATP translocase (ANT) and Histone H3 to examine relationships among taxa. A number of taxonomic changes are supported. Mitochondrial and nuclear data sets are partially in conflict, but are congruent with a putative hybrid zone in Western Australia previously suggested by morphology. Some *Melo* species show an unexpectedly large distribution for animals that have direct development.

Keywords: volute, phylogeny, taxonomic revision, hybridization, distributions

PHYLOGEOGRAPHY OF THE ROCK SHELL *THAIS CLAVIGERA* (MOLLUSCA): EVIDENCE FOR LONG-DISTANCE DISPERSAL IN THE NORTHWESTERN PACIFIC

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The present-day genetic structure of a species reflects both historical demography and patterns of contemporary gene flow among populations. To precisely understand how these factors shape current population structure of the northwestern (NW) Pacific marine gastropod, *Thais clavigera*, we determined the partial nucleotide sequences of the mitochondrial COI gene for 602 individuals sampled from 29 localities spanning almost the whole distribution of *T. clavigera* in the NW Pacific Ocean (~3,700 km). Results from population genetic and demographic analyses (AMOVA, FST-statistics, haplotype networks, Tajima's *D*, Fu's *F*s, mismatch distribution, and Bayesian skyline plots) revealed a lack of genealogical branches or geographical clusters, and a high level of genetic (haplotype) diversity within each of studied population. Nevertheless, low but significant genetic structuring was detected among some geographical populations separated by the Changjiang River, suggesting the presence of geographical barriers to larval dispersal around this region. Several lines of evidence including significant negative Tajima's *D* and Fu's *F*s statistics values, the unimodally shaped mismatch distribution, and Bayesian skyline plots suggest a population expansion at marine isotope stage 11 (MIS 11; 400 ka), the longest and warmest interglacial interval during the Pleistocene epoch. The lack of genetic structure among the great majority of the NW Pacific *T. clavigera* populations may be attributable to high gene flow by current-driven longdistance dispersal of prolonged planktonic larval phase of this species.

Keywords**:** *Thais clavigera*, rock shell, phylogeography, population structure, long-dispersal

INITIAL STUDIES OF THE PHYLOGEOGRAPHY OF THE MUSSEL GENUS *XENOSTROBUS*

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The Indo-West Pacific mussel genus *Xenostrobus* occupies a broad diversity of habitats ranging from open marine waters to the upper reaches of estuaries. We have begun broad- and fine-scale investigations of the genus' phylogeography by examining its Australasian species, including its only marine representative (*X. pulex*) and the widely invasive species *X. securis*. The New Zealand forms of these taxa were found to be distinct species and we have identified a new species of the *X. securis* group from northern Australia. Spatial geographic structure is much greater in *X. securis* than in *X. pulex* and includes genetic partitioning within larger drainages whereby mitochondrial DNA haplotypes from clades that have dispersed globally are preferentially located in upper estuarine reaches in our fine-scale study region in central New South Wales. These clades may have originated here. *X. securis* in the region was found to comprise multiple robustly-supported mtDNA clades, that were mostly very distinct. Frequently, these clades comprised numerous haplotypes that may have evolved *in situ* as few were found in multiple drainages. We also collected fragment size and sequence data from five microsatellite loci. Mantel tests show that there is little correlation between spatial variation in the mtDNA and microsatellite data. The microsatellite data generally do not suggest that localities or drainages are clustered according to geographic proximity. These data conform generally to a "chaotic genetic patchiness" model with intermediate gene flow. The patterns of mtDNA variation do not conform so closely to the chaotic genetic patchiness model and are proposed to reflect not only the re-colonisation of estuaries or lagoons after infrequent local extinction but also the relative ability of haplotypes from nearby (or distant) localities to migrate successfully into established populations in competition with resident haplotypes that have selective or demographic advantages derived from local occupation.

Keywords: Invasive mussel, spatial genetic partitioning, haplotype diversity, microsatellites, mitochondrial DNA

CARDIID BIOGEOGRAPHY, PHYLOGENETICS AND EVOLUTION

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Modern ‘museum’ science incorporates a diversity of methods to tackle some of the toughest questions related to improving our understanding of diversity, distribution and adaptation in the sea. Cardiid bivalves are a generally well-known, moderately diverse and widespread marine molluscan family with a decent fossil record. These attributes make them a viable system to ground-truth biodiversity assessments in remote corners of the world, draw comparisons for biogeographic inference and test hypotheses related to evolution of novel life strategies, such as photosymbiosis. We present work on each of these three fronts. We discuss updated assessments of biodiversity in Western Australia and consider our findings against other work in the region to assess broader biodiversity and biogeography trends. We highlight gaps (e.g. IO, small, deep taxa) and include giant clams in this discussion. We then shift focus to examine photosymbiotic evolution in cardiids and review how integrating transcriptomic approach has improved phylogenetic reconstruction. We scrutinize evidence for nutrient transfer between host and symbiont, and begin to establish identity of photosymbionts in the understudied Fraginae.

Keywords: Cardiidae, cockles, giant clams, biodiversity, Western Australia, Indo-Pacific, gaps, phylogenetics, photosymbiosis, symbionts

BIODIVERSITY OF BIVALVES IN THE LAGOON AREA OF SETIU WETLAND, TERENGGANU, MALAYSIA

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Study on biodiversity of bivalves in the lagoon area of Setiu Wetland, Terengganu was conducted on two months interval for a year (July, September, November 2011 and January, March, May 2012). Bivalve samples were collected from 11 stations within 50 m transect line perpendicular to the coastline along the lagoon area. A total of 10,845 individual of bivalves were collected which classified into 11 families, 21 genera and 34 species with mean total density was 33±17 individuals/m^2. Density of bivalves had significant difference among stations throughout the sampling period ($p<0.05$). However, there was no significant temporal change in abundance of bivalves ($p>0.05$). Density and diversity of bivalves were higher in the brackish subtidal area compared to freshwater subtidal and mangrove intertidal area. Family Corbulidae, which comprised of *Potamocorbula fasciata*, had the highest abundance that contributed 77% from the mean total density of bivalves recorded in Setiu Wetland. Despite relatively small area that was covered during sampling activities, the lagoon of Setiu Wetlands could be categorised as high biodiversity of bivalve's species in the east coast of Peninsular Malaysia.

Keywords: bivalve, biodiversity, lagoon, Setiu Wetland, Terengganu

SPECIES DIVERSITY AND DISTRIBUTION OF GLIDING SCALLOPS IN EXCLUSIVE ECONOMIC ZONE, SARAWAK, MALAYSIA

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Scallops are locally known as 'Kekapis' in Sarawak, Malaysia and they are commonly sold as frozen meat product in hypermarkets with range price of RM80-RM100 (USD 20-25) per kilogram. Samples of scallops were collected from selected stations in Sarawak Exclusive Economic Zone (EEZ) using otter trawl net with stretch mesh size of 38 mm at the cod end. All scallops used in this study were by-catch of trawling activities during survey of Malaysian fisheries resources in Sarawak EEZ. Trawling operations were conducted beyond 12 nautical mile from the coast, and the area were divided into three depth strata, I) 20-50 m, II) 50-100 m and III) 100-200 m. The scallops internal ribs (left and right valve) were counted (n=30) with a category of size range (shell height 50-60 mm). Two species of scallops namely *Amusium pleuronectes* Linnaeus, 1758 (Asian moon scallop) and *Ylistrum balloti* Bernardi, 1861 (Saucer scallop) were found during the two-month sampling period from 16 August until 6 October 2015. Both species shared similar shell ornamentation: i) shell nearly smooth externally, ii) thin shell, iii) both valve convex and iv) shell almost circular in outline. For the left valve, the mean number of ribs for *A. pleuronectes* was 25 (range 21-30), while *Y. balloti* averaged 35 (range 32-39). The mean number of ribs in the right valve of *A. pleuronectes* was 26 (range 21-30), while *Y. balloti* averaged 41 (range 37-47). Specimens of *A. pleuronectes* were found in strata I (17 stations), strata II (13 stations) and strata III (2 stations). However, *Y. balloti* specimens were collected only in strata I (7 stations) with no specimen found in strata II and III. This study provides the first record of scallops sampled from Sarawak EEZ. The findings serve as baseline data for the relevant agencies to further explore the potential of this valuable resource in Sarawak EEZ.

Keywords: scallops, internal ribs, depth strata, Sarawak waters

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RIVERINE RADIATION OR RELICT REMAINDER? – EVALUATING SPECIATION IN *BROTIA* SPECIES ENDEMIC TO THE KAEK RIVER, THAILAND

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Despite much debate the view still persists that allopatric speciation is the usual mechanism involved in the majority of speciation events. Nevertheless, an increasing number of evidence points also at ecologically driven sympatric speciation. While for studies on speciation and radiation mostly vertebrates (such as e.g. birds and fishes) are used so far, actually invertebrates represent the vast majority of biodiversity. Over the past two decades in particular lacustrine gastropods – from several Cerithioidean freshwater families, such as paludomids, thiarids and pachychilids – have proven to be ideal model organisms for studying the diverse mechanisms involved in speciation and the proposed adaptive nature of radiation. While several of these lacustrine models turned out to be more complex than anticipated, riverine radiations remain both infrequent and rarely studied to date. In a unique setting at the Kaek River in northern Thailand, we found and evaluated the existence of less than a dozen endemic taxa of *Brotia* snails, with sym-, para- and allopatric occurrences, providing a perfectly suitable model system to study fundamental mechanisms and factors acting in speciation. We use geometric morphometrics of the shell, morphological differentiation of the radula, life history data (i.e. distinct viviparous reproductive strategies) together with detailed ecological parameters (i.e. habitat, substrate preference) in order to assess any phenotype–environment correlation. These are supplemented by genetic data on intra- and interspecific divergence using the barcoding gene COI, together with next generation sequencing (RAD-Sequencing for the first time in freshwater gastropods). Thus, our project attempts an integrative approach by combining interspecific phylogenetics with intraspecific evolutionary genetics, enabling a comparative assessment of ecological vs. geographical factors as drivers for speciation.

Keywords: morphometrics; morphology; species delineation; RAD sequencing; viviparity; Gastropoda; Pachychilidae

THE ENIGMATIC ROUTES OF DISPERSAL OF MINUTE FRESHWATER GASTROPODS (CAENOGASTROPODA, TRUNCATELLOIDEA, TATEIDAE) ACROSS THE SOUTH PACIFIC.

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Tateid gastropods have an enigmatic distribution in the South Pacific region. Their range covers Sulawesi, Papua New Guinea, Australia, New Zealand, Lord Howe Island, New Caledonia, Vanuatu, Fiji, as well as the Austral Islands of French Polynesia. Except for a few brackish water species from Australia and New Zealand, all tateids occur in fresh water. We reconstructed the evolutionary history of these snails with a particular focus on the island radiations based on dated phylogenies, hypothesis testing, and ancestral range reconstructions. The dominant sources of terrestrial and freshwater biota for colonization of the South Pacific islands are Malesia and Southeast Asia as well as Australia. In contrast, our analyses revealed several enigmatic aspects not in accordance with this pattern. Geographic distance was not an appropriate predictor of relationships. The common ancestor of the South Pacific Tateidae occurred in Australia. Its descendents colonized Sulawesi and Lord Howe Island and gave rise to the radiations on New Caledonia and New Zealand. The more remote archipelagos harbouring the genus *Fluviopupa* were colonized out of New Zealand. *Fluviopupa* evolved on the Austral Islands and colonized the archipelago against the progression rule from East to West. Vanuatu was colonized twice independently from the Austral Islands and served as hub for dispersal events to Fiji and Lord Howe Island. Our findings indicate that the diversity of dispersal routes across the Pacific is more diverse than previously thought. More groups of organisms need to be investigated in order to understand origin and evolution of Pacific island biota.

Keywords: biogeography, dispersal, fresh water gastropods, phylogenetics, South Pacific, Tateidae

VANISHING BEFORE OUR EYES-NATIVE FRESHWATER APPLE SNAILS *PILA* SPP. (AMPULLARIIDAE) OF SOUTHEAST ASIA

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The apple snails of the genus *Pila* (Ampullariidae) are the largest freshwater gastropods in Southeast Asia (SEA), and include some of the earliest taxa described from the region; Linnaeus described *Pila ampullacea* in 1758. Other *Pila* species have been described from SEA since the 1800s, but their taxonomy remains confused, obscuring the true distribution of species. Nonetheless, most species are assumed to be common-all seven SEA *Pila* species are Least Concern on the IUCN Red List. Three decades ago, globally invasive New World ampullariids of the genus *Pomacea* were introduced to SEA, and the newcomers have since caused agriculture losses amounting to US$1.47 billion annually. Understandably, much research has focused on monitoring *Pomacea*. In contrast, basic information on the native *Pila* (e.g., distribution) has been worryingly lacking, despite numerous anecdotal accounts of declining populations. We present an overview of SEA Ampullariidae based on comprehensive surveys in the Malay Peninsula, ad-hoc collections from Vietnam and the Philippines, and literature and museum records. Our results reveal 1) morphological and genetic confirmation of extant *Pila* species in the areas surveyed, which has implications for current taxonomy and distribution data; 2) genetic evidence that *Pila scutata* sensu stricto is likely restricted to Java (while the species in the Malay peninsula and Philippines is provisionally *Pila scutata* sensu lato); 3) limited distribution and extremely low genetic diversity of *Pila scutata* sensu lato in the Malay Peninsula; and 4) presence of *Pomacea* spp. at many historical *Pila* sites, with *Pila* now absent from many of these sites. A concerted regional effort is urgently required to reassess the status of all *Pila* spp, and resolve the taxonomic uncertainty, before they disappear.

Keywords: aquatic; non-marine gastropoda, threatened species, Malaysia, Singapore, Vietnam, Philippines

UNITAS MALACOLOGICA Grant Recipients

ESCAPING FROM ADULTOCENTRISM: ON THE BIOGEOGRAPHY AND LIFE HISTORY OF VIVIPAROUS CERITHIOIDEAN GASTROPODS FROM A FRESHWATER THIARID PERSPECTIVE

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Current understandings and views of biological sciences are essentially focused on adults, only rarely taking early ontogenetic life stages into account. Although, this adultocentristic view is necessary for taxonomic and systematic studies, it often distorts our perception of evolutionary, ecological and biogeographic phenomena. This is particularly true for taxa with larval stages that differ considerable in habitat, mode of life and dispersal ability from their adult stages. Within cerithioidean snails several modes of viviparity have evolved independently, each implying a different life history and adaptation to distinct environmental conditions in larval and adults stages. The "marsupial" brooders within the thiarid snails pose a group of particular interesting case studies on this matter as well as with respect to their distinct biogeography. Thiarids inhabit a plethora of habitats with lotic and lentic freshwater environments as well as brackish water conditions. Furthermore, several thiarid species are widespread throughout the Indo-Australian-Archipelago. In concert with distinct biogeographical patterns, reproductive modes vary between releasing veliger larvae and consecutive juvenile stages, with both these modes frequently being facultative rather than obligatory. We anticipate that different reproductive strategies involving these ontogenetic stages provide better explanations for the varying extend of spatial ranges in individual species, instead of explanations that focus solely on adult properties. Therefore, thiarids with their pronounced differences in ontogenetic stages provide valuable models for more detailed studies on evolutionary systematics.

Keywords: veliger larvae, viviparity, larval ecology, larval development, gastropoda, Thiaridae

THE BIOGEOGRAPHY OF HELICOSTYLINE LAND SNAILS IN THE PHILIPPINES

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The subfamily Helicostylinae is the most species (about 300 species) group of land snails in the Philippines, with a range of shell shapes and color patterns. The archipelago's unique geological history is believed to have played a key role in creating and maintaining such diversity and high level of endemism (about 98%). We attempt to consolidate what is known of the Helicostylinae's biogeography—the distribution of species, faunal boundaries, and possible affinities to Taiwan, Malaysia and Indonesian taxa. Information on their biogeography will be useful in understanding their evolutionary history and will be useful in forest management. Current threats to the known biodiversity are also discussed.

MEDICINAL EFFECT, VEGETATIVE PREFERENCE, DIET, HUNTING AND LIFE CYCLE OF *HELICOSTYLA DAPHNIS,* A POSSIBLY ENDANGERED LANDSNAIL, IN BORBON AND SOGOD, CEBU

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Helicostyla daphnis, an arboreal snail endemic to Cebu was thought to be extinct, but was discovered to be still thriving and even eaten by people. Despite its reported extinction, no government programs have been done to conserve these snails in Cebu, and there is very limited published data about them. In order to formulate effective strategies for conservation of *H. daphnis,* information about the snails is needed. To fill this gap, a survey of the local ecological knowledge (LEK) on the medicinal effect, vegetative preference, diets, hunting, and life cycle of *H.daphnis* was conducted. LEK was gathered among fifteen snail-hunting experts that were previously identified by their peers. Conversations with experts were freely conducted, giving opportunity to deeply explore each informant's knowledge. Base on first-hand experience of experts and their relatives, consumption of *H. daphnis* can alleviate asthma, arthritis and body pains. Twenty-four plants were mentioned by experts to be preferred by *H. daphnis*. Of the 24 mentioned, only one shrub and one vine were mentioned, and all the rest were trees. Base on this information, it can be deduced that the snails are not very specific about their vegetative preference and trees are most preferred. The trees that were mentioned more than thrice by experts were *Ficus leucantatoma* (Merr) and *Artocarpus heterophyllus* (Lam.). From this study, it cannot be concluded what the diet of *H. daphnis* is. Experts mentioned dew, sap, leaves and bark of trees. The snail hunters prefer to hunt snails in the morning between 0700-1000 hrs when the air temperature is still relatively cooler. They would hunt for an average of 2-3 hours, and get an average catch of 45 snails. Snail hunters observed that the timing of laying of eggs of *H. daphnis* does not depend on season and happens all throughout the year. The information gathered from this study, can be used by lawmakers to create policies for the preservation, regulation of hunting, and even programs for the culturing of the snails.

UNITAS MALACOLOGICA Grant Recipients

INTROGRESSIVE HYBRIDIZATION BETWEEN THE MORPHOLOGICALLY DIVERGENT LAND SNAILS *AINOHELIX* AND *EZOHELIX*

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Understanding how phenotypic evolution is associated with speciation and evolution of gene has been a major concern in evolutionary biology. Reliable estimation of molecular phylogenetic relationship is very crucial to address this issue. However, phylogenetic relationships of species and population levels are often difficult to estimate due to insufficient genetic divergence and introgression. Hybridization between different taxa is likely to take place when adaptive morphological differences evolve more rapidly than reproductive isolation. When studying the phylogenetic relationship between two land snails of different nominal genera, *Ainohelix editha* and *Ezohelix gainesi*, from Hokkaido, Japan, using nuclear internal transcribed spacer (ITS-1,2) and mitochondrial 16S ribosomal DNA (16S rDNA), we found a marked incongruence in the topology between nuclear and mitochondrial phylogenies. Furthermore, no clear association was found between shell morphology (which defines the taxonomy) and nuclear or mitochondrial trees and morphology of reproductive system. These patterns are most likely explained by historical introgressive hybridization between *A. editha* and *E. gainesi*. Because the shell morphologies of the two species are quite distinct, even when they coexist, the implication is that natural selection is able to maintain (or has recreated) distinct morphologies in the face of gene flow. Future studies may be able to reveal the regions of the genome that maintain the morphological differences between these species.

Keywords: Bradybaenidae, ancestral hybridization, phenotypic evolution, phylogeny, speciation

MALACOLOGICAL SOCIETY OF JAPAN Grant Recipients

EXPLORATION OF ENIGMATIC ‘DORSAL VESSEL SYSTEMS’ IN PANPULMONATE GASTROPODS

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‘Dorsal vessel systems’ are enigmatic, poorly described systems situated dorsally under the epidermis. In literature they were occasionally mentioned among various panpulmonate groups, e.g. for the freshwater acochlidian *Acochlidium amboinense* already in 1895 and for several shell-less sacoglossan species. However, up to now all observations were based on gross-morphological dissections, and the micro-anatomy and ultrastructure of ‘dorsal vessel systems’ is unknown. Accordingly, the homology assumptions among the different panpulmonate groups are problematic and functional assumptions remain highly speculative. In the present study we provide the first detailed micro-anatomical and ultrastructural data on panpulmonate ‘dorsal vessel systems’ from representatives of freshwater, terrestrial and marine habitats. Recently, 3D-microanatomical data of the circulatory and excretory systems in Acochlidia revealed two types of ‘dorsal vessel systems’. The system is connected to the pericardial complex in freshwater species of the genus *Acochlidium*, but linked to the kidney in (semi)terrestrial Aitengidae and deep-sea Acochlidia. The ultrastructural analyses reveal the ‘dorsal vessel system’ in *Acochlidium* to be the extended pericardium with podocytes. The enlarged site of ultrafiltration is interpreted herein as adaptation to the freshwater environment in order to cope with the increased osmotic stress. In contrast, the ultrastructure of the ‘dorsal vessel system’ in the terrestrial *Aiteng marefugitus* resembles that of the kidney. In this species the ‘dorsal vessel system’ enhances the resorption of water and prevents the animal from desiccation on land. We compare the micro-anatomical and ultrastructural data of the circulatory and excretory systems of the examined acochlidian species with the sacoglossan *Elysia*. Remarkable differences in the ‘dorsal vessel system’ of closely related Acochlidia underline the need of comparative, micro-anatomical and ultrastructural (re)investigation of similar systems in traditional ’Pulmonata‘ for reliable homology assumptions, e.g. with the dorsal pallial vessel systems in *Chilina* (Hygrophila) or in Athoracophoridae (Stylommatophora).

Keywords: Acochlidia, podocyte, Sacoglossa, transmission electron microscopy, ultrafiltration.

ON THE ORIGIN AND BIOGEOGRAPHY OF THE SAP-SUCKING SEA SLUGS GENUS *THURIDILLA*

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The sacoglossan genus *Thuridilla* Bergh, 1872 includes 24 valid species and occurs in temperate to tropical shallow waters. The group reaches its highest diversity in the Indo-West Pacific (18), followed by the Caribbean (4), eastern Atlantic and Mediterranean Sea (2) and Red Sea (1). Interestingly, no species have been reported to date in the eastern Pacific coastline of the American continent. We here present the first molecular phylogeny of the genus *Thuridilla* based on a multi-locus approach combining two mitochondrial genes (COI and 16S) and one nuclear gene (H3) from 19 species using both Bayesian and maximum likelihood criteria. Combining knowledge on the fossil record of sacoglossans, geographical distributions of species, and a relaxed phylogenetic approach together with Bayesian discrete phylogeographic methods we hypothesise on the time, mode, and geography of speciation of the genus.

Keywords: Heterobranchia, Sacoglossa, phylogeny, historical biogeography, speciation

UNITAS MALACOLOGICA Grant Recipients

T LOVES ME, IT LOVES ME NOT: COUNTING SPECIES OF THE "ROSE PETAL SEA SLUG," *POLYBRANCHIA* (MOLLUSCA: GASTROPODA) WITH A MOLECULAR SYSTEMATICS APPROACH

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Polybranchia (Gastropoda: Heterobranchia: Sacoglossa) is a pantropical group of herbivorous sea slugs consisting of eight valid species. During field collections, this genus is consistently overlooked because these organisms tend to find shelter under rocks during the day and will become active mainly at night. As a result, these organisms are considered a rare find making the conduction of phylogenetic analyses on this genus a difficult task. This genus has been used in large-scale phylogenetic studies where only a few species represent the entire group but a detailed phylogenetic study on *Polybranchia* has yet to be conducted. This study investigates the disjunct range of *Polybranchia viridis* and whether the species consists of two populations or two species (one from the Caribbean and another from the Eastern Pacific). Secondly, *Polybranchia orientalis* is the most commonly found species in the Indo-Pacific but collecting reports are lacking for the five other described species from the Indo-Pacific. Therefore, we hypothesize a species complex from the specimens obtained of *P. orientalis*. This investigation used nuclear gene H3 and mitochondrial genes COI and 16S. A Bayesian analysis was conducted on the molecular markers to identify clades and misidentified species. Additionally, scanning electron microscopy was used to examine the morphology of the radulae and penis of each clade. Evidence for diversity in obtained specimens was higher than expected.

Keywords: Sacoglossa, taxonomy, phylogeny, mitochondrial gene, nuclear gene

UNITAS MALACOLOGICA Grant Recipients

MONITORING OF OPISTHOBRANCH BIODIVERSITY IN INDONESIA - AND ITS APPLIED ASPECT

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Coastal areas of Indonesia are considered as the most diverse marine habitats in the world. This comprises also opisthobranch taxa (Gastropoda, Mollusca), which exhibit highest species numbers and also highest diversity with regard to life styles in these tropical areas. Not only scientists are interested in opisthobranch diversity. Tourists, a major economic factor in these areas, are highly attracted by these beautiful gastropods. Actually, many diving centers advertising during the International Exhibition BOOT in Düsseldorf use large pictures of slugs for attraction. Less known is there importance in the search of new drug leads. Antibiotic resistance to traditional products is one of the biggest threats in human health and therefore these organisms have come into focus as novel producers of bioactive metabolites. Mollusk-derived molecules are most promising drug leads and especially opisthobranchs contribute already to several new medical therapies. When the Bundesministerium für Bildung und Forschung (BMBF) advertised their program in spring 2014 (Identifikation und Nutzung in Indonesien natürlich vorkommender Substanzen für die Arzneimittelentwicklung), the authors successfully applied and we started with our project (*Indonesian Opisthobranchs and associated microorganisms -From biodiversity to drug lead discovery*) in summer 2015. Here we present first results from our first collecting efforts, which comprise nearly 100 opisthobranch species and several bioactive strains associated with the slugs

Keywords: marine Heterobranchia, Indonesia, biodiversity, drug leads, secondary metabolites, antibiotics, bacteria

ABUNDANCE, DISTRIBUTION AND ECOLOGY OF SPECIALIST SACOGLOSSANS FROM PALK BAY, INDIA

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Sacoglossan molluscs are specialist herbivores proved to have close evolutionary relationship with the host algae. Most of these sacoglossans are chemically defended. The abundance, distribution, and seasonal variation of commonly available these herbivorous molluscs were studied. Eight species of sacoglossans, i.e., *Costasiella* sp., *Elysia grandifolia*, *Elysiella pusilla*, *Elysia tomentosa*, *Lobiger viridis*, *Oxynoe viridis*, *Plakobranchus ocellatus* and *Polybranchia orientalis* were commonly encountered during the investigation. Among this, the most abundant species was *Elysia grandifolia*. The least observed was *Costasiella* sp. Significant correlation between abundance and frequency of observation was found with the abundance of host algae. Sacoglossans were most abundant during December to April. Experiments were conducted to ascertain the specific host algae. Only one host species was observed for *Costasiella* sp. (*Avrainvillea erecta*), *Elysiella pusilla* (*Halimeda gracilis*), *Oxynoe viridis* (*Caulerpa racemosa*) and *Plakobranchus ocellatus* (*Bryopsis pennata*). Preference for multiple species was observed with *Elysia grandifolia* (*Bryopsis plumosa*, *Bryopsis pennata*), *Elysia tomentosa* (*Caulerpa racemosa*, *Caulerpa taxifolia*), *Lobiger viridis* (*Caulerpa racemosa*, *Caulerpa peltata*), and *Polybranchia orientalis* (*Caulerpa racemosa*, *Caulerpa peltata*). Information on the diversity, distribution and abundance of sacoglossans are hitherto not available from Palk Bay region.

Keywords: mollusc, Sacoglossa, herbivore, abundance, distribution, Palk Bay

KLEPTOPLASTS-STARCH STORAGE FACTORIES IN SOLAR-POWERED SACOGLOSSAN SEA SLUGS?

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The incorporation of chloroplasts in enigmatic sacoglossan sea slugs has been known and studied for a long time. Previous work has shown that both the slugs and their stolen chloroplasts (kleptoplasts) survive for weeks to months when the slug enters a starvation period. Carbon fixation is performed by these plastids, a process which is affected by temperature, irradiance and even slug behavior. The particular algal species also affects kleptoplast survival. Active carbon fixation could prolong a starving slug's life span, likely due to the photosynthates produced, although photosynthate accumulation and degradation have only recently been considered. Therefore, the aim of this study is to investigate the relative amount of photosynthates in sea slugs during starvation. The long-term plastid retaining form, *Elysia timida* and its sole food source, the chlorophyte, *Acetabularia acetabulum* was examined. The main photosynthate produced by *A. acetabulum* is starch, a polysaccharide comprised of amylose and amylopectin. We present here for the first time, a significant increase in amylose concentration, within the slug's digestive gland cells during a starvation period, followed by a sharp decrease. This suggests that kleptoplasts function as both, a nutritive producer and storage device, holding onto the polysaccharides they produce for a certain time until they are finally available and used (as indicated by the concentration decrease) by the starving slug. This directly indicates some benefits provided by functional kleptoplasty to a long-term retaining species.

UNITAS MALACOLOGICA Grant Recipients

MAJOR CHANGES IN AEOLIDIDA SYSTEMATICS: WHEN FIVE FAMILIES BECOME ONE

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Tergipedidae represents a diverse and successful group of aeolids nudibranchs with approximately 200 species distributed throughout most marine ecosystems. However, the systematics of this family remains poorly understood since no modern phylogenetic study has been undertaken to support any of the proposed classifications. The present study is the first molecular phylogeny of Tergipedidae based on partial sequences of two mitochondrial (COI and 16S) genes and one nuclear gene (H3). Maximum likelihood, maximum parsimony and Bayesian analysis were conducted in order to elucidate the systematics of this family. Our results do not recover the traditional Tergipedidae as monophyletic, since it belongs to a larger clade that includes the families Eubranchidae, Fionidae and Calmidae. This clade is here referred to as Fionidae, the oldest name for the clade. In addition, the present molecular phylogeny does not recover the traditional systematic relationships at a generic level, and therefore, systematic changes are required. We recognize the following clades within Fionidae: *Calma*, *Cuthona*, *Cuthonella*, *Eubranchus*, *Fiona*, *Murmania*, *Tenellia*, *Tergipes*, plus some new genera. *Aenigmastyletus*, *Catriona*, *Phestilla*, *Tenellia* and *Trinchesia* are nested within other clades and, thus are here considered as synonyms of the larger clades. The phylogenetic position and validity of *Myja*, *Guyvalvoria*, and *Subcuthona* still need to be tested in future studies.

Keywords: Aeolidida, systematics, biodiversity, Eubranchidae, Fionidae, Calmidae, Fionidae, Tergipedidae

FINE SCALE GEOGRAPHIC DIVERSIFICATION IN THE TROPICAL WESTERN ATLANTIC: THE PHYLOGEOGRAPHY OF *BULLA OCCIDENTALIS*

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The biogeography of the Neotropics is complex and several examples of genetic breaks within species have been illustrated for several groups of organisms (e.g. echinoderms, fish, molluscs). Such divergence is often attributed to oceanographic factors, transient allopatry, as well as ecological factors, but no common biogeographical pattern has been found and mechanisms behind diversification within the region are not fully understood. In this project about 150 specimens of the cephalaspidean gastropod *Bulla occidentalis* covering its entire geographical distribution from Brazil to Bermuda including insular and continental regions of the Caribbean Sea were studied. DNA sequences of the mitochondrial COI and 16S rRNA and nuclear ITS-2 genes were generated and analysed with population genetics, demographic, biogeographic, and phylogenetic methods incorporating molecular clocks and fossil data to reconstruct the phylogeographic history of *B. occidentalis* and discuss the putative historical drivers of marine diversification in the tropical western Atlantic Ocean.

DIVERSITY, SYSTEMATICS AND TROPHIC ECOLOGY OF THE TROPICAL INDO-WEST PACIFIC GENUS *PHANEROPHTHALMUS* (CEPHALASPIDEA, HAMINOEIDAE)

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Phanerophthalmus is a genus of Cephalaspidea gastropods in the family Haminoeidae with a reduced internal shell, occurring on intertidal and shallow waters of the tropical Indo-West Pacific (IWP). All species are very similar in their external anatomy and their taxonomy is poorly understood and have not been studied in a comprehensive manner. There are currently nine nominal species described, seven of which are accepted as valid. We have used an integrative taxonomic approach combining morphology and molecular phylogenetics based on three genetic markers (COI, 16S rRNA, 28S rRNA) to revise the systematics of the genus, define diagnostic characters of species, and establish their relationships. Gut contents were analysed as a proxy to infer the trophic relationships of these snails. Here we present the first phylogeny of the genus *Phanerophthalmus* together with a reassessment of the systematic value of morphological characters such as colour patterns, radula, jaws, gizzard plates, and male reproductive system. An overview of the geography of species is included as well as new data on dietary preferences.

UNITAS MALACOLOGICA Grant Recipients

THE END OF THE COLD LONELINESS: 3D COMPARISON BETWEEN *DOTO ANTARCTICA* AND A NEW SYMPATRIC SPECIES OF *DOTO* (HETEROBRANCHIA: NUDIBRANCHIA)

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Antarctic heterobranch biodiversity remains largely underexplored. In fact, to date *Doto antarctica* Eliot, 1907 is the single species of the genus described from Antarctica. The type locality of the species is Ross Sea and it was characterised mainly using external features. We found *D. antarctica* in the Weddell Sea and Bouvet Island, which strongly suggests a circumpolar distribution. Species affiliation was supported by molecular analysis using cytochrome *c* oxidase subunit I, 16S rRNA, and histone H3 markers. We redescribed *D. antarctica* using histology, micro-computed tomography (micro-CT), and 3D-reconstruction of the internal organs. We describe the sympatric species *D. carinova* n. sp. and provide an anatomical comparison between the two *Doto* species. Furthermore, we describe the egg masses in both species for the first time. Our data will help to identify the Antarctic species of *Doto* and provide a reference data set for future collections. We demonstrate that micro-CT is a useful tool for non-destructive anatomical description of valuable specimens. Our high resolution micro-CT data reveal that the central nervous system of both *Doto* species possesses numerous accessory giant neurons. These neurons were previously described as auxiliary glandular cells of the salivary glands. We consider the giant neurons an autapomorphy of the genus. In addition, the phylogenetic tree of all *Doto* species sequenced to date plus *D. antarctica* reveals trends towards the reduction of the bursa copulatrix as well as the presence of a distal connection of oviduct to the nidamental glands, shedding light on the evolution of the reproductive system of *Doto*. Accurate morphological and anatomical descriptions are still of vital importance for understanding species boundaries.

Keywords: Antarctica, Cladobranchia, Dotidae, Weddell Sea, micro-CT, giant neurons

THE ORIGIN OF SPECIES: EVIDENCE ON BOREAL *DENDRONOTUS* (GASTROPODA: NUDIBRANCHIA) SPECIATION, BY GEOGRAPHIC RADIATION AND ADAPTATIONS TO DIFFERENT FEEDING MODES

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Nudibranch molluscs of the genus *Dendronotus* Alder et Hancock, 1845 (Gastropoda: Heterobranchia) are distributed in the northern Hemisphere, with most diversity in the boreal and Arctic regions. For a long time taxonomy studies of the genus *Dendronotus* were problematic due to a high variability in a colouration pattern, external morphology and anatomy. In this research we focused on the detailed integrative study of systematics, phylogeny and biogeography of boreal and Arctic *Dendronotus* species. Methods and approaches included a detailed study of morphology and anatomy, molecular phylogenetic analysis of 2 mitochondrial and 2 nuclear markers, molecular species delimitation methods, an analysis of radular ontogenetic variations and ecological studies. In boreal and Arctic waters of the NE Atlantic and the NW Pacific a high cryptic diversity has been revealed. The taxonomic status of the NE Pacific species *Dendronotus albus* and *Dendronotus diversicolor* was reconsidered and distribution ranges of the most boreal and arctic *Dendronotus* species were revised. Molecular phylogenetic analysis combined with ancestral area reconstruction analysis support the North Pacific origin of boreal *Dendronotus* species with fast radiation. Further speciation relates with periodical opening and closing of Beringia during Miocene-Pliocene and early Pleistocene. Phylogenetic hypothesis based on four molecular markers reveals six major clades; each clade represents by species with Atlantic and Pacific distribution. A model of morphological evolution of the radula strongly corresponds with molecular phylogenetic hypothesis. The ontogenetic changes of radula through the late ontogenesis are species-specific feature and stand in close interdependence with the feeding modes and the specialization on different feeding objects. These data let us to state that feeding adaptation and geographical isolation were the key factors of speciation within genus *Dendronotus*.

This study was supported by Russian Foundation for Basic Research (grant #16-34-00955).

Keywords: Cladobranchia, Dendronotina, integrative taxonomy, phylogeny, biogeography, Beringia

UNITAS MALACOLOGICA Grant Recipients

DEEP SEA MYSTERIES: A MOLECULAR PHYLOGENY OF NEWLY DISCOVERED NUDIBRANCHS IN THE GENUS *HALGERDA*) FROM LOW LIGHT PHILIPPINE REEFS

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The nudibranch genus *Halgerda* includes 34 described species from the Indo-West Pacific tropics. Recent fieldwork during the 2014 and 2015 California Academy of Sciences expeditions to the Philippines and recent investigations in other parts of the Indo-Pacific have provided material for at least another 12 new species from shallow and deep-water reefs. Advanced SCUBA technology also allowed our research to explore deep reefs of the “Twilight Zone”. Formally called the mesophotic zone, this low light area from 60m-150m contains a wealth of poorly studied or completely undiscovered species. The purpose of this study was to investigate the molecular phylogeny of nine likely undescribed nudibranch species from the genus *Halgerda* collected during this expedition, most of which were collected from the mesophotic zone. Mitochondrial fragments cytochrome c oxidase I (COI) and 16S as well as nuclear fragments H3 and 28S were sequenced from 34 samples of *Halgerda* species, including the nine recently discovered species and previously un-sequenced species such as *Halgerda formosa* (the type species), *Halgerda batangas*, and *Halgerda tessellata*. Outgroups were chosen from among several other discodorid exemplars. The phylogeny was determined using maximum likelihood and Bayesian analyses. The results confirm that eight of the nine suspected new species are indeed distinct from described species. Molecular data were lacking from the ninth species owing to its fixation in a formalin-based fixative. The data also suggest that the undescribed species from the mesophotic zone form a clade nested within *Halgerda*. This also suggests a single invasion of the mesophotic zone by a shallow-water ancestor and subsequent radiation of this lineage within the mesophotic. This is different from what was found with mesophotic fish where new mesophotic species each had a different shallow-water sister species, suggesting multiple isolation events.

ONE SLUG, TWO SLUG, WHITE SLUG, NEW SLUG: DIVERSITY AND SYSTEMATICS OF THE NUDIBRANCH GENUS *GYMNODORIS*

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The Indo-West Pacific nudibranch genus *Gymnodoris* comprises about 35 described species of voracious predators best known for hunting and devouring other sea slugs. The group features intriguing behaviors such as cannibalism and fish-fin parasitism and is ecologically important as one of the few known predators of nudibranchs, yet the genus is plagued by poor species descriptions, unreliable identifications and much undescribed and undocumented diversity. In addition, certain authors place some members of *Gymnodoris* in a separate genus —*Analogium* — based on gill morphology. Here we present a molecular phylogeny for *Gymnodoris* based on two nuclear (H3, 28S) and two mitochondrial (16S and COI) markers. Bayesian and Maximum Likelihood topologies largely agree and the resulting phylogeny fully supports *Gymnodoris* as monophyletic with *Analogium* nested within *Gymnodoris*, and subdivides the genus into three main clades. Within these clades, relationships are still unresolved for the deeper nodes. In addition, we found that gill morphology is not phylogenetically informative, but likely associated with lifestyle evolution. Further, these results reveal extensive undescribed diversity within the genus, suggesting that *Gymnodoris* may represent upwards of 100 species.

Keywords: *Gymnodoris*, nudibranch, phylogenetics, Indo-Pacific, biodiversity, Polyceridae, Gymnodorididae, *Analogium*, opisthobranch

DEVELOPMENT OF SEXUAL CANNIBALISM IN A SIMULTANEOUS HERMAPHRODITE, *GYMNODORIS CITRINA* (NUDIBRANCHIA DORIDACEA)

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Sexual cannibalism is mating behavior in which basically a female preys on her mate during or after copulation, but detailed studies were limited to gonochoristic species such as mantises and orb-weaver spiders. Although Johnson (1992) reported *Gymnodoris citrina* cannibalized its mate after copulation, sexual cannibalism has not studied precisely in any simultaneously hermaphroditic species. We observed mating behavior in *G. citrina* and distinguished developmental stage based on morphology and behavior pattern. Among juveniles, they rarely showed aggressive behavior (11/111), but exhibited escape behavior at most of encounters. They usually reversed their courses by twisting the body as soon as they touched conspecific juveniles. As well as juveniles, most sub-adults exhibited escape behavior, but some showed aggressive behavior (26/259). In a few cases, they bit their mates after performing escape behavior for several times. The behavior patterns after biting were not fixed, and 4 patterns were observed; (1) quit biting and move away without mating and predation, (2) protrude copulatory organ, and result in time-consuming cannibalism, (3) exhibit mating behavior but not complete, then exhaustion cause death to both individuals without cannibalism, (4) start copulation without finishing it, and result in time-consuming cannibalism. Full-grown adults exhibited a fixed behavioral chain of “attack, mate, cannibal’’ in all of 22 cases observed. Whenever adults contacted with mature conspecifics, mating and cannibalism took place. While sub-adults often showed hesitation to attack conspecifics, adults never hesitated to bite. These results suggest that cannibalistic behavior in *G. citrina* is not expressed suddenly when it reaches a certain developmental stage or sexual maturation, but the rate of choosing aggressive response gradually increases with growth. Cannibalism at adult stage in this nudibranch is regarded as sexual cannibalism from the characteristics that it is always composed of mating and predation, though quite different from hitherto known examples.

Keywords: nudibranch, *Gymnodoris*, sexual cannibalism, simultaneous hermaphrodite, mating behavior

A NUDIBRANCH REMOVES ALLO-SPERM AND THROWS IT AWAY ALONG WITH OWN THORNY PENIS AFTER COPULATION

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It is generally understood that simultaneous hermaphroditism has evolved to fully utilize scarce mating opportunities caused by law mating frequency and sexual selection such as sperm competition has little importance. However, many simultaneously hermaphroditic opithobranchs have allo-sperm storage organs, seminal receptacle and copulatory bursa, suggesting the possibility of sperm competition. A nudibranch, *Chromodoris reticulata*, autotomises its penis after every copulation and replenishes it within about 24 h to perform multiple copulation. The autotomised penis was covered with many backward-pointed spines on its surface and a sperm mass was often entangled in the spines. This suggests that the nudibranch removes sperm already stored in a mating partner’s sperm storage organs with its thorny penis. Using 6 microsatellite markers, we clarified that 75 % of the sperm mass samples in this study included allo-sperm originated from individual(s) that had copulated in precedence. We revealed that they performed sperm displacement using the thorny penis. It is thought that they copulate repeatedly in a short time to remove allo-sperm using thorny penis and throw it away along with penis after every copulation. Our results suggest that competition in fertilization is quite intense and mating frequency in the wild is relatively high in this simultaneously hermaphroditic species. It is well known that some dragonflies (gonochorists) perform sperm displacement by sperm removal. As the disposable penis in *C. rerticulata* has similar function with an accessory structure of the copulatory organ of dragonflies, it is reasonable to think that sexual selection works as intense in this species, a simultaneously hermaphroditic animal, as in gonochorists.

Keywords: nudibranch, simultaneous hermaphrodite, sperm competition, sperm removal, microsatellite DNA analysis

NOVEL HYPOTHESES ON HETEROBRANCH EVOLUTION FROM MICROANATOMY AND SEQUENCES

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Historical hypotheses imagined that Euthyneura, comprising opisthobranch and pulmonate gastropods, evolved from inside a stock of minute, prosobranch like snails (termed "lower" Heterobranchia), and that their last common ancestor was a "primitive" burrowing snail similar to recent headshield-bearing Cephalaspidea. Recently, our subsequent addition of hard-to-get and enigmatic taxa to ongoing molecular and morphological analyses unraveled sometimes surprising sistergroup-relationships at the intersection of paraphyletic "lower" Heterobranchia and Euthyneura. In the light of comparative (micro)anatomy and histology, I will present new ideas on the evolution of lower Heterobranchia, the advent of cephalaspidean-like snails, and one potential role of heterochrony in the evolution of the often-claimed "crown-group" of gastropods, the Euthyneura.

Keywords: phylogeny, Gastropoda, Euthyneura, lower Heterobranchia, Cephalaspidea, Opisthobranchia, Pulmonata

UNITAS MALACOLOGICA Grant Recipients

RELAY RACE, THE TURN OF THE RESURRECTED GENUS “*FELIMIDA*” EV. MARCUS, 1971 (HETEROBRANCHIA: CHROMODORIDIDAE), LET'S SPLIT IT!

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In 2012, the genus name “*Felimida*” Ev. Marcus, 1971 was chosen by Johnson and Gosliner as the most conservative choice for naming the eastern Pacific, Atlantic, and Mediterranean species previously included in the genera *Chromodoris* Alder & Hancock, 1855 and *Glossodoris* Ehrenberg, 1831 -except *Glossodoris sedna* (Ev. Marcus & Er. Marcus, 1967), despite to not be recovered as a clade. However, the authors of this proposal also encouraged the idea of a broader taxon sampling to clarify the situation. Thus, our aim was to solve the relationships within “*Felimida*” incorporating more species and specimens from the eastern Pacific (including *Felimida sphoni* Ev. Marcus, 1971, the type species of the genus), the Atlantic coast and the Mediterranean, and using two mitochondrial genes -cytochrome *c* oxidase subunit I (COI) and 16S rRNA (16S)- and one nuclear gene -histone-3 (H3). Accordingly to our results, we found that the genus *Felimida* is valid, with wide distribution and includes species from the eastern Pacific, western Atlantic, and one of the Mediterranean Sea. Nevertheless, our outcomes also showed some extra clades with strong bootstrap values that would include several early *Felimida* spp. Accordingly to that, we proposed several new genera within Chromodorididae Bergh, 1981, which joining also reflects historic hypotheses relationships proposed by earlier authors.

Keywords: phylogenetic analysis, Atlantic species, dorids nudibrachs, gastropods

UNITAS MALACOLOGICA Grant Recipients

EVOLUTION OF DORID NUDIBRANCHS: A CALL FOR INTEGRATION OF MOLECULAR, MORPHOLOGICAL AND DEVELOPMENTAL DATA

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Dorids are a speciose and morphologically diverse group of nudibranch molluscs. Understanding their evolution thus is an important aim for malacology. Morphological and ontogenetic evidences for a cryptobranch (i.e. with closable gill cavity) common ancestor of all dorids were challenged by a recent molecular genetics study. Here we extended this multilocus dataset to more than 100 dorid species representing almost all families with multiple representatives. We also generated novel sequences of some key taxa, such as the genus *Onchimira*. The latter genus shares all apomorphies of the traditional family Onchidorididae, such as unique features of the radula and buccal pump, but simultaneously possesses a true gill cavity with fully closable edges as present in most cryptobranch dorids. Our initial molecular trees did not support an earlier proposed genus *Knoutsodonta* or a separate family Corambidae, a classification which is also in conflict with the unique presence of a special reproductive arrangement in the genera *Onchidoris*, *Adalaria*, *Corambe* and *Loy*. Finally, our trees did not recover an earlier proposed sister relationship between the phanerobranch family Polyceridae and cryptobranch Chromodorididae, but Chromodorididae were in a more basal position. The recent discovery of *Elfdaliana*, a new genus of Polyceridae with cryptobranch gill cavity, further weakens the hypothesis of a phanerobranch ancestral dorid. Although dorid phylogeny clearly needs further study we conclude that the last common dorid ancestor likely possessed a gill cavity with closable edges and that this feature was lost several times independently during dorid evolution.

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Keywords: Gastropoda, Nudibranchia, Doridida, phylogeny, evolution and development

LABORATORY SPAWNING AND EMBRYONIC DEVELOPMENT IN THE FALSE-LIMPET *SIPHONARIA PECTINATA* (GASTROPODA: PULMONATA) FROM THE BIZERTE CHANNEL (TUNISIA)

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Spawning and embryonic development of the gastropod *Siphonaria pectinata* were investigated in the laboratory at 25°C. Individuals were collected in May 2015 from a station located in the northern Tunisia (Bizerte Channel). In the laboratory, specimens were reared in aquaria using small rocks as substratum. The snails were fed on algae biofilm adhering both rocks and aquaria walls. From the first week of July to early September, the females lay their eggs capsules, which were grouped in gelatinous mass in the form of ribbons. The spawning time per female varies from 2 to 19 days according to the number of laid ribbons. The female takes 40 to 107 mn with an average of 58 mn as needed time for achieving the laying of one ribbon. The length of the ribbons ranges from 12.3 to 90.0 mm with an average of 38.25 ± 15.20 mm. Each ribbon contains an average number of ovoid capsules of 12669.61 ± 9749.93. Each capsule contained only one egg and measured on average 238.22 ± 2.33 mm and 158.76 ± 2.82 mm, respectively as length and width. Eggs are spherical, with an average diameter of 80.29µm ± 2.10µm. Eggs start development 3 hours and 30 mn after spawning and take between 9 to 12 days to hatch. Hatched veligers were planktonic with coiled shell and kept alive for ten days before it dead without reaching settlement. This information could be very useful in controlling the spread of this species considered as invasive and recently introduced to the Tunisian coast.

Keywords: *Siphonaria pectinata*, spawning, embryonic development, Tunisia

SHELL REPURPOSING IS AN IMPORTANT CONSIDERATION FOR THE FUTURE SUSTAINABILITY OF MOLLUSC AQUACULTURE

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Shellfish are an important component of the rapidly growing global aquaculture sector. In a changing environment, and under increasing demand, future sustainability is a key consideration for mollusc aquaculture. One regularly overlooked aspect of shellfish food production is shell waste. Shellfish are either sold “in-shell” by restaurateurs and food retailers, or de-shelled prior to sale (common for tinned and frozen produce). Either way, shell waste is most likely discarded as a “low risk” material (Category 3 animal by-product waste in the European Union), which may ultimately end up in a waste pile or landfill site. Materials scientists are still unable to mimic or replicate the strength and toughness of mollusc shells, a testament to this impressive composite biomaterial. Shells are formed mainly of Calcium carbonate ($CaCO_3$) and ~1% organic matrix. $CaCO_3$, in the form of limestone, is mined globally in huge amounts and used widely in many applications including cement production and paper whitening. There is, then, disparity between the discarding of mollusc shells by one sector, and the use of environmentally damaging and costly mined $CaCO_3$ by many other sectors. This project, as part of the EU FP7-funded CACHE network (http://www.cache-itn.eu), considers the increasing issue of mollusc shell waste, highlights where shell waste is already being repurposed, and explores and reviews further potential applications for mollusc shells. Potential applications include the inclusion of shells in; construction aggregates and mortars; in natural coastal protection schemes and reef restoration projects; and as biocompatible materials for use in bone grafting orthopaedic surgery.

Keywords: mollusc shell, calcium carbonate, biomimicry, aquaculture, waste valorization

METAMORPHIC AND PROTEOMIC RESPONSES OF FAST-GROWING AND SLOW-GROWING LARVAL COHORTS OF A PACIFIC OYSTER TO OCEAN ACIDIFICATION AND WARMING

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Ocean acidification and warming have previously been shown to significantly affect the physiological performance of oyster larvae. This could be a serious social-economical problem to China as she produces more than 80% of the overall Pacific oyster in the world. However, those climate change studies were mainly focus on the effect of fast growing larval cohort that represented <20% of the overall population. In many of the oyster farms especially in China, natural seeds were collected and fattening process were performed to grow the oyster to marketable size. Both fast and slow growing larvae contributed significantly to the natural community of seeds. Therefore, understanding both fast and slow growing oyster larval performance under future climate change is very important to the future oyster industry in China. This study investigated comparative larval metamorphic success and molecular responses (iTRAQ protein analysis) of both fast and slow growing cohort of Pacific oyster larvae (*Crassostrea gigas*) to chronic environmental stresses of temperature (24 and 30°C) and pH (8.1 and 7.4) in a >2-week laboratory study. The experiments addressed two hypotheses: (1) fast and slow growing larvae have different proteome profile at the time of metamorphosis; (2) the proteome profile of both fast- and slow growing larvae will be altered in elevated temperature and reduced pH condition. Slow growing larvae showed reduced metamorphosis in all conditions because of the later onset of protein degradation and the reduction of Cathepsin protein when compared to fast growing larvae. Even though the metabolism pathways were highly expressed in slow growing larvae in the warming condition, the metamorphosis signaling mechanism was found suppressed. The results highlight the importance of considering both fast and slow growing cohorts of larvae in experiments to precisely project the situation of future China oyster industry under climate changes and therefore to seek for the best mitigation solutions.

OYSTER AQUACULTURE IN A POLLUTED AND CHANGING CLIMATE: PROBLEMS AND WAYFORWARD

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Oysters are well known for their ecosystem services, aquaculture, and production of nutritious seafood, health supplements, and natural drugs. This precious natural resource is however is under threat due to overexploitation, pollution and climate change. Of these threats, climate change due to rising anthropogenic carbon dioxide is of greatest concerns, and so understanding their impact on commercial oysters is a pressing issue. Globally this issue has become one of the serious socio-economic issues because majority of coasts will soon become unsuitable for oyster aquaculture. This is a stark warning to China, which is not only a center of oyster biodiversity but also accounts for >90% of world's oyster production. We are using the Hong Kong's subtropical climate and its oyster aquaculture practice as model system to develop solutions to mitigate the climate change effect on aquaculture at global scale. This city used to be the home of 12 species of oyster; one of them is culturally linked to the society, cultivated commercially over the past 700 years and it is even called as Hong Kong oyster. Their production is dwindling due to climate change and socio-economical issues pertained to this community. Our large-scale and long-term acclimation experiment in a commercial hatchery setting suggests that larval shell growth rate will be significantly reduced at projected climate change conditions for the year >2100 in the Hong Kong oyster species that supports the livelihoods of millions of people in South China. Nevertheless, the true scientific value of this culturally and climatically sensitive species is yet to be revealed.

Keywords: climate change, ocean acidification, oyster aquaculture, marine shells

THE SHELLFISH BEYOND FISH: INTEGRATING LOCAL ECOLOGICAL KNOWLEDGE IN THE ASSESSMENT OF MOLLUSCAN DIVERSITY AND ABUNDANCE CHANGES

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Ecosystems and societies are facing major challenges as climate changes and ecological services are degrading. The linkage of local knowledge and academic science at all scales has become central in international debates. Molluscs represent a privileged biodiversity compartment to monitor and assess coastal change by combining traditional and scientific knowledge. On one hand, shellfish play a crucial role in the diet of coastal livelihoods; the cumulative and complex bodies of knowledge of shellfish gatherers are dynamic and adaptable, and have been developed through a long history of interactions and reliance on this resource. On the other hand, molluscs are reliable scientific indicators of ecosystem quality and physico-chemical changes; in addition, their ubiquitous nature and broad ecological distribution make them particularly suitable for large scale geographical surveys. Ethno-malacology is a new field of study that aims to understand the relationship between humans and shells through the study of local knowledge, practices and representations. It relies on interdisciplinary approaches combining anthropology, archeology, geography and ecology. The aim of this research was 1) to explore local practices and ecological knowledge among shellfish gatherers in the mangrove forest of Katurai Bay (Siberut Island, Indonesia), and 2) to examine the applicability of local malacological knowledge in climate and coastal change monitoring. We found that knowledge of shellfish gatherers include accurate knowledge of molluscs diversity, lifestyles, habitat and distribution, as well as detailed knowledge on environmental characteristics and coastal ecological changes. This corpus of ethno-ecological knowledge allows local gatherers not only to assess past conditions and survey day-to-day shellfish population dynamics, but might also enable them to comprehend social and ecological vulnerability to climate and environmental change.

Keywords: shellfish, local knowledge, ethno-malacology, coastal ecosystems, monitoring, climate change

UPPER TEMPERATURE LIMITS OF MANGROVE SNAILS: DEVIATION FROM THE GENERAL PREDICTION OF TROPICAL ECTOTHERM VULNERABILITY TO CLIMATE WARMING

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The hypothesis that tropical ectotherms are generally vulnerable to climate warming by presumably living closer to their upper thermal limits lacks comprehensive support for the full spectrum of marine organisms and habitats. While the hypothesis might be appropriate to relatively stable subtidal environments, it is more difficult to comprehend for highly thermally heterogeneous intertidal environments. Intertidal ectotherms often experience extreme temperature fluctuations during aerial exposure, while complex morphological, physiological and behavioural adaptations to counter these conditions may potentially buffer the effects of climate warming. We investigated the upper thermal limits of cardiac function (equivalent to upper lethal temperature, ULT) for 21 species and 7 families of gastropods, cohabiting a tropical mangrove system. Additionally, ULTs were compared with maximum habitat temperatures, and data were partitioned with respect to habitat use (whether snails lived on the mud substratum or occupied the aerial components of mangrove trees) and phylogeny (family level). We found that ULTs were highly variable among species, ranging between 44 and 52°C, and differed among mud-dwellers (44-52°C) and mangrove tree snails (49-52°C). There were also significant phylogenetic differences; for example, the Littorinidae snails, which have recent evolutionary connections to thermally extreme rocky shores, had significantly higher ULTs than the Ellobiidae, which have recolonized mangrove systems from relatively benign terrestrial thermal habitats. The thermal maxima of both habitat types (mud and air) were similar, approximately 35°C, and comparable to the average daily maximum for regional climatically relevant air temperature. Thermal safety margins, which indicate climate warming vulnerability (calculated from the difference between habitat thermal maximum and ULT) thus ranged between 9-17°C. This study highlights the complexity of factors affecting environmental thermal maxima and lethal temperatures in ectotherms, and contests the generalization of vulnerability of tropical marine ecotherms to climate warming.

THE IMPACT OF DIFFERENT TEMPERATURES CONDITIONS ON BEHAVIOR OF *ARION VULGARIS* MOQUIN TANDON 1855 FROM SOME EUROPEAN POPULATIONS IN LABORATORY CONDITIONS

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Arion vulgaris is a serious pest of crops in Europe. This slug species is spreading across the Europe for last 60 years and can be found in almost every country in Europe. The results of research on nocturnal activity of slugs from different European populations in different temperatures are presented. Tested populations are localized in places that were invaded in different time and thus it is possible to compare their behaviour in different stages of invasion. The research was conducted under laboratory conditions in a climatic chamber at a temperature of 10, 15 and 20°C and 12h day length. In translucent plastic containers one slug was placed. The surface of the container was divided into four parts: on the first the shelter for slugs was placed, on the other discs of cabbage. Each container was also equipped with an infrared camera connected to video recorder. For the next 72 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 analyzed in Noldus EthoVision software. Experiments were made in 6 replicates. The residence time in the shelter, slug movement and immobility time differed among the populations. Differences were also observed during feeding time. This research study was supported by The National Centre for Research and Development as part of the Warion project Pol-Nor/201888/77/2013.

Keywords: *Arion vulgaris*, behaviour, temperature condition

GLOBAL INVASION PATTERNS OF NON-MARINE MOLLUSCS UNDER CLIMATE CHANGE SCENARIOS

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Invasive alien species (IAS) are one of the greatest threats to biological diversity, agriculture, livelihoods, human and animal health and forestry after habitat destruction. Introduced either accidentally or deliberately, the invasive species out-compete native and endemic species, pushing many species to extinction as shown in many studies. Invasive species act synergistically with climate change and could have serious implications on ecology and local economies. Hence, identifying suitable habitats, where these species could invade becomes a high priority for early detection, prioritization of regions for conservation and effective management of invasive species. For the present study 10 non-marine molluscs (8 freshwater and 2 terrestrial) that are globally invasive were selected. The distribution data was downloaded from GBIF and ecological niche modeling tool (MaxEnt) was used to predict the possible sites of invasion at the global level under two climate change scenarios (RCP 2.6 and RCP 8.5 for 2080). We have also predicted the present distribution scenario after testing for co-linearity among the variables. For the pooled data, the result indicates that there are four "hotspots" of invasion under present scenarios, which are in southeastern United States, Western Europe, southeastern parts of South America and eastern China. Other parts of the world are less prone to invasion. Under both climate change scenarios, there is an increased area of invasion.. A niche shift was also seen ,particularly in parts of South America, Central Africa, India, and Australia. However, there is a difference in response to climate change at the individual species level. The results of this study can be used to understand how these invasive mollusks respond to climate change and also to prioritize the region for management of invasive species.

USING MOLLUSKS AS ENVIRONMENTAL ARCHIVES

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As major calcareous organisms, globally distributed and with a long fossil record, mollusks provide an excellent archive of past climate events and oceanographic changes thus increasing our understanding of present day conditions, helping with predictions of future trends and facilitating the development of new conservation strategies. Important biomineralizing organisms, mollusks can be heavily affected by current trends in ocean warming and acidification, especially larvae and juveniles. Nevertheless, some studies show a certain level of tolerance especially among intertidal and coastal groups. Mollusks have been widely used as proxies for environmental reconstruction and their sensitivity to changes can provide detailed information on both short-term habitat disturbance and long-term ecosystems' restructuring. Shells in general are important components of benthic communities, contributing to its structure and facilitating settlement of many other organisms. Bivalves in particular are important ecosystem engineers in coastal and estuarine areas. Mollusk faunal composition has been long used in paleoecology to reconstruct ocean dynamics, whereas bivalve life habits provide valuable information on subtract types. This talk will give an overview of the use of mollusks in climate and environmental reconstruction in general.

Keywords: mollusks, climate reconstruction, environmental indicators, archives, paleoecology

SPECIES DELINEATION: COMPARING THE POWERS OF SHELL MORPHOMETRICS AND DNA-BARCODING IN THE TROCHID GASTROPOD GENUS *GIBBULA*

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Roughly 20 species of the genus *Gibbula* s.l. are described from European seashores. Vague original descriptions, misleading type material and considerable intraspecific variability led to problems in identification and delineation of several of these abundant, biofilm grazing species. We attempt to resolve some of the complexities of the genus using DNA-barcoding and geometric shell morphometrics on eleven taxa. We developed standardized methods for the use of landmark-based analyses on trochid gastropod shells. By using a landmark set, which combines new and traditional points of interest on the shell, a comparison with original descriptions and some of the available type specimens became possible. Some species are well resolved with CO1 and ITS data, even if shell shapes do not differ, e.g. in *G. varia* and *G. rarilineata*. The genetic separation of *G. varia* and *G. divaricata* is ambiguous, although shell shape is highly diagnostic. *Gibbula (Phorcus) mutabilis* shows deep genetic and morphometric differentiation among disjunct populations. Although the gene tree supports the monophyly, shells from Crete resemble *G. (Ph.) richardi* and those from Croatia are similar to *G. divaricata*. Thus, combining both methods is the most effective approach to characterizing these species without using sometimes-misleading characters like shell sculpture and colouration. We also address taxonomic issues regarding the status of the subgenus *Phorcus* and the potential para- or polyphyly of *Gibbula*.

Keywords: *Gibbula*, species delineation, geometric morphometrics, landmarks, gastropoda, barcoding

INTEGRATING SHELL MORPHOMETRY WITH MOLECULAR DATA FOR DELIMITATION OF SPECIES

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Landmark-based geometric morphometric techniques constitute a powerful tool, which has been used for capturing effectively both shape and size of biological organisms, including shells. The multivariate datasets of shape coordinates obtained in this way (partial warps and centroid sizes) can be used for the study of the variation of size and shape as a function of different factors. For instance, species and populations can be separated on the basis of existing significant differences in shell shape, or alternatively the observed differences in size and shape can be correlated with ecological factors. The sets of shape coordinates and the resulting distances among individual shell forms (Procrustes distances) can be combined with distances resulting from phylogenetic analyses, or even with similarity distances obtained from other sources: anatomical data (i.e. radula), ecological data, biogeography, etc. Each of the datasets is normalized using Non-Metric Dimensional Scaling (NMDS), and the resulting components taken together are subjected to Gaussian clustering. In this fashion, the delimitation of groups corresponding to distinct species results in general more clear than if data coming from one single source are used. The incorporation of shell shape data to this type of cluster analysis can be performed not only by geometric morphometric methods. Other procedures, ranging from classical morphometric parameters based upon distances and rations to other more sophisticated and accurate (i.e. Fourier ellipsoids, etc.), can be used effectively, as the resulting shape variables will be all normalized once NMDS has been performed. The procedure will be illustrated with geometric morphometric analyses of gastropod shells of members of the family Conidae.

Keywords: geometric morphometry, cluster analysis, non-metric dimensional scaling, Conidae

A METHOD FOR QUANTIFYING, VISUALISING, AND ANALYSING GASTROPOD SHELL FORM

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Quantitative analysis of organismal form is an important component for almost every branch of biology. Although generally considered an easily-measurable structure, the quantification of gastropod shell form is still a challenge because shells lack homologous structures and have a spiral form that is difficult to capture with linear measurements. In view of this, we adopt the idea of theoretical modeling of shell form, in which the shell form is the product of aperture ontogeny profiles in terms of aperture growth trajectory that is quantified as curvature and torsion, and of aperture form that is represented by size and shape. We develop a workflow for the analysis of shell forms based on the aperture ontogeny profile, starting from the procedure of data preparation (retopologising the shell model), via data acquisition (calculation of aperture growth trajectory, aperture form and ontogeny axis) and data presentation (qualitative comparison between shell forms) and ending with data analysis (quantitative comparison between shell forms). In this congress we will discuss how the data that obtained by this method can be used for taxonomy, developmental biology, ecology and evolution studies of gastropoda shell.

Keywords: snail, 3D morphometric, ontogeny, Blender software, geometric morphometric, Elliptic Fourier analysis, CT-scan

FACTORS DRIVING CHANGES IN FRESHWATER MUSSEL (BIVALVIA, UNIONIDA) DIVERSITY AND DISTRIBUTION IN PENINSULAR MALAYSIA

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Freshwater mussels (Bivalvia, Unionida) fulfil important ecosystem functions and are one of the most threatened freshwater taxa globally. Knowledge of freshwater mussel diversity, distribution and ecology in Peninsular Malaysia is extremely poor, and the conservation status of half of the freshwater mussel species presumed to occur in the region has yet to be assessed. We conducted the first comprehensive assessment of Peninsular Malaysia's freshwater mussels based on species presence/absence and environmental data collected from 155 sites spanning all major river catchments and diverse habitat types. Through an integrative morphological-molecular approach we recognised nine native and one widespread non-native species, i.e. *Sinanodonta woodiana*. Three species, i.e. *Pilsbryoconcha compressa*, *Pseudodon cambodjensis* and a putatively undescribed *Pseudodon* species, had not been previously recorded from Malaysia, which is likely a result of morphological misidentifications of historical records. Due to their restriction to single river catchments and declining distributions, *Hyriopsis bialata*, probably endemic to Peninsular Malaysia, *Ensidens ingallsianus*, possibly already extinct in the peninsula, and *Rectidens sumatrensis*, particularly require conservation attention. Equally, the Pahang catchment, the Perak catchment and the northwestern basins are of particular conservation value due to the presence of a globally unique freshwater mussel fauna. Acidification and pollution were identified as the most important anthropogenic factors threatening freshwater mussel diversity in Peninsular Malaysia. These factors can be linked to atmospheric pollution, deforestation, oil-palm plantations and a lack of functioning water treatment, and could be mitigated by establishing riparian buffers for rivers running through agricultural and residential land.

Keywords: acidification, Asia, DNA barcoding, endemic species, land-use change, pollution, rare species, tropical

COMPARATIVE PHYLOGEOGRAPHY OF FRESHWATER MUSSELS IN MAINLAND SOUTHEAST ASIA

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The contemporary river systems of mainland Southeast Asia are a reflection of a series of historic freshwater rearrangements driven by various climatic fluctuations and geological events. Sea level rise and fall dramatically changed the size and course of the rivers in Southeast Asia, while various tectonic events caused major watersheds to become captured by adjacent drainages. We used a molecular approach to explore how such historical events may have shaped freshwater mussel diversity and distribution. Preliminary data resolve a mosaic of phylogeographic patterns, some of which may be explained by historic and modern-day river connections, while others may be products of differences in life history. Our results are discussed in the context of the geological, climatic, and ecological factors that shape freshwater mussel diversity and distributions in Southeast Asia.

UNITAS MALACOLOGICA Grant Recipients

FRESHWATER MUSSELS (UNIONOIDA) OF VIETNAM: DIVERSITY, DISTRIBUTION AND CONSERVATION STATUS

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Vietnam has a high diversity of freshwater mussels in the Indo-Burma area and in the world. Fifty-three freshwater mussel species of Unionoida have been recorded from Vietnam. Forty-three of them were assessed in IUCN Red List 2010 with the taxa falling into the IUCN Categories of Least Concern (20 species, 38%), conservation concern (15 species, 28%), Data Deficient (8 species, 15%) and not evaluated (10 species, 19%). Unfortunately, there has been relatively little research on this group. The status of almost species is unclear or unknown. Under current impacts of human and natural disasters, research on diversity and conservation status of freshwater mussels is very urgently needed in order to propose specific conservation measures for these species in Vietnam. If all of Data Deficient taxa are found to be threatened, with around 60 percent of species threatened, this fauna would become one of the most threatened freshwater mollusc faunas.

Keywords: Unionidae, Margaritiferidae, diversity, distribution, conservation

UNITAS MALACOLOGICA Grant Recipients

A GLOBAL BIOREGIONALIZATION BASED ON FRESHWATER BIVALVES

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In the Indo-Malayan region, in which the venue of the 2016 WCM is located, Alfred Russel Wallace developed his famous concept of global zoogeographic divisions based on the distribution of terrestrial vertebrate species. The bioregionalization reflects the joined influence of geography and ecology on the evolutionary history of taxa. Modern statistical clustering approaches, using vertebrate range maps, confirmed this principle bioregionalization and Wallace' zoogeographic system still serves as framework for comparative macroevolutionary and –ecological studies. However, the underlying drivers of distribution patterns are often incongruent across taxa, life style, and ecosystems. Globally distributed freshwater bivalves, for example, cover a longer phylogenetic history than terrestrial vertebrates and are therefore a suitable model taxon for testing the universality of zoogeographic divisions. For this preliminary study, we matched range maps and georeferenced occurrence records for more than the half (>600 species) of the currently recognized bivalve diversity with respective drainage basins. Almost half of the missing species were described from South and Central America, suggesting a good coverage in the remaining parts of the world. We performed a cluster analysis of similarity in species composition among these >350 drainage basins. This similarity calculation also includes the bivalves' hierarchical taxonomic classification because Wallace criteria for bioregionalization call explicitly for considering ancestral relationships. The drainage basins are grouped in large, spatially coherent clusters with boundaries that largely correspond to vertebrate zoogeographic regions. Moreover, we found a (sub)division of the Oriental region into an Indian and Indo-Malayan region. This emphasize that plate tectonics, indeed, strongly determines the evolutionary history of higher taxa, resulting in major convergence of large-scale biogeographic patterns across phyla and ecosystems. However, the Nearctic was more distinct from the Palearctic than suggested by the vertebrate-based regionalization. This indicates that stochastic cross-regional colonization events may blur biogeographical patterns and result in differences in the specific bioregional relationships among various phyla.

Keywords: zoogeographical regions, geographical clustering, biogeography

FRESHWATER BIVALVE DIVERSITY IN TURKEY

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Near the southern margin of Western Palearctics, zoogeographically Turkey is an interesting study area in terms of freshwater mollusks. Of freshwater bivalves, a total of 30 species from superfamilies Dreissenoidea, Sphaerioidea, Unionoidea, Veneroidea have been recorded from Turkey. Patchy distribution pattern can be observed for many unionid taxa, and 3 zoogeographically different realms (western, northeastern and southeastern) can be discerned due to apparent provincialism. Sphaerioidea, currently represented by 11 species, is the most neglected group and actual species diversity is thought to be much higher than anticipated. With 4 species of Dreissenidae, 3 being endemics, Anatolia is thought to be among speciation centers for the genus *Dreissena*. Of Veneroidea, 2 species of *Corbicula* invasive elsewhere have been recorded as native from southern locations. Future studies on the group, considering the scarcity of taxonomic data available and the small size of the surveyed area, may greatly increase our knowledge of this lesser known part of the malacofauna of Turkey.

MODEL FOR THE CONSERVATION ASSESSMENTS OF THE FRESHWATER BIVALVES IN RUSSIA

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In Russia the total evaluation of the freshwater water bodies in respect bivalves is impossible because of the enormous area and lack of experts. Just few species within a small part of its territory are assessed in terms of conservation biology. The only method for amplification of such assessments is an analysis of indirect evidences: cartographic data on water bodies, data on ecological requirements of species and incidental reports on the local faunas. The recent example is a study of *Margaritifera margaritifera* living in the rivers of the Baltic Sea basin. “Searching rules” for the survived pearl mussel populations were elaborated during 2008-2013. The most significant ones concern the availability of lakes in the river sources and the share of deforested areas in the river basins. About 150 watercourses were evaluated based on these rules that resulted in the discovery of previously unknown viable population (about 50000 individuals) and prove of the absence of pearl mussels in some rivers that traditionally were considered as its habitats. Similar “rules” can be elaborated for the other bivalve species. Such an approach would revise some species assessments of the IUCN red list. Now the distribution areas of some bivalves are overstated there. Islands of the Arctic Ocean are indicated as a part of distribution area of the species from the genera *Unio* and *Anodonta*, while there are no suitable habitats for them. The same is true for the nearest mainland. It is most likely that these bivalves are scarcely distributed over the territory of Russia. In the northern part of the country the water temperature is too low, in the southern part the watercourses often become unsuitable for bivalves because of siltation.

Keywords: Russia, assessment, Margaritifera, *Unio*, *Anodonta*

PHYLOGENY OF THE MOST SPECIES RICH FRESHWATER BIVALVE FAMILY (BIVALVIA: UNIONIDA: UNIONIDAE): DEFINING MODERN SUBFAMILIES AND TRIBES

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Malacologists have been organizing genera assigned to the Unionidae into subgroups for over 200 years. We are still working toward a consensus on which genera to recognize - currently between 131 and 142 genera. A total of 56 subfamily and tribe level names have been described under Unionidae. Three names are unavailable and one is for a fossil group, leaving 52 family group names available. Various schemes to group unionid genera have been developed based on shell-shape, shape of anterior shell margin, umbo sculpture, and marsupial and larval characteristics. In the last several decades, molecular phylogenetic studies of mitochondrial and nuclear gene sequences have helped clarify the family group-level relationships and morphological evolution of the Unionidae. We are presenting our analyses based on sequences of cytochrome oxidase c subunit 1 (COI) and 28S for 66 species and analyzed with Bayesian inference and maximum likelihood. Our analyses resolved 17 major well-supported clades. These clades are interpreted as representing six subfamilies: Unioninae, Anodontinae, Ambleminae, Gonideinae, Parreysiinae and Rectidentinae. The validity and position of *Modellnaia*, assigned to a monotypic subfamily, remains unresolved due to lack of recent tissue samples. Some genera with multiple included species are not monophyletic. We discuss our results in the context of all available subfamily and tribe-level names and the developing higher-level classification of the Unionidae.

PHYLOGENOMICS OF FRESHWATER MUSSELS (BIVALVIA: UNIONIDA) PRELIMINARY RESULTS AND LESSONS LEARNED

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Freshwater mussels of the order Unionida are key elements of freshwater habitats and are responsible for important ecological functions and services. Unfortunately, these bivalves are among the most threatened freshwater taxa in the world. However, conservation planning and management are hindered by taxonomic problems and a lack of detailed ecological data. This highlights the urgent need for advances in the areas of systematics and evolutionary relationships within the Unionida. On the other hand, Unionida freshwater bivalves are quite interesting from the molecular viewpoint, as they transmit their mitochondrial genome (mtDNA) both maternally and paternally. Up to now, the majority of molecular studies use single markers or a combination of a small number of markers to infer the phylogenetic relationships. Due to the recent arrival of high throughput sequencing equipment, sequencing prices have dropped and we are entering the Phylogenomic era. While for some vertebrate taxa the full genome comparison is already undergoing, for other taxa (like bivalves) no full genome is still available. However, more practical and cheaper approaches have become available for phylogeny reconstruction mostly using reduced representations of the whole genome. Our study followed a distinct approach by sequencing big portions (>10 kb) of DNA from three independent regions: the whole Female and Male mtDNA mitogenomes and one nuclear DNA fragment that encompass the 18S and 28S regions. The high order phylogenetic analyses of these three markers show distinct evolutionary histories that when analyzed alone might present conflicting results depending on the analytical

methods used. In the present communication, the best analytical methods and combination of both Mitochondrial and nuclear ribosomal markers and phylogenetic analytical methods are discussed in the context of a new ongoing phylogenomic project for Unionoida mussels.

DISTRIBUTION OF ENDANGERED UNIONID MUSSELS IN RELATION TO HABITAT CONNECTIVITY IN AN AGRICULTURE-DOMINATED LANDSCAPE

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Unionid mussels have a unique life cycle, possessing an obligate parasitic larval stage that requires the attachment to suitable host fish. Human activities can directly alter habitat of mussels but also indirectly the fate of larvae through the modification of fish habitat. We tested the hypothesis that the occurrence of unionid mussels in agricultural drainage channels are partly determined by the connectivity of the sites to downstream larger river channels where major habitat of host fish exists. Fish and mussels were caught at 36 sites (18 each with and without mussels) of drainage channels across 30 km^2 areas in the Nobi plain, central Japan. Sites were selected in such a way that other potentially important determinants of distribution such as elevation and surrounding landuse were similar among sites. The connectivity to the downstream river channels and local habitat-quality environment were also quantified in 2011 and 2012. Logistic regression models with the occurrence of mussels as a response variable demonstrated positive effect of vegetation cover along the sites and negative influences of concrete-based bed substrate. Notably, the connectivity had a significant positive influence on the occurrence and the greatest relative importance (50.6%) among the explanatory variables. The occurrence of fish taxa such as *Nipponocypris* and *Rhinogobius* was positively related to the connectivity as well as mussel presence, suggesting that these taxa are the important host fish whose distribution is affected by the connectivity. Our results suggest that efficient conservation of mussel habitat in drainage channels need to consider both the local habitat as well as host-specific connectivity to downstream river channels.

Keywords: freshwater mussels, habitat protection, lotic species, parasitism

TESTING RELIABLE SAMPLING METHODOLOGIES FOR THE THREATENED FRESHWATER MUSSEL *MARGARITIFERA MARGARITIFERA*

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The freshwater pearl mussel *Margaritifera margaritifera* lives in shallow clear water streams that allow sampling strategies to rely on visual searches. A few attempts have been made to establish standard sampling methods, but no testing of their reliability has been made to date. We registered the location of all mussels that could be located by sight on a low-density population (456 visible mussels over 11 Km river length) and on a high-density stretch of river (3762 mussels over 585 m river length) from northern Portugal. Both populations were represented spatially using GIS. We compared the efficiency of sampling using total counts, transects and quadrates. For sampling simulation purposes we placed a variable number of 100 meter long sampling stations along the river. Transect sampling followed both a systematic and a random sampling strategies. Quadrate sampling followed an adaptive strategy, in which quadrate locations were initially assigned randomly. Differences in sampling efficiency were first assessed by comparing population estimates that were averaged over 100 sampling simulations for random transects and quadrate samplings. Population estimates among these were assessed using a Generalized Linear Mixed Model. Additionally, we assessed the reliability of each approach in describing the spatial distribution of mussels using Spearman correlations of sample estimates at the stations of each method against the estimates from the total counts. The results indicate that quadrate sampling provided slightly higher population estimates and also exhibited slightly higher concordance with the ranks of estimates at each station given by total counts. Nevertheless, all approaches were considered to give reliable population estimates while sampling a similar proportion of the river. The choice of method should therefore be based in the available resources, as significant differences in the effort needed to complete each strategy do exist.

Keywords: freshwater mussel, sampling efficiency, population estimate, quadrate, transect.

CAN MUSSELS FIND A REFUGE IN THE DEPTH OF LARGE LAKES?

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Mussel communities in Lake Maggiore (the second largest and deepest lakes in Italy) profoundly changed over the last ten years with overall densities of the dominant species dramatically decreasing. These changes corresponded with a period of repeatedly low lake water levels caused by a combination of climate patterns (a regional drought) and local water management practices (decreased reservoir releases, water abstraction). Such stress conditions likely exacerbated the competition from alien species that have invaded the lake in the same period. A shift towards assemblages dominated by invasive bivalves is progressively occurring in areas previously occupied by abundant populations of a common species, *Unio elongatulus*. Faced with multiple stressors, unionid mussels have their Achilles' heel in a suite of traits that make them unable to adjust to these changes. Unable to escape unfavourable conditions, with poor ability to recolonize after experiencing catastrophic declines, mussels' only chance of survival is to find a refuge from physical stress and competition from invasive species. The large deep lakes could provide adequate refugia to species able to colonize deeper than the commonly described depth optima (<3 m depth). Little is known on depth limits of unionids in lakes, since studies are generally limited to shallow littoral areas, but the few existing data suggest shifts to greater depths with increasing lake size. To explore the hypothesis that large deep lakes can provide refuge for unionid mussels, the spatial distribution of native and alien mussels along depth transects in Lake Maggiore is being studied. The hypothesis will be discussed in relation to preliminary data from lakes of different size and trophic level.

Keywords: unionid mussels, depth limits, refugia, alien bivalves, large deep lakes, microhabitat features

CHROMIUM ACCUMULATION ON MOLLUSCS IN CIMANUK LAMA RIVER, INDRAMAYU, WEST JAVA, INDONESIA

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The residue of human activities and industrial wastewater of batik around the river waters was allegedly increases the accumulation of chromium and can disrupt molluscs communities in the river. The aim of this study is to assess the impact of human activities around river bodies to the molluscs communities and the accumulation of chromium in the Cimanuk Lama River Indramayu District, West Java. Research has been conducted three times a sampling from April to May 2015 at three different locations research station. The result of this research shows a value the heavy metals heavy chromium on the water in all station still meet of quality standard with the range of 0,010 to 0,016 mg/L, while for chromium in sediment only station 1 that fulfill of quality standard with the range of all stations 11,72 to 46,63 mg/kg and chromium in molluscs (*Bellamya* sp. and *Pilsbryoconcha exilis*) all station was over of quality standard with the range of 2,13 to 37,81 mg/kg. The results of the analysis index community describe the occurrence of a change community molluscs at all stations resulting from pressure environment especially at the station 3 that tends to worse value compared with other station is shown by the low scoring diversity index obtained. The accumulation of the chromium in the waters and change structure molluscs community occurring can result of an activity the use of a stream by humans around the Cimanuk Lama River long as the agricultural sector, fisheries and batik home industry.

Keywords: chromium, molluscs, rivers

HISTOLOGICAL ANALYSIS ON DIGESTIVE GLAND OF *BELLAMYA* SP. AND *PILSBRYOCONCHA EXILIS* FROM CIMANUK LAMA RIVER, INDRAMAYU, WEST JAVA, INDONESIA

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The present study aimed to describe effect of batik industry as human activity in Cimanuk Lama River on chromium heavy metal accumulation around water environment and histology of digestive gland of molluscs (*Bellamya* sp. and *Pilsbryoconcha exilis*). River water and sediment, as well as mollusc samples of three replications each were collected from three stations along Cimanuk Lama River from April to May 2015. Physical and chemical parameters measured and analysed were water temperature, total suspended solids (TSS), dissolved oxygen (DO), pH, biological oxygen demand (BOD_5), chromium in water, sediment and molluscs. This study also analysed condition and change in tissue of digestive gland of *Bellamya* sp. and *Pilsbryoconcha exilis*. Results indicated that chromium heavy metals were already accumulated in water, river sediment and molluscs. Chromium accumulation in water and river sediment was found the highest at station 2 (SK), while *Bellamya* sp. at station 3 (ST). Histological images of the molluscs also indicated change or damage in digestive gland, proven with higher damage level at station 2 and 3. Batik industry around Cimanuk Lama River has increased chromium accumulation in water environment, adversely affecting mollusc's digestive gland.

Keywords: batik industry, *Bellamya* sp., mollusc's digestive gland, heavy metal chromium, *Pilsbryoconcha exilis*.

TRAPEZOIDEUS SIMPSON, 1900 (UNIONIDAE) FROM THE TYPE LOCALITY: AN INTEGRATIVE APPROACH REVEALS THE DOUBTFUL TAXONOMIC STATUS OF A WIDESPREAD INDOTROPICAL GENUS

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Trapezoideus Simpson, 1900 was sectioned based on *Unio foliaceus* Gould, 1843 as the type species (type locality: Tavoy, Myanmar), which now considered as a synonym of another nominal taxon, *U. exolescens* Gould, 1843 (same type locality). Here we report preliminary results of an integrative taxonomic revision of the topotype of *U. exolescens*. During the expedition of 2015 in South-East Asia mussels' samples were collected from Tavoy river basin, Myanmar. These specimens were identified as *Unio exolescens* Gould, 1843 based on morphological distinguishing features. Nucleotide sequences for three gene fragments (two mitochondrial genes – COI and 16S rRNA as well as one nuclear gene – 28S rDNA) were obtained for 6 specimens. Phylogenetic analysis reveals that topotypes collected from the type locality cluster together with representatives of another genus, *Lamellidens* Simpson, 1900 (Bayesian posterior probabilities = 1.00). Based on the molecular data, morphological characters and geographical location, we consider that the topotypes of *Trapezoideus* spp. really could belong to *Lamellidens scutum* (Sowerby, 1868) (type locality: Tenasserim). Taken together, the genus *Trapezoideus* Simpson, 1900 seems to be a synonym of *Lamellidens* Simpson, 1900. The integrative taxonomic approach used in this study highlights that morphology-based identification of unionid taxa from such species-rich region as Indo-China may lead to inaccurate taxonomic solutions because of high morphological variability of the shell characters.

This study was supported by grant from the President of Russia (no. MD-7660.2016.5) and the Russian Foundation for Basic Research (no. 16-34-00638).

Keywords: *Trapezoideus*, *Lamellidens*, taxonomy, COI, 28S, 16S

THE AUSTRALIAN FRESHWATER MUSSELS *HYRIDELLA GLENELGENSIS* AND *H. NARRACANENSIS* (UNIONIDA: HYRIIDAE): TAXONOMY, DISTRIBUTION AND CONSERVATION STATUS

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Hyridella glenelgensis (Dennant, 1898) occurs in south- western Victoria, within the range of *H. narracanensis* (Cotton & Gabriel, 1932) in coastal Victoria and parts of South Australia and Tasmania. Both species favour small- stream habitats. They are of similar size and appearance, with conspicuous umbonal sculpture, but in *H. glenelgensis* (and not *H. narracanensis*) there nominally is sculpture also on the disc. Other work has shown that the disc sculpture varies and may even be absent, suggesting that shell morphology is not always a reliable diagnostic character. We report new analyses based on mtDNA and allozymes, designed to investigate the genetic structure between these two taxa. Analyses of variation in allozymes and fragments of the protein-coding genes cytochrome oxidase subunit I (COI) and 16S rRNA were concordant and showed negligible separation between *H. glenelgensis* and populations of *H. narracanensis* from Tasmania and eastern Victoria (Yarra, Latrobe and South Gippsland River basins). However, allozyme patterns for *H. narracanensis* from rivers in western Victoria and South Australia were distinct exhibiting 2 (possibly 3) fixed allele differences from 53 alleles that were tested. We conclude that *H. narracanensis* as currently defined is comprised of two separate taxa: a morphologically variable, geographically disjunct taxon that includes *H. glenelgensis*, which should be named *H. glenelgensis* by priority, and an undescribed taxon from western Victoria and South Australia. The two taxa differ subtly in shell morphology; *H. glenelgensis* have darker, slightly more robust and elongate shells than the undescribed taxon. Morphological analyses are required to discriminate between the taxa. The undescribed taxon should be considered endangered or critically endangered owing to its restricted distribution in a small number of perennially flowing streams in a dry, western district volcanic plain. The inclusion of the Glenelg River population of *H. glenelgensis* with several additional populations may warrant a downgrading of its IUCN status.

Keywords: Hyriidae, systematics, COI, 16S rRNA, allozymes, threatened species

PHYLOGEOGRAPHY AND GENETIC STRUCTURE OF TWO FRESHWATER MUSSEL SPECIES (BIVALVIA: UNIONIDAE) ALONG HYPOTHESIZED POST-GLACIAL DISPERSAL ROUTES INTO THE LAURENTIAN GREAT LAKES

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Understanding genetic diversity of imperiled freshwater mussel species across large spatial scales is necessary for developing appropriate conservation strategies. Genetic data is important for investigating population connectivity, uniqueness (e.g., Evolutionarily Significant Units), and testing biogeographic hypotheses. Mitochondrial sequences and microsatellite loci were used to analyze the phylogeography of two common and widespread unionid species (*Lampsilis cardium* and *Lasmigona costata*) from the Great Lakes and the historically connected Wabash, Illinois, and Wisconsin river drainages; which may have acted as conduits for mussels from refugia south of the Pleistocene glacial maximum. Approximately 30 individuals of each species were collected 17 sampling locations with a mantle clip being removed from each specimen for genetic analysis. Using standard methods, a fragment of the mitochondrial gene COI was sequenced and a suite of microsatellite loci were genotyped. Using mitochondrial DNA haplotype data and microsatellite allele frequencies, multiple analyses suggest two distinct genetic populations for both *Lam. cardium* and *Las. costata*. A total of seven hypothesized post-glacial dispersal scenarios were compared using an Akaike Information Criterion to test the various models of isolation-by-distance. For both *Lam. cardium* and *Las. costata,* evidence was strongest for multiple post-glacial dispersal routes into the Great Lakes. Ten of the putative *Lam. cardium* haplotypes found in the Maumee (Great Lakes) and Wabash (Ohio River) drainages were revealed to be more similar to *Lampsilis ovata* sequences available on GenBank rather than *Lam. cardium*. Multiple assignment tests using microsatellite allele frequencies were conducted to determine if *Lam. cardium* and *Lam. ovata* are interbreeding. Assignment tests failed to accurately classify individuals to their respective species, suggesting *Lam. cardium* and *Lam. ovata* in this region interbreed freely.

Keywords: freshwater mussels, mtDNA, microsatellites, glacial refugia, population genetics

UNITAS MALACOLOGICA Grant Recipients

LIVING *MARGARITIFERA AURICULARIA* (SPENGLER, 1793) IN ORONTES RIVER BASIN AND AN INTEGRATIVE REVISION OF TAXONOMIC STATUS OF ENDEMIC *M. HOMSENSIS* (LEA, 1865) (BIVALVIA: MARGARITIFERIDAE)

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Since the *Margaritifera marrocana* and *Margaritifera laosensis* were rediscovered *Margaritifera homsensis* is the only pearl mussel species which is known based on shells that were collected in the past solely and deposited in mollusk collections of natural history museums. We found one live specimen of Margaritiferidae in the Karasu River, upper Orontes basin, Turkey. The mussel was buried in silty-sandy substrate beneath shrub. Numerous of fragmented empty shells were collected along riversides at this section of the river. The analysis of the COI gene sequence reveals that the pearl mussel from Karasu river actually belongs to *M. auricularia* (*p*-distance is 1.2%). On the other hand, analysis of substitutions in 18S rDNA and D3 expansion segment of 28S rDNA nuclear genes sequences indicates distinct taxonomic position of the specimen. The 18S gene contains four substitutions per more than 1700 nucleotides pairs. Extremely slow evolving and short D3 expansion segment of 28S contains one substitution per 305 nucleotides pairs. Main conchological features – shell shape, teeth morphology, mantle attachment scars – of the live specimen have not differences with morphology of *M. homsensis* or *M. auricularia*. The analysis of DNA data and morphological patterns shows that the live specimen of pearl mussel from lower Orontes could be considered as a subspecies of *M. auricularia*, *i.e.*, *M. auricularia homsensis*. This suggestion is confirmed based on study of the shell morphology of museum samples, which were labeled as *M. homsensis*, and empty shells that we collected from riversides of Karasu River. Our finding shows that *M. auricularia* is not endemic of Iberian Peninsula and distribution of the species is wider. This study was supported by the Federal Agency for Scientific Organizations (no. 0410-2014-0028) by grants from the President of Russia (nos. MK-4735.2015.4 and MD-7660.2016.5) and the Russian Foundation for Basic Research (no.16-34-60152).

Keywords: pearl mussel, integrative taxonomy, Middle East, morphology

INCIPIENT HYBRID SPECIATION OF DOOR SNAILS IN PREVIOUSLY GLACIATED AREAS IN THE CAUCASUS

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Homoploid hybrid speciation, speciation by hybridization without a change in chromosome number, may be the result of an encounter of closely related species in a habitat that is different from that usually occupied by these species. In the northwestern Caucasus the land snail species *Micropontica caucasica* and *M. circassica* form two distinct entities with little admixture at low and intermediate altitudes. However, at higher altitudes in the Lagonaki plateau, which were repeatedly glaciated, *Micropontica* populations with intermediate characters occur. Admixture analyses based on AFLP data demonstrated that the populations from the Lagonaki plateau are homoploid hybrids that now form a cluster separate from the parental species. The Lagonaki populations are characterized by a mtDNA haplotype clade that has been found in the parental species only once. The fixation of this haplotype clade in most hybrid populations suggests that these haplotypes are better adapted to the cooler conditions in high altitude habitats and have replaced the haplotypes of the parental species in a selective sweep. The fixation of a presumably adaptive mitochondrial haplotype clade in the Lagonaki populations is an important step towards speciation under the differential fitness species concept.

Keywords: AFLP, Caucasus, Clausiliidae hybridization, phylogeography, Pleistocene, speciation

THE LAST GLACIAL TO HOLOCENE HISTORY OF *HELIX POMATIA* IN CENTRAL EUROPE

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Helix pomatia is the largest and one of the most common land snails in Central Europe. Many fossil records show that *H. pomatia* is a typical member of interglacial land snail faunas, known form the region from several consecutive interglacials. However, it remains unknown where *H. pomatia* survived the cold periods. The species has been vaguely considered southeastern European, recently refugia located in northern Italy were proposed. Thanks to a rich fossil record, unparalleled elsewhere, the Czech Republic and Slovakia offer the possibility to study the timeline of the postglacial colonization by this species. The published data indicate surprisingly early postglacial appearance of *H. pomatia* in the Czech Republic, suggesting glacial refugia located nearby rather than in southern Europe. To reconstruct the time-line of the postglacial expansion of *H. pomatia* in Central Europe, we collected all available fossil data from the two countries and using radiocarbon dating of shell fragments we critically revised the oldest postglacial findings of the species. We also used mitochondrial markers to explore the geographic distribution of its genetic variability and locate the potential sources of the postglacial recolonization of the central Europe. In our contribution, we discuss how far north the species could have survived the Last Glacial Maximum and from where it spread postglacially. We argue that the effects of climatic changes on the distribution of snail species depend heavily on local topography and geology.

Keywords: *Helix pomatia*, Holocene, postglacial expansion, radiocarbon dating, phylogeography

LYMNAEID SNAILS FROM GEOTHERMAL SPRINGS ACROSS NORTH EURASIA: ENDEMIC SPECIES OR ECOTYPES OF WIDESPREAD TAXA?

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The molecular ecology and evolution of gastropods that inhabit geothermal streams and springs of Northern Eurasia are poorly known. In the present study, we examined several endemic species of the family Lymnaeidae described from geothermal springs located in the southern parts of Eastern Siberia and the Russian Far East. Four local endemic lymnaeid species have been known from hot springs of Kamchatka Peninsula and two local taxa were described from thermal springs of the Lake Baikal Region (Kruglov, 2005). The alleged species status of these endemics has been re-assessed by means of the integrative approach combining the molecular taxonomic methods with the traditional methods based on shell and soft body morphology. The phylogenetic reconstructions were made by using both mitochondrial (COI) and nuclear (ITS2) DNA markers. We used the topotypic samples of these species as well as specimens sampled from other sites situated around geothermal areas. The results show that these endemic species are nothing but synonyms of two widespread taxa, *Radix auricularia* (Linnaeus, 1758) and *Ladislavella catascopium tumrokensis* (Kruglov and Starobogatov, 1985). However, the geothermal populations examined represent their intraspecific ecological morphs (ecotypes) adapted to living in thermal springs. This study was supported by grants from the President of Russia (nos. MD-7660.2016.5) and the Russian Foundation for Basic Research (nos. 14-04-98801_sever, 15-04-05638_a, 16-05-00854_a).

Keywords: freshwater gastropods, Lymnaeidae, *Radix*, geothermal springs, integrative taxonomy, phylogenetic analysis, comparative morphology, North Eurasia

DEALING WITH PERMANENT IMPERMANENCE: THE ECOLOGY AND PHYSIOLOGY OF ENDEMIC SPRING SNAILS IN AUSTRALIA'S DESERT SPRINGS

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Arid zone springs across the globe provide "islands" of hospitable wetland in a "sea" of aridity that host diverse radiations of aquatic gastropods from a range of families. The Australian arid zone is renowned for its water impermanence and scarcity, yet springs in this region host large radiations of gastropods from three primarily rainforest and creek-dwelling families. I will discuss how so many species of seemingly "misplaced" aquatic snails have found themselves in the desert, and describe their ecological and physiological adaptations for persisting in one of the worlds driest and hottest regions. Snails in Australia's desert springs present a model taxon for demonstrating the importance of springs as wet refugia in a drying continent, and an elegant example of how isolation and selection, over considerable time, can create unparalleled diversity (and some surprising convergences). Each species occupying this system has specific behavioural and physiological adaptations that influence how it persists in such a harsh landscape. This insight, in turn, helps us understand the ecology of this system and highlights the importance of maintaining the functional stability of springs at a national scale in the face of ever-increasing threats to their ground-water source.

MALACOLOGICAL SOCIETY OF LONDON Grant Recipients

TEMPORAL VARIABILITY IN HETEROBRANCH (GASTROPODA: HETEROBRANCHIA) SEA SLUG ASSEMBLAGES ON THREE INTERTIDAL ROCKY REEFS OF THE SOLITARY ISLANDS MARINE PARK, NEW SOUTH WALES

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Heterobranch sea slugs are known for their high species diversity, spatial patchiness and ephemerality. These characteristics are likely to have contributed to the relative paucity of studies into community dynamics for this group. Earlier quantitative work on sea slug assemblages on rocky shores suggested little temporal variability over annual and seasonal scales: however, similar studies have not been performed in Australia. In this study, we explored temporal variation at three adjacent rocky headlands in the Australian subtropics at monthly intervals over a 13-month period. Two hour visual surveys were carried out by snorkeling during which all sea slugs were recorded. Analysis using a range of multivariate routines revealed that, despite the strong differences in assemblages among sites, there was significant seasonal periodicity overall as well as at each site. Seasonal patterns were also evident when species data were aggregated into functional feeding groups. Among the dominant species, seasonal peaks in abundance were often followed by large population reductions. While some species maintained a year- round presence, albeit in lower numbers, the absence of others in winter months may reflect seasonal reduction in food availability. These results highlight the strong bottom-up control exerted by food resource availability and thus the practical challenges associated with using this group for environmental monitoring.

UNITAS MALACOLOGICA Grant Recipients

MOLECULAR PHYLOGENY OF THE ELLOBIIDAE (GASTROPODA: PANPULMONATA) SUPPORTS INDEPENDENT TERRESTRIAL INVASIONS

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Gastropods of the family Ellobiidae are an interesting group in which to study transitions from intertidal to terrestrial realms. However, the phylogenetic relationships within this family still lack resolution. We present a phylogenetic hypothesis of the Ellobiidae based on Bayesian and maximum likelihood phylograms. We used nuclear (18S, 28S, H3) and mitochondrial (16S, 12S, COI) data, increasing the numbers of markers and data, and making this the most comprehensive phylogenetic study of the family to date. Our results support phylogenetic hypotheses derived from morphological data, and provide a supported framework to evaluate the internal relationships within Ellobiidae. The resulting phylogenetic trees support the previous hypothesis that the Ellobiidae are monophyletic only if the Trimusculinae (*Otina*, *Smeagol* and *Trimusculus*) are considered part of this family. In addition, we found that the Carychiinae, Ellobiinae and Pythiinae are reciprocally monophyletic and closely related, with the Carychiinae as sister group to Ellobiinae. Relationships within Melampodinae and Pedipedinae and their phylogenetic positions remain unresolved. Land invasion by the Ellobiidae occurred independently in Carychiinae and Pythia during different geological times (Mesozoic and Cenozoic, respectively). Diversification in the family does not appear to be related to past climate and biotic changes, neither the Cretaceous-Paleogene boundary nor the lowering of the sea level in the Oligocene.

Keywords: Carychiinae, Pythiinae, terrestrial invasion, realm transitions, molecular clock, topology tests

UNITAS MALACOLOGICA Grant Recipients

MOLECULAR PHYLOGENY AND FREQUENT PARALLEL EVOLUTION OF JAPANESE CLAUSILIID LAND SNAILS

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Clausiliidae is one of the most diversified land snail families in Japanese fauna. More than 200 species-level taxa have been described from Japan and approximately 40 generic taxa were proposed for them. Supra-specific classification of Japanese clausiliids was based mainly on the morphology of the shell, in particular morphology of the internal lamellae, plicae, and clausilium. Several different systems of Japanese clausiliids have been proposed to date. Although these systems are based on almost the same morphological characters, they differ largely in the definition of each genus, the subgeneric ranking, and the species composition of each genus. We carried out molecular phylogenetic analysis of Japanese clausiliids and Taiwanese related taxa using nuclear internal transcribed spacer and mitochondrial DNA sequences. This is the first molecular phylogenetic study of phaedusine clausiliids based on comprehensive taxonomic sampling which covers all generic taxa proposed for Japanese and Taiwanese clausiliids. Surprisingly, our molecular phylogeny is largely discordant with all the systems proposed to date. Almost all the traditional genera or subgenera are recovered as non-monophyletic in the molecular phylogeny. On the other hand, some tree topologies recovered in our analysis are concordant with the biogeography, rather than the morphology. It is thus strongly suggested that frequent parallel evolution has occurred in various morphological and ecological characters in Japanese clausiliids.

Keywords: Clausiliidae, molecular phylogeny, parallel evolution, taxonomy, biogeography

MALACOLOGICAL SOCIETY OF JAPAN Grant Recipients

COMPARATIVE PHYLOGEOGRAPHY IN LITTORAL MOLLUSKS FROM SOUTHEASTERN PACIFIC OCEAN: THE IMPORTANCE OF LARVAL DEVELOPMENT STRATEGIES IN THEIR EVOLUTIONARY HISTORY

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Contrasting phylogeographic history in co-distributed species suggests being consequence of different life history strategies. Marine species with planktonic and lecithotrophic larval development have shown different spatial structure pattern, which even suggests have experienced differently the Pleistocene glaciations. In this context the aim of this study is to evaluate the effects of larval development type in the evolutionary history of mollusks species co-distributed throughout the Southeastern Pacific Ocean. The genetic and phylogeographical analyses with the mitochondrial gene COI evidenced that the planktonic species *Siphonaria lessoni* showed high genetic diversity and complex genealogy of haplotypes which contrasted with simpler genealogy and less diversity of lecithotrophic species *Chiton magnificus* and *Fissurella picta*. All species showed a genetic isolation by distance, but differing in that the lecithotrophic species showed greater genetic isolation by shortest distances than the planktonic species. All species showed a genetic structure pattern mostly between north localities and the south, and they showed two genetic populations. The three species showed a sign of population growth, but differ on the date of beginning of the expansion.

Keywords: phylogeography, larval development, mollusks, southeastern Pacific Ocean

PHYLOGEOGRAPHIC ANALYSES REVEAL TRANSPONTIC LONG DISTANCE DISPERSAL IN LAND SNAILS BELONGING TO THE *CAUCASOTACHEA ATROLABIATA* COMPLEX (GASTROPODA: HELICIDAE)

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We investigated the phylogeography and population structure of land snails belonging to the *Caucasotachea atrolabiata* complex in the Caucasus region to obtain a better understanding of diversification processes in this biodiversity hotspot. So far the complex has been classified into three species, *C. atrolabiata* from the north-western Caucasus, *C. calligera* from Transcaucasia and *C. intercœdens* from the eastern Pontus Mountains. Analyses of AFLP data showed that the complex consists of two population clusters corresponding to *C. atrolabiata* and *C. calligera*. The populations assigned to *C. intercedens* in fact represent hybrids consisting of different proportions of the genomes of *C. atrolabiata* and *C. calligera*. The presence of mitochondrial *C. atrolabiata* haplotypes in Turkey can only be explained by passive dispersal across the Black Sea. There is a broad transition zone between *C. atrolabiata* and *C. calligera* in the Pontic Mountains and a second transition zone in Abkhazia. Because of the evidence for gene flow, we suggest to classify them as subspecies. The distribution of *C. atrolabiata* and additional cases of land snails with disjunct Transpontic distribution patterns cannot be ascribed to a common cause, but are results of long-distance dispersal events at different times.

Keywords: Caucasus, Helicoidea, biogeography, hybridization, refugia

CHECKLIST AND EVOLUTIONARY ORIGIN OF THE HYDROBIIDAE (CAENOGASTROPODA: TRUNCATELLOIDEA) FROM THE SOUTHWESTERN MEDITERRANEAN REGION (MOROCCO AND IBERIA)

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The Mediterranean region has been described as a biodiversity hotspot for non-marine gastropods. One of the groups that contribute the most to this species richness is the family Hydrobiidae Stimpson, 1865, whose overall distribution mainly ranges from Neartic to Palearic ecozone. Within this latter region, most of the hydrobiid species are found in European aquatic systems, being the knowledge of the diversity of North African hydrobiids far from complete. In spite of numerous descriptive studies of European hydrobiids, little is known about their origin and the processes that shape their current distribution patterns. Since the western-Mediterranean Gibraltar Strait may have served as a landbridge/barrier between other African and European freshwater fauna, the relationships between Ibero-Balearic and Moroccan hydrobiid species are the subject of our study. Recent field surveys and publications confirm that Hydrobiidae is largely distributed across Morocco and the Ibero-Balearic region, with 23 and 82 species respectively, occurring from headwater springs to brackish estuaries. So far, our morphological descriptions, in combination with preliminary phylogenetic analyses based on mitochondrial sequences, have revealed: (1) that the semi-brackish genera *Mercuria* and *Pseudamnicola* (widely distributed in western Mediterranean territories, including the Iberian Peninsula), are the most species rich in Morocco, with 5 and 7 species, respectively. (2) the presence in Morocco of three new species belonging to the Iberian springsnail genus *Corrosella* and (3) the closely sister relationships between the southern Iberia and Moroccan *Corrosella* species and between the Majorcan (Balearic islands) and Moroccan *Pseudamnicola* species. Our findings underscore the common biogeographic origin between the south Iberian and Moroccan *Corrosella* spring snails, which suggests the implication of the closure/opening of the Gibraltar Strait as zoogeographical barrier. Conversely, transmarine dispersal via water birds may explain the relationships among the *Pseudamnicola* species, as previously reported for other brackish hydrobiids of other regions.

Keywords: biogeography, phylogeny, anatomy, spring snails, Morocco.

UNITAS MALACOLOGICA Grant Recipients

COLOUR POLYMORPHS OF GIANT AFRICAN SNAIL *ACHATINA FULICA* (BOWDICH, 1822) IN SOUTH INDIA: A COMPARATIVE STUDY USING MITOCHONDRIAL 16S R RNA GENE

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The Giant African Snail *Achatina fulica* (Bowdich, 1822) native of East Africa is one of the worst 100 invasive species in the world. The snail was introduced to India from Mauritius in 1847 and spread into many parts. In South India, the snails were first reported around 1900s. We had collected samples of *Achatina fulica* from different localities in South India to identify invasion routes using molecular markers. Only 18 haplotypes of this species were recorded globally and India harbours only two haplotypes C and P. The haplotype C is the most common haplotype in Mauritius and postulated as the source since the haplotype P is a C related haplotype found only in India. We could able to distinguish three distinct body colouration among the Giant African Snails collected from South India *viz.*, black, grey and white. The colour polymorphs are seen in equal proportion with each other. Land snails are known to exhibit polymorphism and African Achatinidae family is remarkable in body colour polymorphism with the existence of contrasting colours ranging from black to white. In this study, we used partial sequence of 16s r RNA gene to identify the haplotypes in South India including the three different colour polymorphs. We had identified a total of 10 new haplotypes along with C and P. The three different colour polymorphs are turned out to be new and different haplotypes. The haplotype P exhibits two different body colors - black and grey. The white-bodied snail is a distinct haplotype and could be possibly introduced from Africa through a different source. Our study shows the existence of body colour polymorphism in the Giant African Snails. The identification of new haplotypes and polymorphs will give insights into the evolution in introduced ranges and fill the gaps in tracking the invasive routes.

Keywords: body colour, invasive species, haplotype, polymorphism

REVISED CLASSIFICATION, NOMENCLATOR AND TYPIFICATION OF GASTROPOD FAMILIES

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We present a second, updated and expanded, version of the "Classification and Nomenclator of Gastropod Families", published a little over10 years ago. The past decade was marked by the profound and broad-ranging impact of the molecular revolution in gastropod systematics, before 2005 limited to selected branches of the gastropod tree, and with limited taxon sampling. A second source of changes in the classification has been the ongoing discovery of brand new taxa, Recent and fossil, necessitating the description of new families. About 2,570 names at the rank of tribe, subfamily, family and superfamily have been proposed for Recent and fossil gastropods. All names are listed in a nomenclator giving full reference, date of publication, and their nomenclatural availability and validity under the International Code of Zoological Nomenclature. Another 765 names, established for categories above the family-group, and not regulated by the Code, are listed separately. Although molecular phylogenies are greatly improving the robustness of the classification, ongoing studies of well-preserved fossil gastropods are still essential to our perception of the evolutionary history of this clade in deep time. In all, the classification recognizes as valid a total of 724 families, of which 248 are known exclusively as fossils and 476 occur in the Recent with or without a fossil record. The present work differs from the 2005 work in a couple of features. In the nomenclator, we have now included the full typification of all family-group names, i.e. we give the type species of the type genus - and not just the type genus. The 2005 classification avoided ranks above superfamily; the development and success of online taxonomic authority lists demonstrate that the use of additional ranks - suborder, order, subclass - is favored by many users, and our classification is thus now fully ranked.

Keywords: recent and fossil gastropods, morphological and molecular characters, type genus, type species, phylogeny-based classification

INVASIVE MOLLUSCAN SPECIES: A CONTINUING THREAT TO THE PHILIPPINE ENVIRONMENT

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Philippines is one of the mega-diverse countries owing to its strategic location within the coral triangle. Unfortunately, it is also facing the greatest threats to biodiversity including climate and non-climate related factors that include: climate change impacts, habitat degradation and transformation, and introduction of exotic species that eventually become invasive. This makes Philippines the hottest of the hotspots and ranking 116th (among the poorest) out of 140 countries surveyed globally. Problems related to biological invasion are often associated to its serious impact not only to biological diversity but also to agricultural economic losses, human health hazards, pollution and algal blooms due to pesticide usage among other things. Of the 148 invasive species recorded in the country, five are molluscan species namely *Pomacea canaliculata* (Golden Apple Snail), *Pomacea insularum* (Channeled Apple Snail), *Achatina fulica* (African Giant Snail), *Bellamya chinensis* (Chinese Mystery Snail), and *Perna viridis* (green mussel). *Pomacea* has been persistent problem since its introduction to the country in 1980's. Recently, the blue mussel *Mytella charuanna* has been observed spreading in the estuaries in the Province of Pangasinan. This paper will be case study of the history, impact, species traits, status and probable management approaches of these six molluscan invasive species in the Philippines to address the fundamental issues concerning biological invasion.

Keywords: invasive species, biodiversity, Philippines, snails, mussels

SEARCH FOR SNAIL-VECTORS OF AN ENDEMIC *SCHISTOSOMA* SPECIES IN HUNGARY

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The *Schistosoma turkestanicum* blood-fluke, formerly known as *Orientobilharzia turkestanica*, was discovered in Hungary, Central-Europe, as an endemic species. This widespread trematode is rather frequent in different ungulate host species in middle belt of Asia from Korea to Turkey but it only lives in red deer (*Cervus elaphus*) in its European area. Although the adult flukes are not able to colonize in the human body, the cercariae of this parasite frequently cause dermatitis. Therefore, *S. turkestanicum* has remarkable zoonotic significance in countries where infected domestic animals (i. e. water buffaloes) are used for plowing paddy fields because its larvae often encounter with people who work on artificially flooded areas. The Hungarian endemic focus of the fluke is a semi-natural swamp forest, where mainly fishermen and tourists experienced the cercarial dermatitis caused by its larvae. Till now only one freshwater snail species (*Radix auricularia*) had been detected as intermediate host for the Hungarian population of *S. turkestanicum*, but 5 other lymnaeid snails living around the swamps might be also involved as hosts. However, despite the extensive research we found *Schistosoma* infected ones among investigated specimens of *R. auricularia* only and none among *Radix balthica, Radix labiata, Galba truncatula, Stagnicola palustris, Lymnaea stagnalis* snails. Interestingly, *R. auricularia* is a rather rare species all around the endemic area of European *S. turkestanicum* population, while the prevalence of schistosome infection of red deer is above 50% in that area. This contradiction may be solved in consequence of habit of deer to walk long distances and stay long time in shallow lakes where the intermediate hosts of *S. turkestanica* occur. Unfortunately, populations of *R. auricularia* are hardly detectable because snails live in the floating seaweed usually far away from lakeshore. We supposed that the cercarial emission into the water reveal the places of infected *R. auricularia* snails – or other intermediate host species – therefore, we tried to find swimming cercariae in lakes and canals. Floating microscopic slides, treated with unsaturated fatty acids had been used to trap schistosome cercariae but no trematode larvae were found on them. Although this method of trapping blood-fluke cercariae was found effective by others for human schistosomes, we could not catch a *S. turkestanicum* larva with this method so far. The lifespan of *R. auricularia* in nature looks like a year as adult snails never survive winter. Young snails can be found in lakes usually in fall and spring. Temporary lakes that almost regularly dry up in summer have to be repopulated by this snail again and again from other permanent water bodies, which keep constant populations. As most temporary lakes are isolated from each other by forests or reed, freshwater snails need to be mechanically carried to reach these lakesfrom time to time. We suppose that young snails either travel by floods or attach to fur coat of wading deer.

In order to investigate the survival and growth of *R. auricularia* snails we tried to rear this species in laboratory. The snail is extremely sensitive species for quality of water and food. So far we have not succeeded in propagating it but we could grow the young to adults. As far as we know, nobody could sustain this species under artificial conditions. Our goal is to select a laboratory strain of *R. auricularia*.

EFFECTS OF HYPOBRANCHIAL GLANDS AND SQUID INK PROTEIN EXTRACTS FROM THREE MEDITERRANEAN MOLLUSKS ON HUMAN GLIOBLASTOMA U87AND HELA CELL LINE EPITHELIA CERVIX CARCINOMA

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The aim of this study is to evaluate the effects of tree Mediterranean mollusks co-product protein extracts on Human Glioblastoma U87 and HeLa cell line epithelia cervix carcinoma. Hypobranchial gland proteins (HGPE) are extracted from the gastropods *Hexaplex trunculus* (HT) and *Bolinus brandaris* (BB). The squid ink proteins are extracted from the cephalopod *Sepia officinalis*. Proteins are extracted by acetone precipitation. Cell viability is measured using MTT assay. Cell adhesion and migration are established using fibrinogen as matrix. Both HGPE HT and BB are non-cytotoxic substances until 20 mg/mL. They decrease by more than 50% at 25 mg/mL. All HGPE significantly impair migration of U87 cells towards fibrinogen in a concentration dependent manner. Concentrations for 50% inhibition (IC_{50}) of male and female HGPE HT are of 3.7 and 4.0 mg/mL respectively. They are of 4.2 and 5.8 mg/mL for male and female HGPE BB respectively. Squid ink proteins block significantly the migration of U87 to fibrinogen in a dose dependent manner. The IC_{50} is about 9.2 µg /mL. This supernatant inhibits also cell adhesion U87 on various types of matrices. Inhibitions are 60% fibrinogen, 25% fibronectin. Similarly HGPE of both HT *a*nd BB inhibit Hela cell adhesion to fibrinogen at 50 mg/mL. Male and female inhibitions significantly impair at 10 mg/mL and continue until 20mg/mL. Squid ink proteins inhibit also HeL*a* cell adhesion. Inhibition significantly impairs at 10 mg/mL and continues until 30mg/mL: HGPE HT, HGPE BB and Squid ink proteins may have the potential to serve as a model for future anticancer-drugs development.

Keywords: Hypobranchial Gland Proteins, *Hexaplex trunculus*, *Bolinus brandaris*, squid ink proteins, *Sepia officinalis*, Glioblastoma U87, HeLa cell, viability, adhesion and migration

DIET AND VENOM EVOLUTION IN CONE SNAILS

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Although diet is believed to be a major factor underlying the evolution of venom, few comparative studies examine both venom composition and diet across a radiation of venomous species. Cone snails within the family, Conidae, comprise more than 700 species of carnivorous marine snails that capture their prey by using a cocktail of venomous neurotoxins (conotoxins or conopeptides). Using venom duct transcriptome sequencing and comparative phylogenetic methods, we test the hypotheses that venom composition should be shaped by (a) prey taxonomic class (i.e., worms, molluscs, or fish) and (b) dietary breadth. In contrast with the dominant paradigm for interpreting Conidae venom evolution, we found that prey taxonomic class did not predict venom composition patterns among species. Our results suggest that cone snails have either evolved species-specific expression patterns likely as a consequence of the rapid evolution of conotoxin genes, or that traditional means of categorizing prey type and conotoxins (i.e., by gene superfamily) do not accurately encapsulate evolutionary dynamics between diet and venom composition. We also found a significant positive relationship between dietary breadth and measures of conotoxin complexity. These results confirm patterns predicted by Van Valen's niche variation hypothesis (1965) and suggest that species with wider dietary breadth utilize a greater number of venom genes for prey capture. Whether this increased gene diversity confers an increased capacity for evolutionary change remains to be tested. Overall, our results corroborate the key role of diet in influencing patterns of venom evolution in cone snails and other venomous radiations.

Keywords: phylogenetics, comparative biology, venom duct transcriptome

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REMARKABLE EXTANT SPECIES DIVERSITY AND CONSERVATION OF LAND SNAIL FAUNA OF PALAU ISLANDS: THE LAST PARADISE OF ENDEMIC LAND SNAILS IN PACIFIC ISLANDS.

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The Palau islands (Republic of Palau), which comprises of more than 500 islands, are oceanic islands locating c.a. 800 km east of the Philippines. Rundell (2010) reported 117 land snail species from Palau and highlighted the need for conservation attention. However, the land snail fauna of Palau is not yet fully studied. I carried out faunal surveys of the islands from 2003 to 2014. As a result of intensive surveys on more than 200 localities in the islands, a total of 170 land snails species were found. 155 species are endemic and c.a. 40 % of them are undescribed species. The high level of species diversity is attributable to endemic radiation of Diplommatinidae, Trochomorphidae, Assimineidae, and Endodontidae. Almost all the endemic species are collected alive or collected as freshly dead specimens. It is amazing that so many endemic species are still extant in Palau, because most of endemic land snails are already extinct or seriously endangered in other area of Pacific islands. It is also notable that land snails of some endangered families, such as Endodontidae and Partulidae, are not rare in some localities in Palau. Palau is the last paradise of Pacific land snails where the diversified species community is still extant. On the other hand, several species are probably extinct within the last 60 years, and environmental destruction is taken place and/or ongoing in some islands. Possible cause for the survival of Palauan land snails and the threatening factors will be discussed.

UNDERSTANDING COMPLEX MOTOR PATTERNS IN THE OCTOPUS MUSCULAR HYDROSTAT: ARM 'SLAPS' AND 'REACHES'

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Octopuses can produce a variety of flexible arm movement patterns using principles that govern muscular hydrostats. Bending and stiffening are two consequences of the key principle that muscular hydrostats maintain constant volume. Various degrees of static localized bending and stiffening of the arm are involved in the most stereotyped movement patterns - 'reach' and 'fetch'. Gutfreund et al. (1996) described reaching as extension of the arm by stiffening and propagating a bend to the tip. Fetching uses quasi-articulated structures to combine localized stiffening with multiple bend points that behave like temporary joints (Sumbre et al., 2006). These movement patterns are examples of what Flash and Hochner (2005) call 'motor primitives' which may be combined to make up more complex movements. We are interested in understanding the relationship between static bending and stiffening in these complex dynamic movement patterns. We investigated two patterns in two species of octopus. One pattern in the octopus *Abdopus sp*. involves the octopus's reaction toward a goby fish by using an 'arm slap', as first described by Mather (1992). The second pattern ('dorsal arm reach') involves whole arm stiffening of one of the anterior arms as a means of catching prey in the Larger Pacific Striped Octopus (Caldwell, Ross, Rodaniche, and Huffard, 2015). Both patterns involve variations in bending and stiffness propagation, resulting in rotational change in the arm and/or the presence of a traveling bend along the arm. Kinematic analysis of the data will show how this unique muscle system is able to produce different patterns for different behaviors using only a few simple principles.

Keywords: octopus, muscular hydrostat, locomotion, motor primitives

REVIEWING THE EASIN CATALOGUE OF ALIEN TERRESTRIAL GASTROPODS IN EUROPE

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The "European Alien Species Information Network" (EASIN; http://easin.jrc.ec.europa.eu/) is an initiative of the Joint Research Centre of the European Community that was launched in September 2012. Its goal is "to facilitate the exploration of alien species information from distributed sources and to assist the implementation of European policies on biological invasions". In this context an initial catalogue of alien terrestrial gastropods in Europe had to be revised. This catalogue was based on a compilation of data derived from 45 online databases. As such, it listed 168 species. However, after revision it appeared that: (1) 6 of these species were not gastropods (3 plants, 2 fungi and 1 moth), (2) 15 species were brackish- or freshwater snails, and (3) 19 species were either misidentified terrestrial snails or were synonyms of other species in the list. Hence, only 128 of the initial 168 species (76%) were retained (with still 6 names being misspelled and 25 needing nomenclatural updating). Moreover, no less than 130 species had to be added to the list, and the work is still far from finished. Hence, currently the list comprises 258 species that at least in some parts of Europe are alien (on a total of 2000-2500 terrestrial gastropod species in Europe). This work illustrates the poor performance of many online databases on alien terrestrial gastropods and the need for more accurate data.

Keywords: alien species, databases, EASIN, Europe, terrestrial gastropods

MALACOFAUNA IN PRACHEENBURI PROVINCE, EASTERN THAILAND (MOLLUSCA: GASTROPODA; BIVALVIA)

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Survey of malacofauna in Pracheenburi Province, Eastern Thailand was investigated from limestone areas and freshwater habitats in 24 selected stations. A total of 2 classes, 10 orders, 22 families, 35 genera and 55 species were recorded. *Ferrissia* spp. is a new record in this study.

Keywords: land snails, freshwater mollusks, Pracheenburi Province, diversity, Thailand

EXAMINING FLASHING AS A SIGNAL IN *CTENOIDES ALES*, “DISCO” CLAMS

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The “disco” clam *Ctenoides ales* (Finlay, 1927) is known for its vivid flashing display which results from light-scattering silica nanospheres. We analysed three hypotheses; that the fitness value of the flashing was used in conspecific recruitment, as a phototactic prey lure, and/or as an aposematic predator display. Conspecific recruitment was tested by examining visual morphology and reactions to stimuli. The display was also tested as a phototactic prey lure for plankton. The flash rate (Hz) of *C. ales* increased significantly when presented with a food stimulus. To test if the flashing in turn induced planktonic phototaxis, plankton density was tested in two experiments; artificial clams with LED lights adhered to both valves (three treatments: LEDs off, on, or flashing) and a flashing playback trial utilizing a tablet display (two treatments: flashing and non-flashing). Plankton density in live *C. ales* was tested in situ using SCUBA in Bali, Indonesia (-8’13”, 114’65”). Samples were taken in high-light (flashing visible) and low-light (flashing not visible) settings. These three experiments did not show significant differences in plankton density between treatments. To test aposematism, predators were identified using video analysis, underwater observation, and dead valve collection. Valve damage type was linked to potential predators, and laboratory interactions were filmed when possible. Predator analyses are ongoing, including the study of potentially volatile sulfuric compounds present in the tissue of the clam.

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TOLERANCE AND RESPONSES OF THE FRESHWATER SNAIL *(THEODOXUS FLUVIATILIS)* TO INCREASING SALINITIES

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The snail *Theodoxus fluviatilis* (Gastropoda: Neritidae) is found in both brackish and freshwater habitats in northern Germany and has formed regional subgroups. These two lineages are closely related, and individuals of both are neither clearly distinguishable by shell size, shell patterning-due to the high variability within each lineage-nor by mitochondrial RNA markers (Bunje (2005), Mol Ecol 14:4323-4340). Despite the high degree of similarity, they differ in their tolerance to changing salinities. Animals of the brackish water lineage struggle when transferred into freshwater and freshwater animals die upon transfer to high salinities (21‰). The low survival of freshwater animals may be explained by a less well-developed ability to accumulate free amino acids (FAA) in their foot muscle as a means of cell volume regulation. This diverging ability between the lineages is associated with characteristic differences in protein expression that show both, lineage-specific (genetic) and environmentally induced (plasticity) expression patterns (Symanowski & Hildebrandt, 2010). To elucidate any responses of these animals to changing salinities, including tolerance limits and experimentally achievable range shifts in reaction norms of freshwater animals to hypertonic environments, individuals were collected at three freshwater sites and exposed to a 22-day transfer and acclimation regime. Survival rate, the amount of accumulated free amino acids as well as protein patterns were recorded and analysed for each individual and each treatment. A control group and 3 treatments of either slow acclimatising or radical transfers to higher salinities were compared. The results showed that range shifts in reaction norms can be achieved by stepwise acclimation of freshwater animals to higher salinities.

Keywords: osmotolerance, *Theodoxus fluviatilis*, physiological responses, range shift, phenotypic plasticity, genetic adaptation

EFFECT OF *MORINGA OLEIFERA* ON BIOCHEMICAL PARAMETERS AND HAEMAGGLUTINATION POTENTIAL OF GIANT AFRICAN LAND SNAIL (*ARCHACHATINA MARGINATA)*

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A study was conducted on the effect of *Moringa oleifera* on haemolymph biochemical parameters of giant African land snail (*Archachatina marginata).* Thirty-two snails (32) with weight range of 100-150g were used for this study. Eight snails (8) were subjected to each of the four treatments (Concentrate only, Concentrate +100g of *Moringa oleifera*, Concentrate +200g of *Moringa oleifera* and concentrate +300g of *Moringa oleifera*). Parameters monitored were: haemolymph Glucose, Total protein, Albumin, Cholesterol and Globulin after nine weeks of the experiment. Result showed that haemolymph Glucose, Albumin, Cholesterol and Globulin were not significantly affected ($P>0.05$) by the treatment. However, treatment effect was significant ($P<0.05$) for total protein. The result also showed that the concentrate with 300g of *Moringa oleifera* had better significant effect on total protein. This is an indication that building block for cells and tissues are been influenced by inclusion at this level. Result for haemagglutination potential further confirmed that inclusion of *Moringa* at this level (200 g/kg) and also at 300 g/kg gave consistent and higher haemagglutination titre which reveals the ability of these two levels to boost immunity of the animal. It was however recommended that inclusion of *Moringa oleifera* at 200 and 300 g/kg into snail feed will enhance snail survivability under intensive cage culture system.

HOW LONG ARE THEY DOWN THERE? THE FOSSIL RECORD OF NEOMPHALID AND PROVANNID GASTROPODS

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Neophalid and provannid gastropods are flagship taxa of deep-water hydrothermal vent communities. Both are endemic to chemosynthesis-based ecosystems where they commonly occur in masses. Several species cultivate chemosynthesizing bacteria as a main source of nutrition. For many years both groups were either considered to be ancient or, in contrast, very modern evolutionary. The intensive research on ancient hydrothermal vents, vertebrate/wood falls, and especially hydrocarbon seeps has revealed that they are old indeed. The oldest record of provannids is known from the Albian (113-100 Myr old) while oldest representative of neomphalids is known now from the Toarcian (183-174 Myr old). Both records are from ancient hydrocarbon seeps, which are relatively common in the fossil record. In contrast, the fossil record of hydrothermal vents is extremely scarce, however, one of the few known vent deposits from Cyprus (Turonian, 91 Myr old) yields numerous shells of pyritized provannids. The origin of the clade Neomphalida remains a mystery. It appears with *Retiskenea*-like species in the Early Jurassic and their ancestors are unknown. On the other hand Provannidae are probably paraphyletic with at least two distinct groups, which appeared already in the Cenomanian (100-94 Myr old). They form with non-seep Abyssochrysidae a clade Abyssochrysoidea. Most likely extinct Paskentanidae and Hokkaidoconchidae (both endemic to seeps and vents) also belong to this clade. The ancestors of entire group probably stem from Zygopleuroidea, which are an extinct clade highly diversified in the Mesozoic times.

Keywords: hydrothermal vents, hydrocarbon seeps, Gastropoda, Provannidae, Neomphalidae, fossil record

GENUS-SPECIFIC SYMBIOSIS OF THE ROVE BEETLE, *ZYRAS* SP. TO ITS LAND SNAIL HOST, *RYSSOTA* (GASTROPODA: HELICARIONIDAE)

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Coevolution between symbiotic organisms is an important mechanism to ensure the survival of species. In this study, the morphological, phylogenetic and behavioral relationship between the endemic land snail, *Ryssota* and its symbiotic rove beetle, *Zyras* from Mount Makiling, Luzon Island and Polilio Island, Philippines were analyzed. Using principal component analysis and geometric morphometrics, data showed that there was significant similarity between the *Zyras* sp. from the Mount Makiling and Polillo Island, while *R. otaheitana* (Makiling) and *R. uranus* (Polillo) were morphologically distinct from each other. Phylogenetic tree analysis based on cytochrome oxidase subunit I (COI) also revealed that *Zyras* sp. found in both locations possibly belong to the same species. However, phylogenetic trees based in COI for *Ryssota* revealed clear separation between the two species and across sampling sites (Makiling, Polillo, Albay and Marinduque). Feeding experiments further showed mucophagy and coprophagy behavior of *Zyras* on its *Ryssota* host. The present data demonstrated that association of the rove beetle, *Zyras* was not species-specific but rather genus-specific to *Ryssota*.

Keywords: land snail, rove beetle, coevolution, COI

LUITFRIED VON SALVINI-PLAWEN AS A SCHOLAR OF MALACOLOGY AND BEYOND – AND MY TEACHER

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Prof. Dr. Luitfried v. Salvini-Plawen (* June 1st 1939 in Vienna, Austria, † Oct. 22nd 2014 in Vienna) has been one of the most influential scientist concerning the phylogeny of Mollusca and invertebrates in general. His main focuses were the aplacophoran taxa Solenogastres and Caudofoveata, where he described about half of all solenogastres species up to now aside from many other studies. However, Luitfried also influenced the original and evolutionary history of Mollusca in general and of Gastropoda in particular, where is first recognized the common origin of Thiele´s Zeugobranchia and Trochacea to Vetigastropoda. In addition, he contributed to our knowledge of various interstitial taxa among the Gastropoda, but also within Cnidaria, Entoprocta (Kamptozoa), Priapulida or Holothurioidea. Luitfried´s papers and ideas on the “grand game of metazoan evolution” revived phylogenetics as a whole and helped to keep the discussion open in the times of the highly popular and seemingly granted “Archicoelomate Theory”. Moreover, his ideas on the acoelomate and non-segmented origin of Bilateria have been supported also by recent molecular data. All in all he published more than 150 papers, many of which are still regularly cited. Usually unknown in the malacological community, Luitfried also owned a degree (Magister) as a historian and had an education as a classic singer. I am myself indebted to Luitfried to introduce me into malacology and for many useful advices how to proceed in hypotheses on molluscan anatomy and phylogeny.

ON THE SOLENOGASTER *WIRENIA ARGENTEA*

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Wirenia argentea (Odhner 1921) is a solenogaster species commonly found at shelf depth along the European Atlantic coast. Specimens of this species were observed by Luitfried Salvini-Plawen during his trips to Norway in the early 1970s. Since then, several of Luitfried's (former) students have based descriptions of solenogaster morphological traits on the species and more recently it has become a model species for studies on solenogaster ontogeny and aplacophoran evolutionary relationships. Here, I sum up our current knowledge on the morphology and biology of this species and its closest relatives, including published results and yet unpublished findings. This presentation is dedicated to the memories of Luitfried Salvini-Plawen, and Amelie Scheltema, our highly valued and sorely missed teachers, mentors, and inspiring colleagues in all things aplacophoran.

EXPLORING SOLENOGASTER (MITO-)GENOMES

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Whole genome sequences provide a backbone for new approaches to elucidate origin and diversification of major clades in the animal kingdom, whose phylogenetic relationships are still controversially debated. Cost-efficiency of modern high-throughput sequencing technologies now allows for genome scale projects beyond model organisms. Available reference genomes for the phylum Mollusca are nevertheless still limited and data on major molluscan clades such as aplacophoran Solenogastres (also called Neomeniomorpha) is lacking. We assembled the first low-coverage genomes of two representatives of cavibelonid Solenogastres from the Antarctic deep sea via whole genome shotgun sequencing on an Illumina HighSeq 2500 platform. Here, we present an initial characterization of the comparably small (approximately 650 Mb) genomes and provide first comparative insights on genome structure. Current data on molluscan mitogenomes indicate convergent evolution of gene arrangements and show sensitivity to taxon sampling in phylogenetic analyses urging the need to supplement missing clades to further explore mitogenome evolution in molluscs. We thus additionally assembled the first mitochondrial genomes for Solenogastres from our datasets and analyze the gene arrangement in comparison to each other and to the currently available molluscan mitogenomes. These solenogaster reference (mito-) genomes will shed light on the evolutionary history of aplacophoran molluscs from a genomic perspective and allow for easier integration of this neglected clade in future phylogenomic analyses.

Keywords: Aplacophora, gene arrangement, phylogenomics

MONOPLACOPHORAN GENOME SHEDS LIGHT ON RELATIONSHIPS AMONG SHELLED MOLLUSCS

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Despite their diversity and importance, evolutionary relationships among the major lineages of Mollusca have long been debated. Recent studies provided the first largely well-resolved phylogeny for Mollusca, showing that there are two major clades: Aculifera (chitons and aplacophorans) and Conchifera (all other shelled molluscs). However, relationships among conchiferan taxa have been inconsistent among studies. Monoplacophora is traditionally viewed as the sister taxon of the rest of Conchifera. Nevertheless, analyses of datasets dominated by nuclear ribosomal genes recover Monoplacophora sister to Polyplacophora and the one phylogenomic study sampling this clade recovered it sister to Cephalopoda. We conducted phylogenomic analyses using deeply sequenced transcriptomes or genomes from all major lineages of Mollusca, including newly sequenced genomic data from *Laevipilina antarctica*. Whereas a partitioned maximum likelihood (ML) analysis recovered Monoplacophora sister to Cephalopoda with moderate support, Bayesian inference (BI) analysis using the site heterogeneous CAT-GTR model recovered Monoplacophora sister to all other conchiferans with strong support. A supertree approach also recovered Monoplacophora sister to the remainder of Conchifera although support for the node grouping other conchiferans to the exclusion of Monoplacophora was weak. ML and BI analyses recovered Gastropoda and Scaphopoda as sister taxa although Gastropoda + Bivalvia was weakly supported in the supertree analysis. A molecular clock analysis based on our Bayesian topology dates the origin of Mollusca to 564±3.51 MYA and the origin of Conchifera to 556±2.88 MYA. Results from this comprehensive phylogenomic dataset largely support a basal conchiferan placement of Monoplacophora and a sister-taxon relationship of Gastropoda and Scaphopoda. Implications of support for a basal conchiferan position of Monoplacophora for understanding ancestral character states of Mollusca and Conchifera will be discussed. Future studies incorporating additional genomes from other molluscan taxa will hopefully continue to solidify our understanding of early molluscan evolution, impacting all disciplines investigating molluscs.

Keywords: Monoplacophora, Conchifera, phylogenomic, phylogeny, molecular clock

NERVOUS SYSTEM CHARACTERS CAN RESOLVE SHALLOW AND DEEP RELATIONSHIPS WITHIN MOLLUSCA

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Molluscs are renowned for their extraordinary anatomical flexibility, an evolutionary trait that underpins their success as a clade but also confounds resolution of the inter-relationships among the various branches within the molluscan phylogenetic tree. Nervous systems represent the direct interface of an organism with its environment, and nervous system and brain features have been used to provide powerful insights to the evolutionary history of many animal groups. This approach, however, is new to the study of molluscs. Molluscan anatomical plasticity extends to sensory systems: the evolution of complex eyes and photoreceptor systems has developed in several classes independently, including the famously vertebrate-like eyes of cephalopods, but image-forming eyes are also present in bivalves, gastropods and chitons. Recent research has shown that the molluscan 'osphradium' has a similarly complex evolutionary history, and many convergent or non-homologous structures have been called by that term. So we understand that sense organs are evolutionarily plastic and molluscs have a great capacity to develop morphological structures. Even the presence or absence of discrete, separate identifiable ganglia in the central nervous system is more flexible than has been previously appreciated. New research shows that the architecture of the central nervous system in molluscs is under higher evolutionary constraint than sensory structures. And these patterns provide a new independent line of evidence to assess conflicting hypotheses about the inter-relationships among the classes of living molluscs. Using neuroanatomical features to infer shared evolutionary history requires detailed descriptive work, and a level of attention to detail that was a hallmark of descriptive work by the late Prof Luitfried Salvini-Plawen.

Keywords: phylogenetics, neurophylogeny, sense organs, Polyplacophora, Scaphopoda, Cephalopoda, eyes, 'osphradium'

SEEING THROUGH ROCKS: THE FUNCTION AND EVOLUTION OF THE SHELL-EYES OF CHITONS (MOLLUSCA: POLYPLACOPHORA)

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New genomic, transcriptomic, and phylogenetic resources for non-model study systems have revealed that light-sensitive cells are distributed more broadly across metazoan taxa and tissue types than suspected previously. Combined with a phylogenetic perspective on the distribution of light-detecting structures across animals, it appears that eyes in different metazoan lineages have evolved separately through the co-option of particular sub-sets of these extraocular photoreceptors. Here, I will discuss how we can use the diverse array of extracephalic visual systems found in mollusks – particularly those associated with the aesthetes of chitons (Class Polyplacophora) – to ask how and why eyes evolve from less complex light-sensitive structures. To study how shell-eyes have evolved in certain chitons, we are first identifying the molecular components of vision in in these animals using transcriptome sequencing and a high-throughput, tree-based approach for sequence annotation. Second, we are studying the patterns of expression of these eye-related genes across taxa. So far, our results indicate that the shell-eyes of chitons may be homologous to light-sensitive, non-visual organs found in eyeless relatives. Third, by building a new molecular phylogeny of chitons and inferring ancestral character states related to eyes and vision, we are constructing a step-by-step account of how the eyes of chitons may have evolved. To address why eyes may have evolved in certain lineages of chitons (and not others), I will discuss the functional benefits, costs, and constraints associated with transitions from non-visual light-sensitive organs to those that provide spatial information about light. As a benefit, spatial vision may help chitons distinguish approaching predators from uniform decreases in illumination, thereby reducing costly defensive responses to non-existent threats. However, by incorporating more elaborate sensory structures into their shell plates, chitons may weaken their armor system's ability to protect them from predators or adverse environmental conditions.

Keywords: phylogeny, transcriptomes, evolution, vision, complex traits, biomineralization

ADVANCES IN THE MITOGENOME CATALOGUE OF GASTROPODS

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With more than 100,000 living species, Gastropoda is the most diverse lineage within Mollusks. Moreover, they show high levels of morphological and ecological diversity, and thus are considered particularly interesting for evolutionary studies. Here, we present new complete mitochondrial genomes from several lineages of Gastropoda including Patellogastropoda, Neritimorpha, Vetigastropoda, and Caenogastropoda that were obtained using massive sequencing technologies. Phylogenies for Gastropoda, Neritimorpha, Vetigastropoda, and Conoidea (Caenogastropoda) were reconstructed using probabilistic methods showing a good level of resolution and congruence with published nuclear-based phylogenies. The existence of some lineages with long branches introduced important biases, and possible ways of ameliorating their effect on the inference of the gastropod phylogeny are discussed. Additionally, we analyze the evolution of gene rearrangements in the mitochondrial genome organization taking into account the reconstructed phylogenies.

Keywords: Gastropoda, Vetigastropoda, Neritimorpha, Caenogastropoda, Conoidea, mitochondrial DNA

HEMOCYANIN-BASED PHYLOGENETICS: THE NEXT GENERATION

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Hemocyanin, first mentioned in 1878 by Leon Fredericq, is the blue respiratory protein of most mollusks. Due to its enormous size, complexity and medical relevance, it is intensely analyzed by electron microscopy, biochemical and other molecular biology methods. Most progress in studying its structure, function and evolution was made during the last 20 years. We unraveled the 3-dimensional structures of several hemocyanins, we sequenced a number of hemocyanin genes, and also functional studies were completed, mainly focused on the differential expression of hemocyanins. We also performed detailed analyses of the evolutionary history of molluscan hemocyanins and tested the phylogenetic potential of these huge hemocyanin gene regions (>20,000 base pairs), cDNAs (>10,000 base pairs), and their associated primary structures (>3500 amino acids). We used hemocyanin data to calculate molecular trees, e.g. for chitons, characterized the hemocyanins of several cephalopods, gastropods and also of Caudofoveata. We discovered the mega-hemocyanin in Cerithioidea, documenting a unique molecular character suite that is synapomorphic for this group, and we sequenced the complete hemocyanin gene of *Laeviplina hyalina* (Monoplacophora). All phylogenetic results, solely based on hemocyanin data, are in good accordance with other current estimates of phylogeny within Mollusca. Thus, with the emerging availability and affordability of the new NGS-methods, we should reconsider an expanded use of hemocyanin data sets for future molluscan systematic or phylogenetic studies.

Keywords: Hemocyanin, Gastropoda, Cephalopoda, Caudovofeata, Polyplacophora, Monoplacophora

MOLECULAR PHYLOGENY OF ACANTHOCHITONINA (POLYPLACOPHORA) REVEALS ENDEMIC RADIATIONS WITHIN THE PACIFIC OCEAN

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Chitons in Acanthochitona are united by an abanal gill placement and cup- or cone-like egg hull shape, and are supported as monophyletic in multi-locus DNA analyses. More taxon-dense sequencing across this suborder with mitochondrial markers, 16S and COI, have approximately resolved species relationships within genera and have contributed to supporting associations of genera within families, but deeper relationships are still partly unresolved probably because these markers evolve too rapidly. Despite these limits, 16S and COI analyses provide compelling evidence to extend the reorganization of genera already initiated in multiple locus and mitochondrial gene order studies. In particular, they have revealed endemic radiations of species flocks in the North Pacific in related genera, and exclusive of other genera not found in the North Pacific that are morphologically similar but only remotely related. A featured example is Lepidochitonidae Iredale, 1914, which in the Pacific include the genus *Nuttallina* Carpenter MS, Dall, 1871 and the genus group, *Cyanoplax* Pilsbry, 1892 + *Schizoplax* Dall, 1878 (the latter formerly in Schizoplacidae Bergenhayn, 1955). These are examples of North Pacific radiations of fairly closely-related lineages, although their last common ancestor has deeper tropical New World affinities, including Caribbean/Panamic species of that are currently placed in *Lepidochitona* Gray, 1821 even though the presented analyses indicate that they are more closely related to *Nuttallina* than they are to North Atlantic *Lepidochitona* species, including the type species of that genus, *L. cinerea* (Linnaeus, 1767). The New World genus *Ceratozona* Dall, 1882 is also here reassigned to Lepidochitonidae based on its affinities to the above-discussed Pacific members of Lepidochitonidae. Likewise, the results support a new concept for Mopaliidae Dall, 1889 corresponding to a monophyletic grouping of mostly North Pacific genera, and excluding the southern hemisphere genera, *Plaxiphora* Gray, 1847 and *Nuttallochiton* Plate, 1899, representing a new concept for this family.

Keywords: chitons, phylogeny, systematics, North Pacific, Lepidochitonidae

MOLLUSCAN PHYLOGENETICS IN THE ERA OF GENOMICS

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Molluscs are impressive organisms, with unparalleled diversity in the oceans and an astonishing body plan disparity. Their origin dates back to the Cambrian and since then molluscs have been a dominant group in our planet. However, despite a rich fossil record and the long-term maintenance of highly disparate lineages, reconstructing the phylogeny of molluscs and their place in the animal tree of life have been, to say the least, challenging, even after the discovery of the first living members of key lineages like Monoplacophora. Numerous hypotheses have been proposed based on morphology and small molecular data sets, and little consensus had been reached. The advent of massive parallel sequencing and its application to phylogenomic analyses has been spearheaded by mollusc work, and after decades of phylogenetic debate, a consensus of the phylogeny of molluscs is finally emerging. This talk, honoring the late Lutfried Salvini-Plawen, elaborates on some of these developments and results, focusing on deep relationships within the molluscan classes, as well as the phylogenies of bivalves and gastropods, two diverse and commercially important molluscan classes.

Keywords: Phylogenomics, genomics, molluscan phylogeny

CELL PROLIFERATION PATTERN AND *TWIST* EXPRESSION IN AN APLACOPHORAN MOLLUSK ARGUE AGAINST SEGMENTED ANCESTRY OF MOLLUSCA

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The study of aplacophoran mollusks (i.e., Solenogastres or Neomeniomorpha and Caudofoveata or Chaetodermomorpha) has traditionally been regarded as crucial for reconstructing the morphology of the last common ancestor of the Mollusca. Since their proposed close relatives, the Polyplacophora, show a distinct seriality in certain organ systems, the aplacophorans have also been in the focus of attention with regard to the question of a potential segmented ancestry of mollusks. To contribute to this question, we investigated cell proliferation patterns and the expression of the *twist* ortholog during larval development in solenogasters. In middle-aged to late larvae, during the outgrowth of the trunk, a pair of uniform, longitudinal bands of proliferating cells is found in a lateral to ventrolateral position. These bands elongate as the trunk grows longer. Likewise, expression of *twist* occurs in two laterally positioned, uniform longitudinal stripes in middle-aged larvae. The position of the bands of proliferating cells as well as that of the *twist* expression domains is always subepithelial, suggesting a mesodermal origin of the cells involved. Both, the pattern of proliferating cells and the expression domain of *twist* demonstrate the existence of extensive and long-lived mesodermal bands in aculiferans, a situation which is similar to annelids but in stark contrast to conchiferans, where the mesodermal bands are usually rudimentary and ephemeral. Yet, in contrast to annelids, neither the bands of proliferating cells nor the *twist* expression domains show a separation into distinct serial subunits, which clearly argues against a segmented ancestry of mollusks.

Keywords: Solenogastres, Neomeniomorpha, development, gene expression, mesodermal bands, last common molluscan ancestor

UNITAS MALACOLOGICA Grant Recipients

EVOLUTIONARY ECOLOGY OF NERITIMORPH GASTROPODS: HOW THEY HAVE MADE EXTRAORDINARY HABITAT TRANSITIONS BUT WITH SO FEW SPECIES?

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Adaptive radiation – the rise of a diversity of ecological roles and attendant adaptations in different species within a lineage – is an important process bridging ecology and evolution. The Neritimorpha (Neritopsina), one of the six main clades of Gastropoda, represent a prime example of animal radiation and adaptation by inhabiting rocky shores, seagrass beds, mangrove swamps, freshwater streams, subterranean waters, submarine caves, deep-sea sunken wood, hot vents and cold seeps, in addition to terrestrial and arboreal ecosystems. Here we provide the first comprehensive molecular phylogeny of the clade based on four gene sequences (4.6 kbp) from 58 species that cover most of the previously recognized genera in the aquatic environments and many of terrestrial ones. The following eight extant families are recovered as valid and exclusive monophyletic groups: Neritopsidae, Neritiliidae, Bourcieridae, Proserpinidae, Helicinidae, Hydrocenidae, Phenacolepadidae and Neritidae. Our phylogeny also illustrates their multiple invasions of each of the intertidal, stream, groundwater, submarine-cave, deep-sea and terrestrial habitats. Such a high degree of ecological radiation, however, has not been accompanied by a significant increase of species richness in the four aquatic families, which comprise a total of only about 500 living species worldwide. We provide several lines of new evidence on how they could invade the various habitats but with so few species: Regardless of where adults occur, the planktotrophic larvae of most aquatic neritimorphs disperse in the surface water of the open ocean for months or perhaps even years, and resulting enormous dispersal faculties contribute to their wide geographic distributions, panmictic structures and low rates of speciation and extinction. Once they become fully terrestrial by losing the connection to the sea and potential for further ecological radiation, vicariance plays a significant role as exemplified by the Helicinidae that arguably encompass 800–1,400 extant species.

Keywords: amphidromy, fossil, hydrothermal vent, larval dispersal, Neritimorpha, phylogeny

SYSTEMATICS OF THE DIVERSE AND GLOBAL GASTROPOD FAMILY FISSURELLIDAE (VETIGASTROPODA) IN A TIME-CALIBRATED PHYLOGENY

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Fissurellidae is a worldwide-distributed family of gastropods comprising more than 450 described species in 47 genera. Traditional classifications have proposed two to five subfamilies depending on the morphological characters used. The only molecular phylogenetic study focusing on the family found a topology compatible with a classification system of four subfamilies, but taxon sampling was limited and results sensitive to analytical methods. We expanded taxon sampling adding 115 new specimens, for a total of 25 genera and 122 species – twice as many genera and more than three times the number of species of the previous study. Five genes (18S rRNA, 28S rRNA, histone H3, 16S rRNA, cytochrome *c* oxidase subunit I) were sequenced, concatenated and analyzed phylogenetically. Our results support the four subfamilies Hemitominae, Emarginulinae, Diodorinae and Fissurellinae. All major genera within each subfamily are not monophyletic, suggesting the need for generic revisions in the group. Several genera traditionally considered as Emarginulinae, such as *Lucapinella, Cornisepta* and *Profundisepta*, were recovered in different subfamilies. We also present a calibrated tree analyzed under the fossilized birth-death model (FBD).

Keywords: phylogenetics, keyhole limpets, slit limpets, Fissurellidae, Vetigastropoda, fossilized birth-death, fossils

ON THE PHYLOGENETIC RELATIONSHIPS OF SCAPHOPOD MOLLUSCS – WHAT ELSE IS NEW?

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The phylogenetic relationships of Scaphopoda with the other major conchiferan taxa remain unclear, although their systematic position is pivotal for our understanding of conchiferan evolution. The ambiguous information from morphology and palaeontology has been supplemented by inconclusive molecular and phylogenomic studies. Scaphopod anatomy shows some resemblance to that of bivalves, e.g. lateral mantle elongation, a burrowing foot, and the organisation of the nervous system. This is likely due to convergent adaptation to a burrowing lifestyle, and the bivalve-scaphopod sister-group relationship is not supported by molecular analyses. Similarities with the cephalopod bauplan include the pronounced and elongated dorsoventral body axis and a single, annular attachment of the shell muscle. A close phylogenetic affinity of Scaphopoda and Cephalopoda is also indicated by mitochondrial and nuclear DNA sequences and developmental gene expression data, although the signal for a sister-group relationship is not robust. However, the absence of unambiguous scaphopods in the fossil record before the Carboniferous remains unexplained. A divergence time analysis of DNA sequences attempts to shed light on the origin of the Scaphopoda and their major subtaxa.

Keywords: anatomy, molecular phylogenetics, evolution

ALL QUIET ON THE EASTERN FRONT? DIVERSITY AND BIOGEORAPHY OF DEEP-SEA SOLENOGASTRES FROM THE SEA OF OKHOTSK

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Solenogastres are a small and understudied clade of worm-shaped molluscs occurring mainly in deep waters. Many species are described from single localities only and their bathymetric and geographic distribution ranges are poorly explored. To our knowledge, there are currently only nine records of Solenogastres from the Far Eastern Seas, with eight of them dating back to the early 20th century. As part of a large scale project aimed at understanding biodiversity and biogeographic patterns in the region of the Northwest Pacific, the 'Sea of Okhotsk Biodiversity Studies' expedition set out in 2015 to explore the deep-sea benthos of the Sea of Okhotsk (Russia). During this cruise, we collected around 100 entire specimens (and additionally several partial and damaged individuals) of Solenogastres from the bathyal Kuril basin at eight stations from 1696 m to 3377 m depth. Preliminary investigations revealed 16 morphospecies, including one lineage with a relatively common occurrence at six stations. Using a combination of morphological methods (i.e., light and scanning electron microscopy as well as microanatomical 3D-reconstructions) and molecular barcoding, we present a first analysis of the hidden molecular and morphological diversity of Solenogastres found in the Sea of Okhotsk. We compare our results with the solenogaster diversity of the Kuril-Kamchatka trench and its adjacent abyssal plains (sampled during the 'Kuril-Kamchatka Biodiversity Studies' KuramBio-Cruise), which are connected with the semi-enclosed Kuril basin via two bathyal straits, the Bussol and the Krusenstern Strait. During the KuramBio-Cruise 35 solenogaster specimens were collected from 4830 m to 5780 m, which represent diverse lineages. Our integrative taxonomic approach not just leads to an immense boost in the hitherto very restricted diversity of Solenogastres in the Far Eastern Seas, but it also significantly raises the global number of Solenogastres from these depths of the world's oceans.

Keywords: Aplacophora, integrative taxonomy, deep sea

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REPEATED ADAPTIVE RADIATIONS IN THE ECHINODERM-PARASITIC GASTROPOD FAMILY EULIMIDAE (CAENOGASTROPODA: VANIKOROIDEA)

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Repeated adaptive radiations are described as parallel diversification with morphological convergence in species of different lineages that live under similar ecological conditions. This pattern is typically found in multiple sets of closed systems, such as islands or lakes, but might also occur in host-parasite interaction if distinct host species or groups work as isolated “islands” for parasites. The gastropods of the family Eulimidae offer unmatched potential to address this hypothesis; they parasitize echinoderms with wide varieties of parasitic strategy and shell morphology and with more or less strict host specificity, although there has been very limited knowledge on their evolutionary relationships. Here, we show the first comprehensive molecular phylogeny of the family based on six gene sequences (ca. 4.7 kb) from 101 eulimids representing more than 50 genera. The resulting, well-resolved tree illustrates that eulimids exploiting each of the five echinoderm classes belong to two or three different phyletic groups. In addition, ancestral character state reconstruction suggests that the teleoconch has been lost more than once and globose to capuliform shells as well as endoparasitism have evolved independently in several lineages. Principal component analysis of conchological characters reveals correlation between parasitic strategies and shell forms: temporary parasites have more slender shells than permanent ectoparasites and endoparasites. With these results, we conclude that the Eulimidae have diversified through repeated adaptive radiations. Respective radiations always started as a temporary parasite with a slender shell, while the broad shell and large attachment area may be adaptive for permanent ectoparasites and endoparasites in reducing the cost of shell construction, and possibly also in avoiding predation and/or dislodging by wave action for ectoparasites.

Keywords: endoparasitism, molecular phylogeny, parallel evolution, shell morphology

AN INTEGRATIVE APPROACH TO RESOLVING AN "IMPOSSIBLE" GROUP – USING ADULT AND LARVAL MORPHOLOGY, BEHAVIOR, SPERM ULTRASTRUCTURE, AND MOLECULAR DATA TO UNDERSTAND THE VERMETIDAE (CAENOGASTROPODA)

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Members of the 'worm-snail' family Vermetidae occur worldwide in temperate and tropical seas and have developed numerous highly unusual traits, including irregular 'uncoiled' shell growth, a gregarious cementing habit (making them important reef builders as well as nuisance species when transported globally), feeding by mucous webs to trap particles from the water column, and a rapid rate of mitochondrial gene-order change compared to most animals. Their 'colonies' also mark former sea level stands, making them important indicators of sea level and climate changes. Their full potential as paleoclimatic indicators has yet to be realized because of unresolved species delineations and relationships. Taxonomic problems are particularly vexing in this group whose members are frequently confused with superficially similar calcareous structures such as polychaete tubes, linings of bivalve burrows, scaphopod fragments, and even fossilized vertebrate bones. Our team has been working on a combined approach of analyzing shell morphology, anatomy, behavior, primary nucleotide sequences and mitochondrial gene orders, sperm ultrastructure, as well as historic literature data and type material, to understand species identities and explore relationships in the group. Using this approach, we have identified several novel morphological characters that may be phylogenetically useful; including previously unrecognized shell structures for modifying the shell aperture and guiding the columellar muscle. Application of the multiple character systems has uncovered a much richer species and genus-level diversity in this family than previously recognized, and suggests that the majority of traditionally recognized genera are not monophyletic. Independent evidence for our supraspecific arrangement based on morphological and nucleotide sequence characters comes from shared mitochondrial gene orders. In addition, some gene order changes are further modifications of earlier rearrangements. These nested rearrangements provide an independent marker of evolutionary direction on the tree, and increase our confidence in the phylogeny.

Keywords: anatomy, invasive species, mitochondrial gene order, phylogenetics, protoconch, revision, shell

CEMENTING MUSSELS TO OYSTERS IN THE PTERIOMORPHIAN TREE: A PHYLOGENOMIC APPROACH

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Mytilida (mussels) is an ancient group comprising some of the most important commercial shellfish worldwide. Mytilida consists of approximately 400 species found in various littoral and deep-sea environments. The multiple adaptive radiations that occurred within Pteriomorphia have rendered phylogenetic classifications difficult and uncertainty remains regarding the relationships among most families. To address this incongruence, novel transcriptomic data were generated to include all five orders of Pteriomorphia represented by a total of 41 transcriptomes. Our results, derived from complex analyses of large data sets and evaluating possible pitfalls affecting phylogenetic reconstruction (matrix occupancy, heterogeneity, evolutionary rates, evolutionary models) consistently recover a well supported phylogeny of Pteriomorphia, with the only exception of the most complete but smallest matrix (51 genes, 90% gene occupancy). Maximum likelihood and Bayesian mixture model analyses retrieve strong support for (a) the monophyly of Pteriomorphia; (b) Mytilida as a sister group to Ostreida and (c) Arcida as sister group to all other pteriomorphians. The basal position of Arcida is congruent with its shell microstructure (solely composed of aragonitic crystals), whereas Mytilida and Ostreida display a combination of a calcitic outer layer with an aragonitic inner layer composed of nacre tablets, the latter being secondarily lost in Ostreoidea.

Keywords: bivalve, phylogeny, transcriptomes, Mytilida, Ostreida, Arcida

OLD CHITONS, NEW TRICKS: A RE-EVALUATION OF THE CENTRAL NERVOUS SYSTEM ACROSS POLYPLACOPHORA, AND ITS POTENTIAL ROLE IN NEUROPHYLOGENY

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Chitons (Polyplacophora) have long been considered to be amongst the most plesiomorphic molluscs. This particularly applies to their nervous system, which is described as simple, ladder-like, weakly centralised and lacking true ganglia, leading to a consensus that chitons lack a brain. However, recent anatomical and electrophysiological work on *Leptochiton asellus* has indicated a higher level of cephalisation than previously appreciated, challenging this consensus. A more complex, organised nervous system could provide new morphocladistic characters and contribute to finally resolving the position of chitons and other groups in deep molluscan phylogeny. Using the historic histological slides of Johannes Thiele, we reconstructed tomographic models of the nervous system of eight chiton species from the major clades across the class to examine its structure and interspecific variation. This material, dating from the late 19th and early 20th centuries, is of outstanding quality and helped form the foundation for much of our modern understanding of chiton anatomy. Through combining this historic collection material with cutting-edge digital modeling, we confirm that there are distinct cerebral, pedal and lateral regions of the anterior nerve ring (homologous to the brain in other molluscs), with the neuropil being constricted into three nested rings. These are not full ganglia, however they do represent a higher level of organisation than previously appreciated, in line with our physiological findings in *L. asellus*. These regions and other features of the nervous system also appear to vary between polyplacophoran clades, providing new morphological characters and contributing to a new neurophylogenetic framework in chitons. With increasing interest in neuroanatomical characters for use in phylogenetics, this could not only enrich our understanding of molluscan nervous systems and their evolution, but also provide a model for a novel phylogenetic approach in Mollusca, which could help to resolve the remaining deep phylogenetic questions surrounding the phylum.

Keywords: Polyplacophora, nervous systems, morphology, neurophylogeny, anatomy, Thiele

UNITAS MALACOLOGICA Grant Recipients

USING ONTOGENETIC VECTORS TO INTERPRET NODES WITHIN A MOLECULAR PHYLOGENY OF ISOGNOMONINAE WOODRING, 1925 [1828]

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I carried out a phylogenetic analysis of Isognomoninae Woodring, 1925 [1828] using both mitochondrial and nuclear genes. This phylogeny supports their monophyly but also reveals unexpected structure within this clade. With the relatively recent revision of the Pterioidea Gray 1847 [1820], (Tëmkin, 2010) combining several families into an expanded Pteriidae, the discovery of intermediate structure within *Isognomon* has presented a both a challenge and an opportunity for taxonomic revision. While species assignments can be guided by well-defined and referenced species concepts, intermediate-level clades have no equivalent framework for assigning genera, subgenera, subfamilies, etc. For my revision of the Isognomoninae, I develop a concept by which to judge deeper nodes for taxonomic significance and a novel application of geometric morphometric ontogenetic analysis to generate optimal data for this method. The criteria I apply is that categories are of maximal utility if they describe only unique information and do not contain information described by a higher or lower taxa. Ontogenetic vectors, high-dimensional algebraic descriptions of whole-animal development are uniquely well suited for this type of comparison, but analogous analyses are possible using nearly any type of data. What ontogenetic vectors allow is a simple, one-dimensional, measure of the redundancy of the information contained in two nodes of the phylogeny - the angle of divergence between the average ontogenetic vector for all specimens within those two clades. At 90 degrees, the developmental pathways of the nodes are independent of each other and describe entirely separate processes of shell-growth. Using this criterion, I find that the Isognomoninae have taxonomically significant changes in shell development at two node levels between the basal node containing the subfamily and the tip-groups containing the species. Therefore, I divide this group into two genera; *Isognomon* Lightfoot, 1786 and *Melina* Philipsson, 1788 each consisting of three subgenera.

Keywords: tropical bivalves, *Isognomon*, phylogenetics, geometric morphometrics, ontogeny, taxonomy

A MOLECULAR PHYLOGENY OF THE TONNOIDEA

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The Tonnoidea is a moderately diverse group, with a little under 400 species living mostly in (sub)tropical waters on the continental shelf, and with a few species living in depths in excess of 2,000 meters. Among biologists, they are known for their teleplanic larvae and for their ability to secrete sulfuric acid; many feed on echinoderms, famously including the crown-of-thorns starfish. Among shell collectors, the Tonnoidea are popular for including the tuns, frog shells, helmets, tritons and other collectables. Tonnoideans are classified in seven currently accepted families - the "classic" Tonnidae, Cassidae, Ranellidae, Bursidae and Personidae, and the little-known, deep water Laubierinidae and Pisanianuridae. We assembled a 4-gene (COI, 16S, 12S, 28S) mitochondrial and nuclear dataset for ~105 species, representative of the morphological diversity of the superfamily, including such rare and elusive genera as *Akibumia*, *Dalium*, *Distorsionella*, *Distorsomina*, *Eucorys*, *Oocorys*, *Personopsis*, *Pisanianura*, *Sconsia* and *Thalassocyon*. Bayesian analysis of the concatenated dataset recovered a monophyletic Tonnoidea, with *Ficus* as its sister group; unexpectedly, *Thalassocyon*, currently also classified in the Ficidae, was nested within the ingroup. Among traditionally included families, Tonnidae, Cassidae, Bursidae and Personidae were also supported as monophyletic but, remarkably, the Ranellidae was not, with cymatiids, *Ranella* and *Charonia* dispersed among three distinct clades. The Laubierinidae and Pisanianuridae together form a monophyletic group. Although not all nominal genera, nor even all currently accepted genera, have been included in the analysis, we believe the new phylogeny is stable enough to establish a revised family-level classification of the Tonnoidea. Molecular characters will continue to impact the systematics of the Tonnoidea at genus and species level, and our preliminary results have already disclosed several species complexes. This suggests that, despite their teleplanic larvae, the circumglobal distribution of several tonnoidean species is the result of excessive synonymy.

Keywords: phylogeny-based classification, Gastropoda, teleplanic larvae, cryptic species

RHODOPEMORPHS AND OTHER MESOPSAMMIC GASTROPODS: STATE OF THE ART

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Professor Luitfried Salvini-Plawen was one of the earliest modern researchers working with mesopsammic gastropods. In the 1970s he started describing several species of tiny sea slugs from European waters, using light microscopy from whole mounts and examining hard structures such as radulae and calcareous spicules. His studies included different opisthobranch groups, such as Acochlidia, Cephalaspidea, Nudibranchia, Sacoglossa and Rhodopemorpha. They provided the taxonomic basis and evolutionary scenarios to be tested and elaborated by his successors, among them Erhard Wawra. One of Professor Salvini-Plawen's latest papers referred to the morphology of the cephalaspidean family Philinoglossidae. Following his footsteps, here we give a brief update on the systematics and global diversity of these mesopsammic slugs using a variety of up-to-date histological and 3D microanatomical methods. We also present novel molecular phylogenies of rhodopemorphs and philinoglossids and discuss aspects of their evolution.

Keywords: Opisthobranchs, microanatomy, phylogeny, meiofauna

MOLECULAR PHYLOGENY REVEALS RELIABLE DIAGNOSTIC MORPHOLOGY CHARACTERS OF SELECTED LAND SNAIL GENUS *LEPTOPOMA* IN SABAH, WITH ADDITIONAL EVIDENCE FROM GEOGRAPHICALLY-INDUCED MORPHOLOGICAL VARIATION

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The operculated land snail of genus *Leptopoma* are a morphologically diverse taxa where their taxonomy could be problematic as their identification was solely dependent on shell morphology and internal anatomy. Lack of diagnostic character, striking variation of shell patterns and undistinguishable shell size and shape among and between the *Leptopoma* species lead to ambiguous species delimitation. The association of geographical variation with *Leptopoma*'s shell morphology in Sabah is also poorly understood. To clarify the ambiguous taxonomy of *Leptopoma*, we investigated the phylogenetic relationship of three *Leptopoma* species from Sabah using mitochondrial genes (16S and COI) by performing maximum likelihood and Bayesian analysis. The shell morphologies of 14 specimens involved in phylogeny analysis were quantified, and mapped across the phylogenetic tree for phylogenetic signal test in order to identify diagnostic character for *Leptopoma*. To explore variation of *Leptopoma*'s shell morphologies in Sabah and their association with geographical variation, we quantified and compared the shell size, shape, and other discrete shell characters for 294 shell samples, represented by *Leptopoma sericatum* and *Leptopoma pellucidum* which collected from Balambangan Island and Kinabatangan. The molecular analysis results suggest that each of the three *Leptopoma* species was monophyletic, and has shown congruence with current morphological-based classification. Through phylogenetic signal test, spiral ridges and presence of inner ring in aperture was significant in delimitation of the monophyletic taxa. Furthermore, inner ring in aperture was not associated with geographical variation. In contrast, shell patterns, shell size and shape were found to have association with geographical variation and are not recommended as key for species identification. Overall, our study provided the first phylogenetic investigation for the genus *Leptopoma* in Sabah. Spiral ridges and presence of inner ring were proposed to be potential diagnostic characters, though further investigation is needed.

Keywords: Cyclophoridae, Borneo, mitochondrial DNA, DNA barcoding, phylogenetic signal

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MOLECULAR PHYLOGENY OF *CANDIDULA* (GEOMITRIDAE) LAND SNAILS INFERRED FROM MITOCHONDRIAL AND NUCLEAR MAKERS REVEALS THE POLYPHYLY OF THE GENUS

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The genus *Candidula* (Geomitridae) consisting of 28 species in western Europe, is disjunctly distributed in the Iberian Peninsula, Italy, Balkan region, the Aegean Islands, and one species in the Canary Islands. Although the genus is well defined by characters of the reproductive system, the relationships within the genus are still unclear and some authors have indicated a possible subgeneric division based on the internal morphology of the dart sac. We present a molecular phylogeny of *Candidula* based on two mitochondrial genes (*COI* and 16S rRNA), the rDNA region (5.8S rNRA + ITS2 + 28S rRNA) and seven nuclear DNA regions isolated specifically to this genus (60SL13, 60SL17, 60SL7, RPL14, 40SS6, 60SL9, 60SL13a). Two major clades were recovered with *Candidula* species, grouped into six monophyletic entities. One major clade grouped species from southern France and Italy with the widely distributed species *C. unifasciata*. The second major clade grouped all the species from the Iberian Peninsula, including *C. intersecta* and *C. gigaxii*. *C. ultima* from Canary Islands was recovered as one separated lineage within the latter clade. The incorporation of additional geomitrid genera allowed us to demonstrate the polyphyly of the genus *Candidula*. Moreover, we showed that similar structures of the dart sac complex of the genital system in different taxa do not necessarily mean a close phylogenetic relationship in the Geomitridae. More genera of the family are needed to clarify their evolutionary relationships, and to fully understand the evolution of the dart sac complex of the genital system within the Geomitridae.

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PHYLOGEOGRAPHY OF A NOVEL EVOLUTIONARY TRANSITION FROM MARINE TO TERRESTRIAL ENVIRONMENT IN NEW ZEALAND ONCHIDIIDAE

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Transitions from a marine to terrestrial habitat are quite rare across the phylogenetic spectrum, so it is therefore of great interest to find a new taxon of terrestrial onchidiid living in rocky areas completely separate from the littoral zone on islands in Southern New Zealand. In addition to the evolutionary significance, this finding is also intriguing in the context of onchidiid biogeography, because no genera other than the exclusively marine *Onchidella* have previously been recorded in New Zealand. New Zealand's oceanically isolated islands also provide an excellent natural system for studying dispersal, being separated by large stretches of open water and yet geologically recent (i.e. have never been connected to mainland New Zealand). Therefore, the biogeography of these recently formed oceanic and tectonic subantarctic islands must rely on trans-oceanic dispersal, which we suggest is facilitated by seabirds in this instance. It seems likely that this rare slug was once widespread and has declined to just a few isolated pockets, possibly due to predation pressure. We present genetic and morphological data to highlight the evolutionary, biogeographic and ecological significance of this exciting find.

Keywords: terrestriality, phylogeography, Onchidiidae, dispersal, subantarctic islands

PHYLOGENY, DIVERGENCE TIMES AND SPECIES DELIMITATION OF *TONICIA* (MOLLUSCA: POLYPLACOPHORA) FROM THE EASTERN PACIFIC OCEAN

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The genus *Tonicia* Gray, 1847 is composed by nine nominal species in the Eastern Pacific Ocean (EPO), but the taxonomic status and geographic distribution at a species level has long been controversial. In this study we compare the species of *Tonicia* from the EPO with a molecular systematics analysis. We used two mitochondrial markers, cytochrome oxidase subunit I (COI) and 16S ribosomal RNA (16S), and one nuclear marker 18S ribosomal RNA (18S) to estimate the phylogeny and divergence times of *Tonicia* species from the EPO using parsimony and Bayesian inference, and we inferred species delimitations using a generalized mixed Yule coalescent (GMYC) approach. We interpreted a clear barcoding gap (using COI) as corresponding to intra- and interspecific divergences. In the phylogeny, we found five monophyletic groups and several nominal species of *Tonicia* in the same clade. The GMYC analysis confirmed five coalescent groups and six species in the gene tree. Genetic distance, phylogeny and coalescent approach confirmed that the nine nominal *Tonicia* species from the EPO belong to six lineages. We suggest that the morphological characters used to identify *Tonicia* species must be re-examined in depth.

Keywords: polyplacophorans, phylogeny, chitons, Chitonidae

THE USAGE OF PHYLOGENIES TO INFER DRIVERS OF DIVERSIFICATION IN THE NON-MARINE AQUATIC FAMILY HYDROBIIDAE (CAENOGASTROPODA: TRUNCATELLOIDEA)

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Hydrobiidae Stimpson, 1865 represents the most diverse family of non-marine aquatic gastropods with a total of 70 genera and ca. 800 species. The striking differences in species richness among genera as well as in body sizes, ecological features and geographic ranges make hydrobiids a suitable model taxon to explore drivers of diversification in continental aquatic ecosystems. Our investigation comprises two case studies, each developed through three phases: 1) inferring the phylogenetic relationships; 2) estimation of diversification (speciation minus extinction) rates that determine the species richness of a clade; and 3) assessing how extrinsic (habitat type, altitude and co-occurrence) and intrinsic (body size) factors influence these rates. The first study focuses on the Mediterranean genera *Corrosella* and *Pseudamnicola*, with 12 and 70 species respectively. Our comparative phylogenetic method revealed that this difference in species richness is driven by a burst in diversification in the latter genus connected to high morphological divergence. The diversification burst is demonstrated to be the result of an altitudinal transition along the headwater/lower-reaches gradient. The high connectivity among lower-reach localities might have facilitated dispersal and the colonization of novel habitats, and ultimately the radiation of *Pseudamnicola*. The second study searched for causes of species richness differences across the entire family. We inferred a phylogenetic tree from mitochondrial sequences of 266 species and revealed that variation in diversification rates depends significantly on habitat type, with headwater species showing lower rates than brackish or lacustrine species. Based on these preliminary results, showing an individual influence of altitude and habitat on diversification rates but not of the intrinsic factors investigated, we aim at using a more complete taxon/gene coverage and novel multifactorial analyses in future studies to quantify the relative effect of multiple drivers of hydrobiid richness differences. This will help to understand evolutionary processes in continental aquatic ecosystems.

Keywords: microgastropods, freshwater, species richness, radiation, multifactorial analysis

MOLECULAR PHYLOGENY OF PHILIPPINE HELICARIONIDS (GASTROPODA: PULMONATA)

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The phylogeny of the terrestrial snail family Helicarionidae is poorly understood. A phylogenetic analysis of Philippine helicarionids was done using the mitochondrial genes, *CO1* (548 bp) and 16S rRNA (374 bp), and the nuclear rRNA gene cluster (1585 bp) for a total of nine species, namely *Hemiglypta moussoni*, *Lepidotrichia luteofasciata*, *Nipponochlamys semisericata*, *Ryssota uranus*, *R. sagittifera batanica*, *R. zeus*, and the Philippine endemic *Hemiglypta semperi*, *R. otaheitana*, and *R. lamarckiana*. A further two genera, *Hemiglypta* sp. and *Lepidotrichia* sp., were also included. Phylogenetic trees were constructed for each gene using the model based methods Neighbor-Joining, Maximum Likelihood, and Bayesian Interference Analysis and the non-model based Maximum Parsimony. All the trees were rooted to the urocyclid *Sheldonia* as the outgroup. Generally, all of the trees showed clustering of the Philippine samples into one big clade. Three major subclades were consistently observed, namely, the *Ryssota* clade, *Hemiglypta* clade and the *Lepidotrichia* clade, with high bootstrap supports. Based on the G1 test, the tree length distributions for all of the genes used were found to be skewed and therefore show phylogenetic signal. The use of other characters such as reproductive anatomy and ecology complemented by such molecular studies would be helpful to better understand the phylogeny of this group.

Keywords: Helicarionidae, COI, 16S, rRNA gene cluster, molecular phylogeny, Philippines

BY MORE WAYS THAN ONE: RAPID CONVERGENCE IN GASTROPOD ADAPTATIONS TO HYDROTHERMAL VENTS

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Deep-sea hydrothermal vents are ‘extreme’ ecosystems, founded on chemosynthesis, where animals face pressures including high temperature and low pH. Vent systems are characterised by a few dominating species, highly modified for a lifestyle specific to vents, and the singular constrained pathway to successful exploitation of energy appears to be hosting symbiotic bacteria. *Gigantopelta* is a recently discovered member of the hydrothermal vent endemic family Peltospiridae, with two species known from the Southern and Indian Oceans. *Gigantopelta* shares a number of unusual features with another peltospirid, the ‘scaly-foot gastropod’ *Chrysomallon squamiferum,* though they are not phylogenetically sister-genera. These gastropods are the only vent molluscs that host endosymbionts in a way other than on their gills, in an enlarged and highly vascularised esophageal gland. Being enclosed within the host body means that all resources required by the bacteria must be supplied by the animal, rather than by direct contact with the vent fluid. The gastropods are also unusually large for the clade. Here, we present new evidence of key anatomical differences between *Gigantopelta* and *Chrysomallon* that demonstrate these two genera acquired a similar way of life through independent adaptive pathways. By comparing *Gigantopelta* and *Chrysomallon,* we show that metazoans are capable of rapidly and repeatedly evolving close-knit relationships with chemoautotrophic bacteria, by achieving the same end-product through parallel evolutionary trajectories.

ARMINID NUDIBRANCHS AND OTHER OPISTHOBRANCHS AS BY-CATCH IN TROPICAL SHRIMP FISHERY

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During the Hong Kong Marine Biology Workshop in 1995 five species of the nudibranch genus *Armina* were collected by the shrimp-trawler hired for the workshop. There were identified and anatomically described by me in the proceedings of that workshop. Subsequently I joined the TMMP and during the post-congress workshops in Vietnam, Cambodia and India I found two species of *Armina* commonly occurring in the piles of trash-fish (by-catch) from commercial shrimp fishery that were always diverse collecting spots visited by TMMP participants. In this paper I will present information on the arminid nudibranchs as well as some other opisthobranch (heterobranch) gastropods found as by-catch during TMMP workshops and subsequent collections involving the TMMP network. The importance of the TMMP for networking and research collaborations in the countries included in the TMMP will be stressed.

MARINE MOLLUSCAN DIVERSITY IN SINGAPORE: THEN AND NOW

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Singapore is one of only a small number of tropical localities where marine molluscs are relatively well-sampled and evaluated over time. Natural historians and scientists from far and near have collected many specimens from Singapore’s shores since the establishment of the British Straits Settlements in the 19th century. Its position as an English colony and port ensured a constant stream of curious conchologists. Over the last century, and particularly over the last fifty years, Singapore has grown into a large city-state with one of the world’s busiest ports supporting a population exceeding five million. In the meantime, large-scale land reclamation has increased the original land area by some 30% at the expense of many natural coastal habitats. This paper examines the changes in the diversity of marine molluscs in key habitats over the last 100 years or so, based on published literature as well as our own observations. We also discuss the challenges in assessing molluscan biodiversity in the Indo-Pacific region despite the seemingly small area that is Singapore.

Keywords: biodiversity, tropics, gastropods, bivalves, Malacca Strait, Singapore Strait, Johor Straits

UPDATED TAXONOMIC LIST OF TEUTHOFAUNA OF THAI-MALAY PENINSULAR: GULF OF THAILAND AND ANDAMAN SEA, INCLUDING MALACCA STRAITS

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The teuthofauna of 2 subclass, 8 orders, 32 families, 68 genera and 134 species from Thai-Malay Peninsular are listed in this study. The fauna comprises 67.2% decapods and 32.1% octopods and 0.8% nautiloid. The decapod fauna include 0.8% spirulid squid, 9.7% sepiid cuttlefish, 9.0% sepiolid squids and 2.2% idiosepiid squids, 11.2% myopsid squids and 34.3% oegopsid squids. The group of oceanic oegopsid squids is the most diverse one and the second rank is the octopods. The percentage of neritic species is 58.2% and of oceanic species is 41.8%. Most of the species, 67.2%, have been recorded from both sides of the Peninsular, 14.2% only in the Gulf of Thailand and 18.6% only in the Andaman Sea. The number of teuthofauna recorded in this region is 87.6% of that reported from the South China Sea. The number of neritic species is also similar indicating the uniformity of ecological conditions throughout the Sunda Shelf. This study also reflects the necessity for taxonomic expertise in the region for this economic group of animal.

Keywords: taxonomic list, teuthofauna, Thai-Malay Peninsular

MARINE MOLLUSK DIVERSITY FROM SOUTHERN MERGUI ARCHIPELAGO SURVEY, THE REPUBLIC OF THE UNION OF MYANMAR

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The assessment coral reef ecosystem and biodiversity survey of Southern Mergui Archipelago Survey, the Republic of the Union of Myanmar was conducted during 3 - 10 February 2014 and 21 - 30 January 2015. Of the 46 stations, the collection by SCUBA diving along the coral reefs was in 45 stations and 1 station by sandy beach survey. A total of 237 species of marine mollusks were recorded in three classes: Gastropoda found 43 families 140 species, Bivalvia found 27 families 97 species and Cephalopoda found only 1 species *Sepia pharaonis*. A mean of 29.1 species was recorded per site. The range was from 2 to 88 species. The highest diversity site was in Kyun Philar Island. *Pinctada margaritifera* in family Pteriidae was the most dominant species then *Chicoreus ramosus* in family Muricidae. The similarity of mollusk species in each station showed in the cluster of survey stations.

Keywords: marine mollusk, distribution, marine mollusk diversity

OPISTHOBRANCH MOLLUSCS IN CORAL REEF HABITATS FROM THE SOUTHERN MERGUI ARCHIPELAGO, THE REPUBLIC OF THE UNION OF MYANMAR

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The Mergui Archipelago, located in the southernmost part of the Republic of the Union of Myanmar, comprises over 800 islands. Most of the islands are uninhabited and reported to be untouched. The Archipelago contains 1,700 km² of coral formations consisting of fringing reefs, submerged pinnacles and seamounts, limestone caves, sheer and sloping rock walls, and reef patch on sand bottoms. The variety of coral habitats supports a high diversity of marine resources. This paper reports 44 species of Opisthobranch molluscs from 45 stations of coral reef habitats in the southern Mergui Archipelago, based on two SCUBA dive survey expeditions undertaken in February 2014 and January 2015. Of those, two are Sacoglossa (Family Plakobranchidae), three Cephalaspidea (Family Aglajidae), and thirty-nine Nudibranchia (Family Chromodorididae, Discodorididae, Phyllidiidae, Flabellinidae, Facelinidae, and Aeolidiidae). The highest diversity was found at Kyun Philar Island (13 species), followed by Pollock Reef (10 species). The most widely distributed opisthobranch mollusc was Phyllidiella pustulosa (Cuvier, 1804). Multivariate cluster analysis shows that opisthobranch molluscs composition and diversity changes between coral habitats.

Keywords: Opisthobranch molluscs, Mergui Archipelago, coral reef habitats

GASTROPODS DIVERSITY IN SEAGRASS MEADOW OF BALANGDATU WATERS, TANAKEKE ISLAND, TAKALAR REGENCY, SOUTH SULAWESI, INDONESIA

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Marine gastropods hold important role in coastal ecosystems including seagrass meadows. The research about biodiversity of gastropod in seagrass meadow of Balangdatu waters, Tanakeke Island, Takalar Regency, South Sulawesi has been conducted. The research aims to know the diversity of gastropod species in Balangdatu waters. Sampling was conducted using quadrate transect method systematically, with three replicates of transect were applied for each station. Gastropods were identified based on main characters according to identification guidebook. Ecological indices such as Diversity, Evenness and dominance indices were applied to assess an environmental condition towards gastropods community. The result indicates that there were 34 species of gastropods from 14 genera and 14 families were found, respectively. Diversity index varies from 1.661 to 2.899 and these values range from low to moderate. The diversity, Evenness, and dominance indices showed that Balangdatu waters were in good condition and sustain habitat for gastropod.

Keywords: Diversity, Molusca, Seagrass meadow, community structure

UNDESCRIBED TAXA OF TRIASSIC AMMONOID, *HUNGARITES* (AMMONOIDEA: CERATITIDA: HUNGARITIDAE) IN SOUTHERN THAILAND

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The undescribed ammonoid specimens of the genus *Hungarites* (Cephalopoda: Ammonoidea: Ceratitida: Hungaritidae) were collected from the Lower Triassic Strata, Phukhaothong Dolomite Member, Chaiburi Formation, Lampang Group in Changwat Phatthalung, southern Thailand. The lobes of the suture of the present specimens are smooth; with only 3 lateral lobes compared to serrate lobes with 4-5 lateral lobes in congeners.

Keywords: undescribed taxa, Triassic, ammonoid, *Hungarites*, Thailand

EGG PLACEMENT HABITAT SELECTION OF CUTTLEFISH, *SEPIA LATIMANUS* (SEPIDAE; CEPHALOPOD; MOLLUSC), IN NORTH SULAWESI WATERS, INDONESIA

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Reproduction success of cuttlefish is promoted by the availability of suitable substrate for egg placement. This study was carried out to gather information on habitat selection of *S. latimanus* to lay their eggs and to describe possible factors influencing this behavior. Dive surveys were employed to pursue collect the data. Results showed that there were 8 species of branching corals selected, *Acropora micropthalma, A. brugemanni, Porites cylindrica, P. nigriscens, Hydnophora rigida, Echinopora horrida, Merulina scabricula,* and *Millepora*. There were also possible active compounds driving this selection.

Keywords: North Sulawesi, cuttlefish, *S. latimanus*, egg placement, habitat selection

REPRODUCTIVE BIOLOGY OF NEEDLE CUTTLEFISH, *SEPIA ACULEATA* (FÉRUSSAC & D'ORBIGNY, 1848), IN PENINSULAR THAILAND

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A total of 966 specimens of needle cuttlefish, *Sepia aculeata* (Férussac and d'Orbigny, 1848), were collected from different 4 localities including 490 specimens from the Andaman Sea and 476 specimens from the Gulf of Thailand. The results revealed that the needle cuttlefish were able to reproduce all year. However, the peak fecundity of females from both waters was in December but the peak of spermatophore numbers in males was in April in the Andaman Sea and in July in the Gulf of Thailand. Moreover, the peak of gonadosomatic index of females in the Andaman Sea was from February to December and in the Gulf of Thailand was February to October. The gonadosomatic index of males was from August to December in the Andaman Sea and from February to October in the Gulf of Thailand, the same period as females. The male to female ratio of the needle cuttlefish in Peninsular Thailand was 1: 2.07 ($P<0.05$).

Keywords: reproductive Biology, *Sepia aculeata*, Peninsular Thailand

THE POTENTIAL OF SYMBIONT BACTERIA IN *MELO MELO* GASTROPOD FOUND IN PEKALONGAN WATERS AS A SOURCE OF MDR ANTIBACTERIAL ACTIVE COMPOUND

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This research aims to discover the potency of symbiont bacteria in the gastropod *Melo melo* with capabilities in producing Multi-drug resistant (MDR) antibacterial compounds. Samples of *Melo melo* are collected from the Pekalongan, Central Java, Indonesia. This research begins with the isolation of symbiont bacteria, screening of symbiont bacteria with potency in MDR antibacterial activities, antibacterial test, and isolation of MDR clinical pathogenic bacteria. These protocols are then followed by antibacterial sensitivity test, and identification of bacterial species active against MDR by biochemical test and molecular analysis. Molecular analyses are carried out sequentially by DNA extraction, DNA amplification by PCR, and DNA sequencing. Results of 16S rDNA are analyzed using Genetix program and then followed by sequence analysis of the 16S rDNA. In this research, 11 bacteria in Melo melo are isolated and there are 4 isolates which show antibacterial activities against MDR bacteria from Pseudomonas sp. and Enterobacter sp species. Molecular analysis of the most active isolates identifies that isolate PM 26 matches in characteristics with *Brevibacterium celere* strain KMM 3637 with 89% homology match. On the other hand, biochemical test shows that isolate PM 26 is identical with Bacillus sp. This research concludes that symbiont bacteria found in *Melo melo* possess antibacterial activities against bacteria of MDR strain.

Keywords: symbiont bacteria, gastropod, antibacteria, Multi Drug Resistant

UNITAS MALACOLOGICA Grant Recipients

FORMING ELEMENTS OF SHELLS AND PEARLS (BLISTER) LAYERS FROM *PTERIA PENGUIN* AND *PINCTADA MARGARITIFERA* CULTIVATED IN NORTH SULAWESI, INDONESIA.

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The development of shells and pearls is not only related to physical formation of the layers but also to the chemical elements forming the layers. However, there is a little study to reveal such elemental compositions from pearl forming oysters. The purpose of this study is to analyze the chemical elements forming the shells and blister pearls of *Pteria penguin* and *Pinctada margaritifera* cultivated in Arakan, North Sulawesi. Samples of shells and blister pearls from *Pteria penguin* were taken from to the third, fifth and ninth month after nucleus insertions and similar sampling was conducted in the second, sixth and ninth month from *Pinctada margaritifera*. Samples were cross-sectioned and analyzed under Scanning Electron Microscope (SEM) and the chemical elements were detected with Energy Dispersive X-ray Spectroscopy. There is a big similarity between the shells and the blisters of *Pteria penguin*. Both have C, K, O, Na and Ca as the main elements. However, there is a difference in the elemental composition from both shells and blisters of *Pinctada margaritifera*. The main elements detected from this species are C, K, O, Na, Mg, Al, Si, Cl, Ca and Fe, but there was a different composition of C and K detected from shells and blisters of this species and both elements (C and K) were reduced during the development time. Chemical elements that are bound with Carbon (C) and CaO are representation of calcium carbonate and these are composed by 69% in the second month of the development of *Pinctada margaritifera*. It was assumed that there was a transfer of elements from shells to the blister layers. Water quality and biomineralization differences may affect the existence of the forming elements of shells and pearls layers.

Keywords: *Pteria penguin, Pinctada margaritifera*, chemical elements, shells, pearl layers

MOLLUSC PREYS ON THE STOMACHS OF WRASSE FISHES (LABRIDAE) CAUGHT BY INDIGENIOUS FISHERMEN IN BUNAKEN NATIONAL PARK, INDONESIA

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Recently abundance of coral polyp eaters and fluctuation of the community structure in the reefs have been related to the fish predator deflation by fishing pressure. On the other hand, studies of the prey-predator relationship were mainly neglected. It is important to notice “who eats who” within the reef ecosystem for the support of coral reef management. The aim of the present study was to identify the diets as well as the prey items of wrasse fishes that are intensively fished in the exploitation zone of Bunaken National Park. The contents of 132 stomachs from a total of nine fish species obtained from indigenous fishermen were examined. Food items were mostly digested, but some hard parts such as skeleton, bones and shell fragments were possible to identify. Food coefficient index revealed that mollusks were the main diet of seven wrasse fish species (Labridae) living in the coral reefs: *Hemigymnus melapterus* (Bloch), *Halichoeres trimaculatus* (Griffith), *Cheilinus chlorurus* (Bloch), *Choerodon anchorago* (Bloch), *Cheilinus fasciatus* (Bloch), *Cheilio inermis* (Forsskål) and *Hologymnosus annulatus* (Lacepède). For the other two fish species, *Novaculichthys taeniurus* (Lacepède) and *Coris gaimardi* (Quoy & Gaimard), mollusks were the second energy source. Mollusks occurring in the fish stomachs included *Mitra*, *Epitonium*, *Rhinoclavis*, *Trochus*, *Cypraea*, *Strombus*, *Tonna* and *Tectus*. Feeding niches of the fishes were discussed.

Keywords: Labridae, fish diets, Bunaken

SHELL RECONSTRUCTION AND TAXONOMY OF *SHIKAMAIA AKASAKAENSIS* OZAKI, 1968 (ALATOCONCHIDAE; AMBONYCHIOIDEA; BIVALVIA) FROM THE MIDDLE PERMIAN OF JAPAN

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The extraordinary large and aberrant-shaped shells of the Permian bivalve family Alatoconchidae (Ambonychioidea) are difficult to extract from the host limestone bodies and have been reconstructed their shape mostly by broken pieces of shell. The alatoconchid *Shikamaia akasakaensis* Ozaki, 1968 from the middle Permian Akasaka Limestone of central Japan, the type species of the genus, was described based on only three incomplete specimens and later reassessed its shell characters with fragmentary specimens from the Neo area, ca. 30 km NNE of the type locality. The type specimens of *S. akasakaensis* are too fragmental, being difficult to diagnose the species and taxonomically unable to compare the specimens to those from the Neo area as well as of other known species. A shell reconstruction based on 19 specimens from the type locality prepared with a grinding method reveals that *S. akasakaensis* exhibits a very large, elongated lanceolate to elliptical shell form, and shows that the shell of *S. akasakaensis* is most similar to the specimens previously allocated to the same species from the Neo area but clearly differs in having higher and longer dorsal crests and more dorsally reflected shell wings in their anterior portion, rendering an establishment of a new species for the latter specimens. The outer shell consists of a very thin outermost prismatic layer that is followed by thick layers of granular crystals, suggesting that the shell was not translucent enough to culture symbiotic algal zooxanthellae in the soft tissue of the animal. Discovery of the presence of a ventral gape, a previously unreported shell character, suggests the extension of the soft body into the sediment through it during alive. The algal symbiosis hypothesis for alatoconchids needs to be reconsidered.

Keywords: Akasaka Limestone, Alatoconchidae, Bivalvia, Permian, *Shikamaia*, taxonomy

MALACOLOGICAL SOCIETY OF JAPAN Grant Recipients

MORPHO-FUNCTIONAL ANALYSIS OF THE BUCCAL COMPLEX IN TWO SPECIES OF NUDIBRANCH MOLLUSCS

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Nudibranchia is a large group of gastropod molluscs, which is remarkable by morphological and biological diversity and can be characterized by especially wide range of feeding spectra. The evolution of nudibranch molluscs is possibly related to their adaptation to feeding objects. Up to now buccal complex's morphology is studied just for several species and it is insufficiently for functional analysis of food-obtaining apparatus. Thus buccal complex of two species of Nudibranchia from different groups (Dorididacea and Aeolidida) were studied for the first time. *Flabellina verrucosa* (M.Sars, 1829) (Nudibranchia: Aeolidida) specimens were collected in the White Sea and *Vayssierea elegans* (Baba, 1930) (Nudibranchia: Doridacea) were collected in the Japan Sea. The detailed examination of general and fine morphology of the buccal complex and cuticular structures was carried out using light microscopy, TEM and SEM. The 3D-reconstruction of the buccal complexes of *F. verrucosa* and *V. elegans* was constructed. According to our data there are three main groups of muscles in the buccal complex of *F. verrucosa* whereas in the buccal complex of *V. elegans* there are two of them. The functional analysis of the buccal complexes was performed and the feeding mechanisms for these species were supposed: suctorial-triturating feeding mode for *F. verrucosa* and drilling-suctorial for *V. elegans*. The obtained data were interpreted in relation to the position of these species on the phylogenetic tree of Nudibranchia. This research was supported by the Russian Foundation for Basic Researches, Grants N-15-04-02580 and N-16-34-00955 and by the Grant of the President N-6178.2015.4.

Keywords: nudibranch molluscs, feeding mode, buccal complex, buccal muscles

UNITAS MALACOLOGICA Grant Recipients

GENUS *HAMINOEA* (GASTROPODA) FROM MAHARSHTRA AND GULF OF KUTCH (INDIA)

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Genus *Haminoea* (Mollusca, Gastropoda, Haminoeidae). is least studied in India in general and in Maharashtra state particular. Field surveys were carried out in intertidal zones from October 2015 to March 2016. The taxonomic features including the shell, external morphology, animal coloration, radula, gizzard plates and penis were studied. Scanning Electron Microscopic images for radula, shell, gizzard plates and penis are provided for first time for many species. DNA profiling is also being undertaken. As of now only six species are currently known from India. Considering the fact that India has approximately 8000 km coastline, the studies on this genus is insignificant. Also being highly cryptic, species complex can be recorded as single species unless detailed anatomical and genetic studies are undertaken. Current work which aims to review Genus *Haminoea* across coastal states of India, a rapid survey along Maharashtra and Gujarat state was conducted. Till now eight distinct species have been recorded. The preliminary studies indicate several cryptic species.

Keywords: *Haminoea*, diversity, SEM, Maharashtra, Gulf of Kutch.

UNITAS MALACOLOGICA Grant Recipients

A SYSTEMATIC REVISION OF *CHONDROCYCLUS* (CYCLOPHORIDAE) REVEALS HIGH LEVELS OF NARROW-RANGE ENDEMISM, WITH IMPORTANT IMPLICATIONS FOR CONSERVATION IN SOUTH AFRICA

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A revision of *Chondrocyclus* was undertaken based on morphology and molecular data. These snails are characterised by an ornate periostracum with axial pleats, expanded into spiral rows of hairs, pointed or rounded flange-like extensions and a horny operculum with a spirally coiled fringe of fused bristles. Worn specimens on which several early descriptions were based lacked distinguishing morphological features leading to taxonomic confusion. Species discrimination, informed by these characteristics together with scanning electron microscope examination of the protoconch, radula and penis, has been extensively revised. Molecular data provided additional evidence guiding species delimitation. Sixteen species are recognised; nine new species are described and existing species redescribed. Several are cryptic species, previously recorded under other names. Most species are narrow-range endemics and the only apparently widespread species was revealed to represent a complex of cryptic species, which requires further study and description of its constituent species. Conservation management and legislation in South Africa are based on species information, but baseline data on terrestrial molluscs and other invertebrate groups is currently inadequate. Hence enhancing knowledge of the composition of molluscan biodiversity, including description of new species, together with accurate spatial information has important implications for conservation.

UNITAS MALACOLOGICA Grant Recipients

NEW MORPHOLOGICAL CHARACTERS RECLASSIFY ALYCAEID SPECIES IN MULTIPLE TAXONOMIC LEVELS (CAENOGASTROPODA: ALYCAEIDAE)

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The Alycaeidae are characterized by a tube-like structure, which runs along the suture between the last and the penultimate whorls. This apparatus opens inside the shell just behind the operculum, as well as similar devises do in other operculated land snails. However, in all the alycaeids, this apparatus appears to be externally closed at the both ends and completely sealed to the shell, whereas those tubes of the other operculated groups consistently have openings. This prompts a puzzle of air intake if the alycaeid devices are also tubes for that purpose. Pre-existing hypotheses speculated the possible presence of microscopic pores in the tube wall. Our examination of microstructure rules out this hypothesis and shows that the outermost shell layer of the body whorl along the suture forms several very slender channels which opens at the umbilicus and continue to the inside of the tube. These channels should allow the air to reach the snail body when the operculum seals the shell aperture. Based on the structure of the tube and corresponding breathing channels the Alycaeidae can be subdivided into three subfamilies. The first includes the Madagascan endemic *Boucardicus*, and the second includes the Southeast Asian *Laotia* and *Helicomorpha*, whereas all the remaining Asian alycaeid genera can be included in the third subfamily. The fine structure of the breathing apparatus and other characters, such as the sculpture of the protoconch and the teleoconch allows us to perform a genus-level revision of the whole family which is paramount since the last revision was published a century ago (Kobelt 1902). The new system we propose probably reflects the evolutionary relationships more accurately than the pre-existing one.

Keywords: operculated snails, Cyclophoridae, breathing apparatus, taxonomy, systematics

CLIMATE-RELATED SHELL VARIATION IN *TROCHULUS STRIOLATUS* (GASTROPODA: HYGROMIIDAE) AND ITS IMPLICATIONS FOR SUBSPECIES TAXONOMY

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The shell size of the land snail *Trochulus striolatus* varies widely within and between populations. Its shells from four biotic zones (lowland, submontane, montane and subalpine) were measured to identify the potential effect of bioclimatic factors and spatial variables (altitude, latitude and longitude) on the shell size and shape. Many of the shell features describing its size were significantly negatively correlated with precipitation parameters, temperature range and seasonality, longitude and altitude, and positively correlated with minimum temperature of coldest month, mean temperature of driest and coldest quarter as well as latitude. The shells were smaller at higher altitudes and in colder environment with larger temperature amplitudes. We propose that the reduced growth period is an adaptive response to the shorter vegetation season in mountainous regions, compared to lowland oceanic areas, where the longer season permits a longer growth resulting in larger mean adult body size. Our results suggest that in temperate climate the synergetic interactions between seasonality, temperature and moisture availability explain best the size variation. The ultimate size of *T. striolatus* is mostly a response to prevailing local environmental and/or climate variables. In this context, we show that the shell measurements and features do not justify the recognition of subspecies. Aperture width and height showed the strongest correlation coefficient with altitude, which was at best described by linear rather than non-linear models. It indicates a continuous cline of these features. However, relationships of most other shell characters were better fitted by non-linear models.

Keywords: altitude, phenotypic plasticity, subspecies, *T. s. abludens, T. s. danubialis, T. s. juvavensis*

HOMOLOGOUS SERIES OF SHELL VARIATION IN LYMNAEID SNAILS AND ITS TAXONOMIC IMPLICATIONS

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The shell morphospace of the lymnaeid snails (fossil and living) is very wide and encompasses a contunuous range of turbospiral morphotypes as well as true limpets (this shell shape has independently evolved in at least two phylogenetically distant lymnaeid clades). The parallel evolution of shell shape has been observed in different genera and species of the family including intriguing cases of very similar habituses arising in unrelated groups belonging to different subfamilies. An explanation of parallel evolution of lymnaeid shell based on Raup's geometric model of shell coiling is proposed. Certain geometric constraints rather than environmentally driven factors seem to induce this parallel evolution. The possible taxonomic implications of it are discussed. It is shown that many alleged "species" or "varieties" of lymnaeid snails introduced in the past are nothing but arbitrarily separated parts of continuous series of variation. Such homologous series of variation (sensu Vavilov, 1922) have been discovered in many species of lymnaeid (especially in widely distributed and ecologically plastic ones) that creates serious difficulties for morphology-based taxonomy. The use of the integrative approach to lymnaeid systematics may help resolve it but this approach is hardly applicable to fossil groups. The cases of parallel variation are not restricted to the family Lymnaeidae. Analogous examples of homologous series can be found in other taxa of freshwater snails with turbospiral (Bithyniidae, Valvatidae) and planispiral (Planorbidae) shells. The breakage of a continuous series of variation into several independent blocks divided by hiatuses seems to act as a possible (though highly speculative) mode of speciation in freshwater snails. Certain geometric constraints rather than environmental factors seem to be responsible for.

Keywords: Lymnaeidae, shell morphology, taxonomy, geometric constraints, Raup's model

SOUTH AMERICA ANCYLINAE (PLANORBOIDEA): SYSTEMATICS AND DISTRIBUTION

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Currently Ancylinae is amember of Planorboidea, but previously it was assigned at familiar rank, Ancylidae. It is encompassing freshwater gastropod limpets. In order to update the knowledge and diversity of ancylids in South America, a taxonomic revision and distribution of species it is being carried out. Eight genera inhabits in South America: *Anisancylus* Pilsbry, 1924; *Burnupia* Walker, 1912; *Ferrissia* Walker, 1903; *Gundlachia* Pfeiffer, 1849; *Hebetancylus* Pilsbry, 1913; *Laevapex* Walker, 1903; *Sineancylus* Gutiérrez-Gregoric, 2012 and *Uncancylus* Pilsbry, 1913 encompassing about 18 described species. The study is being performed considering new data on shell morphology and micro sculpture, anatomy and molecular biology. Records on the distribution of species are being reviewed considering data from literature, museum collections as well as new data from field works and projects in collaboration with other institutions. Preliminary results show the group is highly diverse, with some regional endemism although some species are widespread. The new records of distribution allowed to extend the geographic distribution of many species. Molecular studies, based on COI and 16S confirmed *Burnupia* as a clade outside Ancylidae and Planorbidae and corroborated morphological data, supporting the validity of the so called Neotropical ancylids (*Anisancylus, Gundlachia, Hebetancylus and Uncancylus)* and *Sineancylus*. Based on a comprehensive analysis, including both morphological and molecular methodologies, we were able to identify the examined specimens of different genera and species. With this, we are contributing to increase our understanding of systematic and distribution of ancylids that could be important to support future conservation strategies in South America.

Grants: CNPq/Protax, Faperj, Capes

Keywords: Freshwater snail, Neotropical Ancylinae, pateliforms basommatophorans

IMPACTS OF 2011 EARTHQUAKE AND TSUNAMI ON LAGOON AND SUBTIDAL MACROZOOBENTHOS COMMUNITIES

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Physical disturbances, such as earthquakes and tsunamis, can have drastic effects on marine organisms and marine ecosystem. Especially the benthic animals living in estuaries, lagoon and inner bay, which are strongly associated with soft substrates, were severely affected by the 2011 Great East Japan Earthquake and tsunami. The benthic communities of Gamo Lagoon and Onagawa Bay, located on the Pacific coast of northeastern Japan, were thought to have severely damaged. The aim of the present study is to discover the ecological impacts of the Great East Japan Earthquake and tsunami on the lagoon and the subtidal macrozoobenthos, and to examine the response of the community to a large-scale disturbance. The density, biomass, and diversity of macrozoobenthos decreased after the earthquake and tsunami, and the community structure fluctuated after the disturbance. In this fluctuation period, opportunistic polychaete species occurred initially and abundantly. Following polychaete recolonization, the bivalve *Theora lubrica*, which has a long planktonic larval period, dominated in Onagawa Bay. On the other hand, following continuous topographical changes, although polychaetes and crustaceans recovered sooner in numbers, recruitment of bivalves was delayed. The overlapping effects of the natural and anthropogenic disturbances are considered to have an impact on the macrozoobenthos community. The community in both Onagawa Bay and Gamo Lagoon is still under unstable condition and in the process of succession though 3 years have passed after the tsunami disturbance.

Keywords: macrozoobenthos, community, impacts, earthquake and tsunami, lagoon, inner bay

SHORT-TERM AND LONG-TERM EFFECTS OF THE 2011 GREAT EAST JAPAN EARTHQUAKE ON INTERTIDAL MOLLUSKS

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The Great East Japan Earthquake that occurred on the 11th March 2011 caused a great deal of damage to the organisms that inhabit the coast of the Tohoku district of Japan. In this paper, I mainly focus on the earthquake's impact on bivalves that inhabit the sandy intertidal zone, with specific emphasis on the short-term effects from liquefaction and the tsunamis and the long-term effects of land subsidence. As previous studies have not discussed the details of the separate physical events of this type of natural disaster, this study divided it into three main events; the initial earthquake including liquefaction, subsequent tsunamis and land subsidence. During the liquefaction period, bivalves were brought to the surface with jets of water and were then swept away by the tsunamis. As such, both the magnitude of the tsunamis and length of the liquefaction period were factors critical to the survival of clams. The tsunamis have also contributed to dispersion of benthic organisms. For example, the redistribution of oysters across the mud bottom increased their range. In addition to these events, land subsidence resulted in marked changes to the vertical position of the intertidal zone. These large changes in the physical environment cannot recover in the short term and the re-adjustment of tidal communities is expected to take several decades. However, land subsidence has also formed new intertidal zones, which will ultimately promote the colonization of various organisms. These disturbances to the ecosystem have destabilized these bivalve species resulting in fluctuations in abundance and community structure for at least three years following the earthquake. Finally, continual monitoring studies are needed to understand the ecological impacts resulting from the earthquake, and the artificial seawall and tidal flat that have been constructed since the quake, on benthic organisms inhabiting the coastline of the Tohoku district, Japan.

Keywords: mollusk, earthquake, tsunami, liquefaction, subsidence, disturbance, tidal flat

IMPACTS OF THE 2011 GREAT EAST JAPAN EARTHQUAKE AND TSUNAMIS ON SHELL FORMATION OF THE INVASIVE NATICID GASTROPOD *EUSPIRA FORTUNEI* AND COMMERCIALLY IMPORTANT BIVALVES

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On 11 March 2011, the Great East Japan Earthquake and tsunamis occurred in Japan. It caused huge damage to the marine organisms including mollusks along the Pacific coast of Northern Japan. The invasive naticid gastropod *Euspira fortunei* (*Laguncula pulchella*) introduced with imported Manila clam *Ruditapes philippinarum* from China and Korea has been found living after the earthquake. The growth break like the bivalves was observed on the shell surface in almost all samples collected in Matsushima Bay and Matsukawa-ura Lagoon in Northern Japan after the tsunamis were examined by Scanning Electron Microscope and Electron Probe Micro Analyzer. The shell of *E. fortunei* consisted of three layers before and after the "tsunami" break. The newly formed middle crossed lamellar layer became thinner after the "tsunami" break. It may be the result of rapid change of the mineralization process including quick shell growth and/or repair. Eight elements (C, O, Na, S, Cl, K, Ca, Sr) were detected in all samples analyzed in this study. The concentration of three elements (S, Fe, Si) increased after forming the growth break in the samples from Matsukawa-ura Lagoon where the tsunamis of 9m or more came. However, there was no similar tendency in the samples from Matsushima Bay where large tsunamis did not come. It is suggested that the size of the tsunamis could be involved in the process of shell formation and the level of some elemental concentration. We also observed the microstructures and the elemental concentrations after the tsunamis in some bivalve species such as *R. philippinarum* and *Meretrix lusoria* in Matsukawa-ura Lagoon. The concentration of two elements (S, Sr) increased after forming the growth break. These results suggest that derangement of habitats by tsunami was stressed on *E. fortunei* and commercially important clams. Stop or decrease in the shell formation after the tsunami was a common phenomenon for the mollusks that inhabited tidal flats.

Keywords: earthquake, tsunami, growth break, *Euspira fortunei*, clam, shell structure

MALACOLOGICAL SOCIETY OF JAPAN Grant Recipients

2004 TSUNAMI IN THAILAND: THE IMPACT AND RECOVERY OF REEF COMMUNITIES

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After the 2004 Indian Ocean Tsunami, the impact of the tsunami on reef organisms at Mu Ko Similan Marine National Park and the recovery was investigated. In addition, changes of populations of corals, sponges and molluscs were observed. The overall results showed that the damage to corals and other reef organisms by the tsunami was low, although, the damage was found as deep as 27 meters. In addition, intensive surveys showed that massive coral form was the most susceptible to the tsunami at almost every study site. From the surveys, at Snapper Alley Point, 30m below mean seawater level, we observed a significant amount of sand and rubble up to 2m deep was scoured out from the seafloor by the tsunami. Ten years after the tsunami, monitoring surveys found that rocks and seafloor at 30-meter depth, which were once covered by sand before the tsunami, are now covered with new recruitments of soft, hard coral, sponge, and mollusc communities. Thus, a totally new community has been created out of the chaos of 2004.

KARST ENDEMISM AND THE CONSERVATION OF EVOLUTIONARY HISTORIES

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Isolated karstic outcrops in Southeast Asia are numerous and well known among malacologists and conservationists alike for their rich malacofaunas, in terms of densities, diversities, and degrees of endemism alike. In several snail taxa, single-site endemism is rife, with many species globally restricted to individual outcrops, sometimes of only a few hundred metres across. Such species are often considered endangered or vulnerable, especially if the site is threatened by development. Consequently, arguments for conservation of sites often focus on such vulnerable site-endemics. However, such a focus on the species itself, is shallow and risky. Many site-endemic species of the same genus are ecologically replaceable and could therefore be candidates for ex-situ conservation. Moreover, the focus on the species as a conservation entity ignores the evolutionary reasons for endemism itself. I will highlight a few cases from Malaysian Borneo where detailed knowledge of the evolutionary process that has given rise to endemic species allows not just the end-product (the endemic species) to be valued, but also the evolutionary route by which these species have come into existence.

DYNAMIC EVOLUTIONARY PATTERNS IN LAND SNAILS OF THE GENUS *GEORISSA*

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The study of gastropod shell characters is ideally suited to understand character evolution and evolutionary diversification. In this study I am proposing to explore the shell character evolution of minute land snails from the genus *Georissa* (Family: Hydrocenidae). This poorly known genus occurs throughout Southeast Asia, and is particularly rich in shell-shape diversity in Borneo. The animals are known to occupy limestone hills, and they could also be found at lower density areas such as on rocky substrates. Extensive morphometric study is proposed by using micro-computed tomography on a µCT-scanner and the application of recently developed models for quantifying shell shape. At the same time, molecular analysis is expected to reconstruct the evolutionary history of *Georissa* with the combination of morphological variation through time. This research will be carried out to give insights in the character evolution and diversification, long-term patterns and dynamics of adaptation, and conservation of these minute land snails.

UNITAS MALACOLOGICA Grant Recipients

EFFECTS OF DIFFERENT LAND USE TYPES ON INVASIVE AND NATIVE LAND SNAIL SPECIES IN JAVA LIMESTONE OUTCROP

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We investigated the effects of different land use types on the number and abundance of native and introduced land snail species in South Malang limestone outcrop, East Java. 2919 specimens were sampled and assigned to 55 species of which 8 are introduced. Whereas species richness was highest in primary forest, the highest number of introduced species was found in agroforest. The snail assemblages in different habitat types differ much clearer in composition than in total species richness. Plantations and agroforest are dominated by introduced pulmonates with regard to number of individuals, while primary forest is dominated by native prosobranchs. The habitat requirements of the introduced pulmonates differ from those of the native species. In the study area, the abundance of introduced pulmonate species significantly decreased with increasing density of the canopy cover and increased with increasing human impact, whereas the abundance of native prosobranch land snails decreased with increasing human impact and tends to increase with the availability of deadwood and with increasing canopy cover. Improving the canopy cover and retaining deadwood in plantations and agroforests might help to control the populations of introduced species or even prevent their establishment in these habitats. Dense plantations and agroforests bordering primary forests may protect the latter from introduced species and help to conserve the native fauna by reducing desiccation and buffering the human impact on the primary forests.

Keywords: agroforest, Indonesia, plantation, rainforest, gastropods, invasive

USING PHYLOGENETICS AND BIOGEOGRAPHY OF *ALYCAEUS* LAND SNAILS TO INFORM TROPICAL KARST CONSERVATION IN MALAYSIA

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Tropical limestone karsts are regarded as having high conservation value due to their role as refugia for biodiversity and a large number of endemic taxa threatened by human-induced habitat loss such as quarrying, agricultural land conversion and fires. The management and protection of karst biodiversity can best be served through assessment of the biological and economic value of individual karsts. As such, sound understanding of the taxonomy and phylogeny of karst endemic taxa is a fundamental cornerstone for informing karst biodiversity conservation plans. Here, we present an ongoing case study of using the mostly limestone-obligate land snail genus *Alycaeus* as our model taxa. The genus *Alycaeus* displays remarkable species diversity in Peninsular Malaysia, with 12 species and 1 subspecies recognised currently. Most *Alycaeus* species and subspecies (e.g. *Alycaeus perakensis perakensis*, *Alycaeus perakensis altispirus*, *Alycaeus kapayanensis*) appear to be limestone rock obligates, hence possibly confined to individual karsts. In contrast, some species (e.g. *Alycaeus gibbosulus, Alycaeus kelantanesis*, *Alycaeus liratulus*) appear to be widely distributed across both limestone and non-limestone habitats. We suggest possible roles of species population dispersal and speciation, as well as their relationships with dispersal barriers and facilitators in the formation of high species richness across Peninsular Malaysia. We will then highlight implications to the conservation of limestone karsts in Peninsular Malaysia.

Keywords: terrestrial, Gastropoda, *Alycaeus*, phylogeography, limestone karsts, conservation, Peninsular Malaysia

PROTECTED OR UNNOTICED IN THE LIMESTONE UNDERGROUND? – IMPLICATIONS FROM STUDIES ON EUROPEAN STYGOBIONT *BYTHIOSPEUM* (GASTROPODA: RISSOIDEA)

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The genus *Bythiospeum* Bourguignat, 1882 represents a group of European rissoidean freshwater snails that are obligate stygobionts living in groundwater, caves, interstitial water in river plains and – most closely to the surface and accessible – in springs. Although not exclusively, their known distribution and areas of increased diversity are strongly linked to the occurrence of limestone. The systematic concept within the genus changed significantly over time and the currently accepted version results in a diversity hotspot with a number of endemic taxa expecially in Southwestern Germany. Results of recent systematic studies on Central European species from Germany, Swiss and parts of Austria and France are evaluated with respect to their implications towards conservation. The investigations were based on molecular and morphological data of nearly 200 specimens representing about 26 currently accepted taxa including a significant share of topotypic material. Special attention is given to the relation of diversity and the potential age of habitats in context of the geological past and the range of the respective species. In addition, available IUCN Red List data of 60 accepted species throughout Europe are critically reviewed and discussed with reference to threats to their special habitat.

Keywords: groundwater organisms, systematics, diversity, conservation, limestone, habitat age, IUCN Red List

THE COCKPIT COUNTRY OF JAMAICA: A LIMESTONE FOREST AREA OF GLOBAL IMPORTANCE

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The Cockpit Country encompasses approximately 70,000 hectares of karst terrain in west-central Jamaica. Characterized by its steep conical limestone hills and bowl-shaped valleys (i.e., cockpits), it is the type locality for "cockpit karst" limestone. Home to the largest and most intact primary wet limestone forest and largest aquifer in Jamaica, it is a biodiversity hotspot of global importance. Although about a third of it is a designated forest reserve, it has remained susceptible to human exploitation; Cockpit Country Stakeholders Group identified bauxite mining as the most imminent threat to its ecological integrity. We compiled a list of Jamaican terrestrial gastropod species by parish and region based on biodiversity survey field records, validated museum records at the Academy of Natural Sciences, and published type localities. We found that the Cockpit Country is the most species-rich area in Jamaica; more than 200 species are known to occur within the Cockpit Country, or 40% of all land snail species from Jamaica. Among those, 90% are endemic to Jamaica, and 31 species are endemic to the Cockpit Country itself. We also developed multivariate, spatially explicit, statistical models to uncover major determinants of terrestrial gastropod species richness. The statistical model revealed susceptibility of terrestrial gastropods to human disturbance, as species richness was negative correlated with erosion and presence of secondary forest. Our results reinforce the importance of the Cockpit Country to global biodiversity conservation and the need to strengthen protection of its remaining primary forest.

Keywords: cockpit karst, terrestrial gastropod, species richness, endemism, bauxite mining

THE TERRESTRIAL SNAILS CONSERVATION IN A SMALL UNIQUE ISLAND NUSA KAMBANGAN IN JAVA, INDONESIA

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Nusa Kambangan is a small island located in Indian Ocean and separated by Segara Anakan a narrow strait of the southern coast of Java. The island is very unique adminitratively, its maximum security for prisons but also opened to the public for tourism destination. The eastern side of the bay is a nature reserve area wich is very diverse for fauna and flora but now has been negativelly affected by widespread illegal logging and cement industrial activity that usually by blasting the limestone area. Monitoring study was conducted in 2010 , and found only 18 species of terrestrial snail that most were living in the karst area in central area of the island (Cave Ratu, Sendang Putri, Lawa, Willy and forest track A,B,C). The snails are belong to the family Cyclophoridae, Ariophantidae, Camaenidae, Trochomorphidae, Helicarionidae, Clausiliidae and Subulinidae that were threatened because of the environment damage.

Keywords: Terrestrial snails, conservation, Nusa Kambangan, Java

CROSSED-LAMELLAR LAYER IN EVOLUTION OF THE MOLLUSCAN SHELL MICROSTRUCTURES

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Mollusc shells represent an important portion of the large family of biomaterials. By studying the shell microstructures, we gain a better understanding of how molluscs have developed exceptionally strong protective shells. The nacreous layer and the crossed-lamellar (CL) layer have been shown to be several orders of magnitude stronger than their geological counterparts, aragonite. A large number of proteins are involved in the control of biogenic mineral formation. The CL layer contains much less organic matter compared with in nacre, less energy is required for protein synthesis. This low energy-consuming layer is the most common type of mollusc shell microstructure. We are interested in the comparison of hierarchical architectures and crystallographic form in CL layer and nacreous layer, for getting a better insight of biogenic mineral evolution. The potential use of our understanding of the microstructure in novel bio-inspired and biomimetic applications may be feasible for developing material with high fracture toughness and low cost.

Keywords: Crossed-Lamellar microstructure, nacreous layer, organic molecules

TENACIOUS SUCKERS: AN INVESTIGATION INTO THE ECOLOGY OF ECTOPARASITIC SNAIL (FAMILY PYRAMIDELLIDAE) ON GIANT CLAMS AND ITS CONTROL MEASURES

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Globally, giant clam hatcheries contribute cultured clam stock for food production and conservation efforts. However, the prevalence of *pyramidellid* (pyram) snail infestations has caused detrimental effects for these maricultured clams such as slow growth and low survival rates. Physical removal via brushing, washing, and isolation, are the standard techniques used by researchers and aquarists to control these parasites, but their efficacy is limited. Therefore, this study was aimed at formulating better eradication techniques by examining several aspects of pyram ecology including their behaviour, spatial distribution on clam shells, and resistance to selected chemicals and elevated temperatures. Surveyed pyrams were mostly found on the hinges, byssal orifice and lower half of the clams' shell valves. In a series of trials, snail specimens were submerged in various concentrations of tannin solution, ethanol, and household bleach solution for periods of 3, 5, 10, 20 and 30 minutes. Bleach solution turned out to be the most effective molluscicide of the three tested reagents. Pyrams were also subjected to heat shock treatment at nine temperatures ranging from 39 to 43°C, with increments of 0.5°C. The greatest mortality occurred at temperatures above 42.5°C. Pyram attraction to effluent from conspecifics, and from hosts (giant clams), is currently being tested. Together, our results will contribute towards the development of effective control techniques for pyram infestations on cultured giant clams.

Keywords: *Tridacna*, mariculture, Pyramidellidae, ectoparasites, ecology, eradication methods

RECOGNITION OF SNAIL HANDEDNESS BY A SNAKE PREDATOR, *PAREAS CARINATUS*

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Specialized predator-prey interactions can be a driving force for their coevolution. The Southeast Asian snail-eating snakes of the have more teeth on the right mandible and specialize in predation on the clockwise-coiled (dextral) majority in shelled snails by soft-body extraction. Snails have countered the snakes' dextral-predation by recurrent coil reversal, which generates diverse counterclockwise-coiled (sinistral) prey. However, whether the snake predator in turn evolves any response to prey reversal is unknown. Herein we demonstrate that *Pareas carinatus* living with abundant sinistrals avoids approaching or striking at a sinistral that is more difficult and costly to handle than a dextral. Whenever snake strikes, however, the snake succeeds in predation by handling dextral and sinistral prey in reverse. *P. carinatus* is frequently active on trees where invariably sinistral snails of the subgenus *Syndromus* and also chirally dimorphic snails of the genus *Amphidromus* abundantly co-occur. In this habitat, handedness recognition by the snake to avoid predatory attempts on costly sinistrals should be advantageous. The predator does not evolve to exploit sinistrals by arms race because the easier prey type (dextral) still remains abundant. On the other hand, no sinistral tree snail co-occurs with a congeneric snake *P. iwasakii* on the islands where only one of 23 potential ground-dwelling prey species is sinistral. Thus, it would be of little advantage for *P. iwasakii* to evolve an ability to distinguish between prey enantiomorphs. This explains its frequent failure to capture a given sinistral snail after striking without recognition of prey handedness. Under dextral-predation by *Pareas* snakes, adaptive fixation of a prey population for a reversal gene instantaneously generates a sinistral species because interchiral mating is rarely possible. The novel warning, instead of sheltering, effect of sinistrality benefitting both *P. carinatus* and prey snails could further accelerate single-gene ecological speciation by left-right reversal.

THE ONTOGENY OF SHELL-BORING *OCTOPUS* VERSUS *NAUTILUS* PREDATOR-PREY INTERACTIONS

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To complete our picture of predatory boring by *Octopus*, this study focuses on the rate and pattern of *Octopus* predation in pre-adult stages of *Nautilus*, which encompasses the first 15 years of its life. Dry shells from several natural history museum collections were used for this study. In the 555 examined shells, 334 borings were found. For adult *N. pompilius* 136/242 (56.2%) were bored, while for juvenile *N. pompilius* 41/154 (26.6%) were bored. Of the juvenile *Nautilus* 8/52 (15.4%) have multiple borings while 68/179 (38%) of the adult *Nautilus* have multiple borings. One adult *Nautilus* has 6 borings and one juvenile *Nautilus* has 5 borings, both of which set a new record. In adult *Nautilus*, there appears to be no preference to bore on the left or right side of the shell: 129 borings are on the left side (48%) and 140 borings on the right side (52%). In juveniles, though, there is a clear difference in left and right borings. With 47 borings on the left (75,8%) and 15 borings on the right (24,2%) there is a statistical difference. Not just all species of *Nautilus* are attacked by *Octopus*, their predation also has a big impact on all ages.

MALACOLOGICAL SOCIETY OF LONDON Grant Recipients

PREDATION ON FRESHWATER SNAILS IN MIOCENE LAKE STEINHEIM AS A TRIGGER FOR INTRALACUSTRINE EVOLUTION

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Shells of the freshwater gastropods *Gyraulus trochiformis* (Planorbidae or ramshorn snails) and *Bania pseudoglobula* (formerly *Pseudamnicola*, Hydrobiidae) from Miocene (*ca*. 15 Million years before present) Steinheim Basin in SW Germany contain small holes with a mean diameter of 0.8 mm. Comparable holes are so far unknown from fossil or extant assemblages of freshwater shells. This analysis of the perforated shells suggests that the holes were not formed by post-depositional or pure taphonomic processes. Instead, they were most likely produced by predators. This analysis widens the means for identification of predation on freshwater snail shells that can be used in other palaeolimnological studies. The co-occurrence of fish teeth and perforated shells in the studied samples as well as the perforation features suggest that the predator was tench fish. The correlation between shell sizes and hole diameters suggests a size relationship between predator and prey that may generally be related to gape-limited fish predators. The co-occurrence of perforated shells in these lake sediments with a dominance of large and armoured shells suggest that these larger shells with protuberances and knobs could not be crushed by the gape-limited fish predators. This analysis is the basis for a hypothesis that the endemic evolution of *Gyraulus* in Lake Steinheim, with some varied forms of shell thickness and morphology, was triggered by a predator–prey relationship based on adaptations to avoid shell-breaking predators.

Keywords: *Gyraulus*, intralacustrine evolution, predation, Miocene Lake Steinheim

HOLOPLANKTONIC MOLLUSKS (GASTEROPODA: PTEROPODA AND HETEROPODA) FROM THE GULF OF CALIFORNIA, MEXICO IN AUGUST, 1977 AND FEBRUARY AND OCTOBER, 1978

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Some holoplanktonic gastropods belonging to Heteropoda (superfamily Pterotracheidae) and Pteropoda (Heterobranchia, orders Thecosomata, and Gymnosomata). These mollusks have a significant role in the ecology of the pelagic communities, for example, in the global carbon cycle of the marine ecosystems, as food of many fishes, particularly some species with commercial values, as tuna, herrings, and mackerels, etc., or as indicators organisms of hydrological conditions of some water masses in the oceans. An analysis of the distribution and abundance of species of these gastropods from the Gulf of California, Mexico is presented. Zooplankton samples were collected during three oceanographic cruises (AA7704, AA7802, and AA7810) by oblique tows in the epipelagic region, (between 200 m deepth to the surface), using a standard net of 1.0 m of mouth diameter, 1.5 m long, and 505 µm mesh. A total of approximately 18, 000 specimens were sorted from the total of 45 zooplankton samples, which were determinate on 43 species of mollusks, 72 % of Pteropoda and 28 % of Heteropoda. In a general way, Pteropoda were dominated by *Creseis vírgula* and *Hyalocylis striata*, while, Heteropoda was headed by *Atlanta leuseuri*. Variations of the species richness, distribution, and density of these holopelagic mollusks are discussed in the three periods of study.

Keywords: Holoplanktonic mollusks, Gulf of California, Pteropoda, Heteropoda, seasonal variations

EARLY LIFE DEVELOPMENT OF THE CORALLIVOROUS GASTROPOD *DRUPELLA RUGOSA*

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Muricid gastropods of the genus *Drupella* are corallivorous and widespread throughout the Indo-Pacific region. Population outbreaks of *Drupella* can decimate up to 75% of coral reefs and thus constitute a major threat to reef ecosystems. Little is known, however, about the early life stages of most *Drupella* species. We report the first observation of *Drupella rugosa* egg capsules on the hard coral *Pocillopora damicornis*. Up to 104 capsules were observed on two *P. damicornis* fragments, which were kept together with a pair of randomly selected *D. rugosa* individuals in aquarium tanks. The egg capsules were deposited in clusters directly on the coral skeleton. No capsules were observed on the live coral tissues or inner walls of the tanks. Like its congener *D. cornus*, egg capsules of *D. rugosa* appear kidney-shaped in cross section. The capsules averaged 2.44 mm in diameter and each contained about 60 embryos. The capsules are maintained in outdoor aquaria supplied with flow-through filtered seawater with temperature, salinity and light averaging 29.5°C, 29 ppt and 375 μmol $m^{-2}s^{-1}$ respectively. After 14 days, the embryos hatched into planktonic veligers and the early development of the larvae was documented. The newly hatched free-swimming veligers averaged 328 x 245 μm (width × depth). Our observations indicate that coral skeletons function as substrate for the attachment of *D. rugosa* egg capsules and also support the early embryonic development of the gastropod. With the increase in *Drupella* population densities in recent years, further studies into the early life strategies of *D. rugosa* are necessary to mitigate their impacts on coral reefs.

Keywords: Muricid, coral reef, *Drupella rugosa*, veligers, reproductive ecology

MODEL ORGANISM *LIMACINA HELICINA* (PHIPPS, 1774) - A COMPLEX STORY

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Shelled pteropods (Thecosomata) form a cosmopolitan monophyletic clade of holopelagic euopisthobranch gastropods. The aragonite shell of euthecosomes has been demonstrated to be vulnerable to lowered seawater pH, rendering them a suitable bioindicator for ocean acidification research. In particular the "species" *Limacina helicina* with its extraordinary delicate shell bears a high indicative potential and is thus frequently used to monitor rising acidification in polar and subpolar regions. It is also one of the most abundant pelagic organisms, of major ecological importance, and supposedly threatened by ocean chemistry change. The actual taxonomic status of *Limacina helicina* is confusing. There is a conglomeration of subspecies and "formae" characterized by hardly perceptible differences restricted to shell morphology. Most of these descriptions left the soft body unrewarded and still there is little information on internal morphology and organ functions. Initial single gene approaches indicated high genetic divergence between Arctic and Antarctic clades, which is suggestive for the presence of a species complex. Different species may have different ecological preferences and tolerances to changing environments. This integrative taxonomical study combines modern microanatomical investigation techniques with a multilocus molecular analysis of an extended set of newly generated sequences from specimens representing both hemispheres. 3D-reconstructions based on semithin histological sections revealed an astonishing anatomical resemblance of northern and southern clade. Molecular analyses, in contrast, support the presence of a species complex with at least three species. To provide a reliable taxonomic foundation for any ecological work, it is eminent to explore the actual species diversity of *Limacina helicina* covering its entire geographic range.

Keywords: Pteropoda, microanatomy, 3D-reconstruction, zooplankton, phylogeny

UNITAS MALACOLOGICA Grant Recipients

NEW INSIGHTS INTO ATLANTID TAXONOMY AND BIOGEOGRAPHY

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The Atlantidae is a poorly known family of microscopic, aragonite shelled holoplanktic gastropods. Despite the current interest in shelled pteropods, the atlantids are rarely considered in recent zooplankton research, which is likely due to difficulties in catching and identifying them. However, recent quantitative plankton sampling has revealed that atlantids make up an important part of the calcareous ocean zooplankton. Research on pteropods also suggests that atlantids are likely to be negatively affected by current and future global changes. Therefore, it is important that we improve our understanding of this potentially important and threatened family of gastropods. Until recently, the taxonomy of atlantids has been restricted to morphological characteristics of the shells, eyes, radula and operculum. Combined molecular and morphological techniques are now helping us to examine atlantid taxonomy in more detail. Here we present initial results of the DNA barcoding of atlantids from the Atlantic, Pacific and Indian oceans, as well as an update on current atlantid biogeography. Results have already revealed a new species that is restricted to the narrow circumpolar Sub-Tropical Front and highlights interesting patterns in biogeography, particularly in the Atlantic Ocean. Our overall aim is to improve the availability and quality of taxonomic and biogeographic information for the atlantids, in the hope of encouraging their documentation in future zooplankton research.

Abstracts

POSTER PRESENTATIONS

THE MARINE MOLLUSC COLLECTION AT THE NATURAL HISTORY MUSEUM, LONDON

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The Natural History Museum, London holds one of the largest and most important collections of molluscs in the world with an estimate 8 million specimens. The marine collection includes around 40,000 type lots for the phylum, mainly from the collections of Cuming, Sowerby, Smith, Gray, Adams, Melvill, Hinds, Carpenter, d'Orbigny, to name a few. As well as the scientific importance of the collections, a wealth of material originating with Sloane, Banks, Cook, Darwin, Lyell, Cracherode and Montagu gives an unparalleled historic dimension to our holdings. A dedicated library of over 6,000 bound volumes and 30,000 reprints on molluscs, dating from the 17th century, provides an incredibly accessible source of information to support collections, curation and research.

ECOLOGY OF PINNIDAE FROM CORAL HABITAT IN THE GULF OF THAILAND

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Taxonomically identification showed three species of Pinnidae were collected from field. Only one species, *Atrina vexillum* and two *Pinna*, *Pinna atropupurea* and *P. deltodes* were reported. Thai Pinnid were generally varies distributed among ten study sites of coral habitat. The distribution analysis showed was mainly shallow water depth not more than 4 m that mostly pinnid were commonly clump distributed except Ko Sak was random distribution. Density of pinnid in the Gulf of Thailand was showed varies in each sites, however *A. vexillum* showed the highest density (1.86±0.57 individual/m^2) following *P. deltodes* (0.77±0.17 ind/m^2) and *P. atropurpurea* (0.40±0.11 individual/m^2) respectively. Sai Bay, Chang Island, Trat Province was an important site for *A. vexillum* density that was reported 0.5±0.16 individual/m^2. The highest density of *P. deltodes* was report at Leam Yuon Bay, Lan Island, Chonbui Province (0.27±0.08 individual/m^2). Density of *P. atropurpurea* was maximum at Sabbarod Bay, Chang Island. Percentage of dead shell showed *Pinna* were significant higher than *Atrina* but not significant different between *P. atropurpurea* and P. atropurpurea. Higher density of *Atrina* than *Pinna* in coral habitat of the gulf of Thailand could explained by boring and attachment mechanism of *Atrina* such as shorter distance of the sediment - water interface (3.93±0.41 cm) with longer byssus thread length (8.04±0.46 cm), higher number of particle to attachment by byssus (213.75±9.7 particle/ bundle) and selected smaller size of objective for attachment (0.54±0.09 cm)

Keywords: distribution, density, coral habitat, *Pinna atropurpurea*, *Pinna deltodes*, *Atrina vexillum*, island, Gulf of Thailand

MANIPULATION AND TRANSPORT VELOCITY OF SEQUESTERED FOOD PARTICLES IN BIVALVE MOLLUSCS IN RELATION TO GILL MORPHOLOGY: A SYNTHESIS

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In bivalve mussels suspension feeding by the gill is the principal means by which food particles are obtained. Once captured, particles are moved towards the mouth by means of the ventral food grooves (VFG) and/or the dorsal food grooves (DFG) on the gill, which are essentially channels for transporting food. The use of one or both of these food grooves and the velocity of the particles within them, appear to be associated with the morphological type of the gill. In this study endoscopy, histology and SEM were used to determine the nature of this association in five mytilid species, one ostreid and two pectinids. In species with homorhabdic gills, particles are transported from the gill lamella towards the VFG, in which they travel anteriorly, bound in a mucous cord, i.e. by mucociliary movement, at velocities not exceeding 500 µm sec^{-1}. In species with heterorhabdic gills, however, captured particles are directed towards the mouth in the form of a mucous slurry within the DFG, i.e. by hydrodynamic movement, at velocities greater than 1 mm sec^{-1}. A novel insight into particle transport was found in *Ostrea chilensis* (heterorhabdic), in which particle transport occurred in both grooves simultaneously. In *O. chilensis* particles were transported in mucous cords in both the DFG and the VFG, and at lower velocities than those observed in pectinids. This unusual observation may be attributable to the fact that *O. chilena* is a brooding species which maintains the embryos within the pallial cavity. (Fondecyt-Chile Grant 1141052).

Keywords: gill, food groves, particles, endoscopy, bivalve molluscs

IMPACT OF CLIMATE CHANGE-DRIVEN CORAL BLEACHING EVENT ON CORALLIVOROUS *DRUPELLA CORNUS* DENSITY

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The coral-eating gastropod *Drupella cornus* has been documented to have a preferential diet of stressed acroporid coral tissues and thus contributes to the devastation of coral reefs worldwide at an alarming rate. This study was conducted during coral non-bleaching (2010 and 2011) and bleaching (2016) years during summer in the coastal waters of Flic-en-Flac, Mauritius. The effect of climate change-driven coral bleaching conditions was assessed on the density of *D. cornus* present on the branching coral *Acropora muricata* colonies covered and non-covered by the macroalga *Padina boryana*. The health status of bleached and non-bleached corals was measured using a Diving Pulse-Amplitude-Modulated (PAM) fluorometer and this was quantified as the effective quantum yield (Φ_{PSII}). In 2010 and 2011, the mean density of *D. cornus* on the covered non-bleached coral colonies was significantly higher (17.60 ± 6.07 m^{-2} and 17.00 ± 5.87 m^{-2}, respectively) compared to 2016 (0.80 ± 0.83 m^{-2}). For the non-covered non-bleached coral colonies, the mean density of *D. cornus* was 0.60 ± 0.55 m^{-2} in 2010 and 0.80 ± 0.45 m^{-2} in 2011. In 2016, surface seawater temperature was higher in comparison to 2010 and 2011, and extensive and severe coral bleaching was observed, with almost no *D. cornus* individuals on the bleached colonies irrespective of *P. boryana* covering the corals. In 2016, the climate change-driven thermally induced bleaching of corals, which is also the source of nourishment for *D. cornus*, might have resulted in decline in *D. cornus* density. The variable densities among the size classes of *D. cornus* present on *A. muricata* in the year 2016 implies that elevated temperatures may have a differential effect on *D. cornus* recruits, juvenile and adults. To better understand climate change-driven effects on *D. cornus* ecology further studies are warranted.

Keywords: *Drupella cornus*, recruits, *Acropora muricata*, coral bleaching, climate change

FOOD PREFERENCE AND CONSUMPTION RATE OF THE INDO -PACIFIC TRUMPET SHELL *CHARONIA TRITONIS* (FAMILY RANELLIDAE) UNDER LABORATORY CONDITIONS

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The acceptability of the five invertebrate species (sea star: *Acanthaster planci* and *Protoreaster nodosus;* sea cucumber: *Holuthoria atra;* gastropod: *Lambis lambis* and bivalve: *Annachlamys flabellata* as food, the rate of consumption and the amount of the three accepted species (*A. planci, P. nodosus,* and *H. atra*) out of the five consumed by the marine gastropod Trumpet shell *Charonia tritonis* were studied. Also determined in this study was the duration time of the *C. tritonis* to detect the five invertebrate species first offered as food and the amount of each of the three preferred species consumed by *C. Tritonis*. Experiments were conducted at the facilities of University of San Carlos Marine Research Station (USC-MRS) in Maribago, Lapu-Lapu City, Cebu, Philippines. Four wild live adults of *C. tritonis* (631.6+24.6g weight) were collected by SCUBA diving from a coral reef off the Municipality of Glan, fronting Sarangani Bay, Sarangani Province and Celebes Sea in 2012 and then, transported to USC-MRS. The four live tritons were subjected to feeding preference experiment (four trials run) in the laboratory, their rate of consumption and feeding duration of the three selected species of natural preys; *A. planci, P. nodosus,* and *H. atra*. Based on the means and standard deviation on the three food items offered from four trials, it took *C. tritonis* to detect the food items at an average range of 12.13±3.44 minutes. In terms of preference, as expected *C. tritonis* preferred *A. planci* with an average amount consumed ranging from 2.66.46±34.80g; 219.75±49.34g for *P. nodosus* and 3.87±1.08g in *H. atra* respectively. The above results showed that food items preferred and consumed by *C. tritonis* differed significantly at 95% confidence level. It was also recorded that the bigger the size of the food item offered, the longer for *C. tritonis* to consumed it. One way analysis of variance (ANOVA) used to test for significant differences in average consumption rate for *C. tritonis* to consume each three food items. If significant ($P < 0.05$), Tukey's multiple-comparison test was applied to identify groups that were significantly different. All three food items offered were consumed with the highest consumption rate for *A. planci* (35.00±9.12 min) followed by *P. nodosus* (34.5±8.81 min) and least for *H. atra* (19.50±4.20 min). It was relatively longer for *C. tritonis* to consume *A. planci,* followed by *P. nodosus* and *H. atra*. From the results it is consistent with previous observation that *C. tritonis* prefer larger echinoderms such as *A. planci* and *P. nodosus* while least with the relatively smaller sea cucumber *H. atra*.

THE DISTRIBUTION OF HORSE MUSSEL *MODIOLUS* SP. AT KO MAPHAO, PHUKET, THE ANDAMAN SEA

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The horse mussel, *Modiolus* sp. is recognized as one of bivalves in the shallow coastal communities in Phuket, the Andaman Sea. It is an important fishery target for local communities as it is easily collected during the low tide. Understanding on population biology of this horse mussel in Thailand is limited. This study aimed to investigate the distribution pattern and abundance of *Modiolus* sp. in supralittoral, littoral and sublittoral zones at Ko Maphao, Phuket, the Andaman Sea in the year 2015. Diving and a random quadrat method were used to examine the number of live individuals present. The study on size class distribution of this mussel was also conducted. Most individuals of *Modiolus* sp. were observed at the sublittoral zone in where seagrasses were found. The population densities of *Modiolus* sp. were negatively correlated with the median grain size and positively correlated with the organic content. The size class 2.1 - 2.5 cm. was the most abundant group. The small size class (1.1 - 1.5 cm) was also obviously recorded, indicating high potential recruitment of this mussel along the coastline of Phuket. This study provides important baseline data on distribution and abundance of *Modiolus* sp. in Phuket. Further studies on population biology of *Modiolus* sp. along Thailand’s Andaman Sea coast are needed to enhance knowledge on its population ecology and applications for improving mariculture of this mussel in Thailand.

Keywords: bivalve, Modiolus, distribution, abundance, intertidal, Phuket

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PATTERNS OF DISTRIBUTION OF SUBTIDAL MOLLUSC ASSEMBLAGES AT THE ENSENADA DE BAIONA (GALICIA, NW IBERIAN PENINSULA)

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Baseline studies based on reliable quantitative data about composition of benthic assemblages are paramount when testing hypotheses about distribution, importance of abiotic variables and human impact on the biota. Furthermore, soft-bottom faunas, including molluscs, may serve as ecological indicators of marine environment health because of their sensitivity to alterations in hydrodynamism, granulometric composition or organic matter content. The Galician rías (NW Iberian Peninsula) are particular marine environments in regard to its peculiar geological origin, topography and hydrodynamic regime, which include strong seasonal upwellings. This results in high benthic biodiversity in a variety of subtidal soft-bottom habitats. Concentration of human population on their shoreline has, however, resulted in alterations of the benthic environment, mostly related to the proliferation of coastal defense infrastructure, shellfish harvesting and increase of the organic load. For instance, the Ensenada de Baiona (Ría de Vigo) has been impacted, in the last 40 years, by the construction of the harbour's jetty, increase of recreational boating and establishment of rafts for mussel culture. In order to assess the actual state of its benthic fauna and sediments, quantitative sampling was done across the inlet in summer 2015 at 19 subtidal sites; depth ranged between 2 and 12 m and sedimentary types from coarse sand to silt/clay. Samples were obtained by means of a Van Veen grab (0.056 m^2) and sieved through a 0.5-mm mesh. This communication summarizes the results about diversity, composition and trophic structure of the mollusc assemblages; potential changes in sediments and biota are assessed by comparison to previous data obtained in the 90's, including presence of exotic species.

Keywords: NE Atlantic, benthos, subtidal, distribution, sediment

EFFECT OF THE EXPLOITATION OF CLAMS *RUDITAPES DECUSSATUS* ON THE DISTRIBUTION AND DENSITY OF RAZOR CLAM *SOLEN MARGINATUS* IN SOUTHERN OF TUNISIA

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In Tunisia two of the most common bivalves are the clam *Ruditapes decussata*, who has an important economic issue, up to 1800 tons produced yearly, with more than 8000 fishermen and a high level of the trade balance. The second specie is the Razor clam *Solen marginatus* recently appeared among edible bivalves eligible for a large economic interest, subject of an occasional collection, some 1,2 tons/year used as fishing bait. Field investigation confirm the distribution of the two species on almost all the coast, especially in the Gulf of Gabes (681km of coast length), buried in clean or muddy sand of intertidal and infra-littoral zones, the mean density reach 48 and 17 specimens per square meter, respectively for the Clams and the Razor clam. Although the two species live in the same areas, they have different biological cycle and they was collected differently, dig out with sickle for the clam or using salt excitation techniques for the Razor clams. Thus, the indiscriminate and unregulated collection of clams outside the regular open season affects the availability of this resource due to overexploitation and contributes, to the depletion of the stock and the disturbance of the habitat. With the aim to reduce the clam collecting pressure on exploited areas, limiting overfishing and protect the species, two action are developed: a rational exploitation of Razor clam performed according to its bioecological characteristics, and an intertidal on growing culture of small clams based on fields experiments conducted in a pilot area.

Keywords: clam, *Ruditapes decussates*, Razor clam, *Solen marginatus*, Southern Tunisia, Gulf of Gabes, exploitation

SPATIAL AND TEMPORAL VARIATION IN POPULATION DENSITY OF THE GIANT CLAM *TRIDACNA SQUAMOSA* ON CORAL COMMUNITIES IN MU KO CHUMPHON NATIONAL PARK, THAILAND

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Giant clams are recognized as the largest sessile mollusk in coral reefs and lagoons and an important food item in the Indo-Pacific region. Number of giant clams is remarkably reduced because of overharvesting. They are under the protection of the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES). Proper management of giant clams is an important aspect in many tropical countries. In Thailand, giant clams represent an important component of coral communities and are ecologically important. They are also a major fishery resource for local coastal communities. The data on status and dynamics of population density of giant clams are limited, particularly in the Gulf of Thailand, although several giant clam restoration projects have been carried out for a few decades. The present study aimed to study spatial and temporal variation in population density of the giant clam *Tridacna squamosa* on eight coral communities in Mu Ko Chumphon National Park, Chumphon Province, the Western Gulf of Thailand following the mass coral bleaching event in 2010. Field surveys were conducted in permanent belt-transects during 2014 to 2016. The population densities of *T. squamosa* were significantly different among the coral communities and the study periods. Lower population densities of the giant clams were observed at the study sites in Ko Ngam Noi and Ko Phao while higher population densities were observed at Ko Mattra, Ko Rad and Ko Rang Ka Jiu in 2016. The results imply that the previous giant clam restoration projects may enhance population density of the giant clam on some coral communities. Aquaculture of *T. squamosa* in Thailand should be highly supported for enhancing fishery products and coral reef restoration projects with involvement of local communities.

Keywords: giant clam, population density, coral community, restoration, Gulf of Thailand

MOLLUSC DIVERSITY ASSOCIATED WITH THE NON-INDIGENOUS MACROALGA *ASPARAGOPSIS ARMATA* HARVEY, ALONG THE ATLANTIC COAST OF THE IBERIAN PENINSULA

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Asparagopsis armata is a widespread non-indigenous macroalgae along the Atlantic coast of the Iberian Peninsula. Previous studies showed that *A. armata* harbours a diverse assemblage of Crustaceans (particularly Amphipods) along the Atlantic coast of the Iberian Peninsula but the diversity of mollucs associated with this macroalgae remains unexplored. The principal aim of this study was to study the diversity of molluscs associated with *A. armata* in two different biogeographical areas of the Atlantic coast of the Iberian Peninsula. For this aim, we sampled four intertidal shores in two areas: North-west coast of the Iberian Peninsula (i.e. Galicia) and the central-south coast of Portugal. At each rocky shore six individuals of *A. armata* were collected and preserved in formalin (4%). Each sample was washed in a sieve of 0.5 mm mesh size and mollusc were sorted and determined to species level. We found 1296 individuals and determined 30 species, 22 of gastropods, 7 of bivalves and one of Polyplacophora. The number of species estimated by Chao 1 (33 species) and Chao 2 (33 species) were very similar to the observed number. Permanova analysis showed significant differences in structure of mollusc assemblages between the two studied biogeographical areas. Permdisp analysis showed that significant differences between assemblages were due to their different structure rather than for different degree of dispersion of the data. Finally, Simper analysis found an average dissimilarity of 83% between the two studied biogeographical areas. The main responsible of this dissimilarity were 14 species (10 of gastropods and 4 of bivalves).

Keywords: NE Atlantic, Iberian Peninsula, diversity, non-indigenous macroalgae, intertidal

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INFLUENCE OF SEASONAL VARIATIONS ON ANTIOXIDANT ENZYMES IN ROCK OYSTER, *SACCOSTREA CUCULLATA*, ALONG THE IRANIAN COAST OF PERSIAN GULF

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Antioxidant enzymes are useful biological markers to display the integrity of marine ecosystem's species but the markers are strongly affected by different factors like seasonality. To show how much the enzymes fluctuate in oyster S*accostrea cucullata* over a year, we assayed the antioxidant enzymes superoxide dismutase (SOD, EC 1.15.1.1), catalase (CAT, EC 1.11.1.6), glutathione peroxidase (GSH-Px, EC 1.11.1.9), glutathione reductase (GR, EC 1.6.4.2) and the phase II biotransformation enzyme glutathione-S-transferase (GST, EC 2.5.1.18) in whole body of *S. cucullata*. The oysters were collected in winter and in summer at two localities in the Persian Gulf: T-pier and Shoghab Park. Our results showed that the activities of SOD, GSH-Px and GST were seasonally dependent on higher activities in winter. GR activity was also higher in winter, but only in oysters from T-pier. In oysters from Shoghab Park, GR activity was lower in winter compared to summer. In addition, a decrease in CAT activity in oysters from T-pier compared to those from Shoghab Park was found. It can be concluded that seasonal variations should be incorporated into interpretation of environmental biomonitoring studies in oysters

UNITAS MALACOLOGICA Grant Recipients

POPULATION AND DISTRIBUTION OF BIVALVES AT THE INTERTIDAL ZONE OF PULAU GAZUMBO, PENANG

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A study had been conducted focusing on the population and distribution of bivalves at the intertidal zone in Pulau Gazumbo, Penang. The samples collected from the island brought back to the laboratory for identification. Three 50m transect lines were set up on the intertidal zone at five different sampling sites. Five quadrats of 1m x 1m and five cores with 15 cm diameter were used to collect bivalves and soil samples from each transect line at all sites. The population and distribution of bivalves were analysed using Shannon-Wiener Diversity Index (H'), Dominance Index (D) and Evenness Index (J'). Site 4 recorded the highest H' value (1.5494) and J' value (0.9627). Meanwhile, Site 1 recorded the highest D value, which is 0.2004. The bivalves' identification was done following Arnold and Birtles (1989), Abbott (1955) and Poutiers (1998). It was done to family level and a total of eight families were found. The families that were found are Family Arcidae, Mytilidae, Pandoridae, Pectinidae, Pinnidae, Solenidae, Tellinidae and Veneridae. Pearson correlation coefficient was done to find the relationship between soil particle size and organic content with the abundance of bivalves. However, the result showed that there is a weak correlation between soil particle size (r=-0.2408) and organic content (r=0.015) with the abundance of bivalves.

TURUT MEKAR SDN. BHD. Grant Recipients

SPATIAL VARIATION OF PLANKTONIC MOLLUSC ABUNDACE ON CORAL COMMUNITIES IN THE EASTERN GULF OF THAILAND

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Coral reef zooplankton is an important trophic link between primary producers and consumers on coral communities, particularly corals and fishes. Understanding on the structure of zooplankton community is necessary for explaining marine ecosystem processes and also contributes for prediction of recruitment for commercially exploited marine organisms. Studies on zooplankton composition and abundance on coral communities, especially planktonic molluscs, are relatively limited. This study aimed to investigate the abundance of planktonic molluscs on coral communities at Ko Baidung, Ko Yak Lek, Ko Yak Yai and Hin Kurkma in Mu Ko Chang, Trat Province, the Eastern Gulf of Thailand. The coral communities at Ko Baidung, Ko Yak Lek and Ko Yak Yai are in shallow areas while the coral community at Hin Kurkma is on a pinnacle in deeper area. The zooplankton was collected with a standard 120 µm mesh plankton net by vertical haul in a day time. The most abundant planktonic mollusc group was gastropoda. The densities of planktonic gastropods were significantly different among the coral communities. The lowest density of gastropods was observed at Ko Yak Lek while the highest one was found at Hin Kurkma. Juvenile bivalves were also main components of the planktonic molluscs. The densities of juvenile bivalves were also significantly different among the study sites. The high densities of juvenile bivalves were found at Ko Baidung and Hin Kurkma while the low densities were observed at Ko Yak Lek and Ko Yak Yai. This study highlights the importance of spatial variation of planktonic mollusc abundance on the coral communities in the Eastern Gulf of Thailand. Further studies are required to explain the relationships between environmental factors and zooplankton composition and abundance in coral communities, particularly larvae of economically important marine species.

Keywords: zooplankton, gastropod, bivalve, abundance, coral community, Gulf of Thailand

ISOLATION-HYPOXIA AND RE-OXYGENATION OF THE PALLIAL CAVITY OF FEMALE *CREPIPATELLA DILATATA* DURING ESTUARINE SALINITY CHANGES REQUIRES INCREASED GLYOXYLASE ACTIVITY AND ANTIOXIDANT METABOLISM TO AVOID OXIDATIVE DAMAGE TO FEMALE TISSUES AND DEVELOPING EMBRYOS

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The estuarine slipper limpet *Crepidula dilatata* is a gastropod that can survive prolonged periods of low salinities (< 24 PSU) caused by tidal changes and/or prolonged periods of rain. During low salinity events, *C. dilatata* can isolate its body from the outside environment, by sealing its shell against the substrate on which it grows. Prolonged isolation periods from the surrounding environment can greatly lower available oxygen levels inside of the pallial cavity, impacting on the physiology of both females and their incubated encapsulated embryos. When salinity levels return to normal, isolation is terminated and the inflow of seawater results in re-oxygenation. In this study we show that when re-oxygenation of the pallial cavity takes place, oxidative damage, in the form of increased levels of lipid peroxides and protein carbonyls, occurs in both maternal tissues and in incubated embryos. To avoid terminal oxidative damage both females and their embryos increase their levels of the glyoxalase pathway enzymes Glyoxylase I and Glyoxylase II and general antioxidant metabolism (SOD, CAT, GR, GPox and GST). As a result the levels of oxidative damage decline to basal levels within 24 hours of reoxygenation. Thus the combination of isolation, a behavioral strategy, combined with encapsulation of embryos and a capacity to up regulate relatively rapidly the glyoxylase pathway and general antioxidant metabolism, play major roles in facilitating the survival of *C. dilatata* in the small estuaries of Southern Chile. Fondecyt-Chile Grant 1141052.

Keywords: estuary, tidal changes, hypoxia-anoxia, antioxidant defenses, oxidative damage

ABUNDANCE OF CORAL-ASSOCIATED BIVALVES IN RELATION TO CORAL CONDITION FROM THE WESTERN GULF OF THAILAND

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The study of spatial variation of benthic community is a very important aspect in marine ecology. The community structure of coral-associated invertebrates exhibits substantial spatial variability. Understanding on distribution patterns of coral-associated fauna is necessary to assess the impacts of natural and anthropogenic disturbances of coral communities. The severe coral bleaching events in 1998 and 2010 caused mass mortality of corals in the Gulf of Thailand. Some coral communities along the Western Gulf of Thailand were also degraded by heavy sedimentation, land-based pollution, tourism impacts and uncontrolled fishing activities. The present study aimed to examine the abundance of two common coral-associated bivalves, i.e. *Arca ventricosa* Lamarck, 1819 and *Beguina semiorbiculata* (Linnaeus, 1758) along the coral condition gradient in the Western Gulf of Thailand. Coral community structure and abundance of *A. ventricosa* and *B. semiorbiculata* were investigated from the field surveys in permanent belt-transects during 2014 – 2016. The most dominant coral species was massive Porites species complex. The highest percentage of live coral cover was observed at Ko Mattra (75%) while the lowest one was observed at Ko Maphrao (57%). The highest percentage of dead corals was also found at Ko Maphrao (24%). The highest population densities of both *A. ventricosa* and *B. semiorbiculata* were observed at Ko Mattra while the lowest ones were found at Ko Maphrao. This study highlights the importance of studies on coral reef-associated invertebrates as ecological indicators to evaluate the coral reef conditions, particularly the impacts from coral bleaching events, and implies the impacts of global change on coral reef biodiversity and ecosystem services.

Keywords: *Arca ventricosa*, *Beguina semiorbiculata*, abundance, coral community, Gulf of Thailand

COMPLEX FEEDING CHOICES IN THE OBLIGATORY SEAGRASS FEEDING SNAIL *SMARAGDIA SOUVERBIANA*

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By amalgamating all seagrass-associated grazing invertebrates into an assumed epiphyte-feeding guild, the currently accepted model of seagrass trophic dynamics ignores the diverse range of invertebrates that feed directly on, and do considerable damage to, seagrasses. Of the wide range of invertebrates documented to damage seagrass directly, the gastropod genus *Smaragdia* has adaptations and ecology that suggests it could be a specialized seagrass-feeding group, of which at least two species are known preferentially to consume seagrass. This paper investigated the dietary associations of *Smaragdia souverbiana* (one of the most widely distributed but least studied species of the genus) in the subtropical eastern Australian part of its range. Using field-based assessments of grazing damage and targeted laboratory feeding trials, we assessed the dietary associations, digestive ability and feeding preferences of *S. souverbiana* with local seagrasses (*Halophila ovalis*, *Zostera capricorni* and *Cymodocea serrulata*). *Smaragdia souverbiana* readily consumed and digested all three seagrasses, though digestibility was contingent on the cell size of the seagrass. Rather than the simple preference for *Z. capricorni* we once proposed, recent findings regarding variance in phenol content of seagrasses from different sites in Moreton Bay and extended preference tests suggest the feeding behaviour of *S. souverbiana* is a complex set of trade-off's between local availability, cell size and chemical protection of their seagrass prey. These findings highlight the potential importance of seagrass grazing invertebrates and potential complexity in their feeding behaviour.

CURRENT STATUS OF THE DIVERSITY OF BENTHIC MOLLUSCS IN THE STRAIT OF MAGELLAN, CHILE: A PATH TOWARDS A COMPARATIVE REGIONAL BIOGEOGRAPHY

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Phylum Mollusca is the most diverse marine group in the world, and in Chile is represented by about 1,000 described species, augmenting to high latitudes (with over 600 species south of 42°S), indicating an increase in the diversity of molluscs towards the south pole on the east coast of the Pacific Ocean. This may be due to the complex system that the biogeographic ecoregion of Magallanes presents (42°-55°S), also known as channels and fjords ecosystem. Within this complex system of sub-Antarctic fjords, the most important is the Strait of Magellan, a channel with more than 500 km long and high influences of the Pacific, Atlantic and Southern Oceans. The objective of this study is to investigate the current status of the diversity of benthic molluscs in the Strait of Magellan, measuring its alfa, beta and gamma diversity, nestedness and degree of endemism. Thus, the regional biogeographic panorama will be complemented, giving an initial standing for prospective comparisons with the Antarctic. To carry out this study, a literature review with samplings at several sites of the strait was made, adding a custom sample in Punta Arenas. Calculations were analyzed qualitatively (presence/absence of species), using the software Primer. With the presence/absence matrix, nestedness and parsimony analysis of endemicity (PAE) were performed. Total richness was 154 species in 306 records. Gastropoda was the most represented class with 91 species, followed by Bivalvia and Polyplacophora, with 46 and 17 respectively. The most diverse families for each class were Buccinidae (Gastropoda), with 12 species, Mytilidae (Bivalvia) and Chitonidae (Polyplacophora), both with 6 species. The most common species were the gastropods *Pareuthria plumbea*, *Fissurella oriens* and *Trophon geversianus*, and the polyplacophoran *Plaxiphora aurata*. This work corresponds to the first report of diversity measurements and ecological analysis of benthic molluscs of the Strait of Magellan.

Keywords: Sub-Antarctic region, biogeography, alfa diversity, beta diversity, gamma diversity, nestedness, PAE.

SPATIAL SURVEY OF IMPOSEX, TENTACLE AND PENIS MALFORMATIONS IN WESTERN MEDITERRANEAN BASIN AND NORTHEASTERN ATLANTIC OCEAN

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Decades of research in biomonitoring of aquatic environments have shown the usefulness of using certain species of marine mollusks in these approaches. Indeed, some species of bivalves are good bio-indicators of oil pollution, pesticides and heavy metals. Gastropods especially muricids are a good bio-indicators of pollution by organotin compounds such as Tributyltin (TBT). This biocide induces change in sexuality called imposex by imposing sexual male characteristics (penis and vas deferens) in females. Assessment of the intensity of the development of malformation provided an indication of the state of marine pollution by these compounds. In this study, a spatial survey of imposex deformity in *Stramonita haemastoma* was conducted in 12 stations in the Western Mediterranean basin and five in the Atlantic Ocean. Imposex incidence varies from 0% in Arcachon Bay (France), Faro (Portugal), Thau (France), Tarragona (Spain), Kelibia (Tunisia), Palermo (Italy) and 95% in Bizerta Channel (Tunisia). In addition to imposex deformity we had identified several malformations affecting tentacle and males' penis. The causal factor of these malformations is still unidentified, but is probably due to water pollutants. This hypothesis was enforced by the spatial assessment of the tentacle malformations in 17 stations. Penis malformations were however linked to TBT used in antifouling paints. However, this assumption should be supported by bioassays.

Keywords: *Stramonita haemastoma*; tentacle malformation; penis malformation; Bizerta Channel; Western Mediterranean basin; North-Eastern Atlantic Ocean

MORPHOLOGICAL IDENTIFICATION AND POPULATION DENSITY OF *TRIDACNA MAXIMA* AND *TRIDACNA SQUAMOSA* AROUND MAURITIUS ISLAND

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Giant clams have been subjected to both natural and anthropogenic impacts for decades leading to the rapid decline of these 'vulnerable' classified (CITES) species. This study investigated the spatial and temporal population density of giant clams in the months of April and May in 1999 and 2010 at seven sites around the island of Mauritius. Two species of giant clams were morphologically identified as *Tridacna maxima* and *Tridacna squamosa*. The number of *T. maxima* and *T. squamosa* individuals were quantified along 50 m x 10 m belt transects (n=3) at the different sites and the individuals recorded were classified into two main length size classes; recruits (≤50mm) and adults (≥51mm). The findings revealed that there has been a significant ($P < 0.01$) decrease in *T. maxima* abundance (adults and recruits) in 1999 compared to 2010 at all studied sites. Similar results were obtained for the *T. squamosa* recruits ($P < 0.01$); however, no significant difference was observed for adult *T. squamosa*. Moreover, the study showed a strong positive relationship between the adult and recruit classes in *T. maxima* ($r=+0.930$, $p=0.01$), which indicated that a decrease in the adult populations may result in a decrease in the recruits, as compared to *T. squamosa* ($r=-0.347$, $p=0.360$) which showed a non-significant negative correlation between its adult and recruit classes during the period studied. The results of this research indicate that pressure on either one of the size classes may affect the other one over time and could lead to declines in giant clam populations around Mauritius Island. Further investigations on impacts of exploitation and environmental changes over time are needed to identify the causes of such declines in these threatened Tridacnid populations.

Keywords: giant clams, *Tridacna maxima, Tridacna squamosa,* Mauritius, morphological identification, population density

RELATION BETWEEN GROWTH RIBS AND REPRODUCTIVE CYCLE LEADING TO POSSIBILITY OF SEXUAL DIMORPHISM OF *SWIFTOPECTEN SWIFTII* (BIVALVIA: PECTINIDAE), BASED ON STABLE CARBON AND OXYGEN ISOTOPIC COMPOSITION AND MORPHOLOGICAL ANALYSIS

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Swiftopecten swiftii (Bernardi, 1858) belongs to Pectinidae, Bivalvia, and is living in rocky and gravel bottoms, within 50m deep of Northwest Pacific (Tohoku and northward) and Japan Sea (Oga Peninsula and northward). It is known as a dioecious mollusca. *S. swiftii* has a unique character of its shell form: very significant periodic growth ribs are observed when accretionary growth occurs. In this study, there are two findings. First of all, it was discussed the relationship of shell growth and reproductive cycle, based on stable carbon and oxygen isotopic composition and changes in the volume of the soft part. The first finding is that the seasonal growth pattern and reproductive cycle are reflected on the form of the growth ribs on valves. Secondly, it was examined that the female bulge of valve is slightly greater than that of male bulge suggesting that the female growth ribs develop slightly greater than those of male. This assumption is led by the fact that the size of Pecitinidae's female ovary is generally larger than that of its male's testis in gonad. The examination was considered by using 134 samples (male 74, female 60) of *S. swiftii* were taken from Sea of Okhotsk. The second finding suggests the possibility of sexual dimorphism of *S. swiftii*.

Keywords: *Swiftopecten swiftii*, Pectinidae, sexual dimorphism, growth rib, reproductive cycle

THE ABUNDANCE OF MEIOFAUNAL GASTROPODS AND BIVALVES FROM CORAL COMMUNITIES IN THE GULF OF THAILAND

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Meiofauna have not been extensively examined, particularly in Southeast Asian countries. Coral reef is one of typical habitats in tropical areas, which is especially interesting for studying meiofauna communities. Two major groups of benthic mollusk, the bivalvia and the gastropoda, are commonly found in marine and freshwater sediment. Nearly all of the benthic bivalvia are temporary meiofauna in the early stages of their life history while the gastropoda are both temporary and permanent meiofauna. They may provide a significant food source for fishes and large invertebrates. This study aimed to examine the spatial abundance of meiofaunal gastropods and bivalves from coral communities in the Gulf of Thailand. The meiofauna samples were collected from 20 study sites at Ko Kut and Ko Mak (Trat Province), Mu Ko Samet (Rayong Province) and Mu Ko Angthong (Suratthani Province) in the Gulf of Thailand during August 2014 – April 2015. The samples were collected by SCUBA divers using a hand corer (3.5 cm diameter). The densities of meiofaunal gastropods were significantly different among the study sites. The lowest density of meiofaunal gastropods was observed at Ao Prakarang, Mu Ko Samet while the highest one was found at Ao Wong Duen, Mu Ko Samet. The densities of meiofaunal bivalves were also significantly different among the study sites. The low densities of meiofaunal bivalves were observed at Ao Platom, Mu Ko Samet, Ko Sam Sao (north) and Ko Sam Sao (east), Mu Ko Angthong while the highest one was also found at Ao Wong Duen, Mu Ko Samet. The densities of meiofaunal gastropods and bivalves at all study sites in Mu Ko Angthong were relatively low and showed negative correlation with the grain sizes. Further research on meiofauna in coral reefs for bioindicator approaches on global climate change is required.

Keywords: meiofauna, gastropod, bivalve, abundance, coral community, Gulf of Thailand

EFFECTS OF FRESHWATER MUSSEL (BIVALVIA: UNIONIDA) COMMUNITIES ON WATER QUALITY IN TWO PENINSULAR MALAYSIAN HABITATS

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Freshwater mussels (order Unionida) are known to provide key-functions in temperate ecosystems, but their role in tropical systems is poorly understood. In a controlled and replicated experiment, we assessed the rates at which tropical mussel communities at a mesotrophic stream (inhabited by two native species) and a eutrophic lake (inhabited by the non-native *Sinanodonta woodiana*) remove nutrients and algae from the water column. Experiments were carried out during four days in dry season in July 2015 (Sungai Muar) and May 2016 (Tasik Semenyih), respectively. Each day, three pairs of black plastic bins with the bottom removed (area = 0.13 m^2) were firmly wedged into the substrate at three randomly selected sites, so that the surface water within the bins was isolated from the surrounding surface water. Mussels were removed from one bin per pair, which served as the control. Five water quality parameters were monitored in 15-30 min intervals using a YSI-multiprobe. Changes in nutrient, chlorophyll and organic and inorganic suspended solids-concentrations were assessed on water samples taken at the start and end of the experiments. Statistical analyses showed significant associations between mussel presence/absence and/or density and a decrease/increase in concentrations of chlorophyll, dissolved oxygen, total ammonia nitrogen, total and reactive phosphorus, organic suspended solids as well as pH and temperature. The two mussel communities differed particularly with respect to their effect on total ammonia nitrogen concentrations.

Keywords: filtration, ecosystem services, functional ecology, invasive species, water quality

FISH HOSTS FOR *ANODONTA ANATINA* AND *UNIO DELPHINUS* AND THEIR ROLE IN STRUCTURING THE MUSSELS' POPULATIONS

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Freshwater mussels' (order Unionoida) larvae, called glochidia, are obligatory parasites of certain species of fish. *Anodonta anatina* and *Unio delphinus* have been regarded as generalist concerning the hosts for their glochidia. We studied the natural infection of the fish community at the river Tâmega (Douro basin, northern Portugal) with glochidia of both species, estimating prevalence (proportion of fish infected) and intensity (number of glochidia per fish). Additionally the mussel and fish community were studied along the river, estimating the abundance of each species at each sampling station. The relation between both communities was studied by means of analyses of correlation, using the abundance of each fish species, of all species combined and of each species weighed according to their estimated prevalence and intensity of infection. Glochidia from both species were found in a wide variety of fish species, confirming previous observations. However, the prevalence and intensity of the infection varied greatly between species. For *A. anatina* prevalence ranged from 50% in *Lepomis gibbosus* to 100% in *Pseudochondrostoma duriensis*, while average intensity ranged from 0.7 glochidia per fish in *L. gibbosus* and *Gobio lozanoi* to 8.18 in *Luciobarbus bocagei*. For *U. Delphinus* prevalence ranged from 27% in *P. duriensis* to 92% in *Squalius carolitertii*, while average intensity ranged from 0.3 in *G. lozanoi* to 4.6 in *S. carolitertii*. *A. anatina* abundance was significantly correlated to total number of fish (r_s=0.93, $p<0.05$) supporting its host generalist status. For *U. Delphinus* a statistical significant correlation between its abundance and all *Squalius* species combined was found (r_s=0.75, $p<0.05$), suggesting fishes from this genus are its primary hosts. The results show the importance of studying freshwater mussels' host-parasite relations in natural conditions, and strengthen the importance of coupling *Squalius* conservation to the conservation strategies of western Iberian *Unio* species.

Keywords: freshwater mussel, glochidia, host-specific, natural infection, fish community

MIGRATION AND SPREADING OF *SINANODONTA WOODIANA* IN POLAND

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The Chinese pond mussel *Sinanodonta woodiana* (Lea, 1834) becomes more and more widespread in all parts of Europe. In Poland it has been reported for many years in standing waters (like fish ponds or lakes affected by heated water discharge from a power plant) and running waters (rivers and a discharge canal with warmer water of a power plant). The species has been recorded in at least 25 places and this number tends to increase. The presentation is aimed at showing how *S. woodiana* has spread across Poland for recent years. The information includes also statistical data related to the population condition taking into consideration the shell dimensions, weight, age and parasitic infections of found individuals. The richness of the species was also evaluated in the function of parameters that describe water reservoirs. During the research an attempt has been also made to trace an eastbound migration path of *S. woodiana* to Poland. To do it genetic comparisons of populations were done considering specimens from Hungary. Two routes of spreading were identified. The presented outcomes of the field surveys confirm that the species spreads easily colonizing waters of various types, which in the future can lead to appearance of its large populations.

Keywords: *Sinanodonta woodiana*, invasive species; migration, field research, parasite, rivers, lakes, ponds

THE UNIONIDS OF TUNISIA: DIVERSITY, ECOBIOLOGICAL AND CONSERVATION STATUS

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Unionid bivalves are the most diverse family of freshwater mussel, with over of 670 species distributed worldwide except South America and Australia. They play an important ecological role in lotic and lenitic ecosystems. Despite their importance, freshwater mussels have decreased in recent decades, with some species declining faster than potential rates of recovery. In Tunisia, the diversity of unionid mussels is much lower, with only five species currently recognized. The geographic distribution of Unionids in Tunisia is limited to the humid and sub-humid bioclimatic regions and they are spread over four watersheds in the north. The parasitic stage of the glochidium is ensured by the barb *Barbus callensis*, known as an endemic common host teleostean fish in North Africa. Three of them are of the genus *Unio*: *U. ravoisieri* (Deshayes, 1847), *U. durieui* (Deshayes, 1847) and *U. gibbus* (Spengler, 1793). The other two species of the unionid family recorded in Tunisia are represented by the monotypic genus *Potomida: Potomida littoralis* (Cuvier, 1798) and *Anodonta anatina* (Linnaeus, 1758) of the genus *Anodonta*. Despite its endemism, *U. ravoisieri* is the most frequent freshwater mussel species in North Africa. However, *U. durieui* is in Endangered status according to the International Union of the Conservation of Nature (IUCN) Red List of Threatened Species 2010. The latter has been assessed the Least Concern status by the IUCN as this species has a very large distribution encompassing almost all of Europe and a part of Asia. However, *P. littoralis* has been recently added to the Red List of Threatened Species as Endangered species in 2014. Despite their relative stability, unionids population of Tunisia undergoes various anthropogenic pressures due to hydraulic and agricultural development and eutrophication.

Keywords: Tunisian freshwaters, unionid bivalve’s, distribution, diversity, threatens

A PCR-RFLP KEY FOR THE FRESHWATER MUSSELS (BIVALVIA: UNIONIDA) OF PENINSULA MALAYSIA

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Accurate species identification is a prerequisite for most scientific and applied biological research, but the extreme morphological variability of freshwater mussels often leads to inaccurate species identification by morphology alone. Molecular techniques have been proven as a powerful alternative tool for identification of freshwater mussels in North America and Europe. PCR-RFLP and other molecular identification keys developed for freshwater mussel faunas in these regions have additionally facilitated quick and reliable identification of host fish species. Unfortunately, no such tools are currently available for tropical mussels, which are subject to particularly severe habitat alteration and destruction. We developed a PCR-RFLP key for all Peninsular Malaysian freshwater mussels (Bivalvia: Unionida), covering nine native and one non-native species from seven genera and three unionid subfamilies (Gonideinae, Rectidentinae and Anodontinae). The key allows identification of all species from six genera through 2-3 digestion steps of a 374bp PCR-fragment of Histon H3. Unambiguous identification of the three *Pseudodon* species of this region additionally requires one digestion of an ITS-1 fragment. Reliability of the key was tested on 80 specimens from over 50 populations sampled from all major river catchments. The key will subsequently be used to identify the most important host fish species through molecular identification of parasitic larvae found on fish sampled across the peninsula.

Keywords: Freshwater mussels, molecular identification key, restriction fragment length polymorphisms (RFLP), Bivalvia: Unionida

ALLOMETRIC GROWTH OF *KURTIELLA BIDENTATA* (MONTAGU, 1803) AND ITS RELATION WITH SEDIMENT CHARACTERISTICS IN A GALICIAN RÍA (NW IBERIAN PENINSULA)

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The montacutid bivalve *Kurtiella bidentata* (Montagu, 1803) is a common species in shallow sedimentary bottoms in the NE Atlantic and the Mediterranean. It reaches high densities in fine sediments, from fine sand to mud, and it frequently inhabits the burrows built by the brittle star *Amphiura filiformis* (O.F. Müller, 1776). Its shell can reach lengths of up to 5mm and growth has been reported to be slightly allometric, with variations in shape associated to different kinds of sediment. For this work, two fine-sediment bottoms in Ría de Aldán, a small bay in NW Iberian Peninsula, were studied: an 18m-depth muddy sand bottom (Site A) and a 17m-depth organically enriched muddy bottom (Site B), both in the inner part of the embayment. Five replicate samples were taken monthly at each site from May 1998 to May 1999 by means of a Van-Veen grab with an operating surface of 0.056m^2. After sorting and identification, length and height were measured by means of a stereo microscope and an image analysis software in all individuals of *K. bidentata* with at least one of their valves unbroken. A total number of 1934 shells were measured, 763 from Site A and 1171 from Site B. Lengths (L) ranged from 0.53 to 4.01mm, while height (H) values were between 0.47 and 2.75mm. Average H/L ratio was 0.72±0.04, with slightly different values for each site when they were considered separately. On average, individuals from Site B, the one with the finest sediment, were larger and more elongated. These differences were also observed in the regressions based on shell dimensions, which indicate a slightly more allometric growth in Site B. The subtle differences between our study sites agree with previous studies on this species, thus supporting the influence of sediment characteristics over shell dimensions in *K. bidentata*.

Keywords: *Kurtiella bidentata*, size, growth, sedimentary bottoms, sediment effects, NorthEast Atlantic

THE FOOD HABITS OF THREE NEW GYMNODORID NUDIBRANCHS (GASTROPODA: OPISTHOBRANCHIA) FROM OKINAWA ISLAND, JAPAN

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Gymnodoris Stimpson, 1855 are known as opisthobranchs eaters, except for *G. nigricolor*, which apparently lives on some species of goby such as *Amblyeleotris japonica*. Of the gymnodorids that feed on opisthobranchs of various orders, some feed exclusively on particular groups. There are 27 described and at least 60 undescribed *Gymnodoris* species in the Indo-Pacific Ocean including Okinawa, Japan. In the present study, the food habits of three undescribed *Gymnodoris* species were investigated in the vicinity of Okinawa Island. This *in situ* observations are consistent with previous records; three gymnodorids showed stenophagous. *Gymnodoris* sp. 1 is characterized as the brownish body with a series of yellow longitudinal lines. *Gymnodoris* sp. 1 lives on the sand and feeds on small cephalaspideans such as *Metaruncina setoensis* on/in the sand. *Gymnodoris* sp. 2 has translucent white body with many pinkish dots and opaque white pustules. *Gymnodoris* sp. 2 lives in the shallow rocky shore; it feeds on *Odontoglaja guamensis*. *Gymnodoris* sp. 3 has purple body with big gill looks like a polyp of octocoral *Clavularia inflata*. *Gymnodoris* sp. 3 lives near the colony of *C. inflata* and feeds on small arminids such as *Dermatobranchus fasciatus, which* feeds on *C. inflata*. The descriptions of these *Gymnodoris* species are in preparation.

Keywords: *Gymnodoris*, opisthobranchs eater, food habit, stenophagous, *Metaruncina setoensis*, *Odontoglaja guamensis*, *Clavularia inflata*, arminids, *Dermatobranchus fasciatus*

AN ANTARCTIC OPISTHOBRANCH CLADE IS SISTER TO ALL OTHER CEPHALASPIDEA (GASTROPODA: HETEROBRANCHIA)

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For a long time Diaphanidae has been considered a basal family within Cephalaspidea, based on the presence of plesiomorphic morphological features within this taxon. Traditionally the family contained the genera *Bogasonia*, *Colobocephalus*, *Colpodaspis*, *Diaphana*, *Newnesia*, *Toledonia*, and *Woodbridgea*. Some phylogenetic analyses of several of these genera support the basal position of Diaphanidae within Cephalaspidea *sensu stricto*. However, the family is presently confirmed to be a polyphyletic taxon in which only the genus *Diaphana* is included. Several genera previously embraced within the family, such as the monotypic *Newnesia*, have never been previously analyzed in molecular studies. Here we provide an extensive morphological, anatomical, and histological description of a new species of *Newnesia* from Antarctic deep waters (967-1227 m depth) in the Drake Passage. We also discuss the similarities to the traditional Diaphanidae genera to try to shed light into this phylogenetic conundrum. We sequenced cytochrome *c* oxidase subunit I, 16S rRNA, 28S rRNA, and histone H3 markers of *Newnesia antarctica* and *Newnesia joani* n. sp. We analyzed a comprehensive dataset of genes to evaluate the placement of both *Newnesia* species within the cephalaspidean families. Maximum likelihood and Bayesian phylograms support the monophyly of *N. joani* n. sp. and suggest cryptic speciation in *N. antarctica* specimens. *Newnesia* is recovered as the most basal offshoot of Cephalaspidea, suggesting the establishment of a new family restricted to Antarctic waters, named Newnesiidae n. fam., to hold both species. The possible Antarctic origin of Cephalaspidea is also discussed.

Keywords: Diaphanidae, Antarctica, taxonomy, Newnesiidae, *Newnesia*

TESTING THE COLOUR VARIABILITY OF *EUBRANCHUS FARRANI* (ALDER & HANCOCK, 1844): REALLY A SINGLE SPECIES?

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Variation in pigmentation is in nudibranchs (Mollusca, Gastropoda) sometimes hiding cryptic species complexes. Actually, aeolids seem to be a rich group in terms of cryptic species: in the last four years more than 20 of these were detected and/or described. *Eubranchus farrani* (Alder & Hancock, 1844) is a common aeolid species distributed from Norway to the Western Mediterranean. Several different morphotypes, distinct in colour from each other, have been traditionally attributed to this species. In order to investigate the genetic structure and diversity of this species, a phylogenetic approach was used based on fragments of two mitochondrial (COI and 16S) and one nuclear gene (H3) from specimens obtained from different European localities. Bayesian Inference (BI) and Maximum Likelihood analyses (ML) were performed to infer the phylogenetic hypothesis. This study was complemented with Automatic Barcode Gap Discovery method (ABGD) for species delimitation and network analyses. Sampled individuals revealed that they belong to two distinct and geographically partitioned lineages. Therefore, *Eubranchus farrani* is indeed a species complex composed of two congeneric species.

Keywords: Nudibranchia, cryptic diversity, species complex, systematics, marine biodiversity

ARION VULGARIS (MOQUIN-TANDON, 1855) IN EUROPE – ONE WIDELY DISTRIBUTED SPECIES OR A CRYPTIC COMPLEX?

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Arion vulgaris (Moquin-Tandon, 1855) is regarded as one of the 100 most invasive species in Europe. For many years it was believed that it came from south-west Europe, but a recent study showed that there probably was no such expansion of this species. The newest data suggest that *A. vulgaris* is not an invasive species but it is native to Central Europe. In the presented study 27 *Arion vulgaris* populations from Europe were investigated: Polish (9), Norwegian (10), Danish (3), German (3) and French (2). Species identification was done by anatomical section and morphology of internal organs. Moreover, the mitochondrial marker COI was used for barcoding and to investigate genetic variation between and within populations, plus to conduct a phylogenetic analysis. Relatively high genetic differences in this DNA fragment were discovered. On the basis of all obtained sequences, 37 distinct haplotypes were revealed and a comparison between them shows that the number of SNPs range from 1 to 11. For the phylogenetic analysis, alongside with our sequences of *A. vulgaris,* sequences of 19 other *Arion* species were downloaded from GenBank. The average genetic distance between haplotypes is 1.06%, and ranges between haplotypes from 0.2% to 2.6%. The average genetic distance between species in *Arion* genera is 17.67%. The results indicate that there are no cryptic species within the studied populations and *A. vulgaris* is indeed one wildly distributed species exhibiting a relatively high genetic variability within Central Europe.

Keywords: COI, molecular taxonomy, phylogeography

UPDATING THE SYSTEMATICS OF THE AEOLID GENUS *BULBAEOLIDIA* CARMONA, POLA, GOSLINER AND CERVERA, 2013 (HETEROBRANCHIA: AEOLIDIDA)

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The genus *Bulbaeolidia* Carmona, Pola, Gosliner & Cervera, 2013 was erected for those species of the genus *Aeolidiella* Bergh, 1867 with oral tentacles constricted at the midpoint and rhinophores with a pair of prominent bulbous swellings. In addition, Carmona et al. (2013) rendered as *Bulbaeolidia* sp. A and *Bulbaeolidia* sp. B a cryptic species of *Bulbaeolidia alba* and an undescribed species from Hawaii respectively. Lately, Caballer & Ortea (2015) added two new species, *Bulbaeolidia sulphurea* Caballer & Ortea, 2015 and *B. oasis* Caballer & Ortea, 2015, to this genus. In the present contribution we described *Bulbaeolidia* sp. A and *Bulbaeolidia* sp. B, and improve the original descriptions of *B. alba*, *B. japonica* and *B. sulphurea*.

Keywords: Aeolidiidae, Nudibranchia, Cladobranchia, new species, biodiversity

DIVERSITY AND SYSTEMATICS OF THE INDO-WEST PACIFIC GENUS *HALOA* (EUOPISTHOBRANCHIA, CEPHALASPIDEA)

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The genus "*Haminoea*" occurs exclusively in shallow habitats associated with sea grass, algae, or coral reefs. Preliminary molecular analysis of the family Haminoeidae (presented at the 5th International Workshop on Opisthobranchs - Porto, Portugal) showed that contrary to traditional view the genus is apparently not monophyletic, with Atlantic/East Pacific (AEP) and Indo-West Pacific (IWP) species forming two distinct groups, the true *Haminoea* (type species *H. hydatis*) and "*Haloa*". The IWP clade "*Haloa*" is more closely related to the intertidal IWP rocky-shore genus *Smaragdinella* rather than to the highly similar AEP *Haminoea*. Preliminary work recognized over 100 worldwide nominal species names of *Haminoea*; however, the majority of these (ca. 65) refer to IWP species. These species would thus likely belong to "*Haloa*", but most were described based exclusively on shells, which are too similar and thus raising doubts about the exact number of valid species. Morpho-anatomical characters together with multi-locus relaxed molecular phylogenetics based on mitochondrial (COI, 12S rRNA, 16S rRNA) and nuclear genes (Histone-3, 18S rRNA, 28S rRNA), will be used to discriminate between species, infer relationships, and estimate the time of cladogenesis and historical biogeographic patterns. Here we present an overview of the diversity of the genus *Haloa* and a preliminary molecular phylogeny including samples from several regions of IWP: East Africa, Indo-Malaya, West Pacific, Central Pacific and Oceania.

Keywords: Cephalaspidea, Haminoeidae, *Haminoea, Haloa,* Indo-West Pacific

CLARIFYING THE TAXONOMIC STATUS OF TWO PROBLEMATIC *NEMBROTHA* TAXA (NUDIBRANCHIA, NEMBROTHINAE)

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Nembrotha Bergh, 1877 is a genus of nudibranchs belonging to the subfamily Nembrothinae Burn, 1967. During the past ten years this subfamily has been the focus of several complete and detailed studies based on both morphological and molecular data. As a result of these studies, the genus *Nembrotha* was found to be clearly monophyletic, *Nembrotha caerulea* Eliot, 1904 was considered as *Nomen dubium* and two new species, *Nembrotha rosannulata* Pola, Cervera & Gosliner, 2008 and *Nembrotha aurea* Pola, Cervera & Gosliner, 2008 were described from the Indo-Pacific. However, the understanding of this genus is far from being complete as pictures of specimens with slightly different colorations become available in new field guides and webpages. This is the case of two well-photographed taxa but not studied until today. Here, we try to clarify the taxonomic status of two mysterious *Nembrotha* taxa. We performed detailed morphological descriptions and sequenced two mitochondrial (COI and 16S) and one nuclear (H3) gene for several specimens. Comparison of morphological characters and molecular sequences with their closest relatives solve the mystery and help us continue to unravel the evolutionary history of this fascinating group of nudibranchs.

Keywords: Mollusca, *Nembrotha*, Nudibranchia, phylogeny, new species, systematics.

A NEW SPECIES OF *OKENIA* MENKE, 1830 (NUDIBRANCHIA: GONIODORIDIDAE) FROM THE AZORES ISLANDS (PORTUGAL): MORPHOLOGICAL DESCRIPTION AND MOLECULAR DATA

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The genus *Okenia* Menke, 1830 is a controversial taxon of nudibranchs belonging to the family Goniodorididae, and is in need of a deep morphological, ecological and molecular revision. In 2004, Gosliner published the first phylogenetic study based on morphological characters. He concluded that *Okenia* was a monophyletic taxon only when *Hopkinsia*, *Hopkinsiella* and *Sakishimaia* were considered as synonyms of *Okenia*. Ten years later, Pola et al. (2014) presented the first molecular data with genetic distances between some species of *Okenia*. To date, the genus *Okenia* is comprised of 52 species, from which eight where described since 2005. Surprisingly, there are no published records of *Okenia* species found from the archipelago of the Azores (Portugal). In the present study we describe a new species of *Okenia* from the Island of Pico using morphological and molecular data. We include information about the external morphology obtained from photographs of living animals and laboratory observations. The complete description of the internal anatomy includes detailed drawings of the reproductive system, and scanning electron microscopy pictures of the radula and penis. The description is complemented with molecular data obtained from the mitochondrial gene cytochrome c oxidase (COI). The new specie is compared with other *Okenia* regarding geographic distribution, morphological characters as well as genetic distances. A preliminary phylogenetic tree based on COI sequences including all *Okenia* available is also included. The material examined will be deposited in the Museo Nacional de Ciencias Naturales (Madrid) and the molecular sequences in GenBank.

Keywords: Mollusca, *Okenia*, Nudibranchia, phylogeny, new species, systematics

FREQUENTLY FOUND BUT NOT FAMILIAR – 3D REDESCRIPTION OF THE MINUTE SEA SLUG *EMBLETONIA PULCHRA* (EMBLETONIIDAE, NUDIBRANCHIA) FROM THE NORTH ATLANTIC

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The phylogenetic relationships of the family Embletoniidae among cladobranch Nudibranchia remains an unresolved mystery and knowledge on the morphology of the two valid species within the family is still scarce. Based on modern methodology, we provide the first detailed microanatomical study of all organ systems of *Embletonia pulchra* (Alder & Hancock, 1844), a tiny and potentially mesopsammic living sea slug with wide distribution range in North Atlantic and Mediterranean waters. Several specimens were extracted from shallow subtidal coarse sands near Kristineberg, Sweden. A series of histological semi-thin sections was prepared for the 3D reconstruction of a 1.5 mm specimen, giving first insights into complex structures. The compact and post-pharyngeal central nervous system consists of paired cerebropleurovisceral, pedal, buccal and rhinophoral ganglia and additional precerebral ganglia. The triaulic hermaphrodite genital system bears a remarkable muscular prostate and a small penis with an inconspicuous cuticular groove at the tip. Presumably mature oocytes and sperm cells occur simultaneously. The digestive system is characterized by a short oral tube lined by oral glands, a muscular pharynx containing jaws and radula, paired salivary glands and a short esophagus widening into the histologically undifferentiated stomach from which the ciliated intestine and the typical cladohepatic digestive gland branch off. Cnidophages filled with nematocytes are found in the swollen cerata with rounded tips. Findings of the reproductive, circulatory, excretory and digestive systems are supported by ultrastructural examination via transmission and scanning electron microscopy (SEM), including SEM micrographs of systematic key features like radula and jaws. The results are compared to the morphology of its only congener *Embletonia gracilis* Risbec, 1928 to generate a reliable basis to discuss the systematic affinities of Embletoniidae among cladobranch Nudibranchia from a morphological perspective.

Keywords: Gastropoda, Cladobranchia, microanatomy

FIRST RECORD AND 3D-RECONSTRUCTION OF A MARINE MESOPSAMMIC ACOCHLIDIAN GASTROPOD FROM GUAM

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Acochlidia is a group of Panpulmonata with a high morphological and biological diversity and a unique evolutionary history. Whereas only a few species succeeded to colonize freshwater systems and even invaded the land, most of the species are marine mesopsammic inhabiting coastal sands worldwide. In this study we present the first record of an acochlid species from the island of Guam. Three specimens were collected from subtidal reef flat sand areas in Bile Bay in the South of Guam during the 1970s and 1980s. An image of a living specimen was posted on the "sea slug forum" and assigned to the genus *Microhedyle* (with possibly affinity to *Pseudunela cornuta* (as *Microhedyle*)) based on external characters only. The body length of living specimens is 3.5 – 5.5 mm long. The external morphology shows the typical division in a head-foot complex and a separated visceral sac. The paired, curved rhinophores are as long as the labial tentacles and held forward in crawling animals. The visceral sac is long and, interestingly, highly coiled. Recently, one specimen was embedded in epon and a series of histological semi-thin sections was prepared. All organ systems were three-dimensionally reconstructed with the software Amira® in micro-anatomical detail. The pre-pharyngeal central nervous system is euthyneurous and consists of paired rhinophoral, cerebral, pedal, pleural and buccal ganglia and three distinct ganglia on the visceral nerve cord. The radula is hook-shaped and approx. 100 µm long. The reproductive system is hermaphrodite and shows a male copulatory organ. The classification into marine hedylopsacean Acochlidia is discussed.

Keywords: Amira®, Hedylopsacea, micro-anatomy, Panpulmonata

HOPING FOR RESOLUTION: APPLYING NEXT GENERATION SEQUENCING DATA TO LONG STANDING QUESTIONS IN "OPISTHOBRANCHIA" (HETEROBRANCHIA)

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The shell has undoubtedly contributed to the success of gastropods, the most species extant class within Mollusca with approximately 40,000 described species, and an estimated 85,000-105,000 that remain undescribed or undiscovered. Despite the protection afforded by a shell, multiple lineages of marine and terrestrial gastropods within the gastropod clade Heterobranchia have evolved alternative defense mechanisms, such as toxin sequestration, and have lost or reduced their shells. The phylogeny of heterobranchs has been researched extensively, but has been problematic because of the independent evolution of many morphological features, and remains largely unresolved at the generic and familial levels due to a lack of sufficient genetic data. With next-generation sequencing (NGS) technologies, we are generating large quantities of data in the form of transcriptomes, to address these questions. Recent studies[1,2] have applied transcriptomic data to address the relationships within Gastropoda, including some members of Heterobranchia. However, due to limited taxon sampling, many relationships remain unresolved and this approach has yet to be applied to Heterobranchia on a large scale. Sampling at the family level across Heterobranchia, we are generating transcriptomes to use for phylogenetic inference to resolve the evolutionary relationships in this charismatic group. Answering long-standing questions of phylogeny in Heterobranchia will enable better study of the evolution of myriad characters and behaviors including shell-loss, toxin sequestration, gill placement, kleptoplasty, and diet.

Keywords: Opisthobranchia, Heterobranchia, phylogenomics, Next Generation Sequencing, phylogeny, systematics, sea slug

SHELL MORPHOSPACE OF MID-PALEOZOIC GASTROPODS: A REVIEW OF SHELL COILING AND HETEROSTROPHY

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Recent studies focused on phylogenetic relationships among the Paleozoic gastropods revealed existence of large, highly diversified and long lasting gastropod clades being now extinct. Most of those clades have hitherto uncertain phylogenetic relationships to post-Paleozoic, and thus also to living gastropod clades. On the other hand, pattern of shell morphologies of the extinct Paleozoic gastropod clades seems to be similar to living gastropod groups. In our contribution we review a distribution of two general shell features, shell coiling and shell heterostrophy, in the mid-Paleozoic (400 Ma) gastropods. Our data revealed the same morphological disparity in the both extinct mid-Paleozoic and living gastropods. Development of the same shell morphologies in unrelated clades, thus in the extinct mid-Paleozoic and living gastropod clades, suggests that these shell morphologies probably represent optimal solutions to common adaptive problems.

Keywords: shell coiling, shell heterostrophy, mid-Paleozoic

PHYLOGENETIC ANALYSIS OF CLASS GASTROPODA USING COMPLETE MITOCHONDRIAL GENOME GENE ORGANIZATION

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Mitochondrial genomes provide phylogenetic information at the level of the sequences of its individual genes and the organization of the genes across the genome. All available species from class Gastropoda with complete mitochondrial genome sequences in GenBank as of September 2015 (93 species from three major groups: Heterobranchia, Caenogastropoda, and Vetigastopoda) were downloaded and aligned per gene. The gene organization of these species was also tabulated. The Xia Test was conducted for every aligned gene (except the tRNA's) to identify which genes are not oversaturated with multiple hits. Neighbor-joining (NJ) and maximum parsimony (MP) trees were then constructed for each selected gene and for the concatenated dataset while bootstrap values were tabulated to evaluate the support of clades. Tabulation of the gene organization between all the species showed three main clades with unique base gene arrangements; these clades correspond to the Heterobranchia, Caenogastropoda, and Vetigastopoda. Eight genes were found to be unsaturated for multiple hits: *cox1, cox2, cox3, cytb, nad1, nad3, nad5*, and *atp6*. The concatenated dataset (6,531 nucleotides) supported Heterobranchia (100% bootstraps) and Caenogastropoda (63% bootstraps) in its MP tree, but only Heterobranchia (100% bootstraps) in its NJ tree. Except for the *nad3* gene, all other genes provided bootstrap support (>50%) for Heterobranchia in NJ and MP trees. However, Caenogastropoda and Vetigastropoda appeared to be polyphyletic as members of each clade overlapped. These results necessitate the need to re-evaluate the taxonomic designation of the Caenogastropoda and the Vetigastropoda using nuclear markers. The Patellogastropoda must also be evaluated since the group is not represented in this study.

Keywords: Mitochondrial genome, Gastropoda, molecular phylogeny, gene order, maximum parsimony, neighbor joining

FIRST WELL-PRESERVED MID-PALEOZOIC *PLATYCERAS* LARVAL SHELL: WHAT WE KNOW ON ORIGIN OF THE CLADE NERITIMORPHA (GASTROPODA)?

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The Neritimorpha (=Neritopsina) represents an ancient gastropod group, which colonized many different marine (shallow- and deep-water), freshwater, and terrestrial environments. Living Neritimorpha can be characterized by several synapomorphies, including its anatomical features and its unique protoconch morphology. The latter character is the only feature that can be used to identify neritimorph gastropods in the fossil record. Based on the protoconch morphology the Neritimorpha can be traced back to the Triassic time (250 Ma) when their diversity was even much higher than nowadays. However, the Paleozoic evolution as well as origin of the clade Neritimorpha is still quite mysterious. Recent phylogenetic analyses based on morphological, anatomical, and molecular data have placed the Neritimorpha as sister group of the Vetigastropoda, or the Apogastropoda (Caenogastropoda + Heterobranchia), and/or the Vetigastropoda + Apogastropoda. Among several presumed Paleozoic neritimorph gastropods, members of highly diversified clade Platyceratoidea, occurring from the Ordovician to the Permian (time span from 480 to 250 Ma), have been considered as one of the most probable neritimorph stem group. Recent discovery of the first well-preserved larval shell in the type genus *Platyceras* coming from the mid-Emsian Chýnice Limestone (400 Ma; Early Devonian; Prague Basin) makes a new re-evaluation of the platyceratoid affinity possible. In our contribution we summarize data on protoconch morphologies of the presumed Paleozoic neritimorph gastropods and discuss an origin of the clade Neritimorpha.

Keywords: Neritimorpha, Platyceratoidea, Paleozoic, phylogeny

MOLECULAR PHYLOGENY OF THE GENUS *SCHILEYKULA* AND RELATED GENERA INDICATE PARAPHYLY IN THE LAND SNAIL FAMILY ORCULIDAE (STYLOMMATOPHORA, PULMONATA)

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According to the current taxonomy, the land snail genus *Schileykula* comprises ten species; all distributed in Turkey, with the exception of the subspecies *S. scyphus crassa* from Iran. All the taxa are dextral except for sinistral *S. trapezensis contraria* and *S. inversa*. We investigated their systematic relationships within the genus and if sinistrality has evolved one or two times. For this study, material of nine species (and most subspecies) was collected and investigated by means of molecular phylogeny based on partial sequences of mitochondrial *COI*, *12S* and *16S*, nuclear *H4* and *H3* genes and the intermediate non-coding spacer region. Most taxa are clearly differentiated in the mitochondrial and nuclear trees, however *S. trapezensis* is polyphyletic with *S. trapezensis neuberti* being closest related to *S. aculeata*. Left-right reversal independently evolved twice within the genus. Our preliminary phylogeny of the family Orculidae provides evidence that the subfamily Orculinae *sensu* Pilsbry, 1918 is not monophyletic. It is closely related to the genus *Pyramidula* whereas *Pagodulina* forms a distinct lineage.

Keywords: left-right reversal, phylogeny, systematics, land snails

EYE LOSS IN DEEP-SEA SNAILS FOLLOWS VARIABLE MORPHOLOGICAL TRAJECTORIES

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Eye loss or reduction is known in many troglobitic, fossorial and deep-sea animals but there is no clear consensus on its evolutionary mechanism or the extent of convergence. This phenomenon is also under-studied in molluscs, despite a large number of deep-sea taxa, which could offer superior study systems in terms of both phylogenetic and morphological diversity. Solariellidae is a family of marine trochoid gastropods found from the shore to more than 2,000 metres in seas around the world. The phylogeny of this clade has recently been clarified and loss of eye pigmentation appears in several deep-sea species scattered throughout the family. In order to study the occurrence and evolutionary trajectory of eye loss in this family, we examined gross eye morphology of 67 species throughout the family from preserved specimens and selected nine representative types, drawn from five of the eight deep-sea groups, spanning five genera. In these species, we studied ocular microanatomy in order to compare the nature and extent of eye reduction across their taxonomic and ecological range. Using three-dimensional tomographic reconstruction from serial semi-thin histological sections, we described their eye structure in detail and, importantly, identified multiple distinctive anatomical forms of eye reduction. These are variable not only within the family, but two different forms can occur in individual genera. Characteristics typically associated with eye loss such as loss of retinal pigmentation, reduction in size and envelopment of the eye by surrounding tissue are observed, but in a variety of combinations. From ancestral state reconstructions in the context of our time-calibrated phylogeny, we conclude that eye losses have occurred at least six times independently within Solariellidae. In some cases this is convergent. However, our results indicate that there are multiple possible anatomical paths to loss of vision, supporting a significant role for neutral evolution alongside directional selection.

Keywords: Solariellidae, eye loss, nervous systems, vision, morphology, anatomy

THE FIRST SIMROTHIELLIID SOLENOGASTER FROM THE FAR EASTERN SEAS – SCANNED, SECTIONED AND BARCODED

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Although Solenogastres are an important clade for our understanding of the evolution of Mollusca, their morphological and molecular diversity is still poorly investigated. During a deep-sea benthos biodiversity expedition to the Sea of Okhotsk (SokhoBio) around 100 specimens of Solenogastres were collected with an epibenthic sledge at eight mainly bathyal stations ranging in depth from 1696 to 3377m. Based on light-microscopic examination, the SokhoBio Solenogastres were preliminarily assigned to 16 morphospecies. One of the most common species was found at three different stations ranging in depth from 3350 to 3366m. Here we present a first characterization of this novel lineage combining detailed morphological investigations (i.e., 3D reconstruction of the microanatomy based on histological semithin serial sections and scanning electron microscopy) with molecular barcoding. Molecular barcodes 1) ensure conspecificity between the morphologically analysed specimens, 2) provide first insights into the intraspecific genetic diversity of deep-sea Solenogastres and 3) will enable much easier re-identification in future research. The morphologically investigated mature specimens reach a size of up to 3 mm. Their worm-shaped body is covered in various layers of hollow acicular spicules and interspersed double-bent ones, all embedded in a thick cuticle. There is a common atrio-buccal opening lined with probably sensory papillae. The radula is biserial with numerous small denticles and the large foregut glands belong to the *Simrothiella*-type. Muscle packages lateral to the pallial cavity enclose a pair of two copulatory stylets. Large respiratory folds are present. Based on our microanatomical examination, this lineage can be unambiguously classified within the family Simrothiellidae (Order: Cavibelonia). We further comparatively evaluate the taxonomic characters of the various simrothielliid genera and discuss the generic assignment to *Kruppomenia* Nierstrasz, 1903.

Keywords: Aplacophora, integrative taxonomy, deep sea

ONGOING SPECIATION AND GENE FLOW BETWEEN TAXONOMICALLY CHALLENGING *TROCHULUS* SPECIES COMPLEX (GASTROPODA: HYGROMIIDAE)

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Geographical isolation, selection and genetic drift can cause the geographical diversification of population and lead to speciation. Due to the lack of a clear morphological diversity and complicated taxonomy, land snails of the genus *Trochulus* is an ideal object to study the evolutionary processes. An identification of the *Trochulus* species remains problematic because of big shell similarity of many taxa and a significant influence of environment on variation in their shell size, which lead to recognition of extremely distinct morphological forms in the same species. Recent studies revealed very complicated relationships among some taxa and still raised questions about the status of forms resembling *T. hispidus*, such as *T. sericeus*, *T. plebeius* and *T. coelomphala*. Another poorly known species that can be involved in this taxonomic Gordian knot is *T. graminicola*. Adopting an integrated approach, that utilises both morphological and molecular markers (COI and microsatellites), as well as ecological preferences, we show an intricate evolutionary history within the genus, which includes frequent inter-specific gene flow and the permeability of species barriers. We suggest an incomplete speciation coupled with rapid morphological divergence within the genus. The current isolated populations could also inherit the same markers from an ancestral widespread population and are differentiated in shell morphology because of local environmental conditions.

Keywords: canonical discriminant analysis, c, cytochrome c oxidase subunit I, ecological preferences, microsatellites, phylogenetic analyses, land snail, species delimitation

DUE SOUTH: AN INTEGRATIVE APPROACH TO THE SUB-ANTARCTIC AND ANTARCTIC TRITONIIDAE (GASTROPODA: HETEROBRANCHIA)

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Southern Ocean tritoniids are macroscopic and commonly sampled, but their taxonomy has not yet been well established. Incomplete morphoanatomical descriptions, unknown ranges of variation, apparently wide distributional ranges of currently valid species, and the lack of molecular data contribute to taxonomic uncertainty. Due to several glaciation cycles, organisms from Magellanic and Antarctic waters were subjected to alternating periods of population decrease, fragmentation or extinction, and subsequent range expansion. In Antarctica, this complex history supposedly induced the so-called biodiversity pump, which has lead to multiple phenotypically similar but ecologically and genetically specialized species. We do not know much about the exact position and role of refuges and ways of dispersal of hardly mobile direct developers, and there is no molecular data available on southern nudibranchs having a planktonic larval stage. In this work, we explore the species level taxonomy, phylogenetic relationships and geographic distributions of the nudibranch family Tritoniidae, including members with planktonic larvae. During numerous expeditions, specimens from southern South America, subantarctic islands and Antarctica were collected, documented alive and fixed for anatomical description, and comparison with type material. Tissue samples were analyzed under scanning electron microscope or embedded for histological study. DNA from more than 170 specimens was extracted and sequenced for mitochondrial (COI, 16S) and nuclear (H3, 28S) markers. ML trees from particular and concatenated genes and species delimitation analyses suggest a number of separately evolving units which do not coincide with traditionally recognized species limits. Southern *Tritoniella* and *Tritonia* species rather split into several morphologically cryptic or at least previously unrecognized species. This result is remarkable because of the supposedly good dispersal abilities of some southern tritoniids.

Keywords: Nudibranchia, sea slugs, cryptic speciation

STATUS AND PROSPECTS OF THE SYSTEMATICS OF FAMILY NASSARIIDAE IN INDIA.

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Nassariids are prominent components of the sandy or muddy intertidal fauna. Although currently included biodiversity inventories, the actual number of species of the family Nassariidae is still unknown. The morphological characters used to define nassariids species might be difficult to interpret, and the intimidating list of synonyms complicates any taxonomical decision. Indian costs are especially interesting for nassarid fauna, in one hand, because they provide numerous habitats in favor for nassariid diversification, and on the other, because Indian costs are the type locality of plenty nominal species described during the late 18th century and never revised again. The main objective of the study is to revise the systematics of family Nassariidae from India, based in an integrative approach to species delimitation. The COI barcode gene was accessed for >100 specimens to: (1) confirm species previously defined using morphological and radula characters, (2) as evidences to propose new species hypotheses, and (3) to evaluate Indian nassariids fauna in a phylogenetic context. Until now, we have been able to correctly discriminate 30 taxonomic units, including seven cryptic species and 12 new species mostly from genus *Nassarius*. As expected, Indian nassariids form a paraphyletic group, indicating multiples colonization events. This result will become the modern reference on taxonomy of family Nassariidae from India. Moreover, high cryptic diversity and zoogeography suggests there is still ample opportunity for new discoveries within the group.

LAND SNAILS GENERA DIVERSITY IN SEWU MOUNTAINS KARST, JOGJAKARTA, INDONESIA

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Indonesia covers the widest karst area in Southeast Asia and saves an irreplaceable ecological benefit. The high calcium carbonate content supports the specificity of the residence flora and fauna; therefore many tend to be endemic. Economy prospective from quarrying had caused countless karst exploitation without pondering the sustainability of karst and its biodiversity. An explorative research in one of the largest karst areas in Java (Sewu Mountains karst, Gunungkidul Regency, Special Region of Jogjakarta) had been conducted in August 2014 to March 2015. The research aims to discover the abundance, diversity and describe the land snail genera fauna, which highly depends on calcium carbonate and potentially endemic in karst area. Collection methods were conducted by direct observation in 20 plots (each 10m x 10m per hour per two persons) and sorted 100L of soil and leaf litter (5L per plot). In total of 2595 specimens of land snail, from 20 families and 29 genera were collected. The genus *Macrochlamys* was found most abundant in the area. Genus *Gyliotrachela* (*Gyliotrachela fruhstorferi*, endemic Java species) was found 8% from the total specimens. Two potentially endemic genera –*Diplommatina* and *Opisthostoma*- were also found in Gunungkidul. The diversity index (Shannon-Wiener) of land snail genus in Gunungkidul are in moderate level with H’= 2,377. The lowest diversity index was recorded from mouth Rancang Kencono Cave (H’= 1,1708), whereas the highest was from surrounds Srigethuk waterfall (H’= 2,3749). Further biodiversity research in Gunungkidul and other karst areas are vital for sustainable karst management.

Keywords: Biodiversity, Sewu Mountains, Karst, land snails

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A SURVEY ON LAND SNAIL SPECIES COMPOSITION BASED ON THEIR MICROHABITAT IN SUKOLILO KARST AREA, CENTRAL JAVA, INDONESIA

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Karst region is an area where contains high calsium carbonate, therefore it tend to have endemic biodiversity, such as land snail. One of these areas in Indonesia is Sukolio Karst Area. We investigated the land snail composition in Sukolilo karst area, District Grobogan dan Pati, Central Java, and recorded its microhabitat. Twenty plots of 10m x 10m were explored by applying time search method (2 hours/person/plot) and 100L soil and leaf litter samples were sorted and sieved. The land snails were catagorised by micohabitat type i.e, on soil surface (H1), beneath the soil (H2), on leaf litter (H3), on low vegetation or herbaceous (H4), on rock with moss (H5), on rock without moss (H6), and on deadwood (H7). In total of 1157 specimens from 13 families, 33 species and two subspecies were recorded. Most specimens were recorded on the soil surface (H1) and inside the soil or below the surface (H2) with 552 and 440 specimens respectively. The least specimens were found on deadwood where only single specimen were recorded. On the other hand, H2 inhabits more species richness compare to H1, with 27 and 24 species respectively. There were more species recorded on rock without moss (16 species) compare to rock with moss (5 species). Also, more species were recorded on leaf litter (8 species) in comparison to low vegetation or herbaceous (5 species). More thoroughly study on land snails as well as other taxa in Sukolilo karst area is highly recommended. The karst area had suffered massive limestone quarry. Fortunately, the Sukolilo karst is supported by environment-aware local people and community. This data is hopefully usefull for Sukolilo karst's conservation management.

Keywords: land snail, Sukolilo Karst, microhabitat.

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LAND SNAIL OF SEMPU ISLAND NATURE RESERVE, EAST JAVA, INDONESIA

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Sempu island is one of the nature reserves in Indonesia and located 800 meters from the southern coast of Malang, East Java. It covers 788 ha of limestone outcrops with altitude ranges from 50 to 100 meters above sea level. In June 2014, we explore the land snail fauna in Sempu Island, taxa which favors limestone habitat. Eight plots 10m x 10m were randomly sampled within the area by conducting time search method (2 person/hour/plot) and sorting-sieving 40 L of soil and leaf litter samples (5L from each plot). A total number of 647 specimens were found in the island. The specimens represent 12 families, 23 genera, and 34 species (including three undetermined species and one possibly new to science). Two species and one subspecies endemic to Java were recorded in the area i.e., *Microcystina subglobosa* (Möllendorff, 1897), *Gyliotrachela fruhstorferi* (Möllendorff, 1897), and *Alycaeus crenilabris crenilabris* Möllendorf, 1897 respectively. Whereas two invasive species were also recorded in the nature reserve i.e., *Allopeas clavulinum* (Potiez & Michaud, 1838) and *Allopeas gracile* (Hutton, 1834) both are Achatinidae. There were neither previous records nor publication on land snails from Sempu Island. This first record will hopefully beneficial for the management of the nature reserve in particular and the inventory of Java and Indonesian biodiversity in general.

Keywords: Land snail, Sempu Island, limestone, nature reserve

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SPECIES PREVIOUSLY UNREPORTED FOUND IN A DISTINCT BRACKISH ENVIRONMENT IN THE PHILIPPINES

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Limestone formations from the Miocene epoch are widely found all over the islands of the Philippine archipelago such as Siquijor Island in the Visayas region central Philippines. Because limestone permeate water and is easily eroded, numerous springs and anchialine caves can be found in Siquijor. There has been increasing interest about mollusks living in unique brackish environment such as underground springs (e.g., Kano 1998). Our survey on March 2016 revealed three notable species in a brackish spring in Siquijor. This is a preliminary report of the anatomy and living environment of these three species and suggestions for conservation. 1. *Aiteng mysticus*: Two individuals were found inside a coastal cave on the east side of the island. The presence of freshwater seeping through the walls of the cave suggests preference for brackish conditions by this species. Although its external anatomy is very similar to *Aiteng mysticus* as reported by Neusser et al. (2011), further analysis is needed. This is the first report for a species of the family Aitengidae to be found in the Philippines. 2. *Neritilia littoralis*: Three individuals were found under a rock in a coastal area fed by an underground spring on the east side of the island. This is also the first report of this species in the Philippines. 3. Assimineidae sp.: One individual was found under a submerged rock inside an anchialine cave on the west side of the island. External anatomy suggests a species in family Assimineidae, but there is need for further detailed analysis. In addition, although Assimineidae are commonly found in brackish environment, there has been no report of any individual found in an anchialine cave. Our discovery of previously unreported species clearly indicates that mollusk biodiversity in the Philippines is underestimated.

Keywords: Siquijor Philippines, *Aiteng mysticus*, *Neritilia littoralis*, Assimineidae

VIETNAM'S BIODIVERSE LIMESTONE KARST OUTCROPS: DO THEY HARBOUR CRYPTIC *CYCLOPHORUS* SPECIES?

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Vietnam is characterised by countless limestone karst outcrops, which form functional islands for a rich diversity of calcium-dependent organisms. The evolutionary processes that have shaped the diversity of these taxa, however, remain largely unknown. One of the most prominent groups of limestone-bound organisms in Vietnam is the terrestrial caenogastropod genus *Cyclophorus*. Most South East Asian species of this genus have relatively restricted distribution ranges. But in Vietnam, two very widespread morphotypes can be found. These two morphotypes are herein called the "*dodrans*" and "*fulguratus*" groups. Specimens from the "*dodrans*" group have large, thick and relatively compressed shells and a typical colour pattern. The "*fulguratus*" group is characterised by medium sized and relatively round shells with a circular aperture, and by highly variable shell patterns within and among populations. Phylogenetic analyses based on mitochondrial DNA sequence data revealed that both the "*dodrans*" and the "*fulguratus*" group do not form single monophyletic groups but consist of multiple distantly related evolutionary lineages. This finding suggests that both widespread *Cyclophorus* morphotypes in Vietnam contain several cryptic species, which might result from convergent evolution among the isolated limestone karst outcrops.

Keywords: Convergent evolution, cryptic species, *Cyclophorus*, functional islands, land snails, limestone karst outcrops, Vietnam

MALACOLOGICAL SOCIETY OF LONDON Grant Recipients

DIVERSITY AND DISTRIBUTION OF DOOR SNAILS AROUND THE RED RIVER IN VIETNAM

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Vietnam exhibits a very rich diversity of terrestrial gastropods. Door snails (Clausiliidae) are especially speciose and several endemic taxa have been described from the country. The highest species numbers are found in regions around the Red River in northern Vietnam. This river has been supposed to form a major biogeographical barrier for various taxa. Despite their remarkable species richness, the phylogenetic relationships of Vietnamese Clausiliidae and the mechanisms involved in the development and maintenance of their diversity remain largely unknown. Terrestrial gastropods from Vietnam have been collected on several recent expeditions by scientists at the Natural History Museum, London. Based on this material, a study of door snail distribution around the Red River was carried out in order to quantify the strength of this putative barrier. The results of this ongoing research revealed highly different faunal compositions north and south of the river. The Red River might thus act as or coincide with a major dispersal barrier for these gastropods. Furthermore, phylogenetic relationships of Clausiliidae from this region have been reconstructed based on mitochondrial DNA sequence data. The restriction of dispersal due to barriers is considered to be the most frequent, if not necessary, first step in the process of speciation. Besides, barriers dividing a certain region can also allow for coexistence of ecologically similar taxa by leading to separate, non-overlapping distribution ranges of the taxa at both sides of the barrier.

Keywords: biogeography, Clausiliidae, phylogenetics, Red River, Vietnam

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THE BIOCHEMICAL COMPONENTS IN THE GONADAL STAGES OF THE TROPICAL OYSTER, CRASSOSTREA IREDALEI: AN OCEAN ACIDIFICATION PERSPECTIVE

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Oysters are luxury seafood and considered a delicacy throughout the world. Due to the high nutritional values and economic importance nowadays, oysters have been widely cultured around the world. However, this resource has not been optimally utilized in some parts of the world such as Malaysia, Thailand, Indonesia and Philippines. The issue with oyster aquaculture is ocean acidification; increased of atmospheric CO_2 absorption in marine ecosystem alters the ocean pH. Ocean acidification is likely to affect oysters as low pH levels increase the solubility of the shell structure. However, will the biochemical components in the oysters decreased if the oysters were to be cultured in the ocean acidification condition? The aims of this study is to compare the biochemical components (total carbohydrate, total lipid and total protein) in the gonadal stages of the tropical oysters, *Crassostrea iredalei* at two cultures sites. One of the sites is located at Pulau Betong, Penang Island, which is an open sea culture site (with normal sea condition; pH: 8.0 ± 0.2) and at Sungai Merbok, Kedah which is a river estuarine with a lower pH (pH: 7.3 ± 0.1). The ripe female and male *C. iredalei* from Sungai Merbok showed the highest biochemical content among all in the gonadal stages. The biochemical contents in *C. iredalei* cultured in low pH were significantly higher compared to *C. iredalei* from Pulau Betong. The storage and the utilization of biochemical components of the oysters were different in different culture sites. Overall studies revealed the impact of ocean acidification on biochemical components of the tropical oysters and this can provide valuable information on the nutritional and edible values of the oysters to the consumers and also to ensure the food safety and security of such oysters' consumption.

Keyword: pH, total carbohydrate, total lipid, total protein

LEE KUM KEE Grant Recipients

FIRST DESCRIPTION OF THE HERMAPHRODITIC REPRODUCTIVE CYCLE OF THE COCKLE *CARDITES ANTIQUATUS* COLLECTED FROM THE BIZERTA CHANNEL (TUNISIA)

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Cardites antiquatus is a sediment-dwelling bivalve with economic interest. It is found in abundance in the northern Tunisian coast. Monthly samplings of this bivalve from the communication channel, which connects the lagoon of Bizerta to the Mediterranean Sea, were carried out from July 2008 to July 2009 by diving at a depth of 12 m (40 specimens/month). Once in the laboratory, morphometric parameters and weight of thirty specimens of a size ranging from 30 to 35 mm, were measured. These samples were used to calculate two indices relating to reproduction: the condition index of Walne and Mann (1975) CI = (soft tissue dry weight / shell dry weight) * 100 and the gonadosomatic index of Laruelle (1999) GSI = (dry weight of the digestive gland-gonad complex / shell dry weight) * 100. The 10 other specimens were used for histological study. The calculation of the two indices showed that the bivalve has not sexual rest. We recorded a spreading mass spawning occurring in the end of winter and ending in early summer. We also recorded intermittent emissions, of low amplitude, in late summer and autumn. The observations of smears and microscopic sections, stained with hematoxylin-eosin, showed the presence, at the same time, of the two sexual lines (functional) in the same gonadal section. The rate of hermaphrodite specimens observed on the sections is of 59.62%. This rate should be reviewed following the completion of other sections at different levels of the gonad. Oocytes of females, with an average size of 120 to 150 µm are wrapped, each, with a thick envelope of 25 to 40 µm.

Keywords: *Cardites antiquatus,* Reproduction, Hermaphrodism, Chanel of Bizerta, Tunisia

TEMPERATURE-DEPENDENT DIFFERENTIAL SURVIVORSHIP OF THREE EXPLOITED MOLLUSC SPECIES: IMPLICATIONS FOR BARACHOIS-BASED TROPICAL AQUACULTURE IN AN ERA OF CLIMATE CHANGE

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Marine mollusc aquaculture is expanding worldwide with a wide variety of commercially important and exploitable species. This activity is often limited by area available, conflicting uses and the impacts of climate change. It is reported that there are 33 barachois in the tropical island of Mauritius. However, limited studies have focused on their suitability for mollusc aquaculture with respect to the challenges of climate change. In this study, the survivorship of three marine molluscs, namely the oyster *Saccostrea cucullata*, the mussel *Modiolus auriculatus* and the clam *Gafrarium tumidum,* was assessed for a period of 3-4 months from November 2015 to March 2016 in the natural setting of the Poudre D'Or barachois, north-east of Mauritius. The survivorship of the molluscs was estimated by recording the percentage of live and dead molluscs out of a population of 50 per species at each of the five experimental stations within the barachois (S1 & S2 - near inlet/south; S3 – mangrove/west; S4 - no mangrove/west; S5- near outlet/north; S6 – Mangrove/east). Water quality in terms of physico-chemical parameters (temperature, pH, salinity, and turbidity), light levels, nutrients level (nitrate, phosphate, and silicate), chlorophyll *a* and phytoplankton density was also determined. Results indicated that only S3 showed unexpected increases in SST above 35°C in December 2015 leading to low survivorship of the molluscs as compared to other stations with a maximum temperature of only 34°C. Among the three species, *G. tumidum* showed lowest survivorship (< 10%) as compared to *S. cucullata* (> 90%) and *M. auriculatus* (> 90%) at S3. Total phytoplankton density at the stations varied significantly among the months except for December. It is suggested that differential thermal regimes in the barachois affected the survivorship of the marine molluscs, especially *G. tumidum,* and can have implications for barachois-based aquaculture production in an era of changing climate.

Keywords: mollusc, aquaculture, climate change, barachois, Mauritius

MOLECULAR PHYLOGENY OF MARINE SNAIL GENUS *MONODONTA* IN JAPANESE COASTAL AREA

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Intertidal marine gastropods of the genus *Monodonta* are one of the most common intertidal snails with wide distribution, while systematics of *Monodonta* remains unclear in Japan. Accordingly, taxonomic confusions occur in some Japanese species. Clarifying systematics and phylogeny of *Monodonta* is essential not only for using these species as model systems for ecology and evolutionary biology but also for conservation of intertidal ecosystems. In this study, phylogenetic relationships among *Monodonta* species and populations in Japan are clarified by molecular genetic analysis. The present phylogenetic analysis of comprehensive Japanese samples shows that *M. labio* includes two genetically and morphologically distinctive species, *M. labio* and *M. confusa* in Japanese archipelago. These species coexist in the western parts of Japan, while hybridizations between these seem to occur in several sites. High level of genetic divergence is found among different geographical regions in *M. labio*, and this species is separated into three genetically distinctive lineages. As *M. labio* prefers more sheltered habitat like inner bay than *M. confusa*, larva of the former is more likely to be isolated geographically due to limitation of opportunity of larval transportation and scarcity of preferable habitats. *M. australis* of the Ogasawara Islands is phylogenetically distantly related to *M. australis* of other regions, and is an endemic species of Ogasawara that is closely related to *M. confusa* of the mainland of Japan. *M. perplexa* has two genetically distinctive lineages between Kuchinoerabu Island and Akuseki Island of the Tokara Islands. It suggests that *M. perplexa* have criptic species. The present study suggests that *Monodonta* has genetically highly diversified within Japan. Finally, taxonomic revision for genus *Monodonta* is needed ranging from East Asia to Australia.

Keywords: molecular phylogeny, genetic structure, genus *Monodonta*

CLIMBING GASTROPODS FROM SETIU WETLAND, TERENGGANU

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Studies on gastropod diversity are scarce in Malaysia. Climbing gastropods has got even less attention among local researchers. This poster reports a few species of climbing gastropods from Setiu Wetland, Terengganu on the east coast of Peninsular Malaysia. From a three-month survey, we collected and identified seven genera from three sampling plots in the area i.e. *Assiminea, Cassidula, Cerithidea, Clithon, Dostia, Littoraria and Neritina*. These gastropods were observed with different population sizes among the plots, and show some kind of microhabitat preference among the three sampling plots. Further analyses on the existing data and also a further study will be carried out in the area to get a clearer picture of the biology and behaviour of these climbing gastropods.

CHITONS FROM THE MALAYSIAN COAST OF NORTHERN STRAITS OF MALACCA

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The chiton fauna of the Malacca Strait has been poorly known. Only five species were reported from this area. The authors collected 171 chiton specimens from the coasts of Penang Island and Langkawi Islands in 2015 and 2016, among which nine species of five genera in four families were found. The identification has not yet been completed, but preliminary results are presented: *Callochiton* cf. *klemioides* Leloup, 1937; *Ischnochiton bouryi*, Dupis, 1917; *Ischnochiton winckworthi* Leloup, 1936; *Ischnochiton* sp.; *Rhyssoplax* cf. *burmanus* (Carpenter in Pilsbry, 1893); *Acanthopleura gemmata* (Blainville, 1825); three species of the genus *Acanthochitona*. Among these species, *I. bouryi*, *I. winckworthi*, and *A. gemmata* were previously reported for the region, while all others are newly recorded. The three species of *Acanthochitona* appear to be undescribed and this genus was never previously recorded in the region.

Keywords: chiton, Polyplacophora, taxonomy, Malaysia, Malacca Strait, Indo-Pacific

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ON THE ONTOGENY STUDIES OF *TAREBIA GRANIFERA* (LAMARCK, 1816) FROM INDONESIA (GASTROPODA: CERITHIOIDEA: THIARIDAE)

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The freshwater gastropod genus *Tarebia* H. Adams & A. Adams, 1854, commonly are living in rivers, lakes, and other limnitic habitats. In Indonesia, only *Tarebia granifera* (Lamarck, 1816) were found to have a wide distribution. Systematics and identity of this spesies is still doubtfull due to high variation of shell morphology. To determine the valid identity of *Tarebia granifera* in Indonesia, the ontogeny studies have been conducted. The results showed that *Tarebia granifera* has a fairly high reproductive capability. One single individu of *Tarebia granifera* able to produce 9 to 200 progenies which remained in broodpouch in various stages of 0.22 mm to about 5 mm in size.

Keyworlds: *Tarebia granifera*, Thiaridae, ontogeny, progeny, broodpouch

MOLECULAR PHYLOGENY OF *NIPPONACMEA* (PATELLOGASTROPODA: LOTTIIDAE) FROM JAPAN: REEVALUATON OF SPECIES TAXONOMY AND MORPHOLOGICAL DIAGNOSIS

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Nipponacmea circumscribes a group of patellogastropod limpets widely distributed throughout East Asia. Its geographic range is centred in the Japanese Islands, where the highest species diversity has been recorded. Species identification of lineages within *Nipponacmea* is challenging owing to high variation in shell morphology. In this study, we attempted to revise the taxonomy of this genus using 130 individuals representing 43 localities (including type localities) by the following three steps: (1) molecular phylogenetic analysis based on four mitochondrial DNA genes, i.e. cytochrome oxidase I (COI), cytochrome b (Cytb), as well as the 12S and 16S rRNA sequences; (2) comparison of genetic distances among and within species; and (3) confirmation of the validity of morphological characters and species taxonomy from sequenced specimens. Results of the molecular phylogenetic analysis revealed that (1) *N. gloriosa*, the sole species in this genus that inhabits the subtidal zone, represents the most basal independent branch; (2) the remaining species are divided into two large clades with lower- and higher-apex shell profiles; and (3) the high-apex morphology was derived from low-apex type. The terminal clades defined using the molecular data are consistent with nine morphospecies and had 100% bootstrap values, strongly supporting the conventional taxonomy of *Nipponacmea*. The maximum values of intraspecific genetic distance of all four genes examined were smaller than the minimum values for this species. Although morphological similarities do not always reflect phylogeny, the set of morphological characters used in the current taxonomy were proven to be adequate diagnostic characters. In conclusion, this study provided solid evidence upholding the monophyly of known species of *Nipponacmea* in Japan and demonstrated the usefulness of morphological characters for species diagnosis.

Keywords: *Nipponacmea*, limpets, phylogeny, taxonomy

PHYLOGENY OF FRESHWATER VIVIPARID SNAILS IN NORTHEAST ASIA

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We extensive incongruence between molecular phylogeny and the current taxonomy of the freshwater gastropod family Viviparidae in Northeast Asia. Both the nuclear ITS and 18S genes were not informative for species identification. A phylogeny based on the mitochondrial COI and 16S rRNA genes for viviparids comprises five major clades. In Northeast Asia species, *Sinotaia quadrata histrica* includes several lineages whose geographical distribution and shell morphology are largely incongruent with their phylogenetic relationships. Several individuals identified as *Heterogen longispira* are nested within a clade of *Cipangopaludina japonica*. In contrast, *Cipangopaludina chinensis laeta* and *C. c. chinensis* are both monophyletic, but the two are not supported as sister taxa. In addition, *C. c. laeta* is devided into at least three subclades. The observed incongruence between phylogeny and taxonomy may be due to incomplete lineage sorting, introgressive hybridization and/or phenotypic plasticity.

Keywords: Viviparidae, Northeast Asia, phylogeny, morphological diversity, Japan

MOLECULAR PHYLOGENY AND BIOGEOGRAPHY OF *CELLANA* (PATELLOGASTROPODA: NACELLIDAE)

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Patellogastropod limpets are abundant and familiar inhabitants of intertidal rocky shores throughout the world oceans. The identification of patellogastropod limpets is difficult due to their highly variable shell colour and shape. Recent molecular analyses revealed that intraspecific variation of the shell morphology and colour are much more common than previously thought, and recognized many cryptic species. The genus *Cellana* is widely distributed in Indo-West Pacific region. Several species of *Cellana* also have variable shell morphology and colour pattern. We conducted molecular analyses using more than 200 specimens collected from 75 localities in Indo-West pacific including Japan to clarify the species boundaries of *Cellana* species. As a result, *Cellana nigrolineata* and *Cellana grata* are consisted of three clades, and *Cellana toreuma* have at least six clades. Based on the examination of detailed morphological characters, the clades of *Cellana nigrolineata* are intraspecific variation, however, those of *Cellana grata* and *Cellana toreuma* are distinct species. *Cellana toreuma* complex has wide distribution in Indo-West Pacific region. Further extensive sampling is needed.

Keywords: limpets, intraspecific variation, species boundaries

PHYLOGEOGRAPHY OF PHILIPPINE SCALLOPS USING MITOCHONDRIAL AND NUCLEAR GENES

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The Philippine archipelago as part of the Coral Marine Triangle is home to many species of mollusks including the bivalved scallops in the family Pectinidae. A phylogenetic study was conducted for eight scallop species collected from various islands in the Philippines to determine their evolutionary relationships. We collected DNA sequence from two mitochondrial markers, 12S rRNA and 16S rRNA, and a nuclear marker (histone H3). Further comparison with similar scallop species from other neighboring islands within the Indo-Pacific region was made to trace geographical patterns in scallop evolution. These data was analyzed using Bayesian inference. Our study revealed that *Decatopecten radula radula* from Palawan Island, Philippines is more closely related to *D. radula radula* from Sulawesi, Indonesia as compared to *D. radula radula* samples from other Philippine islands. These results provide evidence in support to the geological tectonic origin of Palawan Island which was formerly not part of the Philippine Mobile Plate but was connected through land bridges to Borneo Island during the Pliocene period.

UNITAS MALACOLOGICA Grant Recipients

PALEODIVERSITY OF MOLLUSK SPECIES DURING THE FORMATION OF THE SEA OF JAPAN

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The Sea of Japan is a semi-enclosed marginal sea that is geologically young. Its formation is a major geologic event that occurred primarily during the Neogene and has influenced the biodiversity of marine species in the region. Other than changes in water depth, the sea has also undergone fluctuating salinity, temperature, and oxygen levels, all of which contribute to the kind of marine organisms present. By reconstructing range distribution of mollusk species in the region over this period of time, the impact this formation had on marine biodiversity can be examined. We will use GIS methods to reconstruct species ranges, which coupled with geospatial analyses will give a quantitative analysis of mollusk diversity over time. This study aims to further enhance our understanding of the relationship between biodiversity and environmental changes. Results will contribute to a better knowledge of how present day environmental changes will impact future diversity in shallow water areas.

Keywords: Sea of Japan, paleodiversity, mollusks,

THE DIPLOMMATINIDAE (GASTROPODA: CYCLOPHOROIDEA) OF JAVA

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The Diplommatinidae (Gastropoda: Cyclophoroidea) from Java is revised based on 4576 specimens from 429 lots, both from recently collected materials and museum's collections. Twenty seven species of four genera (*Arinia, Diplommatina, Opisthostoma,* and *Palaina*) have been recorded. A new *Arinia* species is the first record of this genus in Java. The most diverse genus is *Diplommatina* with 19 species, of which six are new to science. Three of the five recorded *Opisthostoma* species are also new. Two *Palaina* were already known from Java. Nineteen of the Diplommatinidae species (70%) are endemic to Java, of which 10 are restricted to small areas. Key characters are given and the geographic ranges of the Diplommatinidae species on Java are illustrated in distribution maps.

Keywords: taxonomy, distribution, Diplommatinidae, land snail, Java

USE OF THE IUCN CATEGORIES AND CRITERIA FOR EVALUATION OF RISKS OF EXTINCTION OF CONTINENTAL MOLLUSKS: THE CASE OF BRAZIL

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In order to provide resources for the conservation of the Brazilian continental mollusks, the ICMbio (Chico Mendes Institute for Biodiversity Conservation) has been coordinating workshops since 2004, in conjunction with SBMa (Brazilian Society of Malacology), aiming to update the Red Book of Endangered Brazilian Fauna. It will be presented how the analysis is been conducted. The last review of the Red Book listed nine species of freshwater mollusks: two bivalves and seven gastropods. The previous edition, 2008, listed one gastropod and 26 freshwater bivalves. These changes could suggest an improvement in the quality of waterbodies, in addition to an enhancement of the conservation measures on limnic mollusks. The lack of data, which does not allow an accurate assessment of the state of conservation and the more rigid application of the IUCN criteria explain this. Most bivalves were classified as DD (Data Deficient) or NT (near threatened), many of them formerly included in one of the categories of threat. Even among terrestrial and freshwater gastropods, whose number of threatened species increased, many were classified as DD or NT. Most of the species are included on the Red List just based on incomplete distribution data, in addition to areas not exhaustively searched for mollusks. To the evaluation of risks, it is usually considered that, if there are populations of a particular species within a Conservation Unit, it is well protected. However, recent examples such as the disaster in the Rio Doce, flowing through Rio Doce State Park, that sometimes species are not safe forever. Furthermore, in most cases the reserves in Brazil are not planned aiming water catchment areas at all, but the terrestrial environments. To get an assessment of threatened species really consistent with the size and environmental diversity and degradation of our country, we need to face challenges as to amplify basic research on biology, taxonomy and distribution.

Support: ICMBio, SBMa

Keywords: threatened species, conservation, Brazilian Red Book

THE DIVERSITY AND DISTRIBUTION OF VERTIGINIDAE (MOLLUSCA: GASTROPODA) IN THE LANGKAWI ISLANDS, STRAITS OF MALACCA

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A study was conducted on the diversity and distribution of microsnails from the family Vertiginidae at 16 locations that spreads across the limestone outcrops of the Langkawi Islands in the northern Straits of Malacca. A total of 10 species of vertiginids from three genera were identified with seven species from the genus *Gyliotrachela*, namely, *G. depressispira*, *G. hungerfordiana*, *G. luctans*, *G. salpinx*, *G. transitans helioscopia*, *Gyliotrachela* sp. 1 and *Gyliotrachela* sp. 2; two species from genus *Paraboysidia*, namely, *P. frequens* and *P. serpa*; and one unknown species from genus *Nesopupa*. Identification and confirmation of the snails was done using the reference collection at the British Natural History Museum in London. *Gyliotrachela hungerfordiana* was found to be the most common Vertiginidae species in Langkawi having been found in ten sampling locations. This study also revealed that the morphological variations within vertiginids species at Langkawi Islands might be caused by the geological separation of the limestone formation.

Keywords: microsnails, limestone, Vertiginidae, *Gyliotrachela*

IMPACTS OF TOPOGRAPHIC CHANGES OF TIDAL FLAT BY 2011 MASSIVE EARTHQUAKE AND TSUNAMI ON THE INTERTIDAL MOLLUSK COMMUNITY IN MATSUSHIMA BAY, NORTHEASTERN JAPAN

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The 2011 off the Pacific coast of Tohoku Earthquake that measured 9.0 on the Moment Magnitude Scale on March 11, 2011 generated huge tsunamis. Tidal flats and its ecosystems in northeastern Japan were greatly affected by the tsunamis and the habitat alteration by coseismic land subsidence up to about 1.2 m. This study examined the changes in the species and the density of mollusks in Hatsutsu-ura tidal flat in Matsushima Bay, northeastern Japan from February 2015 to January 2016. Samples were collected using 20 cm quadrat and sieved through a 1 mm mesh. All collected mollusks were identified, counted, and measured the shell length. At the same time as the sample collection, ground height was measured by using virtual reference station real time kinematic-GPS, and sediment hardness was also assessed by the cone penetration resistance and vane shearing strength. In the study area, fluctuating ground height and sediment hardness indices were observed and the results indicating the topographical instability of the tidal flat. Denudation of sediment and unnatural topology in the tidal flat were also observed and it indicated the changes of tidal flat topology by the 2011 tsunami deposit. The density of mollusks was 0 to 2,825 inds m^{-2} and the communities were usually dominated by the Manila clam *Ruditapes philippinarum* and the trochid gastropod *Umbonium moniliferum* during the study period. The shell length growth of the Manila clam was extremely low and most of the clams in the tidal flat were seemed to disappear within a year from their settlement. The tidal flat has not yet reached a stable state even 5 years after the tsunami and instability of tidal flat topography continuously affected the tidal flat ecosystems.

Keywords: Large-scale disturbance, tidal flat, molluscan community, tsunami, topological instability

EFFECT OF TEMPORARY SEDIMENT COVERING THE INTERTIDAL MOLLUSKS IN THE VOLCANIC ISLAND, IZU OSHIMA, JAPAN

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In October 2013, a big typhoon came to Japan. Debris flow from the mountain has reached the coast in Izu-Oshima Island off Tokyo Bay. The rocky coast was temporarily covered with mountain sediment and the turbid water was temporarily residence. The purpose of this study is to clarify the impact of debris flow and covering sediment on the mollusks inhabited in the rocky coast on a volcanic island. During our research in 2014, we confirmed 45 species of mollusks still living the shore after the disaster, the number of umbrella-type species such as the pulmonate limpet *Siphonaria japonica* and some limpets were less after the sediment covering. From May to October in 2015, we performed quantitative and qualitative research at the intertidal zone of the shore A (with covering sediment) and shore B (without sediment covering). We confirmed 39 species of mollusks in shore A, and 30 in shore B. A few species of ark clam and infaunal clam, *Ruditapes variegata* were confirmed on shore A in 2014. But in 2015, we found a relatively a high density of specimens from the bottom sediment and from the lower side of the boulder. From this, it is suggested that these populations were temporarily decreased by the influx of sediment, and it had been recovered in 2015. We also confirmed the laying eggs of the pulmonate limpet *S. japonica* that was reduced in numbers in 2014. Both *S. japonica* and *Thais clavigera* were able to crawl to the surface from the bottom of 2cm of sand. Most of the limpets did not return to the original from the overturned state on the covering sand. It is suggested that the repetition of temporary covering of mountain sediment on the rocky shore is a negative effect on the survival of limpets.

Keywords: typhoon, debris flow, rocky shore, covering sediment, pulmonate limpet

CHANGES IN MOLLUSK COMMUNITY AROUND UDAGAWA RIVER MOUTH BY THE REED BED LOSS OF THE 2011 GREAT EAST JAPAN EARTHQUAKE

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The coastal environment was drastically changed by the tsunamis of the 2011 Great East Japan Earthquake in Northern Japan. Around the Udagawa river mouth in Fukushima Prefecture, most of the reeds were lost by the tsunamis. Parts of the lost reed have not recovered until now. The purpose of this study is to confirm the effect of the presence or absence of the rhizome reed to the survival of the tidal flat organisms. We chose the following three points as a comparison location. St.A was the point that only rhizomes of reed remained after the tsunamis. St.B was the point that reeds were remaining. Whereas, no reed was observed before and after the tsunamis in St. C. Sampling was carried out every month from June to November in 2014 and from March to November in 2015. Samples were collected using quadrats for quantitative survey. Although the species richness (No. of species) was similar between St. A and St. C, the number of individuals of St. C was more than St. A. There is a possibility that the presence of the rhizome is suppressing an increase in the number of individuals in infaunal species. *Assiminea japonica* was only observed in St, B, but bivalves were fewer than other two points. The disappearance of the reed by the tsunamis, led to the expansion of the habitat of some bivalves and also the disappearance of the organisms that depends on the reed. The presence of the rhizome of reeds is sometimes bad and sometimes good for the organisms. Although the rhizomes occupy the living space of intertidal organisms, they help the survival of some organisms to stabilize the sediment. In this way, underground structures likes the rhizomes had some important roles for survival of infaunal species.

Keywords: tsunami, reed, rhizome, disappearance, bivalve, habitat change

CONSERVATION AND MANAGEMENT ACTION PLAN FOR THE RECOVERY AND EXPANSION OF *VERTIGO ANGUSTIOR* AND *V. MOULINSIANA* SPECIES IN BANYOLES LAKE SYSTEM (NE-IBERIAN PENINSULA)

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Vertigo moulinsiana and *V. angustior* are two of the four species belonging to the genus *Vertigo* (Gastropoda: Vertiginidae) included in the Council Directive 92/43/EEC on the conservation of natural habitats and of wild fauna and flora, otherwise known as the "Habitats Directive". Since 2014 a LIFE Nature project "LIFE Potamo Fauna (LIFE12 NAT/ES/001091) is being carried out at the Banyoles lake system which includes some plan actions with the aim of the recovery and long-term conservation of these two *Vertigo* species in their habitat. The main objective defined within this project for these species is the "Expansion and consolidation of the populations of *Vertigo moulinsiana* and *V. angustior* in the Natura 2000 site Estany de Banyoles (ES5120008) via translocations from within the site". For that, the following specific objectives are being developed: To delimitate the area of occupancy of both species across the lake and ponds; To determine the species abundance, population structure and habitat requirements; To asses sampling methods for each species; To establish measures to ensure the conservation and management of both species; To devise a protocol for monitoring each species that will be used during the period 2014-2017. In this work we present the preliminary results obtained for each of these objectives. Nowadays there is no a standardized methodology for monitoring and recovering natural populations of both species in the Iberian Peninsula. Therefore the development of a package of protocols and methodologies with this purpose are of great interest to define the guidelines to be followed in future work of monitoring and management of these two species of Community interest. To *V. moulinsiana* and *V. angustior* this is the first major project developed in the Iberian Peninsula focused on their conservation and management, and it will allow consolidating some of the main Iberian populations.

Keywords: Gastropoda, *Vertigo*, conservation, management, Iberian Peninsula

3D-AMP, A NEW FIJI - IMAGE J PLUGIN THAT RELIABLY QUANTIFIES OBJECTS FROM BI-COLOR IMAGE STACKS

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Numerous scientific disciplines rely on the accurate counting of small objects. The advent of technologies such as confocal microscopy allow the acquisition of large image sets detailing objects in 3D, making the historical methods for quantifying these objects, manual counting or small-scale counting and estimating the true value, time intensive and cumbersome. A number of automated tools have been previously developed to count objects, most of which rely on object recognition software, however this software is severely limited in terms of accuracy, reliability and reproducibility, when the objects it attempts to count lie in close proximity to one another and/or lack clear borders. To alleviate these problems, we developed and present here a new plugin, 3D-AMP, which relies on pixel based counting methods instead of object recognition tools. Up to 3 channels can be analyzed, allowing the quantification of multiple types of objects. User input data allows the raw pixel counts to be converted to area measurements, and the user can control which pixels are counted by applying a threshold. A region of interest can be defined where the objects inside and outside are separately counted. Users can also apply an alignment function to stabilize stacks taken of moving samples. Test data was analyzed and the output was compared to manually counted samples, verifying that 3D-AMP is a reliable and valuable tool in the quantification of objects in bi-color images.

AN ATTEMPT TO CRYOPRESERVE TROPICAL OYSTER, *CRASSOSTREA IREDALEI* SPERMATOZOA IN MALAYSIA

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The tropical oyster typically spawns all year round during the on-set of the raining season. However, the male and female oysters tend to spawn asynchronously, leading to the non-availability of both male and female gametes for fertilization in the hatchery. Maintaining a steady and sustainable gamete stock is crucial in the success and continuity of the oyster aquaculture industry. As a solution, cryopreservation of tropical oyster was carried out on *Crassostrea iredalei* spermatozoa. *C. iredalei* gametes were stripped separately from mature oysters, sieved off debris and the spermatozoa were then immersed in marine Ringer's solution. The spermatozoa were left to equilibrate in Dimethyl Sulfoxide (DMSO), sucrose, egg yolk and honey for 15 minutes before being suspended in liquid nitrogen vapour for 10 minutes prior to direct immersion and storage in liquid nitrogen for 24 hours. The spermatozoa were then thawed at 40°C and fertilized with fresh oocyte. The fertilization was monitored and upon formation of the first polar body, fertilization of the frozen sperm is considered successful. All data were arcsine transformed prior to one-way ANOVA test. The fertilization percentage for the control was 66.38±16.07%. The highest fertilization was found in DMSO 10% and DMSO 15% with 67.01±17.67% and 57.45±33.15% fertilization percentage respectively, which is not significantly different from the control. This study demonstrates that cryopreservation could be adapted on the tropical species of oysters as a gamete stock storage solution.

Keywords: tropical oysters, *Crassostrea iredalei*, cryopreservation

SKY GROUP OF COMPANIES Grant Recipients

CZECH QUATERNARY PALAEOMALACOLOGICAL DATABASE

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The database of all quaternary mollusc succession sites sampled by standard modern techniques in the area of the Czech and Slovak Republics (Central Europe) was completed. Quaternary malacological research has a long tradition in the area starting with first pioneer studies more than hundred years old. The quality of data is certainly discussed in the context of the history of the research and methods used. For data to be included in database strict requirements were determined: standardised stratigraphic sampling, sampling of deposits with consequent extraction of shells in the laboratory, and detail information about site and lithology. Almost all these successions are younger than 1950. Radiocarbon dating has been continuously adding using mollusc shells. Currently, 253 Pleistocene and 353 Holocene mollusc successions were sampled in this area during the period 1948 to 2016. The database contains species, climatic, geographical, geomorphological and other important site information. This dataset is globally unique and can be used for palaeoecological environmental reconstructions and other regional synthesis.

Keywords: Holocene, Pleistocene, mollusc succession, Central Europe, fossil gastropods

DESCRIPTION OF A NEW SPECIES OF *FELIMARE* EV. MARCUS & ER. MARCUS, 1967 (HETEROBRANCHIA: CHROMODORIDIDAE), BELONGING TO THE BLUE CHROMATIC GROUP

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Ortea et al. (1996) defined the blue chromatic group as species included in the Chromodorididae Bergh, 1891 family with dark blue color (from pale blue to navy) with spots, blotches, or lines of white, blue, or orange colors. This group was originally comprised by species from five different genera: *Glossodoris* Ehrenberg, 1831, *Hypselodoris* Stimpson, 1855, *Chromodoris* Alder & Hancock, 1855, *Risbecia* Odhner, 1934, and *Mexichromis* Bertsch, 1977. Nowadays, these species are considered to belong to only two genera; the provisional genus "*Felimida*" Ev. Marcus, 1971 and *Felimare* Marcus & Marcus, 1967 (Johnson and Gosliner, 2012). Here, we describe a new species of *Felimare* belonging to this chromatic group from Cape Verde. Our description is based on traditional characters, such as the radula and the reproductive system, as well as molecular analyses using two mitochondrial genes -cytochrome *c* oxidase subunit I (COI) and 16S rRNA (16S)- and one nuclear gene -histone-3 (H3).

Keywords: Phylogenetic analysis, Atlantic species, dorids nudibrachs, gastropods

DIGITIZING MOLLUSCAN BIODIVERSITY AT THE UNIVERSITY OF MICHIGAN MUSEUM OF ZOOLOGY (UMMZ)

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The Mollusk Division of the Museum of Zoology, University of Michigan, has long been recognized as one of the most important freshwater and land mollusk collections in the World. It is most notable for the excellent taxonomic and geographic coverage, type collection and also for its relative age. The Mollusk Division is currently digitizing approximately 250,000-catalogued lots that roughly comprise 5 million specimens through the help of two National Science Foundation awards, ‘InvertEBase’ and ‘Great Lakes Invasives’ Thematic Collections Networks. The primary goals of these projects are to enter all of the cataloged lots into an online Specify database and to capture high-resolution images of specimens of Great lakes non-indigenous species and their congeners. Networking of georeferenced locality data will form a solid foundation for distribution mapping and for tracking/monitoring change over time. Digitized data and images will be available through Symbiota web portals (invertebase.org and greatlakesinvasives.org) and the national resource (iDigBio.org).

Keywords: UMMZ, InvertEBase TCN, Great Lakes Invasives TCN

MARINE MOLLUSK RESOURCE BANK OF KOREA (MMRBK)

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The Marine Mollusk Resource Bank of Korea (MMRBK) was accredited in 2010 by the Ministry of Oceans and Fisheries of Korea with financial support from the government. The MMRBK houses approximately 600 marine mollusk species collections (wet collections preserved in 70% ethanol) collected from Korean seacoast as well as northwestern Pacific including Japan, and China Sea coasts. Comprehensive inventory information such as GPS data, specimen images, number of specimens are available online and curated under the specimen database system of the MMRBK. Currently the MMRBK has undertaken multiple missions that include (1) research for taxonomy, biodiversity and phylogeny of northwestern Pacific mollusk species, (2) management of mollusk collections and taxonomist education program, and (3) providing taxonomic information and specimen loan to researchers, environmental NGOs, and the general public. The current state (including major tasks) of the MMRBK will be presented in detail in this report.

Keywords: MMRBK, marine mollusk, northwestern Pacific mollusk, biodiversity

DIFFERENT IMPACT OF PREHISTORIC HUMAN COLONISATION TO HOLOCENE MOLLUSC SUCCESSION IN CENTRAL EUROPE

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Although general trend of central European Holocene mollusc succession is well known, the impact of prehistorical colonisation to natural forestation is still being discussed. Some central European areas were attractive for the first agricultural settlements due to their suitable natural conditions. The Holocene development of such areas was thus under long-term human pressure. Our data suggest that steppe habitats of such area can be viewed as a direct continuation of the late Pleistocene and early Holocene natural steppe rather than a purely cultural steppe developed only after deforestation of a continuously forested mid-Holocene landscape by humans. Forest mollusc assemblages of such areas used to be fragmentary developed probably because of many human activities connecting with agriculture. Here we presented such case of České Středohoří Mts. On the other hand, another area of continually documented human presence hosted fully developed forest communities during the whole Holocene giving evidence of completely different landscape use. Succession of mollusc fauna in Moravian Karst is presented as such example. Although there is an evidence of human activity in majority of caves in this area, no impact to forest in immediate surroundings of the caves was recorded. Thus, continual presence of prehistoric human activities predicates nothing about the forest fauna development.

Keywords: Holocene, human colonisation, forest refugia, steppe refugia

PHYLOGEOGRAPHY OF THE BIVALVE *CERASTODERMA GLAUCUM* DETERMINED USING THOUSANDS OF RAD MARKERS

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Next-generatiom (NGS) techniques have become key tools in the investigation of genome-wide variation in natural population. In this study we used restriction site-associated DNA sequencing (RADseq) to genotype 197 individuals of the lagoon cockle *Cerastoderma glaucum* from 14 locations sampled throughout its distribution range. Past studies, using mtDNA (COI) sequences and microsatellite markers, have differed according to each marker in the strength and locations of the major genetic divisions. The large number of RAD markers - 2,701 SNPs, allowed us to infer fine-scale phylogenetic relationships, not achieved in previous studies. Population genomics analysis revealed two deeply divergent lineages of *C. glaucum* in Ionian Sea and Aegean-Black Sea. These two lineages clustered together against Western Mediterranean-Atlantic-Baltic group. At a finer scale diversity among populations is principally organized by geography, with Baltic and North Sea, Atlantic and several Western Mediterranean groups.

Keywords: RADseq, *Cerastoderma glaucum,* genome-wide SNPs, phylogeography

MALACOFAUNA IN SRAKEO PROVINCE, EASTERN THAILAND (MOLLUSCA: GASTROPODA: BIVALVIA)

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Survey of malacofauna in Srakeo Province, Eastern Thailand was investigated from limestone areas and freshwater habitats, which are Khao Chakan, Petphothong Cave, Subthavonniwake Tample, Phuheeppanaram Temple, Subnoi Temple, Petpananikom Temple, Khaophaphueng Temple, Khaosumpung Temple, Klongkarntubtimsiam, Namprasiwa Cave Pangsrida National Park, Khaolone Tower Khaosamsib Reservoir, Praplong Reservoir, Khaochakan Dam, Petpananikom Dam, Talangnai Dam, Klongphomhod, Bantanglung, Klongwangsaew, Huymahod and Klongnamsai. From this study, 11 families, 24 genera and 56 species of land snail and 11 families, 21 genera and 35 species of freshwater mollusks were recorded.

Keywords: land snails, freshwater mollusks, Srakeo province, diversity, Thailand

SOME BEHAVIOR AND DEVELOPMENT OF FRESHWATER MARGINELLID SNAIL (*RIVOMARGINELLA MORRISONI* BRANDT, 1968) OBSERVED IN LABORATORY

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The observation on the embryonic development and some behavior of freshwater marginellid snail, *Rivomarginella morrisoni* Brandt, 1968, was done in laboratory. The result shows the patterns of nocturnal movement and diurnal shelter site. Snails feed primarily on shrimp carcasses, and occasionally hunt on small gastropods as prey, which can be classified as scavenger and predator in ecosystem. According to the development, snail lays a single plano-convex egg capsule attached to the substrate. The snail embryo undergoes direct-development, 50-55 days hatching from egg and growing from juvenile into adult snails within 7-8 weeks.

Keywords: freshwater marginellid snail, *Rivomarginella morrisoni* development, behavior

GOOD LITTLE MOVER: GLOBAL PHYOGEOGRAPHY OF *ONCHIDELLA* (SYSTELLOMATOPHORA: MOLLUSCA)

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The intertidal slug *Onchidella* has a broad global distribution that includes many remote oceanic islands, although is absent from the tropical Indo-Pacific where most onchidiid diversity is found. This widespread distribution occurs even in the absence of an obvious means of dispersal (e.g. direct-development is common), which raises interesting evolutionary and biogeographic questions that we sought to address using a newly constructed species phylogeny (C01, 16S, 12S, H3, 28S). Representative samples were collected across five continents and fifteen countries – a comprehensive taxonomic coverage that encompassed almost all known species. As well as resolving *Onchidella* taxonomy, our data of species relationships within this monophyletic genus show that *Onchidella* spp. are typically geographically widespread, with populations often distributed across different landmasses/islands. High genetic similarity and frequent sharing of haplotypes across oceans suggests that recent dispersal rather than vicariance explains the present day biogeographic pattern. Consistent with this, species on the same continent do not necessarily share the same evolutionary history. For example, a widespread species found in West Africa (Cameroon, Senegal, Ghana) shares a closer evolutionary relationship to taxa on the other side of the Atlantic (Brazil and the Caribbean), than to those in South Africa. Taxa from NZ, South Africa, Australia and South America form a 'southern' clade. Diversity also appears higher in the southern hemisphere compared to the northern hemisphere, possibly due to longer periods of continuous colonization. Notably, very few examples of sympatry can be found within *Onchidella*, the exception being some southern hemisphere locations (e.g. southern NZ, South Africa/Chile). Low diversity across populations of the northern hemisphere species, *O. borealis* (Aleutian Islands, Alaska, Canada), mirrors the findings of a previous study of *Onchidella marginata* (NZ, subantarctic islands, Chile, Falklands) in the southern hemisphere and could be indicative of recent expansion and/or post-glacial recolonisation.

Keywords: *Onchidella*, global phylogeography, marine dispersal, evolutionary history

MALACOFAUNA IN NORTH COAST OF EGYPT

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Malacofauna surveying still insufficiently known in Egypt, and need further studies. There is little shortage in the database of some main land Mollusca species, which contributing in the Egyptian ecosystem except for *Eobania vermiculata* (Müller), *Monacha obstructa* (Müller), and *Theba pisana* (Müller), which are common crop pests. Different biological and ecological studies as well as survey, population dynamic, movement, daily activity and dispersal of land snails have been studied by many researchers. This investigation was conducted during early of April till mid of May 2014 in the Mediterranean Coast from Alexandria till El-Sallum village in the west of the Egyptian-Libyan border which is one of the longest Mediterranean shores in North Africa. This study is an initial review to throw spot light on Malacofauna of the North Coast region of Egypt which start from Alexandria, city extending about 32 km along the coast of Mediterranean sea in the north central part of Egypt, till El-Sallum village at the east border of Libya and around 145 km from Tobruk. Thirteen land snail species had been collected from this region, belonging to five gastropod families. Helicidae presented with the six species *Theba pisana* (Müller), *Eremina desertorum irregularis* chilembia (Bourguignat), *Eremina desertorum desertorum* (Forskäl), and *Eobania vermiculata* (Müller), *Eremina zitteli* Boettger, and *Cornu aspersum* (Müller). Hygromiidae recorded with the three species *Xeropicta krynickinii* (Krynicki), *Xerocrassa* sp., *Xerocrassa tuberculosa* (Conrad) and *Xerocrassa tunisaii*, one species of each family, *Cochlicella acuta* (Müller) from Cochlicellidae, *Rumina decollata* (Linnaeus) (Subulinidae) and *Sphincterochila boissieri* (Charpentier) (Sphincterochilidae) *Eremina zitteli* (Helicidae), *Xerocrassa* sp., *Xerocrassa tuberculosa, Xerocrassa tunisaii* (Hygromiidae), *Rumina decollata* (Subulinidae) and *Sphincterochila boissieri* (Sphincterochilidae) were found as empty shells in in the same locations with no indication of alive specimens. This investigation will contribute the capacity building for biodiversity studies in Egypt.

Keywords: Mediterranean coast, malacofauna, survey, Egyptian ecosystem

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THE IDENTITY OF *DARWININITIUM SHIWALIKIANUM* BUDHA & MORDAN, 2012 (GASTROPODA, STYLOMMATOPHORA)

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Darwininitium shiwalikianum Budha & Mordan, 2012 was originally described as a terrestrial snail species and genus from the Lesser Himalaya of Nepal. It was assigned to the Cerastidae, implying a significant northward range extension of this family. It was also supposed to be the first orthurethran species having a fully pseudosigmurethrous pallial system. However, conchologically, *D. shiwalikianum* is similar to *Helix capitium* Benson, 1848, type species of the camaenid genus *Ganesella* W.T. Blanford, 1863. Moreover, COI and 28S rDNA sequences show that *D. shiwalikianum* and *G. capitium* form a mixed clade, with *G. rhombostomus* (Pfeiffer, 1861) as strongly supported sister taxon. Hence: (1) *D. shiwalikianum* is a junior synonym of *Helix capitium* Benson, 1848, (2) *Darwininitium* Budha & Mordan, 2012 is a junior synonym of *Ganesella* W.T. Blanford, 1863, (3) *D. shiwalikianum* is a camaenid, not a cerastid, (4) it therefore does not imply a cerastid range extension, and (5) it has a sigmurethrous, instead of a pseudosigmurethrous, pallial system. Conversely, with the description of *D. shiwalikianum*, the anatomy of *Helix capitium* is now available to supplement the diagnosis of the genus *Ganesella*.

Keywords: Camaenidae, Cerastidae, *Darwininitium shiwalikianum*, DNA, *Ganesella capitium*, nomenclature, phylogeny, pseudosigmurethry, taxonomy

FIRST OBSERVATION OF SEA HARE MATING BEHAVIOUR AND EARLY EMBRYONIC DEVELOPMENT IN SABAH, MALAYSIA

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Sea hares are gastropod molluscs belonging to the clade Aplysiomorpha. They are named “sea hare” because of the pair of rhinophores on their head that resembles ears of a rabbit. Two species of sea hares were found in a seagrass nursery tank at Marine Ecology Research Centre (MERC) in Sabah, Malaysia, namely the lined sea hare (*Stylocheilus striatus*) and green sea hare (*Petalifera punctulata*). The sea hares were collected together with seagrasses and sediments from Gaya Island, Sabah. Mating pairs of *S. striatus* and *P. punctulata* were collected from seagrass nursery tank and kept separately to observe their mating behaviours and early embryonic development of the eggs. The mating behaviour was monitored every half an hour for 24 hours. *S. striatus* pairs mated for two to seven times during this period, ranging from 15 minutes to one hour. The pairs started to lay eggs in the morning 85 minutes after their last mating. It took about 30 minutes for the sea hares to complete depositing an egg mass. *S. striatus* laid clusters of stringy egg masses ranging from 8.4 cm to 53.4 cm long with string diameter of around one millimetre, either attached to tank wall, seagrass leaves or stems. The colour of egg mass varied from light brown, reddish brown to dark brown. Depending on the length of egg strings, there were about 3040 to 6150 egg capsules per egg mass, each egg capsule enclosing two to seven individuals. The embryos took four to seven days to develop into veligers and ready to hatch from the capsule as free-swimming larvae at approximately 102 µm in body length. Comparatively, *P. punctulata* pairs were less active and stayed in pair on the same seagrass leaf blade for hours during the mating process. They only started to move around after laying eggs. The pair started to lay eggs in the morning 7 hours after their last mating. The duration to complete depositing an egg mass was about 50 to 60 minutes. *P. punctulata* were observed depositing eggs in the form of flat, light green egg masses on seagrass leaf blade of both *Enhalus acoroides* and *Cymodocea serrulata*. The length of egg masses varied from 1.0 cm to 3.0 cm and the width was about 0.5 cm. There were about 10000 to 20000 egg capsules per egg mass, each capsule containing only one individual. The embryos developed into veliger stage (approximately 110 µm in length) in the capsule and hatched after four to five days. The development of the early embryonic stages of both the sea hare species will be described in this paper.

Keywords: veliger, trochophore, Aplysiomorpha, *Stylocheilus striatus, Petalifera punctulata*

TRANS-ATLANTIC RAFTING BIVALVES – AMERICAN MOLLUSCS ON BRITISH & IRISH SHORES

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American molluscs attached to plastic debris were recently discovered on British and Irish beaches. Violent storms pounded the shores of the UK and Ireland in 2013-2014 resulting in anthropogenic waste to be churned up and cast ashore. Bait pots, fishing spools, buoys and other items were discovered on beaches in western Ireland and Cornwall and Devon in England. Attached to these ‘rafts’ were numerous invertebrate species that were later identified as originating from the southeast coast of the United States. The majority of molluscs were byssally attached bivalves that are able to hang on to objects making excellent rafters.These molluscan non-natives are currently unable to breed in our chilly British waters as they require higher temperatures to do so. However, recent records indicate rising sea temperatures in parts of Britain. Are these rafting species potential invasives?

Keywords: Rafting, invasive, non-native, plastic debris, Britain and Ireland

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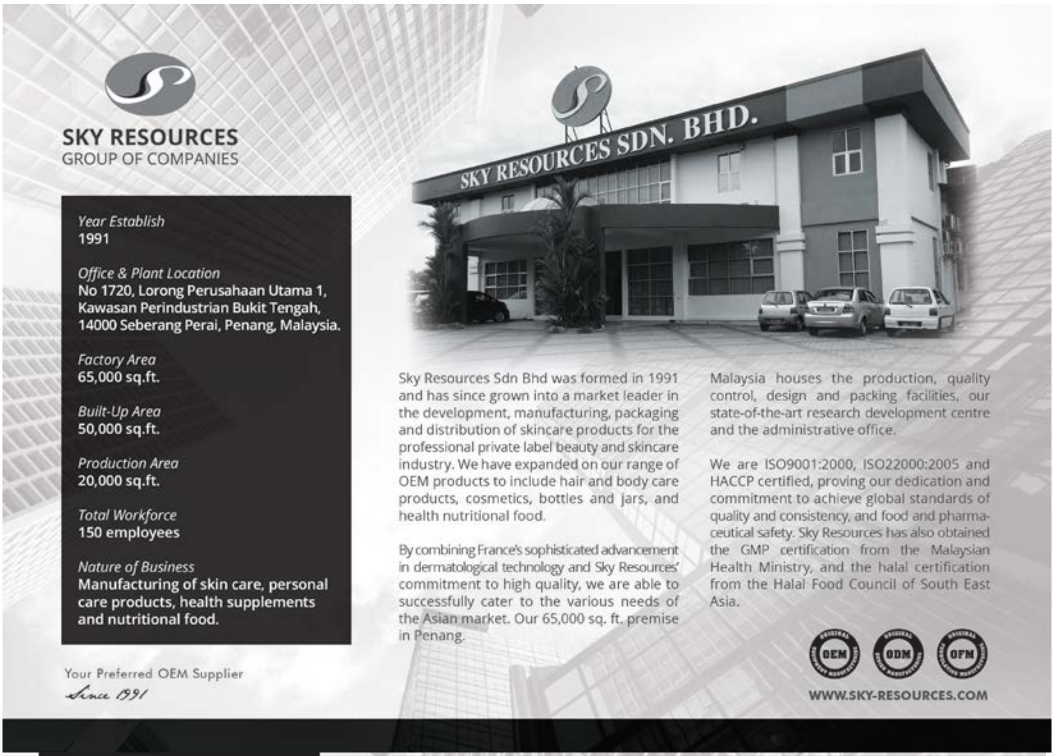

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GROUP OF COMPANIES

Year Establish
1991

Office & Plant Location
No 1720, Lorong Perusahaan Utama 1,
Kawasan Perindustrian Bukit Tengah,
14000 Seberang Perai, Penang, Malaysia.

Factory Area
65,000 sq.ft.

Built-Up Area
50,000 sq.ft.

Production Area
20,000 sq.ft.

Total Workforce
150 employees

Nature of Business
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Sky Resources, a GMP, ISO 9001-2000. ISO 22000 certified company presents you a wide range of OFM, ODM, Health Food & Skin Care products. We maintain high consistency and performance in providing the best quality products and services.

SKY RESOURCES
GROUP OF COMPANIES

WHAT WE DO?

- **Hair** Care
- **Skin** Care
- **Body** Care
- **Cosmetic**
- **Health** Care
- **Others**

OUR EXPERTISES

RESEARCH & DEVELOPMENT

Since 1991, our R&D team has been delivering innovations and breakthroughs that helps the growth for our businesses.

PRODUCTION

Our compounding equipment is capable of blending a variety of products - from the most delicatte emulsions and serums to the most basic shower gels and lotions.

QUALITY CONTROL & ASSURANCE

With stringent quality controls and assurances in place at every step of the way, we maintain the excellent quality that has come to be expected of us.

PACKAGING & DESIGN

We provides designing services to create the desired look for our customers and ensure your product stands out in the mass market.

AWARDS & CERTIFICATIONS

GMP CERTIFIED
CERTIFIED ISO 22000:2005
CERTIFIED ISO 9001:2008

OEM ODM OFM

Your Preferred OEM Supplier
Since 1991

Sky Resources Group of Companies
No. 1720, Lorong Perusahaan Utama 1, Kawasan Perindustrian Bukit Tengah,
14000 Seberang Prai Tengah, Penang, Malaysia.

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TURUT MEKAR was incorporated in 2013 to venture into oil and gas industry, plantation, real estate & properties business and looking forward to expand into other kind of business opportunities. We are the people, who make our vision closer and our dream into reality.

TURUT MEKAR SDN BHD is offering special product and services to meet the requirement of the client and the region

- Oil & Gas supply and services
- Real estate & housing developers services
- Agriculture supply and services
- Aquaculture supply and services
- Forest plantation
- LED billboard & big screen supply & services
- Official merchandise supply for TITO brand
- Food & beverage supply & services

TURUT MEKAR SDN BHD offers a very high level of practical experiences, know-how, quality and confidentiality.

We deliver only a trusted and high quality products and services in an international context with a local understanding of environment. Our company is a team of dynamic and experienced professional working with passion and full commitment to our client's goal.

TURUT MEKAR SDN BHD is a strong financial background company and very highly supported with strategic business partners such as ATB Tanjung Bin Sdn Bhd, Perbadanan Islam Johor (PIJ) Holdings Sdn Bhd, Nadi Marine Sdn Bhd (NMSB), University Malaysia Terengganu (UMT), Complete Oilfield Stimulation Services Sdn Bhd (COSSSB), AsSaffa Design Practice (Malaysia), Future Richmark Sdn Bhd, Leader Formation Sdn Bhd, Azam Sahabat Sdn Bhd, Ekuiti Maksima Sdn Bhd and Empayar Armada Sdn Bhd.

At TURUT MEKAR SDN BHD, our philosophy has always been and continues to provide excellent and timely assistance by providing better quality services and product.

Turut Mekar

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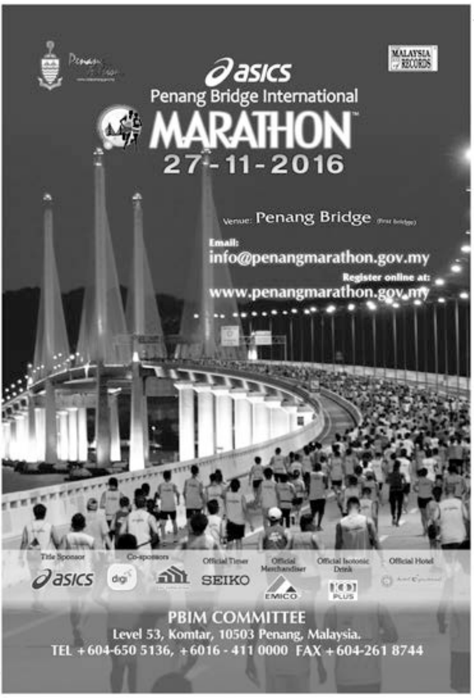

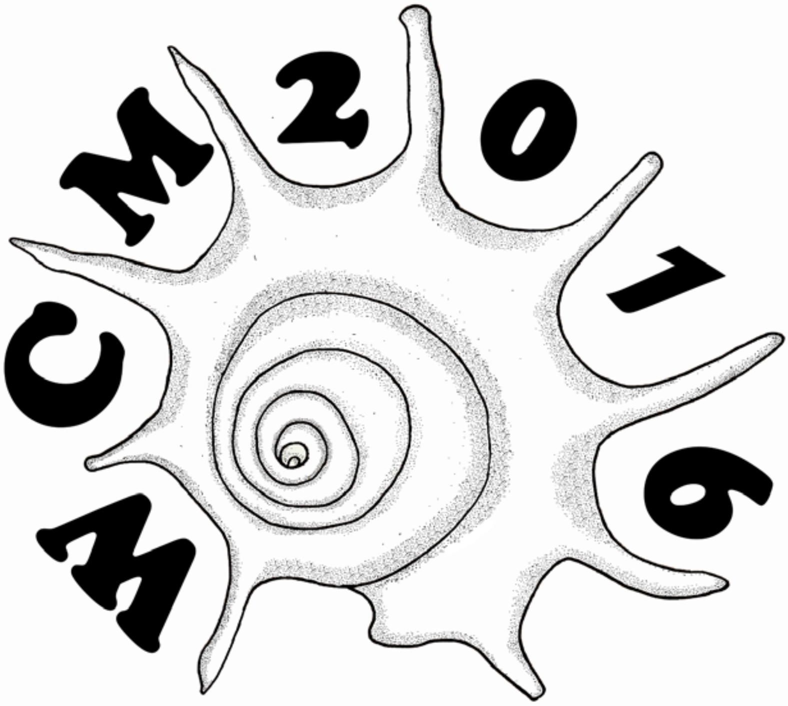
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