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Molluscan Forum 2018

Last November young malacologists from across Europe took part in the 20th Malacological Forum at the Natural History Museum. The abstracts of the twenty nine presentations start inside on page 8.

Molluscan Forum 2018

20th Anniversary

Flett Theatre
Natural History Museum, London
22nd November 2018



ORGANISED BY:

THE MALACOLOGICAL SOCIETY OF LONDON
THE NATURAL HISTORY MUSEUM, LONDON



EDITORIAL

David Reid was editor of the *Journal of Molluscan Studies* from 2002 to 2018, in which year he began the process of retiring from his editorial role. Before completely retiring, David managed an extended handover to the new editor Dr Dinazarde Raheem so that she would be fully *au fait* with all the complicated issues which underly the production of the Journal. During his tenure, the Journal developed its reputation for the quality of its production and aesthetic values, and the science presented in the Journal continued to be first class. The Council was sorry to see the end of David's editorship and offered him heartfelt thanks for the excellent work he has done to further the objects of the Malacological Society of London. David's contribution to the Society was not just as editor. He was the Society's president from 1997 to 2000 and is an Honorary member of the Society. We wish him the very best in the future.

The 2018 Forum was particularly productive. A large number of young presenters from thirteen countries in and out of Europe once again made this an eclectic and exciting meeting. Since it was the 20th anniversary of 'the Young Malacologists' Forum, some of the original presenters were invited to talk about how their careers had progressed between then and now. Their talks were a heartening confirmation that it is possible to have a productive and satisfying career based on molluscs.

A major function of the MSL is to provide funding for malacological research and travel. It is encouraging to see the fruits of this investment in the form of reports in *The Malacologist* and papers in the *Journal of Molluscan Studies*. In this issue of *The Malacologist*, there are research reports from R.Salvador, R.Fernandez-Vilert (Harvard), S.Lundquist (Cambridge) and K.Hendriks (Groningen) and a travel report from F.Bergmeir (Munich). Will the Society only be funding British students after Brexit? Hopefully we will continue to fund good science both in and out of these sceptered isles.

Prof. Georges Dussart
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TAXONOMIC/NOMENCLATURAL DISCLAIMER

This publication is not deemed to be valid for taxonomic/nomenclatural purposes [see Article 8b in the International Code of Zoological Nomenclature 3rd Edition (1985), edited by W.D. Ride *et al.*].

News and notes

Thank you, David, for all you have done for the Journal!

The screenshot shows the homepage of the *Journal of Molluscan Studies*. At the top, there is a navigation bar with links: Issues, More Content, Submit, and Purchase. Below this, on the left, is a featured article titled "One or many diversity in nitidulum Lo" by Nina T Mikkelsen, published on 27 March. To the right of the article is a large photograph of a man with a beard and a cap, wearing a jacket. Below the article, it says "Volume 84, Issue 2 May 2018" and "Impact factor about 1.3".

Disastrous fire at the National Museum of Brazil

From: Vinicius Padula <viniciuspadula@yahoo.com>

Sent: 09 September 2018 01:12

Subject: Malacology - Museu Nacional, Brazil

Dear colleagues,

I think all of you already know about the regrettable fire that destroyed, last Sunday, the main building of the Museu Nacional, Rio de Janeiro, Brazil. Apparently, most of the circa 20 million items of the collection housed in this building were lost, including anthropological, archaeological, paleontology, linguistics and zoological objects.

One thing I would like to clarify is that in addition to the palace, the main building, the Museu Nacional comprises also few other smaller buildings situated nearby. These buildings are preserved and include: the main Library with more than 1,500 rare documents and books; the Herbarium, one of the largest scientific collections of fungi and plants in Latin America with approximately 600,000 voucher specimens and 7,400 nomenclatural types; the sections of Herpetology, Ichthyology, Mammalogy and Ornithology, covering, in total, more than 780,000 specimens of which 2,500 are types; and the collections of many invertebrates groups such as Porifera, Cnidaria, Platyhelminthes, Annelida, Bryozoa, Echinodermata, Crustacea and other less representative groups, including also unique specimens from the deep sea, in a total of more than 80,000 lots of millions of specimens.


Unfortunately, the entire Entomology department as also the Arachnology and Malacology sections, with their large collections, were housed inside the main palace. Until now, we haven't access to the debris resulted from the fire and it can take weeks before we have permission to start a search for any remaining specimen. But by what we can see until now, we are unfortunately not optimistic.

Before the fire, the Malacology Collection consisted by more than 44,500 lots and a countless number of specimens. In addition, more than 25,000 lots were waiting for records to be included in the collection. These includes samples of molluscs from terrestrial, marine and fresh water environments. A shorth breath is that at least 80% of our collection of type specimens composed by around 530 lots - being at least 106 holotypes - related to 285 species names (Pimenta et al., 2014, please see attached), was recovered by our lab technician and colleagues during the fire. Each of these people deserve, in my opinion, a tribute for this act. Along the next days we will make a checking on this precious material to provide further information to the scientific community.

Next Monday, 10th of September, I'll officially begin my activities as professor and curator of the Malacology Section of the Museu Nacional, Universidade Federal do Rio de Janeiro. I'll join the current curator, Professor Alexandre Dias Pimenta. I could never imagine such dramatic scenario and such challenge in the beginning of my history, as a curator, in the Museu.

In addition to the rescued type specimens, we will probably need to start the construction of a new malacological collection. I would like to thank very much some of the colleagues that already offered help and samples. Indeed, any small contribution from you concerning specimens, bibliography and other data will be very welcome. (However, for now we are organising, at least, a new space to work in the labs of our colleagues in the museum. As soon we obtain a minimum of condition to receive contributions and donations, we will inform you.

To get an idea
of the extent of
the malacological
loss, follow
up this article

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Article

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Catalogue of the type specimens deposited in the Mollusca Collection of the Museu Nacional / UFRJ, Rio de Janeiro, Brazil

ALEXANDRE DIAS PIMENTA^{1,4}, JÚLIO CÉSAR MONTEIRO², ANDRÉ FAVARETTO BARBOSA³,
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Abstract

A curatorial revision of the type specimens deposited in the Mollusca Collection of the Museu Nacional / UFRJ, Rio de Janeiro, Brazil (MNRJ) revealed the existence of 518 lots of type specimens (holotypes, neotypes, syntypes and paratypes) for 285 names of molluscan taxa from 88 families, including 247 gastropods, 30 bivalves, three cephalopods and five scaphopods. A total of 106 holotypes and one neotype are deposited in the MNRJ. Type material for ten nominal taxa described as being deposited in the MNRJ was not located; the probable reasons are discussed. Some previously published erroneous information about types in the MNRJ is rectified. A total of 37 type specimens are illustrated.

Key words: types, malacological collection, mollusc, malacology, nomenclature



European survey: volume, scope and digitisation of private collections

From: Emily van Egmond <emily.vanegmond@naturalis.nl>

Sent: 18 July 2018 12:55

We will soon distribute a questionnaire on the volume, scope and level of digitisation of private collections within Europe. In addition, we would like to know what kind of resources private collection owners need for digitisation and dissemination of their private collections. As many association members have a private collection, we hope you are willing to help us reach these private collection owners by forwarding and drawing attention to this questionnaire. The survey is scheduled to be sent out by the 31st of July, contains 20 questions and takes less than 15 minutes to complete. This survey is part of the ICEDIG (Innovation and consolidation for large scale digitisation of natural heritage) project, a design study for the DiSSCo (Distributed system of scientific collections) research infrastructure (icedig.eu and disscos.eu).

DiSSCo is a new pan-European Research Infrastructure initiative with a vision to position European natural science collections at the centre of data-driven scientific excellence and innovation in environmental research, climate change, food security, health and the bioeconomy.

When it comes to privately owned natural history collections, these are often 'hidden' and may harbour highly valuable specimens for a specific taxon or (local) geographic range. On a European scale, these private collections combined are expected to form a significant part of the natural history collections as a whole. Therefore, it is important to include private collections in Europe's digitisation efforts of natural history collections. The outcomes of the questionnaire will be used to write guidelines for the digitisation of private collections, to perform a couple of pilot digitisation pilots of private collections and to present information about private collections to policy and decision makers. If we can show that there are many interesting private collections in Europe, we can make a strong case to focus on these natural history collections as well. It is therefore of great importance to reach as many private collection owners as possible via associations.

If you are interested to participate in spreading the word about this questionnaire on private collections, you do not have to take any action right now. You will receive the questionnaire with an accompanying mail to send out to your members by the end of July. These will be offered as much as possible in the national language to compel as many people as possible to participate in the questionnaire. Otherwise, you can reply to this message and indicate you wish not to participate.

Luc Willemse (Head of Entomological and Geological Collections) and
Emily van Egmond
Naturalis Biodiversity Center, Leiden, the Netherlands
emily.vanegmond@naturalis.nl www.naturalis.nl

If you are aware of any private collections to which this initiative might apply, please contact Emily van Egmond



Status paper on mollusk collections in the U.S. and Canada

A survey-based paper on the status on mollusk collections in the U.S. and Canada has been published in the American Malacological Bulletin and an online version has just become available. The article follows up on a similar project that was published by Alan Solem in 1975.

Mobilizing mollusks: Status update on mollusk collections in the U.S.A. and Canada *Amer. Malac. Bull.* 36(2): 177–214 (2018) Petra Sierwald, Rüdiger Bieler, Elizabeth K. Shea, & Gary Rosenberg

We have provided open access to the paper on BioOne:
<https://bioone-org.proxy.uchicago.edu/journals/american-malacological-bulletin/current>

Rüdiger Bieler, PhD
Curator of Zoology/Invertebrates, Field Museum of Natural History rbieler@fieldmuseum.org



Travel grants for 2019 World Congress of Malacology, California



Applications are invited for travel grants to support participation at the World Congress of Malacology, 11-16 August 2019, at Asilomar conference grounds, Pacific Grove, California. The awards will be in the range of 1000-1500 each, and award notifications will be available 1 April (earlybird registration rate ends 15 April). Eligibility for these awards includes research students and non-student researchers in positions that do not support their research (e.g. museum collection managers, hobbyists, etc). All applicants must submit the application form, and a letter of support from their supervisor (or equivalent). Forms available at <http://www.unitasmalacologica.org>
Deadline for applications is Sunday 10 March.

The application form should be returned by email to <j.sigwart@qub.ac.uk> by 10 March. Letters of support can be sent separately or with the application, but must be received by the deadline for an application to be eligible for consideration.

Dr Julia D Sigwart, Queen's University Belfast, Marine Laboratory j.sigwart@qub.ac.uk



Western Society of Malacologists' James McLean grant for collections-based research, 2019

The Western Society of Malacologists (WSM) offers a financial stipend for students to study fossil or recent malacological specimens in collections to further their research. This award honors the late James H. McLean, Curator of Malacology at the Natural History Museum of Los Angeles County from 1964–2001 and Emeritus Curator until 2013.

Eligibility: Graduate, undergraduate, and exceptional high school students may apply.

Research Scope: The applicant's research project must be collections-based and focus on extant or fossil western North American mollusks (freshwater, terrestrial, or marine).

Funding: The maximum award is \$1000 (US dollars) and should be used to support travel and accommodation costs. Applicants need not apply for the full \$1000 if it is not necessary.

Museum(s): Visits to any University-based or Natural History Museum collection (domestic or international) are eligible.

Deadline: Proposals and recommendations are due March 1st, with announcement and notification of awardees in May or June. Funds are available for use until May 15th of the following year.

Proposal Submission: Proposals are to be sent electronically (as one document) to:

Jann Vendetti at: jannvendetti@yahoo.com or jvendett@nhm.org, using the subject line: James McLean Student Grant

Application: Two pages (single-spaced) with a title, description of the planned research, specific collection(s)/institutions proposed to be visited and why, anticipated visit dates (and length), and a budget justification. Personal information including the applicant's name, address, email address, and student enrollment status (where enrolled, major, degree program, anticipated graduation date) should be included. One recommendation from one graduate, undergraduate, or high school advisor should be sent separately to jannvendetti@yahoo.com with "NAME OF APPLICANT: WSM McLean Student Grant" in the subject line.

Jann Vendetti, Ph.D. Twila Bratcher Endowed Chair in Malacological Research jvendett@nhm.org,
<http://westernsocietyofmalacology.org/grants/james-h-mclean-student-grant-in-collections-based-research/>



Marine Biological Station Vostok (Vladivostok), Russia, 17–27 September 2019

Course on Systematics, Morphology and Evolution of Marine Molluscs



The University Museum of Bergen (University of Bergen, Norway), Shirshov Institute of Oceanology (Russia), National Scientific Center of Marine Biology, Russian Academy of Sciences (Russia), and ForBio (Research School in Biosystematics) jointly offer an International Course on Marine Molluscs. The course will cover a wide range of taxa and lectures will address questions in molluscan biology, morphology and systematics. During the lab work we will study external and internal morphology of selected Mollusca taxa and perform anatomical dissections. Species used in the course will be collected by professional divers but also by the students during the intertidal and small boat field trips in the vicinity of the Station. PhD candidates will be given priority, but based on availability MSc students and postdoctoral researchers on the beginning of their careers may also be considered. Deadline April 1st, 2019

Contact: Nataliya Budaeva (nataliya.budaeva@uib.no) - ForBio coordinator
https://www.forbio.uio.no/events/courses/2019/Molluscs_Vladivostok



2019 edition of *2,400 Years of Malacology*

the 2019 edition of "2,400 Years of Malacology" – a catalog of biographical and bibliographical articles about those who studied and collected mollusks and related files – is now on the website of the American Malacological Society:

<https://ams.wildapricot.org/2400-Years-of-Malacology>

The 2019 edition is 1,710 pages. It includes four additional documents containing (1) collations of a number of important references for malacological systematists (111 pages); (2) collation of the Systematisches Conchylien-Cabinet (1837-1920) (65 pages); (3) collations of significant malacological journals (62 pages), and (4) an updated version of the "Annotated Catalog of Malacological Meetings, Including Symposia and Workshops in Malacology" (145 pages).

We appreciate receiving your suggestions as to additional citations, or your comments on these publications. As always, we remain grateful to numerous colleagues who continue to provide us with their comments and information on relevant papers. We also thank the American Malacological Society for their continued posting of these publications, and AMS Webmaster Chris Hobbs for taking over maintaining the website.

Please note that the home of the AMS website has recently changed, so any links or bookmarks will need to be updated.

Alan Kabat and Gene Coan
alankabat@aol.com



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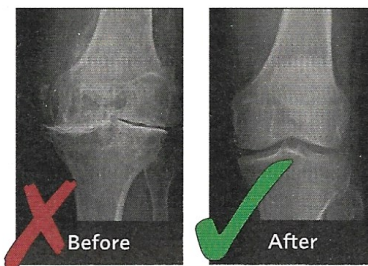
With the high concentration of pure allantoin secreted in snail elixir, the Elixir of Helix Snail Elixirs liquid formula will envelop your joints like a bandage. This will allow the allantoin to immediately act in the healing process of your fissured and eroded, arthrosis-afflicted cartilage (Fig. 1). By repairing your cartilage, the allantoin will replace one of the main causes of your pains from osteoarthritis.

REGENERATION

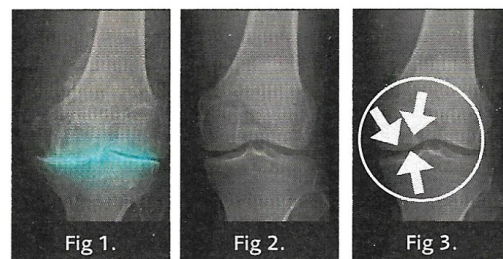
The glycoproteins contained in snail slime are like the glucose that supplies energy to your system: they will provide your cartilage with the necessary energy for its quick, deep and lasting self-regeneration (Fig. 2). As your cartilage progressively regenerates, you'll feel how your mobility and joint-health improve considerably.

CONSOLIDATION

The formula of Elixir of Helix Snail Slime is extremely rich in collagen and elastin, two key substances in the structural integrity of joint tissue, both of which are naturally found in snail slime. Once nourished and bathed in these substances thanks to the Elixir of Helix Snail Slime, your cartilage will become supple and resistant again (Fig. 3). Your joints will quickly regain flexibility and robustness.



Nb



Of course, as an enthusiastic member of the malacological community, you should be able to make your own.

Molluscan Forum 2018

Natural History Museum, London
30 November 2018

Convened by

ANDREIA SALVADOR, Organiser

Curator of Marine Mollusca, Natural History Museum (email: a.salvador@nhm.ac.uk)

Dr J.W.GRAHAME, Organiser,

University of Leeds,

President of the Malacological Society of London (email: J.W.Grahame@leeds.ac.uk)

Schedule

ORAL PRESENTATIONS

09.00 - 09.45 Registration, coffee & set up poste

09.45 - 10.55 Session I

- 09.45 JOHN GRAHAME: Welcome and introduction to the day
- 09.55 FRANZISKA S. BERGMEIER: Bathyal slope to hadal trench: diversity and biogeography of Solenogastres (Mollusca) in the Northwest Pacific
- 10.10 PAUL ZAHARIAS: From one wastebasket to another: an exon-captured based phylogeny of Turridae (Gastropoda, Conoidea)
- 10.25 VALENTIN RINEAU: A new cladistic insight at the comparative anatomy, phylogeny and systematics of rudists (Bivalvia, Hippuritida)
- 10.40 HILDUR MAGNÚSDÓTTIR: Morphological and mtDNA divergence in common whelk, *Buccinum undatum*, across the N-Atlantic
- 10.55 ERIKA LORENCOVÁ: Drivers of mollusc assemblage diversity in a system of lowland lentic habitats

11.10 - 11.40 Coffee & poster viewing

11.40 - 13.00 Session II

- 11.40 ALEXANDER D. BALL: 20 years later, what is state of the art in imaging and analysis now?
- 11.55 HAYLEY JONES: Gastropod research at the Royal Horticultural Society
- 12.10 CESSA RAUCH: Sea slugs of Southern Norway; an example of citizens contributing to science
- 12.25 CHARITOS ZAPITIS: Behavioural responses of the freshwater mussels *Anodonta anatina* and *Unio pictorum* to light availability and their ecological and management implications
- 12.40 MALCOLM T. SANDERS: Frog shells through time: a dialogue between mitogenomics and Palaeontological data
- 12.55 JOHN GRAHAME: Announcements, Arrangements and Awards etc.

13.00 - 14.00 Lunch break

14.00 - 15.15 Session III

- 14.00 KATRIN LINSE: 21 years as a Malacologist
- 14.15 GIZELLE A. BATOMALAUQUE: Beyond the shell: systematic revision of the Helicostylinae using genomes, genitalia, and geography
- 14.30 WERNER DE GIER: Micro-CT scanning Africa's streptaxids – revealing the insides of *Ptychotrema* shells
- 14.45 JAKE GOODALL: Evolution and regulatory control of shell colour polymorphism in the common whelk, *Buccinum undatum*
- 15.00 LISETTE MEKKES: Decline in shell thickness of shelled pteropods along a natural ocean acidification gradient

15.15 - 15.45 Tea break & poster viewing

15.45 - 17.15 Session IV

- 16.00 CRISTINA VINA-HERBON: Innovative and practical uses of bivalve and gastropods species data on the development of marine biodiversity indicators
- 16.15 KASPER P. HENDRIKS: Long-distance dispersal largely explains patterns of endemism in Bornean land snails
- 16.30 RADOVAN COUFAL: Remnants of spring fens in the Bohemian-Moravian Highlands: the occurrence and coexistence of (not only) molluscan glacial relicts
- 16.45 TOMÁŠ NĚMEC: Specific damages recognized at land-snail shells can document the rate of predation: differences among predators and habitat types
- 17.00 JOHN GRAHAME: Closing remarks.

17.15 - 18.30 Wine social & final poster viewing

POSTERS

- MERI ARZUMANYAN: Main Threats to a Critically Endangered *Vertigo angustior* Jeffreys, 1830 in Armenia
- EDGAR BARAJAS LEDESMA: Analysis of the stability of gastropod mucus protein by Infrared Spectroscopy
- PETER D. BARFIELD: First evidence of *Arcuatula senhousia* (Benson, 1842), the Asian date mussel in UK waters
- BASTIAN BREZINGER: How many groups of meiofaunal Cephalaspidea?
- IMOGEN CAVADINO: Garden gastropods: slug and snail diversity in UK gardens
- ELIZABETH CLUTTON: Identification of sources of C, N and S for marine wood boring bivalves
- M. CARMEN COBO: New data on the biodiversity of Mollusca Solenogastres in the Caribbean Sea
- CHRISTOPHER HOBBS: Population genetics of the Shining Ramshorn Snail, *Segmentina nitida*- post-glacial colonisation, bird-mediated dispersal or separate species?
- DANIEL A. HORTON: Drug screening to investigate the effects on *Biomphalaria glabrata* susceptibility to infection by *Schistosoma mansoni*
- ALISON IRWIN: The evolution and diversification of eyes in strombid gastropods
- OPHÉLIE LASNE: Habitat preferences of *Vertigo geyeri* Lindholm, 1925 in the Jura Mountains, France
- HANNAH M. PARRY-WILSON: Biogeographic range shifts of two northeastern Atlantic intertidal limpet species *Patella vulgata* and *Patella depressa*; comparisons of boreal and lusitanian responses to changing climates
- JUSTINE SIEGWALD: A new *Scaphander* species from the deep sea of Argentina

Molluscan Forum 2018

ABSTRACTS

Invited speakers - they were original student presenters at the 1998 Forum

20 years later, what is state of the art in imaging and analysis now?

Alexander D. Ball

Imaging and Analysis Centre, Core research Laboratories, Natural History Museum, London, UK

Email: a.ball@nhm.ac.uk

Twenty years ago John Taylor encouraged me to start the Molluscan Forum as a place for early career researchers and students to come together and discuss our research. At that time I was an early career post-doc, just wondering what to do with myself, but who had unexpectedly gained a lot of experience with imaging molluscs and working on 3D reconstructions from serial sections. Since then I have become the head of the Imaging and Analysis Centre at the Natural History Museum. Over the past twenty years the possibilities for imaging and analysis of biological samples has expanded enormously. In this presentation I compare some of the work that I did twenty years ago: reconstructing 3D models from serial sections, scanning and transmission electron microscopy with some of the results coming out of the laboratories today. Most of my examples will not be drawn from Mollusca, but the general principles remain the same. We are in a golden age for morphological studies. Instruments are more flexible, more powerful and easier to use now than they ever have been. The possibilities that they open up to us as researchers, whether experienced, or just starting out in our careers, are incredibly exciting.



21 years as a Malacologist

Katrin Linse

British Antarctic Survey, Cambridge, UK

Email: kl@bas.ac.uk

In 1997 I published my Diploma thesis on the biodiversity of the epibenthic molluscs of the Beagle Channel and gave my first conference talk in English at the 1st Molluscan Forum held at the NHM on 25th September – since then I call myself a Malacologist. During my PhD thesis, I continued with research on Magallanic molluscs and as part of it, analysed biogeographic links to the Southern Ocean malacofauna. This shaped my further career in Antarctic science as, since 2000, I work as a marine biologist at the British Antarctic Survey studying the biodiversity, phylogeography and evolution of Antarctic marine invertebrates. I led the team designing the first georeferenced Antarctic benthos database based on molluscan data, resulting in new Antarctic provinces and an updated biogeography for the Southern Ocean (SO), which is now applied to different taxa. These biodiversity data and their application form the basis for marine conservation efforts towards policy measures. I am considerably involved in research on phylogenetic relationships of current SO species and their evolutionary histories and have significantly contributed to the discovery of high biodiversity in the Antarctic deep sea. In recent years, I was part of the teams discovering of the SO hydrothermal vents and methane seeps, sampling the abyssal and hadal area of the tropical Atlantic as well as studying deep-water coral and barnacle habitats of the North Atlantic. While my general research interests include all SO and deep-sea invertebrates, my personal focus are still the shelled molluscs. And throughout these years I stayed in touch with the Malacological Society of London, first as a member, then joined the Society's Council and currently I am the Treasurer.



Innovative and practical uses of bivalve and gastropods species data on the development of marine biodiversity indicators

Cristina Vina-Herbon

Joint Nature Conservation Committee, Monkstone House,
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Marine biodiversity indicators are an effective tool to assess status of species, habitats, and functional traits in marine conservation and policy. This information is essential not only to understand the effects and threats to marine biodiversity from human activities, such as fishing, aquaculture, navigational dredging, and coastal development, but also indirect pressures, such as those driven by climate change (e.g. increasing surface water temperatures). This area of work is, however, challenging due to the complexity of interactions between different parts of the ecosystem, data gaps and limited understanding of cumulative effects from multiple pressures. Data and evidence from gastropods and bivalve species are a key part of the development and use of indicators to assess the status of seafloor communities. For example, habitat forming species, e.g. *Modiolus modiolus* reefs which are an important food source, refuge and nursery grounds for many species; consequently the distribution and condition of those habitats indicates the health and diversity of

reefs communities, and their resilience to threats such as smothering by suspended sediment caused by anthropogenic activities. Species such as the long lived bivalve *Arctica islandica* or *Atrina fragilis* provide essential information on the sensitivity of benthic infaunal communities and their resilience to potential impacts and chronic effects from pressures. The application of biodiversity indicators to meet marine policy and conservation demands is developing rapidly in the management realm. The presentation will provide an overview on the type of bivalve and gastropods data used within the current and proposed biodiversity indicators, and how this helps inform the status of marine benthic ecosystems.



Alphabetical by contributor

Main Threats to a Critically Endangered *Vertigo angustior* Jeffreys, 1830 in Armenia

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The Narrow-mouthed Whorl Snail *Vertigo angustior* is one of the most endangered *Vertigo* species in Armenia. *V. angustior* is a widely distributed species in Europe and Asia, yet it is included in the Red Lists of many European countries. Moreover, it is included in the Red List of the IUCN as a Near Threatened species. In the Armenian Red Book, this species has in the category of being Critically Endangered. *Vertigo angustior* occurs in Armenia in only one place. near to the city of Stepanavan in Lori province. *V. angustior* requires a narrow range of conditions. It prefers marshy ground at high elevation and humidity, with flowing groundwater but subject neither to deep or prolonged flooding nor to periodic desiccation. and lives amongst short vegetation, composed of grasses, mosses or low herbs. The current distribution of the species was investigated to identify the main threats. We analysed seven different sites near to the city of Stepanavan that could be an appropriate area for *V. angustior*. The main threats for this species were found to be habitat modification, livestock grazing, drainage and agriculture activities.



Analysis of the stability of gastropod mucus protein by Infra-red Spectroscopy

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Gastropods can adhere to different surfaces, and due to their mucus remain in horizontal or vertical positions without falling. However mucus is not just an adhesive, it is also a lubricant and facilitates movement. Therefore mucus requires certain specialisations for performance in a range of environments and as such it is expected that its constituents, both proteins and carbohydrates, have adapted specifically to achieve this through their state of hydration. To better study these constituents, we introduce Fourier Transform Infrared Spectroscopy (FTIR) which allows for rapid and convenient chemical comparison between species and the possibility to place results into a phylogenetic context. In this study, native mucus produced by 12 terrestrial slugs and snails, and aquatic snails including: *Achatina fulica*, *Cornu aspersum*, *Cepaea nemoralis*, *Lymnaea stagnalis*, *Marisa cornuarietis*, *Pomacea diffusa*, *Arion ater*, *Arion hortensis*, *Limax flavus*, *Limax maximus*, *Veronicella sloanei*, and *Laevicaulis haroldi*, was analysed. Furthermore by subsequent heating of mucus samples, it is possible gain further insights into for protein stability and function within a particular secretion type which will ultimately inform us about their evolution and ecological specialization.

Our results show that FTIR was successful in identifying relationships between species, families and orders, with more closely related species producing more compositionally similar mucus. Furthermore, we show that gastropod mucus proteins present different degrees of glycosylation, as evidenced by absorption at 1534 cm^{-1} . When looking at the response of these materials to heating, the land snail *C. nemoralis* shows no significant changes in absorbance bands corresponding to amide I peak ($1654\text{--}1632\text{ cm}^{-1}$) and amide II peak (1534 cm^{-1}). However, mucus from the slug *A. hortensis*, shows clear changes in its amide I and amide II absorption bands, indicating changes in its protein secondary and tertiary structures. Overall these results indicate how well the mucus is able to resist dehydration and how they may be optimised for performance in different environments. In summary, uncovering the basis for this multi-functional material will not only shed light onto the biology of these organisms but also provide insights into protein function outside the body, a group of materials entitled ecto-secretions.



First evidence of *Arcuatula senhousia* (Benson, 1842), the Asian date mussel in UK waters

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An articulated shell of *Arcuatula senhousia* was found loose on sand in the intertidal mid-high shore area of a site in the Solent, on 25th October 2017. The specimen was not living but was generally in good condition. Subsequently, many more specimens both living and dead have been recovered from the same locality. The species can be found in intertidal and shallow subtidal habitats wherever it occurs. It can settle on soft sediments or hard substrata including man-made structures, but shows a preference for the former. On 15th February 2018 a live specimen was found buried just beneath the surface with its posterior end very slightly exposed. This is a feeding orientation allowing its siphons free access to the water column. The animal was partially surrounded by a fluffy sediment cocoon. These cocoons are considered protective and are constructed using fine byssal threads. The native range of *A. senhousia* extends from the type locality of Zhoushan, China (near Shanghai) north to the Kuril Islands and the Siberian coast and southwards through the Sea of Japan, the Yellow Sea, the East China Sea, and the South China Sea to Singapore. Outside of the native range the northerly extent is exceeded in at least one location. In the Pacific North West there is a record from Savary Island in the Strait of Georgia, British Columbia ($N49.94^\circ$). The UK find pushes the northerly extent higher to 50.82° North. The closest record to the UK prior to the current find was reported in 2009 from Arcachon Bay, in the southern Bay of Biscay. It is therefore considered most likely that the Solent population originated from an introduction event somewhere nearby. The specimens have been compared with images of the type specimen provided by the Natural History Museum, London. A visual comparison indicates minor morphological differences as might be expected from phenotypic variation due to local environmental conditions. It is hoped that future work will include molecular analysis as well as management considerations of relevance to ecologists and regulatory authorities.



Beyond the shell: systematic revision of the Helicostylinae using genomes, genitalia, and geography

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Helicostylinae, a camaenid subfamily with a centre of diversity in the Philippines, is known for having a variety of shell forms. Species have been traditionally classified based on shell morphology, and generic classifications vary between authors due to the overlap in conchological characteristics. We present a taxonomic revision of the Helicostylinae using exon-capture data and examination of the genital anatomy. We determined 12 of the current accepted genera to be well-supported. Furthermore, we resurrect three old genus names, raise three subgenera to genus rank, and plan to introduce four new genus names. *Obba* (classically under subfamily Camaeninae) is now included in the Helicostylinae, while *Chloraea* (classically under Helicostylinae) is transferred to Hadrinae. Genera that tend to be co-distributed exhibit shell-form convergence among species belonging to different genera, and a divergence of shell forms among species belonging to the same genus. This pattern may correspond to adaptive radiation. On the other hand, genera that have a more restricted distribution (i.e. endemic to one island) tend to have uniform shell forms, which may represent morphostatic radiation. The factors that drive such conchological diversity in different genera remains unclear as there are yet no studies of adaptive significance of particular characters in Philippine land snails.



Pfeifferia micans (left) and *Helicostyla virginea* (right),
Northeastern Luzon, Philippines.



How many groups of meiofaunal Cephalaspidea?

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At least six lineages of microscopic and worm-shaped slugs living between the interstices of marine sands are known to have evolved within Heterobranchia and occur in all oceans, especially in tropical and subtropical waters. We here present first molecular data on meiofaunal Cephalaspidea, focusing on the aberrant families Philinoglossidae and probable members of Philinidae *sensu lato*. We found that a combination of fragmentary COI, 16S and H3 sequences prove informative in teasing apart philinoglossid diversity, but so far fail at disentangling the second group. Philinoglossidae fully lack a shell or a gizzard and have modified morphology to the constraints of interstitial life. Molecular phylogeny shows a distinct Indo-Pacific and Eastern Atlantic clade (“Philinoglossinae” with at least 4 species) and another group on both sides of the Atlantic and tropical Southern America (equal to “Plusculinae”, also 4 species, possibly paraphyletic), largely reflecting traditional taxonomy of Philinoglossidae. On the other hand, several morphospecies of meiofaunal “philinids”, collected at various localities in the Indo-Pacific, are largely undescribed: these are 1-3 millimeter-sized, “typical”, meiofaunal worms that bear a peculiar posterior shell and asymmetric gizzard plates, similar to equally meiofaunal *Philine exigua* Challis, 1969 from the west Pacific but also benthic *Spiniphiline* Gosliner, 1988 from Africa and the Caribbean. The present taxon sampling still fails to accurately resolve closer relationships and placement within Philinoidea, but monophyly of the groups is suggested, indicating existence of an unnamed lineage at family level. Marine interstitial Cephalaspidea thus may be the second most diverse group of interstitial heterobranchs, besides panpulmonate Acochlidia (Acochlidimorpha). They also present an interesting target for ongoing study of the phylogeny and evolution of Cephalaspidea as a whole.



Bathyal slope to hadal trench: diversity and biogeography of Solenogastres (Mollusca) in the Northwest Pacific

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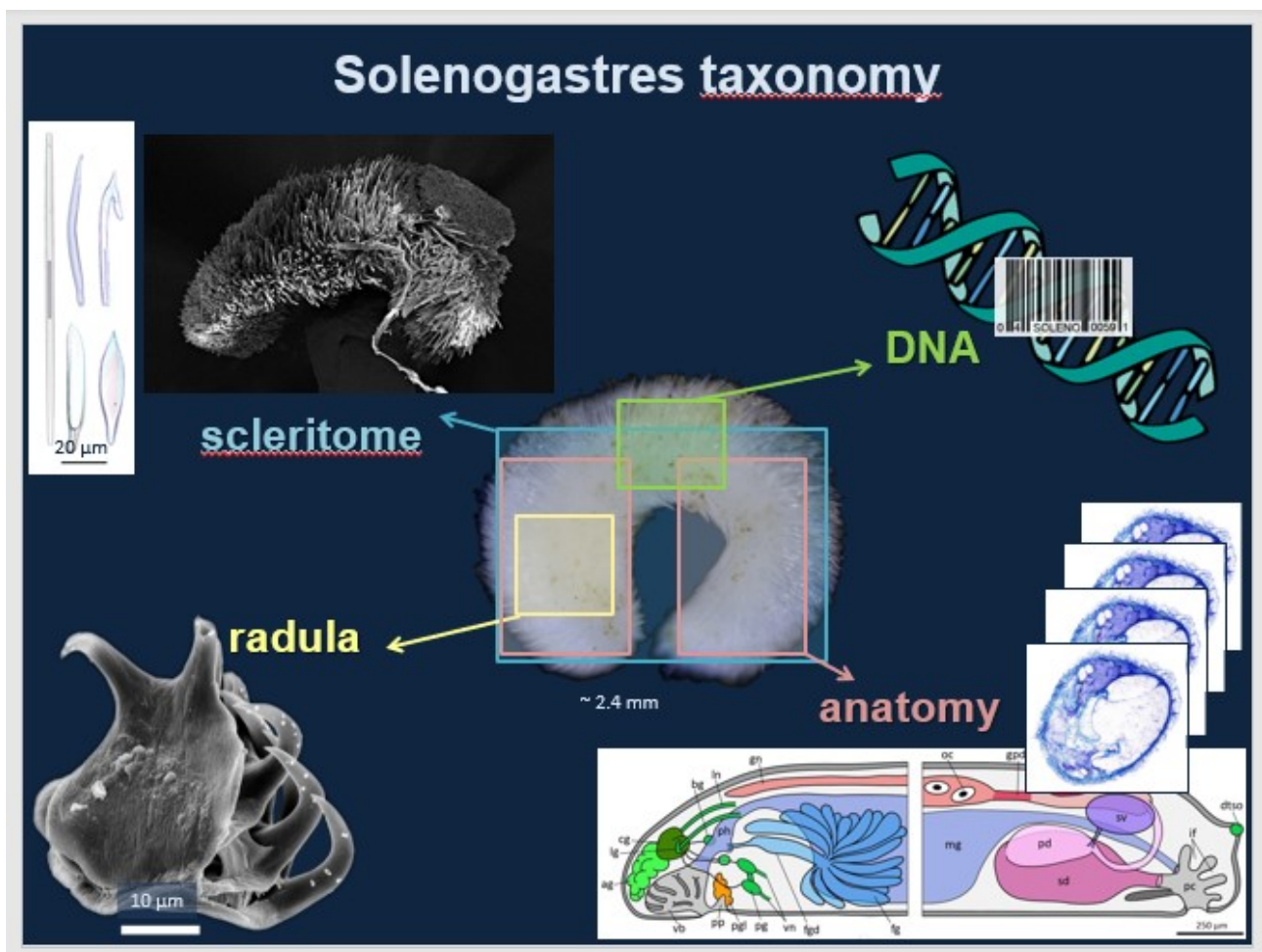
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Several recent joint German-Russian research cruises investigated the deep-sea benthos in the Northwest Pacific with the aim of identifying biogeographic links or isolating factors between the semi-enclosed Sea of Okhotsk and the open Pacific. Solenogastres are a clade of shell-less, worm shaped molluscs and a frequent, albeit not overly abundant, component of the collected deep-sea fauna. Due to their inaccessibility and complex taxonomy, Solenogastres are generally understudied and underestimated – the latter at least in regard to their diversity, which is estimated to be at least ten-fold above the currently known 300 species. Many of these species are based on single findings and as a consequence vertical and horizontal distribution ranges of the group are poorly explored. We studied approximately 150 specimens of Solenogastres, collected from the bathyal slope and basin of the Sea of Okhotsk, the abyssal plain of the Northwest Pacific, and hadal depths of the Kuril-Kamchatka Trench. We used an integrative taxonomic approach combining multiple mitochondrial markers, 3D-microanatomy based on histology, and scanning electron microscopy to delimitate different lineages and investigate their bathymetric and biogeographic distribution ranges. In total, we discovered close to 50 species in the region, largely new to science, and by far exceeding the previously known solenogaster diversity in the area. Solenogastres have rarely been reported from hadal depths, but we discovered several lineages at 9,500 m. Overall there is a unique solenogaster fauna in each of the sampled regions with few lineages present on both sides of the Kuril-Kamchatka Trench, which we think might act as a barrier to their dispersal. This is the first comprehensive study evaluating phylogenetic relationships, population genetic patterns and distribution ranges in Solenogastres on a regional scale. It provides a reliable barcoding library for easier identification in future faunistic surveys and therein a first baseline for beta-biodiversity comparisons.



Garden gastropods: slug and snail diversity in UK gardens

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Slugs and snails are significant horticultural pests, and are frequently the most common pest enquiry to the RHS Gardening Advice service. Domestic gardens are a mosaic of varying habitats, which may be suitable for a range of different slug and snail species. Not all species of slug and snail found in the UK are considered plant pests however, with many thought to play important roles in breaking down decaying material and other aspects of the garden ecosystem. In domestic gardens the presence of these pests is usually recognized by feeding damage, with the culprit species not identified. Very few studies of diversity of slugs and snails in UK gardens exist, with the majority of studies based in agricultural settings. This means little is known about which slug and snail species are present in UK gardens, their abundance, and which are responsible for causing damage to plants.

This project seeks to use a citizen science survey of gardens to recognize which species of slug and snail are found in UK gardens and ascertain which are responsible for damaging plant material. By identifying which species are present in gardens at different times of year, we hope to be able to advise gardeners of more targeted control methods for locally abundant pest species. *Suggestions, comments and feedback on this early stage project are welcomed.*



Shipworms embedded in wood

Identification of sources of C, N and S for marine wood boring bivalves

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Wood makes a significant contribution to the flow of organic matter from land into the marine environment. Once in seawater, wood is rapidly colonized and consumed by isopod crustaceans and by bivalves. These organisms ingest wood and contribute to carbon fluxes by converting a substantial proportion of the wood into animal tissue and faecal matter while releasing dissolved organic matter. Field studies of wood borers are hampered by a lack of information about whether these animals obtain their carbon and nitrogen from wood or whether there are also other significant sources. In particular, the source of nitrogen for marine borers is the subject of speculation, as wood contains only limited amounts of organic nitrogen. Bivalve wood borers harbour endosymbiotic bacteria on their gills. These have been shown to fix dinitrogen and to pass fixed nitrogen to cells of the host, but the importance of this route for nitrogen uptake has not been measured to date. The present investigation quantified the C, N and S stable isotopic signatures of selected wood boring organisms found in the intertidal and subtidal ecosystems. Shifts in C and N signatures show clear trajectories from wood through digestive tract contents and on to faeces and animal tissue. The C, N and S signature shifts from wood to tissue are in some cases too large to be explained only by direct trophic transfer

from wood to animal. Initial findings with signatures of amino acids show the promise of this approach for refining the interpretation of evidence for the sources of these key elements.



Mass spectrometer used to analyse stable isotopes in wood boring organisms.



New data on the biodiversity of Mollusca Solenogastres in the Caribbean Sea

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The known distribution of the solenogastres is highly biased due to dramatically differential sampling effort with respect to geography and bathymetry. To date, there are 285 known species, but many are waiting to be formally described. New species are still found in relatively well-studied areas (as the Mediterranean Sea, the European Atlantic Ocean or some Antarctic areas), although the most recently discovered species come from remote localities. Due to this, along with Caudofoveata (the other Aplacophora clade), the Solenogastres is one of the lesser-known molluscs group and the diversity is considered to be underestimated. They are, in general, small animals so that the analysis of the diagnosis characters imposes a delicate methodology that requires thorough training, which is time consuming. Classification of this group is based mainly on internal anatomical characters, although for a first approximation, it is necessary to study the sclerites. Their study is fundamental for identification at the suprageneric level and even generic level in some groups. In addition, there are sometimes clear interspecific variations. So the first step for classification is through study of the sclerites and habitus and sorting the specimens in distinguishable morphospecies. The present work aims to contribute to the knowledge of solenogastres biodiversity with the first data on the study of a collection from the Caribbean Sea. These molluscs are loaned from the vast collection of the Muséum National d'Histoire Naturelle (Paris). Currently there are no known species in this geographic area so they constitute the first solenogaster records in the Caribbean Sea. In addition, the study of these molluscs in little known areas usually involves the description of new species. Furthermore, the selected specimens were collected in the littoral zone and it must be taken into account that most of the known Solenogastres come from abyssal depths. This contribution is part of the project "*Solenogastres from remote locations, a step forward in the knowledge of aplacophora*", partially funded by a Research Award from the Malacological Society of London and by a Ruth Lee Kennedy travel grant (Fulbright programme). Thank you to Kevin Kocot of the University of Alabama who is the supervisor of the scholarship project. The solenogastres collection is on loan from the Muséum National d'Histoire Naturelle. We want to thank Dr. Philippe Bouchet and all his team for their welcome and also to all those who participated in the expeditions and in the sorting of the samples.



Examples of Caribbean solenogastres.
Photo by Phillipe Maestrati
Museum d'Histoire Naturelle, Paris



Remnants of spring fens in the Bohemian- Moravian Highlands: the occurrence and coexistence of (not only) molluscan glacial relicts

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Fens are groundwater-fed wetlands distinctive by a constant moisture and low productivity of vegetation. These rare and ecologically specific habitats are still frequently distributed across the boreal zone, chiefly in Scandinavia, however southwards they have become highly fragmented and isolated. Some of these are of refugial nature and host isolated populations of cold adapted species, considered as glacial relicts. So far, most of the mollusc research on fens of the Czechia and Slovakia has been focused on the Western Carpathian fens, especially calcareous tufa forming sites, being rich in molluscs and frequently hosting snail glacial relicts, e.g. *Pupilla alpicola* and Geyer's whorl snail (*Vertigo geyeri*). Until recently, malacologists have been overlooking fens in Bohemian-Moravian Highlands, which are slightly acidic to neutral in terms of water pH. Likely because of lack of calcareous sites, mollusc communities at these fens were expected to be poor in species without any rare or protected species. However, in 2011, Geyer's whorl snail was discovered in the area followed



Vertigo geyeri
Photo by MicMichal Horsák

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by *Vertigo lilljeborgi* in the following year. Such findings have started systematic research, as many of these fens are known to harbour several glacial relicts of vascular plants (e.g. *Carex chordorrhiza* and *C. diandra*) and brown mosses (e.g. *Paludella squarrosa* and *Scorpidium scorpioides*). Potentially suitable sites for glacial relict snails were identified based on relict plant and moss occurrence. 55 fens have been examined, with 31 snail species recorded in total (22 terrestrial and nine aquatic). Geyer's whorl snail was found at 23 localities and *V. lilljeborgi* at four. *Nesovitrea petronella*, a denizen of fen and meadow wetlands and also considered a relict species, was found at five sites. These findings indicate a historical continuity of fens in the Bohemian-Moravian Highlands, though recently surviving in only several small fragments out of the original notably higher extent if compared with the situation 70 years ago. Therefore they deserve the highest level of protection and further research is needed, both ecological and palaeoecological.



Protected area Reka (Photo by Radovan Coufal)



Micro-CT scanning Africa's streptaxids – revealing the insides of *Ptychotrema* shells

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Members of the genus *Ptychotrema* are hunter snails (Gastropoda, Pulmonata: Streptaxidae) with a tropical African distribution. The speciose genus was re-defined by Pilsbry in 1919 mainly using characters of the shells' apertural dentition. Pilsbry's classification with various subgenera

"sections" (now mostly, but not universally, treated as subgenera) was designed to classify the streptaxid fauna of the former Belgian Congo (now Democratic Republic of the Congo). This classification is still often used but the various (sub)genera appear

to be artificial and in need of revision in order to deal with the heterogeneous assembly of *Ptychotrema*-like species in Africa. Since anatomical and molecular characters are presently not available for the majority of *Ptychotrema* species, shell morphology is studied in more detail than previously in an attempt to reach a more satisfactory classification of the species. Micro-CT scanning (Computerized Tomography) was applied to virtually cut and 3D-figure shells of more than 40 different species of *Ptychotrema*, focusing on the internal shell structures. Micro-CT scanning technology made it possible to find new morphological characters inside the shells without damaging the material.



An African streptaxid (*Ptychotrema* sp.) being scanned in a desk CT-scanner.



A 3D-printed African streptaxid (*Ptychotrema* sp.), 5x the original



Evolution and regulatory control of shell colour polymorphism in the common whelk, *Buccinum undatum*

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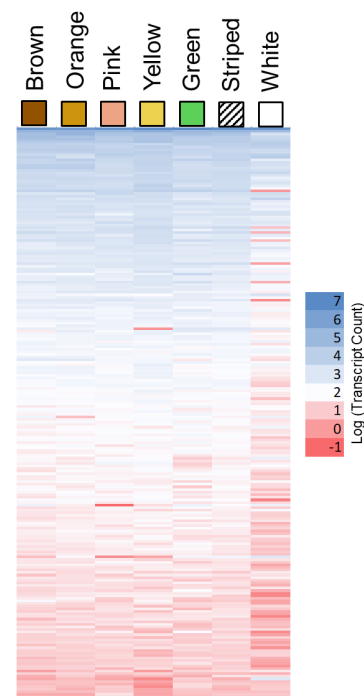
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Colour polymorphisms have long been of interest to biologists for their role in population differentiation, natural selection, adaptation, and speciation. The study of molluscan shell colour polymorphism, in particular, has made significant contributions to our current understanding of evolutionary theory. This is mostly due to the tractability of scoring shell morphs but also due to the shell originating from a single conserved tissue – the mantle. To date, the overwhelming majority of molluscan research has focussed on a narrow range of terrestrial and marine intertidal species, with a conspicuous lack of attention given to subtidal species. Emerging transcriptomic and proteomic studies have highlighted markedly dissimilar molecular profiles across even closely related mollusc species (both phylogenetically and morphologically). Thus, subtidal mollusc species represent largely unexplored systems for the discovery of novel mechanisms and evolutionary processes associated with colour polymorphism. Within the Bay of Breiðafjörður (West Iceland), the subtidal gastropod *Buccinum undatum* (Gastropoda; Mollusca), represents a unique study system with regard to the interplay between colour polymorphism and the area itself. Breiðafjörður's *B. undatum* populations exhibit extreme colour polymorphism over small geographical distances relative to that typically observed across its N-Atlantic distribution. Factors underlying the extreme colour polymorphism in Breiðafjörður remain unresolved. Mitochondrial and morphological analyses however, indicate the potential for population stratification based on depth. The following presentation details emerging results from RNA- and RAD- sequencing analysis aimed at characterising the underlying regulatory control and population structuring of Breiðafjörður's *B. undatum* populations. In particular we focus on key biomineralisation and pigmentation genes associated with the evolution and regulation of shell colour polymorphism in molluscs.



RNA-Seq Analysis
A total of 217 transcripts demonstrate associations with shell colour



Long-distance dispersal largely explains patterns of endemism in Bornean land snails

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Islands are often hotspots of endemism due to their isolation, making colonization a rare event, and as such facilitating allopatric speciation. Dispersal usually originates from nearby locations according to a stepping stone model. We aimed to elucidate colonization and speciation processes in an endemic-rich system of land-based islands that do not seem to follow the obvious stepping stone model of dispersal. We studied the phylogenetic and biogeographic relations within several island radiations of three unrelated taxa of land snail (the microsnails *Georissa similis* E.A. Smith, 1894 s.l. and *Plectostoma concinnum* (Fulton, 1901) s.l., and *Allycaeus jagori* Von Martens, 1859).



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Each of these taxa is common within five land-based habitat archipelagos of limestone outcrops in the floodplain of the Kinabatangan River in Sabah, Malaysian Borneo. We applied a combination of techniques from the fields of population genetics, demography, phylogenetics, and biogeography and found spatial genetic structure among nearby locations to be highly pronounced for each taxon. Spatial-genetic correlation was present at small scales, but disappeared at distances of five kilometers and above.



Plecostoma at Kinebatangan

With most archipelagos having been colonized multiple times over the past three million years, we found evidence for different, usually distant, islands within the region being the source of origin, in each of the three taxa studied. Gene flow in these Bornean land snails has been affected both by small-scale dispersal, where it leads to isolation-by-distance, and by long-distance colonization. Our results demonstrate that island endemic taxa only partially follow a simple stepping stone model; long-distance dispersal, and resultant colonization, is frequent and seems the origin of endemism in our study system. The formation of highly localized, isolated “endemic populations” forms the onset for a complex radiation of endemic taxa.



Population genetics of the Shining Ramshorn Snail, *Segmentina nitida*- post-glacial colonisation, bird-mediated dispersal or separate species?

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The Shining Ramshorn Snail, *Segmentina nitida*, a rare freshwater snail found predominantly in drainage ditches and marshland, has seen a marked decrease in population (~80%) over the last 100 years in the UK. This has mainly been attributed to the over-dredging of drainage ditches as part of land management, as well as eutrophication caused by run-off of fertilizer from agricultural land. *Segmentina nitida* is a priority species for the UK Biodiversity Action Plan, and further research was recommended in the plan to inform reintroduction and translocation for the conservation of *S. nitida*. This presentation offers population genetics analyses of microsatellite, nuclear (ITS2) and mitochondrial (COI) markers for *S. nitida* individuals from Poland, Germany, Sweden, and the UK, to identify genetic patterns and differences within and between populations. Two distinct genetic lineages of *Segmentina nitida* were identified, one present in eastern Europe (Poland, Sweden), and one in western Europe (UK, Germany). No genetic admixture was observed in German populations containing both lineages. Inferences as to these patterns are explored, focussing on post-glacial recolonization from different glacial refugia, movement of populations by migratory water birds, and the existence of a potential separate species or sub-species, *Segmentina clessini*. These could all have implications for the reintroduction or translocation of *S. nitida* individuals from European populations to existing and historical sites in the UK. This work is part of a larger PhD project looking at various aspects of *S. nitida* including 2D geometric morphometrics, breeding, and improved sampling for *S. nitida*.



The evolution and diversification of eyes in strombid gastropods

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The marine gastropods within Strombidae are highly variable with respect to their shell morphology. However, the eyes which extend from stromboid notches on the outer lip are even more intriguing than the elaborate sculptures and colourful patterns of the shells. These large, camera-type eyes have independently evolved a similar optical design to the eyes of fish and cephalopods, which often rely on vision for prey capture. This presumably provides surprisingly good vision for a family of slow-moving, herbivorous gastropods, but there have been limited investigations into exactly what strombids can see. This PhD will therefore combine molecular phylogenetics, morphological studies using traditional histological methods and innovative methods, such as computed tomography, and behavioural studies to explore how and when complex eyes in Strombidae have evolved and test strombid visual abilities, examining visual acuity and contrast thresholds.

The first aim of this project is to recover the phylogenetic history of the family Strombidae and to use this as a framework to investigate the evolution of their eyes. We will build a phylogenetic framework using molecular markers (obtained via Sanger sequencing and mitogenomics) to identify transition points in the evolution of camera eyes. Strombid eyes are typically marked with colourful rings in orange or yellow; these and other traits associated with eye morphology will be mapped onto the phylogeny. The strombid fossil record is excellent, which will allow for fossil calibrations in the phylogenetic framework allowing us to determine the timing for the origin of complex eyes. The project also aims to identify genes associated with vision for key taxa within Strombidae, via transcriptomics. This will enable us to determine how these animals see their own uniquely coloured shells and their surroundings. The final aim of the project, to explore visual adaptations in Strombidae eyes through behavioural studies such as optomotor drum experiments, will enhance this new understanding of strombid vision.



Gastropod research at the Royal Horticultural Society

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Slugs and snails cause significant damage to ornamental and crop plants in UK gardens and are one of the most common pest enquiries to the RHS Gardening Advice service. A wide array of control methods are used by gardeners but these have problems. For example their efficacy is unclear (cultural methods), there may be effects on non-target species and the environment (chemical controls), or there are perceived barriers to their successful use (biological methods).

In order to address gaps in our knowledge, and help gardeners to use integrated pest management strategies against gastropods in their gardens, the RHS has developed a programme of research.

A two year field experiment in collaboration with BASF assessed the effectiveness of metaldehyde, ferric phosphate or a gastropod-parasitic nematode when combined with a cultural control (mulch). The synthetic pesticide metaldehyde performed well most consistently, but the more environmentally friendly options, such as the nematode biological control or the organic slug pellet ferric phosphate gave intermediate or good control, particularly when combined with mulch.

Citizen science approaches offer much potential in this area since both gastropods and gardening are accessible to the general public and generate significant interest. A preliminary project with a small number of schools tested the effectiveness of five barriers to gastropods in a simple experimental design using potted lettuce. A complementary field trial tested barriers both in pots and around lettuces planted in the ground. The results of these studies demonstrated that the barriers are mostly or entirely ineffective. More work is planned to ascertain whether these methods can be effective depending on geographical location and garden conditions.

Summer student projects have tested techniques such as night time searching to observe which plants gastropods feed on and DNA barcoding for non-destructive identification of species. These techniques and skills will facilitate further research at the RHS. Two PhD students have been recruited to start this autumn, working on nematode biological control of slugs, and surveying gastropod species in gardens.





Erika Lorencová & Michal Horsák

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PhyFon

PlaPla

Number of sensitive species

AniSpi

LymSta

PhyCor

Canopy cover

AniVos

PisSub

PisHer

N-Connect

Y-CorDet

Y-Lemna

Y-Leave

Y-Connect

Y-EloCan

Y-Fish

HipCom

BitTen

DrePol

GyrAlb

AcrLac

Transparency

Substrate roughness

pH

N-CorDet

RadAur

N-EloCan

N-Lemna

N-Fish

PhyAcu

Cyanobacteria

Chlorophyll-a

NMDS 2

NMDS 1

VivAce

Number of species

Hildur Magnúsdóttir^{1,2}, Snæbjörn Pálsson¹, Kristen Marie Westfall^{1,3,4}, Zophonías O. Jónsson¹ & Erla Björk Örnólfsdóttir²²Department of Aquaculture and Fish Biology, Hólar University College, Hólar, Iceland

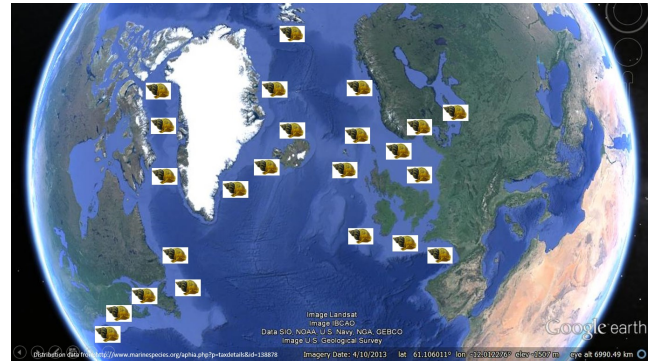
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Preceding work on the phylogeography of the common whelk (*Buccinum undatum*) revealed distinct mtDNA lineages in Canada, Greenland and Europe, suggesting that these populations have diverged since the onset of the first major glacial period of the last Ice Age (2.6 Mya). The aim of the current study was to evaluate the species status of *B. undatum* across the N-Atlantic, based on COI data and morphological differentiation based on shape analyses and morphometrics, both among wild populations and individuals raised in controlled conditions.

Genetic distances based on COI between populations of *B. undatum* from Canada, Greenland and Europe were similar to distances observed between several other *Buccinum* species. The ratio of divergence between and within the populations exceeded the species screening threshold which has been proposed for COI, for all three populations, supporting cryptic species or evolutionary divergence among the populations. Analysis of the morphological variation support the genetic split between Icelandic, Greenland, Faroe Islands and Canadian populations, however the population from the English Channel (UK) did not differ in shape from the Canadian population, possibly due to more similar environments.

Next steps in the study will include further analysis of controlled condition experiments with Icelandic and Canadian *B. undatum* juveniles with regard to shape, as well as analysis of existing RADseq data from Icelandic and Canadian populations in order to shed further light on the species status of the common whelk.



Decline in shell thickness of shelled pteropods along a natural ocean acidification gradient

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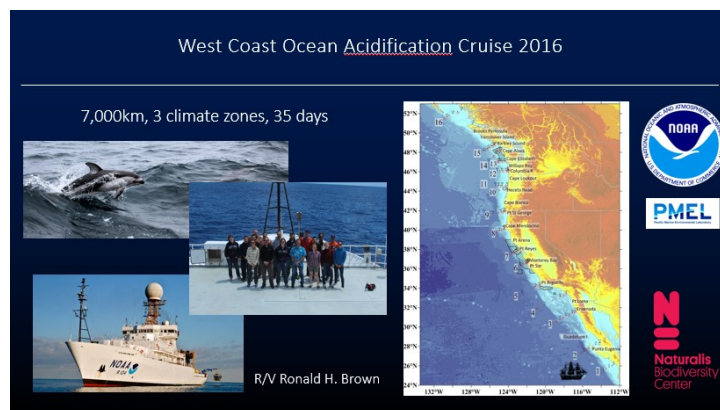
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Rising atmospheric carbon dioxide concentrations lead to a decrease in ocean calcium carbonate saturation, referred to as ocean acidification, which is known to negatively affect marine calcifying organisms. Shelled pteropods, a group of holoplanktonic gastropods, have delicate aragonitic shells (a form of calcium carbonate), which can be damaged or even partially dissolve in waters with low aragonite saturation levels. Therefore, they are widely regarded as bio-indicators of ocean acidification. To date, studies on the responses of pteropods to ocean acidification have mainly been based on experimental work on short time scales. Little is known about natural variation in the calcification of shelled pteropods, hence, for this study we sampled *Limacina helicina* f. *pacifica* pteropods along a natural ocean acidification gradient in the California Current Ecosystem. Shell thickness, a proxy of calcification, was measured using Micro-CT scanning. genetic diversity, and potential population structuring, was assessed based on partial sequences of the mitochondrial Cytochrome Oxidase I gene. Low levels of genetic diversity ($\pi=0.26\%$) were found, indicating a homogenous population of *Limacina helicina* f. *pacifica* in the California Current Ecosystem which consist of the same (sub)species. We found that average shell thickness declined by 33.7% with decreasing pH along natural ocean acidification gradients. This is consistent with the hypothesis that it is more costly for pteropods to calcify in lower pH conditions. Our results suggest that increasing acidification in the California Current Ecosystem would negatively impact on *L. helicina* f. *pacifica* populations, because of reduced calcification along gradients of decreased pH due to ocean acidification.



Biogeographic range shifts of two northeastern Atlantic intertidal limpet species *Patella vulgata* and *Patella depressa*; comparisons of boreal and lusitanian responses to changing climates

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Intertidal habitats in the north-eastern Atlantic face stressful environmental impacts from semi-diurnal tides that result in both immersion and emersion of organisms to oceanic and atmospheric conditions respectively. As well as daily and seasonal temperature changes, global climate change is affecting intertidal habitats causing changes in sea surface and atmospheric temperatures, ocean acidification, and increasing storm conditions. Long term datasets are essential to better our understanding of how intertidal organisms are affected by climate change, monitoring a mainly polewards movement of marine species from increasing sea surface temperatures. Data from the Marine Biodiversity and Climate Change (MarClim) project, globally the longest time series of its kind, have highlighted several intertidal ectothermic gastropods as indicator species for climate change due to their importance for ecosystem biodiversity; changes to their abundance impact on higher trophic levels.

Two species of native limpet, boreal-cold temperate *P. vulgata* and lusitanian-warm temperate *P. depressa*, co-exist within mid and low intertidal zones on rocky shores, where the latter species has been observed expanding its range northwards, currently reaching its northern range limits in North Wales and north-eastern range limits in south-eastern England. A lack of suitable natural habitats in the south-east may previously have been a restriction to further northwards expansion at this range edge, although the deployment of artificial structures such as sea defences may provide opportunities. It is not yet fully understood what species-specific environmental requirements will aid the expansion of *P. depressa* at either of its northern range edges, possibly including habitat suitability, hydrology affecting larval dispersal, temperature affecting survival rates, genetic adaptability or a combination of these factors amongst others.

This research is investigating (a) physiological tolerances of *P. vulgata* and *P. depressa* to the effects of climate change through mesocosm and field biomimetic experimentation, (b) the changes to biogeographic distributions of comparative boreal and lusitanian gastropod species using newly collected MarClim and other historical data to explore expansions at their northern range edge and contractions (if any) at their southern limits, and (c) correlative and/or mechanistic approaches of modelling to predict future ranges of both species in response to rapidly warming sea surface temperatures.



Specific damages recognized at land-snail shells can document the rate of predation: differences among predators and habitat types

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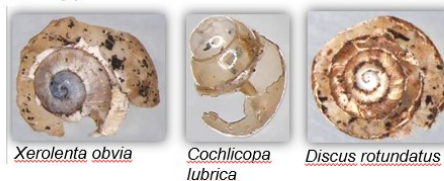
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In certain environments, land snails can be relatively numerous and therefore can potentially become a frequent prey of various predators. The most common predators of terrestrial gastropods include beetles, dipterans, carnivorous gastropods, harvestmen, some vertebrates, and terrestrial flatworms. Snails can retract their bodies into the shell very quickly, along with the production of sticky mucus, which is in a combination with the presence of shell their main defensive strategy. Therefore, various predators have had to

adopt a variety of techniques to overcome the barrier represented by a shell. The main attack strategies include reaching a snail body through the aperture of shell or breaking the shell apart. Because shells can persist in some environment for a long time, we can determine, depending on the type of specific shell damages or the presence of exuviae left in a shell, whether and who has killed the prey. Based on litter samples collected at 30 sites of five different habitat types, the intensity and type of predation were assessed in relation to these habitat types. The minimum predation rate varied between 1 and 21%, on average 9%. The highest rate was observed at steppes (on average 15%). Beetles were found as the most common

Results - evidences of predation

• type 1 - carabid beetle



• type 2 - Drilus beetle



• type 3 - snail



CONTINUED>

adult shells. On the contrary, the sciomyzid fly *Pherbellia limbata* and *Drilus* beetles preferred the adults. It was detected that the intensity of predation by carabid beetles increased linearly with the population size of the prey, while no pattern was observed for the parasitoid fly *P. limbata*. predators of terrestrial snails at all studied sites (the proportion of shells indicating the predation by beetles ranged from 0 to 15%), however, predation by snails was a more common feature in fen samples. Predation by some vertebrates and dipteran flies was observed at a minor rate too. Additionally, preferences, intensity and type of predation were also evaluated in relation to the population size and developmental stage of *Granaria frumentum* from 24 steppe sites. Beetle taxa that break shells strongly favoured juveniles compared with adult shells, chiefly because of the presence of a thickened aperture in adult shells. By contrast, the sciomyzid fly *Pherbellia limbata* and *Drilus* beetles preferred adults snails. The intensity of predation by carabid beetles increased linearly with the population size of the prey, while no pattern was observed for the parasitoid fly *P. limbata*.



Sea slugs of Southern Norway; an example of citizens contributing to science

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Citizen scientist are volunteers who help scientists by collecting data as a hobby in their spare time. The concept originated from the States and UK during the 1990s in an attempt to open up science to the public. Some examples of very successful projects are the online platform iNaturalist with around 1.0 million users, Zooniverse with 1.7 million users and eBird with roughly 411K users (as of July 2018). Although Citizen Science also has its pitfalls, it's due to its success that the concept is extensively spread, also here in Norway: sea slugs of Southern Norway is such an example of a Citizen Science project, with a tiny but tight community of around 135 active members.

The project focusses on sea slugs that live along the coast between the Bergen area southwards to the Swedish border. For nearly 80 years, almost no dedicated survey and scientific work on these animals took place in southern Norway and this part of the country is especially vulnerable for the arrival and establishing of alien species. The goal is to establish an image and genetic library of all collected species, explore the occurrence of cryptic species complexes, and monitor the presence of alien species. Southern Norway alone has a coastline of about 8000 Km, which makes it a particularly challenging task to get a proper overview of the sea slug diversity. But thanks to our established network of Citizen Scientists, the project has already registered 90 different species and a total of 1400 new entries in our database. This successful relationship results from the fact that we actively involve Citizen Scientists in the project by providing sea slug courses, regular updates and discussions via our online Social Media platforms, and participation in club gatherings where we present our work. The "Sea slugs of Southern Norway" research project is a prime example of how citizens can decisively contribute to the success of a scientific endeavour, making the all experience much more challenging, dynamic and rich!



Hi there! Welcome to Sea slugs of Southern Norway and thank you for your interest and support :). The project relies heavily on our dedicated citizen scientists, and we are very happy to welcome you to the team! In order to make the project a success, we made a step by step scheme on what to do when collecting sea slugs

Step 1. Check if your sampling kit is complete

- 10x 20 ml Jars
- 10x 60 ml Jars
- 21x labels
- 1x USB with 2 folders:
 - 1 excel file folder
 - 1 photo folder
- 2x 500ml 29% 2-propanol
- 2x pair of gloves

Step 2. When diving, bring some collecting jars

(this can be anything, some divers like to use Blender Bottle, GoStak for collecting)

Step 3. When you see a sea slug, before collecting, take a picture of it in its natural habitat and more importantly remember the depth of your find!

Step 4. If you were not able to photograph the collected sea slug while diving, make a picture of it after the dive

(this way we can see the distinguishable colours, which will vanish once the sea slug is transferred to 2-propanol)

Steps continue on the other side :)

Step 5. Transfer your sea slug with seawater to a dedicated yellow capped jar, write down the details of your finding on the label (with pencil) and put it together with the sea slug

Step 6. Freeze the sea slug in your freezer overnight. This way the sea slug relaxes, falls asleep and slowly dies

(If you put the sea slug immediately in 2-propanol, it will curl up and this makes it difficult to study afterwards)

Step 7. Go to your computer and open the USB. Transfer your pictures to the photo folder and fill in your findings in the excel sheet

Step 8. The next day you can unfreeze your sea slug and replace the seawater with 2-propanol

Warning: Please handle 2-propanol with care and use gloves

Step 9. Send your samples. Your return will be paid by us (select the option that sending costs will be covered by the recipient). You can choose to send your digital files either with your samples on the provided USB or via e-mail (see step 10)

Manuel Malaquias
Department of Natural History
University Museum of Bergen
PB7800 5020 Bergen

Step 10. Do you have questions? Or in need of more jars and 2-propanol? Please don't hesitate to contact us! Thank you for your help! manuel.malaquias@uib.no and cessa.rauch@uib.no

Did you know?

1. That with help of citizen scientists we were able to identify already 60% of the Norwegian sea slug species during the first month of the project, and every day the list grows!
2. That sea slugs are truly incredible! Some species are able to produce chemicals that are used for anticancer drugs and a few species are solar-powered as they are able to photosynthesize!
3. That we have a dedicated platform for citizen scientists to discuss their findings and to update them on the project; login to Facebook and become a member of the Sea slugs of Southern Norway Facebook group!



A new cladistic insight at the comparative anatomy, phylogeny and systematics of rudists (Bivalvia, Hippuritida)

Valentin Rineau¹, Jean-Pierre Masse² & Loïc Villier¹

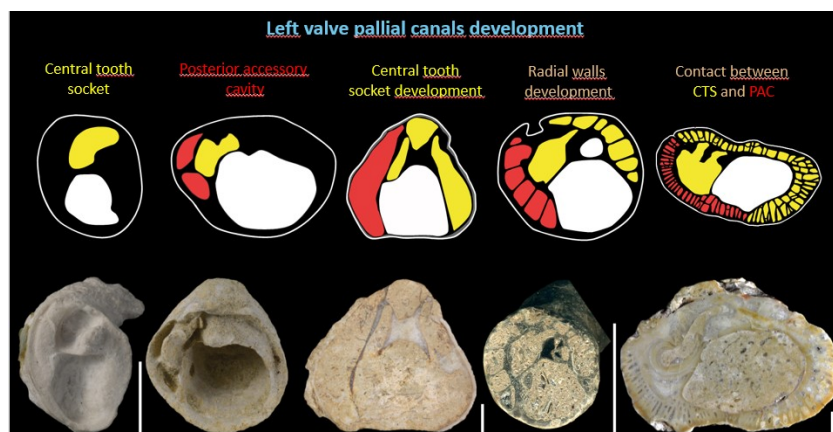
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The rudists (order Hippuritida) are a taxon of bivalve animals that are now extinct, characterized by a pachyodont hinge composed of three thick teeth. Appearing in the Jurassic (Oxfordian, 164 Ma), the diversification of rudists occurs in warm shallow seas, on the carbonate platforms of the Tethys and Atlantic, until they completely disappear during the Cretaceous/Palaeogen crisis (66 Ma). The history of rudists spreads over nearly 97 Ma and counts more than 2000 species. The phylogeny of the rudists is however very poorly known, as only one complete cladistic analysis has been produced to reconstruct the kinship relationships between families. The aim of our work has been to bring new elements to the understanding of the history of rudists by applying new approaches and developing new methods of phylogenetic analysis. The phylogenetic method used here is three-taxon analysis. The use of triplets (three-taxon statements) has also allowed us to develop a new metric, the 'nodal retention index', which we use to describe evolutionary trees. We propose a new phylogeny, based on 40 arborescent characters. The evolutionary scenario of the rise of pallial canals is completely reviewed and now involves nine derived states, compared with two in the previous analysis. This new phylogeny completely overhauls relations between the rudist families. For example, the large Hippuritidae family becomes a sister group of the Radiolitidae, a kinship relationship which had never been proposed before. Of the thirteen rudist families, only four are found to be monophyletic, and both of the two superfamilies are found to be polyphyletic. Two major episodes of diversification were found, respectively during the Hauterivian and Albian. These initial results are a starting point for addressing other issues, such as whether these radiations are adaptive or linked to episodes of maximal extension of carbonate platforms.

New hypothesis: pallial canals are complex structures with several evolutionary innovations



A new *Scaphander* species from the deep sea of Argentina

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Scaphander Montfort, 1810 is a genus of deep-sea soft-bottom gastropods composed of approximately 18 species distributed worldwide. Eilertsen and Malaquias (2013) revised the systematics of the genus in the Atlantic, and recognized eight valid species. The present study describes a new *Scaphander* species from novel samples obtained from the abyssal plains off Argentina, using morphological and molecular data. Shells, gizzard plates, radulae, and male reproductive systems were studied by optical and scanning electron microscopy, and compared with data from all other known *Scaphander* species. Bayesian molecular phylogenetics based on two mitochondrial (cytochrome c oxidase sub-unit I and 16S rRNA) and one nuclear (28S rRNA) genes together with the molecular species delimitation method Automatic Barcode Gap Discovery were used to compare the novel samples with all known Atlantic species. Our results revealed that the Argentinian specimens have a distinct shell and penial papilla and molecularly were 13.1–13.9% distinct (COI uncorrected p-distance) from their closest relative, the northern amphi-Atlantic species *Scaphander punctostriatus*.



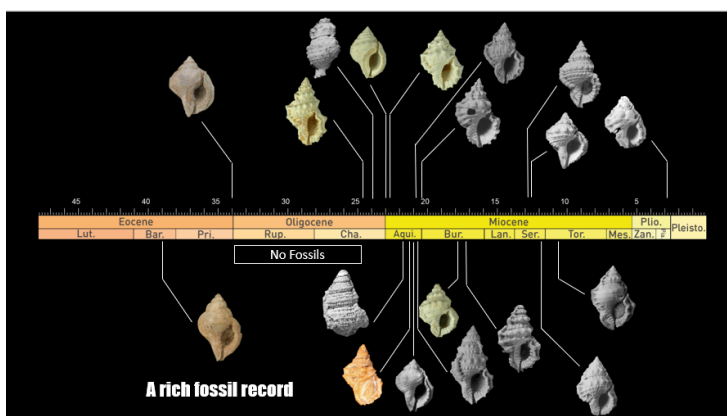
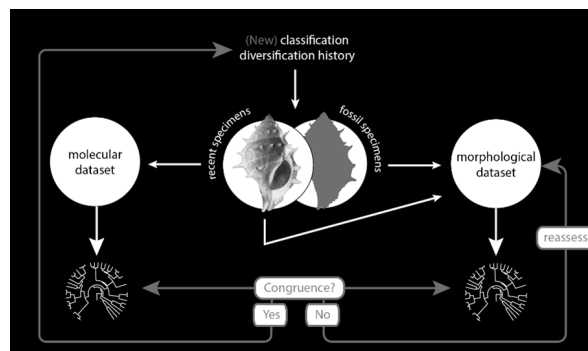
Frog shells through time: a dialogue between mitogenomics and palaeontological data

Malcolm Sanders^{1,2}, Didier Merle¹ and Nicolas Puillandre²

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Frog shells (Bursidae, Tonnoidea,) are a rather small monophyletic family of highly dispersive marine gastropods with poorly known phylogenetic relationships and a poorly defined fossil record, with an origin around the Bartonian (~40Ma). Strongly ornamented, hence potentially bearing numerous shell characters, contrary to many other molluscs, bursids are a good model for comparing and combining morphological and molecular data in a phylogenetic context. We reconstruct a phylogeny covering 50 to 70% of the accepted Recent and fossil species (depending of the analysis). At first we analyse separately a molecular dataset (partly based on complete mitochondrial genomes) and a shell character dataset, then combine both in a single total-evidence analysis. This analysis leads to reconsider the genus limits in the Bursidae, in particular to eliminate the non-monophyly of *Bursa*, necessitating the erection of four new genera. A cali-



brated time-tree is reconstructed using 21 node and tip calibrations. Comparison of divergence events with climatic curves suggests a link with Paleogene thermal maximum (both hot and cold). Additionally, the inclusion of the fossils sheds new light on the historical biogeography of the family, otherwise hidden by considering extant species only. One of the particularities of this work lies in the constant dialog between morphological and molecular approaches and between extant and extinct taxa. At each step, taxonomic hypotheses emerging from molecular analyses allow a reinterpretation of morphological characters, especially by modifying primary hypotheses of homology. Conversely, morpho-

logical approaches, especially on fossils, consolidate hypotheses resulting from the analyses of the molecular characters, allowing us to propose a time-tree based on a robust analysis of bursid paleodiversity.



From one wastebasket to another: an exon-captured based phylogeny of Turridae (Gastropoda, Conoidea)

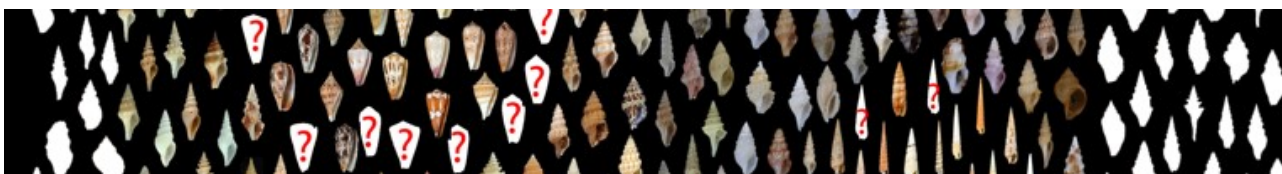
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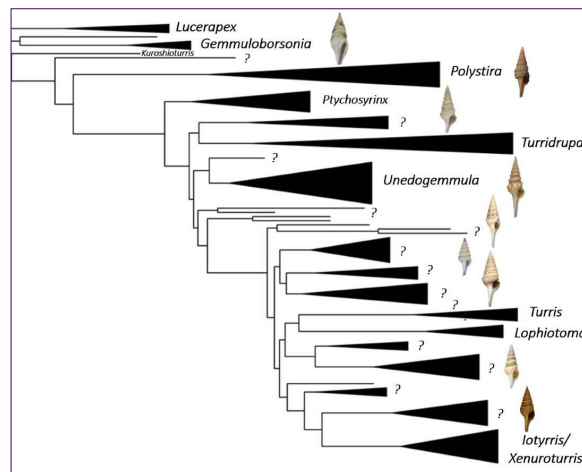
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The turrids (Gastropoda, Conoidea) have often been referred to as a “taxonomic nightmare”, because of their huge diversity (4000 described species, with an estimate of more than 10000 living species), characterized by a variety of forms that seems to be an endless continuum where drawing lines between taxa seems unachievable. Ten years of molecular phylogenetics greatly contributed to a redefinition of the family boundaries and their relationships. In particular, the name Turridae, traditionally applied to all conoideans except terebrids and cone snails, is now used for a restricted group of 15 genera and 200 species. But a big wastebasket often hides a smaller one, and several genera in the Turridae seem to be also non-



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monophyletic. Moreover, the classical “Sanger approach”, based on a few genes and often used to establish gastropod phylogenies, proved to be unable to infer robust relationships with the Turridae. We applied a transcriptome-based exon capture approach to recover thousands of genomic DNA loci for 120 samples in the Turridae family. We particularly focussed on rare lineages and poorly known deep-water species (most of them undescribed) from the large collection of alcohol-preserved specimens of the MNHN. The resulting tree is a robust phylogeny that confirmed the paraphyly of some genera and can be used to redefine several genera and identify new ones. Furthermore, later studies can use this phylogeny to test evolutionary hypotheses such as anatomical changes, radular and protoconch type, depth and geographical range in correlation with diversification rates.



Behavioural responses of the freshwater mussels *Anodonta anatina* and *Unio pictorum* to light availability and their ecological and management implications

Charitos Zapitis¹, Petra Parmová² & Andrew Ramsey¹

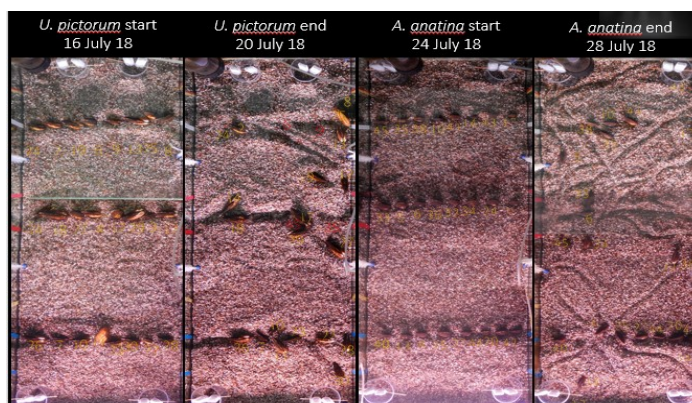
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The water purification potential of mobile benthic filter feeders, such as the freshwater mussels of the Order Unionoida, relies on the balance of filtration, biodeposition, excretion and bioturbation. The environmental factors driving unionid locomotion, resulting in sediment mixing and nutrient release, are highly under-researched, creating a significant gap in the knowledge associated with bioturbation. Empirical data on unionid locomotion are essential for modelling the species-specific purification potential. Light availability is among the least studied physical attributes. This study examines the behavioural responses of *Anodonta anatina* and *Unio pictorum* to a gradient of light availability, ranging from 1630 to 170 lux, during 96 hour laboratory experiments. 8 specimens of each species were placed in a tank parallel to the light source in 3 rows (n=24) at high (29.0 cm distance, ~ 1085 lux), intermediate (80.2 cm, ~ 437 lux) and low (115.4 cm, ~ 232 lux) intensities. From 06:00 to 22:00, light was provided by a fluorescent tube placed on the side of the tank. Vertical photographs were taken daily at 13:00 before feeding the mussels *Chlorella vulgaris* at a concentration of 0.1 mg of Ash Free Dry Weight l⁻¹. Mussel opening, location and angle in relation to the light source were derived by image analysis. Both species showed positive phototaxis, with the low intensity groups showing the strongest net movement and the high intensity groups the weakest net movement towards the light source. This inverse relationship suggests that light intensities between 200 and 300 lux are more likely to trigger locomotion responses towards light than higher intensities. *U. pictorum* showed weak positive phototaxis —strongest negative phototaxis 14.6 cm, median 3.3 cm, mean 3.5 cm, strongest positive 18.7 cm. *A. anatina* showed prominent positive phototaxis — strongest negative 21.8 cm, median 1.3 cm, mean 11.3 cm and strongest positive 102.5 cm. The significantly different responses within and between the two species are discussed in relation to their ecological niche, light and darkness, relevance for unionid monitoring programmes, as well as in the context of habitat restoration and their remediation potential in eutrophic ponds.

Phototaxis of
Unio pictorum
over time



Reports of research funded by the Malacological Society of London

Palaeogene land snails of Europe

Rodrigo Brincalepe Salvador

This project had a duration of 2 months in mid-2017. The aim was to review the fossil land snail fauna of the Eocene and Oligocene of several outcrops within western Europe (Germany, France, Switzerland, UK, and Spain). Since this topic has received little work since the late 19th and early 20th century, most species need revision, especially to clear potential synonyms between countries. While this kind of work is currently out of vogue, it is crucial to first establish a solid taxonomic foundation, as it paves the way to further and broader questions: for instance, these fossils are critical from a biogeographical standpoint, as they suggest affinities between the European and American faunas.

Therefore, visiting collections that harbour specimens is the essential first step. The grant from the Malacological Society of London allowed me to visit several German institutions that hold not only fossils from that country, but also from other localities in Europe. Having access to material from elsewhere is critical for comparison and for a meaningful revised classification. Presently, alongside my collaborators, I am revising the German fossils from the following localities: Amerbach, Arnegg, Bachhagel, Ulm/Eselsberg, and Weilheim/Monnheim. In the future, I intend to conduct a palaeobiogeographical analysis to uncover how these fossil faunas were related to each other and to other localities within Europe and neighbouring places (*e.g.*, Algeria) and also to identify possible sister-taxa relationship between Laurasian taxa.

Moreover, the grant from the MSL allowed me to analyse other specimens in the collections that could be used for other projects, including Miocene fossils from Germany, and sub-fossil and Recent snails from South America. They have been or are being used in further publications.



Tylodinae species complex in the Mediterranean Sea and Eastern Atlantic

Robert Fernandez-Vilert

Department of Organismic And Evolutionary Biology, Harvard University

The initial goal of the project was to work on the nudibranch family Dotidae, for which we have gathered several genes for a bunch of species. Nonetheless, due to the limited amount of time during my internship and the complexity of the group, we decided to focus on the Tylodinae species complex in the Mediterranean Sea and Eastern Atlantic. For this group, we have gathered fewer samples (34 in total) and the specimens were larger, thus easier to dissect and learn about their anatomy. Throughout all these years of collecting samples we have noticed that the type species and only recognised species in this geographical area, *Tylodina perversa*, presented, at least, two different morphotypes. The original species had a flattened shell, while the second morphotype presented a conical shell and different ecological habits (feeding on a different sponge species of the genus *Aplysina*, only found in caves).

During my internship, I have compiled all relevant bibliography in order to know if the two morphotypes were described before. Once we checked all the descriptions and synonymized names, we realised that some authors had synonymized at least two species of *Tylodina*: the original *T. perversa* (Gmelin, 1791) with the flat shell with *T. rafinesquii* Philippi, 1836 having a conical shell. Meanwhile, I began to take ventral, dorsal, and lateral pictures, as well as some details such as the protoconch or the gills, of each specimen under the Keyence VHX-6000 digital microscope in order to be able to identify the necessary characters for later taxonomic descriptions.

Once all samples were photographed, I started with the DNA extractions using the DNeasy Tissue Kit and following the manufacturer's protocol. Since all the individuals were large enough, we only cut a small piece of the foot, so we could dissect the rest of the body and study the digestive, reproductive, nervous, and circulatory systems. After DNA extraction, we amplified fragments of the mitochondrial genes cytochrome c oxidase subunit I (COI) and 16S rRNA and the nuclear H3 gene, carried out through polymerase chain reactions (PCR). After that, I did gel electrophoresis to see if the PCRs had amplified the gene of interest as well as looking at whether the amplification had been contaminated or not. After the amplifications we purified the DNA with the ExoSap protocol, genes were sent to be sequenced by Genewiz. We checked the species identity of each sequence using the BLAST algorithm against the GenBank database and sequences were edited and assembled in Geneious Pro 8.1.5. Genes were individually aligned using the MUSCLE algorithm. We made extra sequencing and the costs were paid by the PI of the Giribet Lab, Gonzalo.

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Bayesian inference and maximum likelihood analyses were used on each gene (i.e. Figure 1), in order to check for contamination, and to the final concatenated alignment of the three genes and the sequences obtained from GenBank. Finally, a tree has been constructed from both analyses. Species delimitation tests (i.e., ABGD, GMYC, PTP) were also conducted on the aligned COI to further test for monophyly in the studied species. Our results demonstrate that the two morphotypes are, in fact, two different species. In order to test this hypothesis, we started the dissections to unravel the internal anatomy and find morphological differences. The buccal mass and the shell of all specimens were immersed in 50% Bleach for up to one hour to dissolve the organic tissues and then rinsed with distilled water. The radula, the shell and the crop content were mounted on metallic stubs with carbon sticky-tabs and coated with platinum-palladium for scanning electron microscopy (SEM). Other samples like the crop or the penis were critically point dried before SEM.

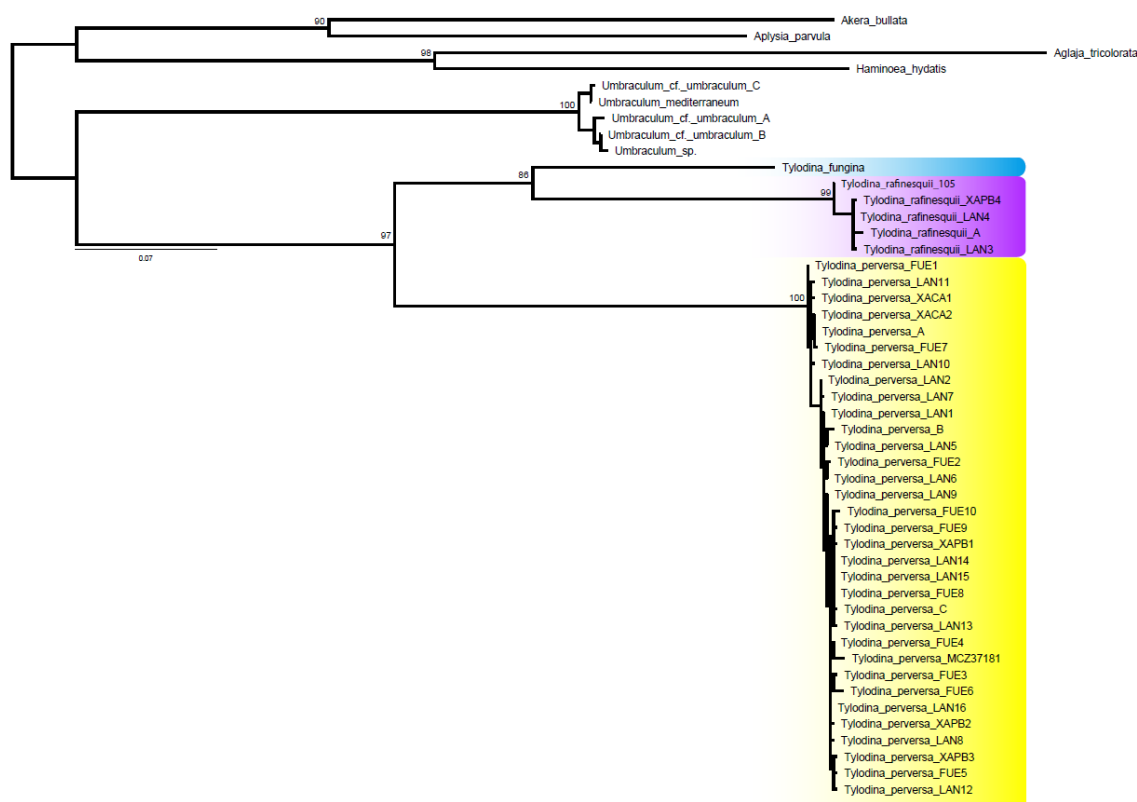


Figure 1: Phylogenetic relationships of Umbraculida inferred by maximum likelihood (ML) based on the partial mitochondrial COI gene (690 bp). Values listed on branches refer to bootstrap support. The tree is rooted with two species of Anaspidea and Cephalaspidea each.

We are now working on the morphological description from both species using live pictures and the morphological data gathered from the preserved specimens, as well as the SEM pictures and the anatomical drawings of the reproductive and nervous system. We will accurately describe the internal anatomy of the type species of the genus -*Tyloclina*, and described a second species living in sympatry with this one, i.e. *T. rafinesquii*. Overall, our integrative molecular and morphological data will shed light into the systematics and diversity of this group of molluscs. The results will be published in an international and peer-reviewed journal.



Freshwater mussels as environmental indicators in UK river systems using a sclerochronological approach

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Introduction

Sclerochronology, the analysis of variations in accretionary tissues of an organism within a temporal context, can be a useful tool to study and create paleoenvironmental and paleoclimatic records of aquatic ecosystems. Since external factors drive the growth of the accretionary hard tissues of many aquatic organisms, the growth increments on these organisms often document changes in the environment (Helama *et al.*, 2006; Rypel, Haag & Findlay, 2008). Mussels are particularly useful for storing environmental data due to their dark, external annual bands called annuli, as well as their high filtration rates, ecological roles as 'engineers', abundance, global dispersal, and sensitivity to environmental changes (Neves & Moyer, 1988).

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Although many sclerochronological studies have been implemented using marine bivalves (Scourse *et al.*, 2006), the use of freshwater mussel annuli as proxies to build records on various water parameters is scarce. Freshwater ecosystems are currently facing a 'global crisis' (Strayer & Dudgeon, 2010) due to anthropogenic stressors, climate change, and habitat fragmentation, and therefore require immediate monitoring and restoration. This study uses the annuli of freshwater mussel species *Unio pictorum*, *Anodonta anatina*, and *Unio tumidus* from along the River Medway in Kent, UK to investigate the relationship between mussel annuli measurements and seasonal water temperatures.

In order to get an even clearer understanding of the relationship between temperature and growth, this study also looks at long-term annuli growth of *U. pictorum* from the River Thames, UK using live mussels collected in 2018 from a single paired site (marina and river sampling) in Caversham as well as historic mussel shells obtained from the Museum of Zoology (CAMZM) collected in 2007 from five paired sites along the River Thames, including Caversham. The use of two separate mussel cohorts allowed us to build a longer chronology of mussel growth at a single site, investigate the effects of long-term seasonal climate patterns on growth, and predict how future climate change may affect freshwater ecosystems based on temperature-annuli relationships.

Methods

Between 15 and 30 individuals of each mussel species at each site were collected by hand sampling. For the short-term study in 2017, *U. pictorum*, *U. tumidus*, and *A. anatina* were collected at three sites along the River Medway: Haysden (the most upstream site), Watlington, and Ringlestone (downstream). For the long-term study, *U. pictorum* were collected at five paired sites (sampling from the river and from an adjacent marina 800m away) along the River Thames in 2007. In 2018, additional *U. pictorum* were collected at one of these five paired sites, Caversham, both in the marina and the river, in order to extend the chronology. Both the River Thames and the River Medway embody UK lowland lotic systems. External growth rings, identified as continuous dark bands around the entire shell (Aldridge, 1999), were non-invasively measured to the nearest mm using a Vernier caliper (Fig. 1).

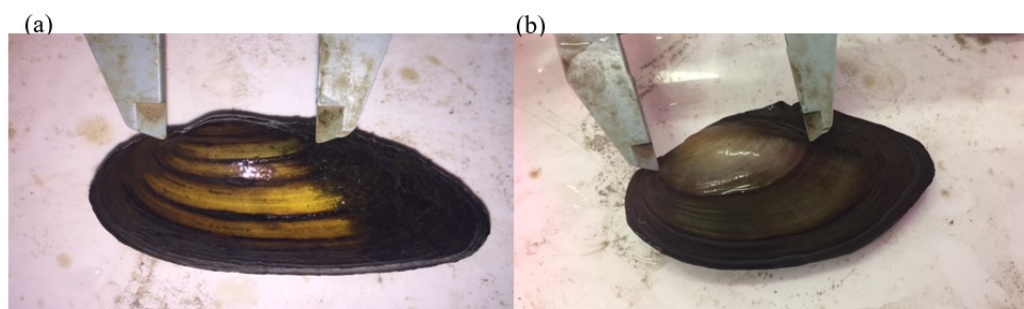


Fig. 1. Measurement of mussel annuli using a Vernier caliper; (a) *U. pictorum* from Ringlestone, (b) *A. anatina* from Ringlestone.

Individual growth parameters were determined using the Walford plot model (Walford, 1946) assuming von Bertalanffy growth curves (Aldridge, 1999). To account for declining growth increments as mussels age and to plot individual mussel growth trends, the natural logarithm of all the raw growth data was taken (Scourse *et al.*, 2006). Each mussel ring was then plotted as the deviation from a standardised index with a defined mean of 1.0 (Fritts, 1976; Cook *et al.*, 1995).

Results and Conclusions

The first study revealed that annual mussel length-at-age curves, growth constants (k), and asymptotic growths (L_{∞}) increased downstream. Between species, *U. pictorum* had the lowest asymptotic lengths and the highest growth constants, and *U. tumidus* had the highest asymptotic lengths and the lowest growth constants. In these two species, a higher asymptotic length corresponded with a lower growth constant, meaning it would take individual mussels a longer period of time to reach larger asymptotic lengths. *A. anatina* had the highest length-at-age curves of all species, resulting in larger individuals. The mean standardised annual growth increments (SIs) revealed significant effects of site, species, and seasonal temperatures on mussel growth. *U. tumidus* had the highest SIs overall and showed annual deviations from the growth patterns of the other two species, especially during years 2011 and 2014. Increasing spring, summer, and winter water temperatures all had a positive impact on SIs, while warmer temperatures in autumn had a negative impact (Fig. 2).

Due to these significant effects, mussel annuli can successfully be used as proxies to document changes in temperatures, especially during spring and summer, as long as species and location are considered in the analyses. The second study revealed that mussels from all of the marina habitats had higher annual length-at-age curves, larger asymptotic lengths, and lower growth constants than mussels from paired river habitats (Fig. 3). Since all marina sites were about 0.5°C warmer than river sites (Aldridge, 1999), this suggested that mussels grew larger in warmer conditions. Additionally, *U. pictorum* collected from Caversham in 2007 were larger than those collected in 2018. Again, mussels were larger downstream, and warmer winter and summer water temperatures significantly increased mussel growth. Significant differences in SIs between sites, species, and seasonal temperatures further support the use of site- and species-specific mussel annuli to document annual and seasonal environmental changes in freshwater ecosystems. Building a long-term chronology at Caversham enabled us to better determine which seasonal temperatures have the most impact on mussel growth over time.

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Since freshwater mussels act as 'ecosystem engineers', controlling water quality, taxon richness, sediment composition, and habitat availability, any change in their size, population dynamics, or dispersal could have major impacts on entire freshwater ecosystems (Gutiérrez *et al.*, 2003). Therefore, it is important to keep track of mussel growth patterns and understand the timing and cause of any changes. The results from this sclerochronological study suggest that mussel annuli can be implemented as a tool in the future to build long-term chronologies on past mussel growth patterns, to study paleoenvironmental changes in areas where records are lacking, and to date fossils and subfossils of mussels from around the world through cross-matching. The establishment of freshwater mussels as environmental indicators could also have global utility to river managers and make the conservation of mussels worldwide easier to justify and implement.

Acknowledgements

This work was funded by the Malacological Society of London [Early Career Research Grant 2018]. I wish to thank my supervisor, Dr. David Aldridge, for his guidance throughout my master's degree and Dr. Thomas Worthington for his help on statistics and modelling. Thanks also to the Museum of Zoology in Cambridge, Dr. Richard Preece, and Matthew Lowe for loaning the 2007 Thames mussel collection and to Thames and Kennet Marina for sampling access.

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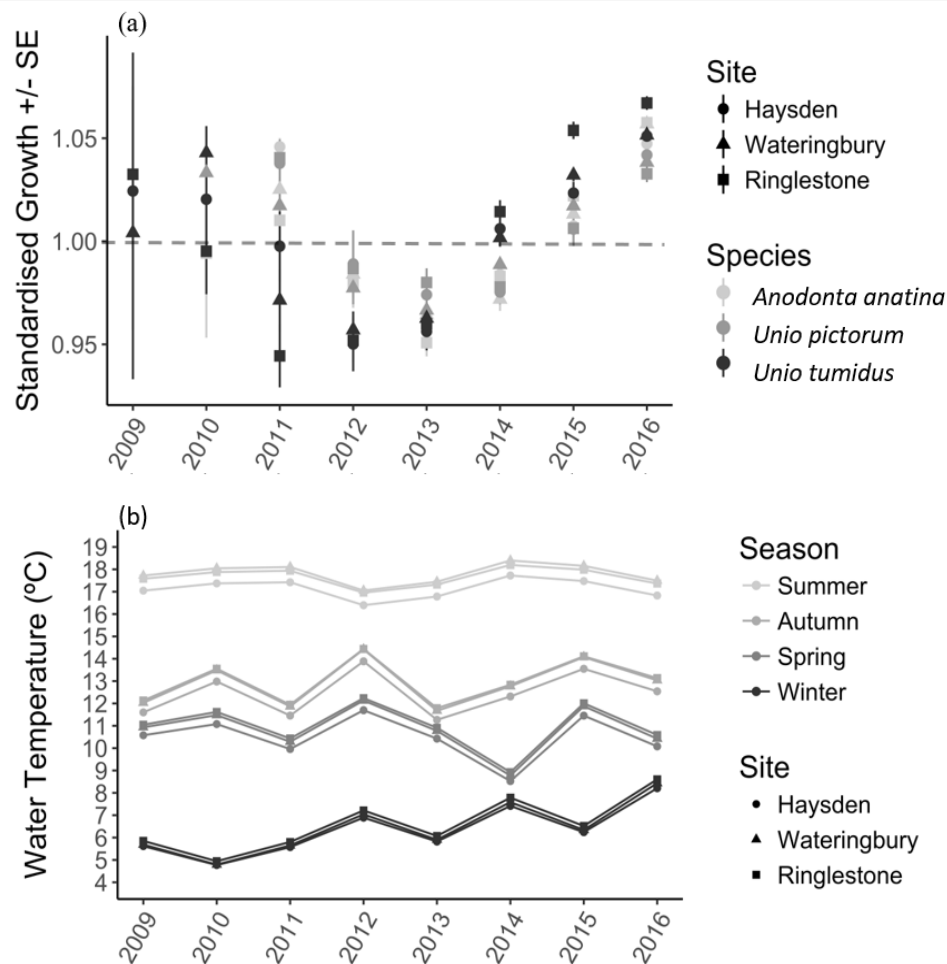


Fig. 2. Mean annual standardised mussel growth indices (SIs) compared with the corresponding mean seasonal water temperatures in the River Medway; (a) SIs for all three *Unionidae* species at all three sites over a period of eight years; (b) seasonal water temperatures for each site across the same time period; error bars represent standard error.

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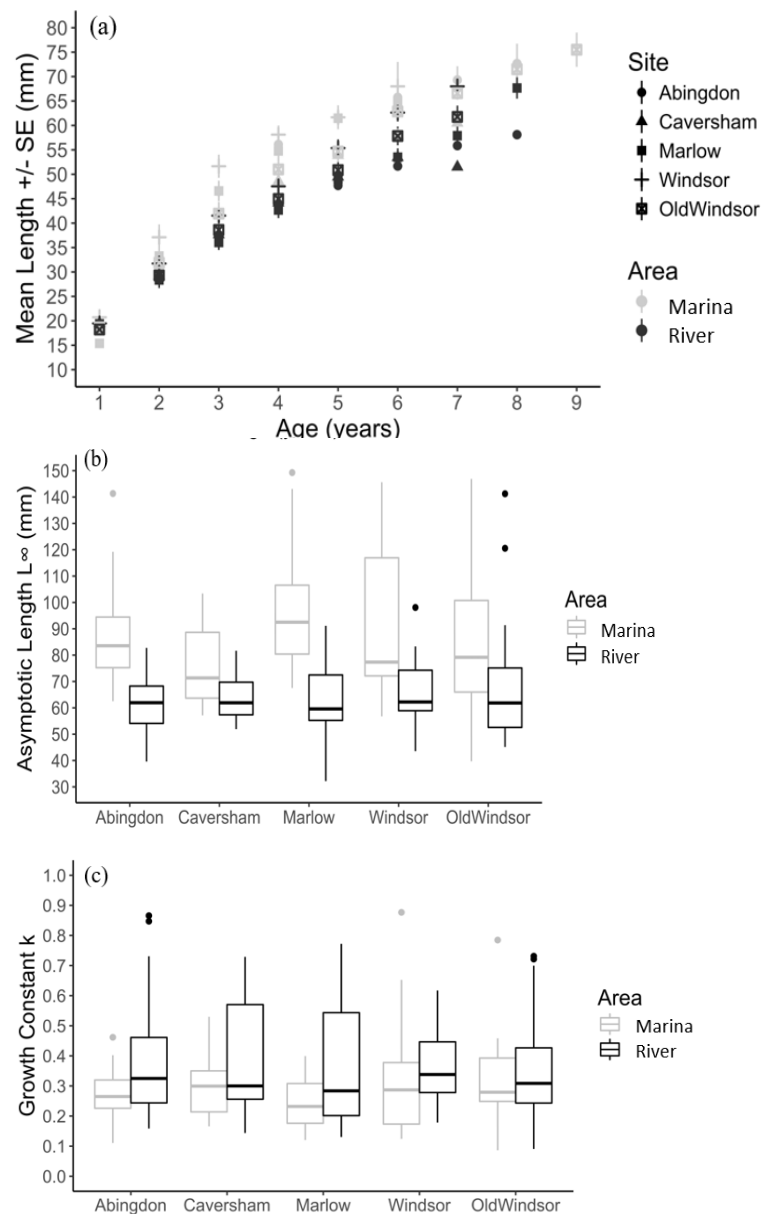


Fig. 3. Growth parameters for *U. pictorum* collected in 2007 from five paired sites along the River Thames; (a) length-at-age curves; sites are ordered from upstream to downstream and error bars represent standard error; (b) boxplot of the asymptotic lengths L_{∞} ; (c) boxplot of the growth constants k ; boxes are based on mean, 1st and 3rd quartiles, error bars represent 95% confidence intervals, and dots mark outliers.



Fieldwork to sample microsnails for diet and microbiome studies along the Kinabatangan River, Sabah, Malaysian Borneo

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Introduction

Over the last 30 years, land snails in snail communities on limestone outcrops in the Kinabatangan River floodplain in Sabah, Malaysian Borneo have attracted the attention from several malacologists, most notably Jaap J. Vermeulen, Menno Schilthuizen, and more recently, Liew Thor-Seng. Much of their research has focussed on taxonomy and systematics (Vermeulen, 1991; Vermeulen, Liew, & Schilthuizen, 2015), evolution and sexual selection (Schilthuizen, Cabanban, & Haase, 2005; Schilthuizen *et al.*, 2006), and biogeography (Schilthuizen, Rosli, *et al.*, 2003; Schilthuizen *et al.*, 2006). Based on published community data (Schilthuizen, 2011; Schilthuizen, Chai, Kimsin, & Vermeulen, 2003) R.S.E. and M.S. hypothesized that these snail communities, with the ecology of the different species seemingly highly similar, might assemble following simple neutral community assembly rules. Such neutral community assembly was described and modelled by Hubbell (2001), where “neutrality” was defined as “ecological similarity in species” from the same trophic level and living sympatrically. This contrasts with niche-based assembly, where assembly rules are dictated by complex species-specific interactions between individuals (Hutchinson, 1961). It is useful to know if communities indeed follow neutral assembly rules, because neutral theory can make useful, powerful predictions, such as on relative abundances, species-area-relationships, and beta-diversity (Rosindell, Hubbell, & Etienne, 2011).

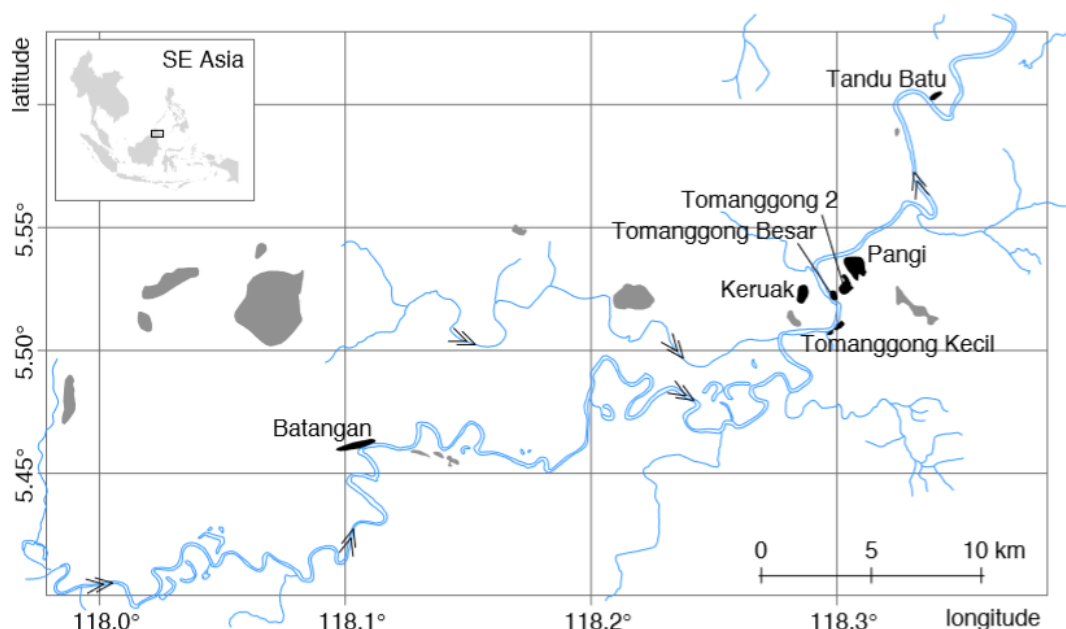
In 2014 a PhD project was started to study the evolution and ecology of Bornean microsnails, carried out by K.P., and supervised by R.S.E. and M.S. While part of the PhD project is based on empirical community data (snail shells sampled from standardized plots as a proxy for the community abundances) and theoretical analyses of these data, we also set up a project to study possible influences of traits on the community assembly, at which point K.B. became involved. More specifically, we have started to apply modern metabarcoding techniques that allow the reconstruction of snail diet and gut microbiome based on genetic data (Taberlet, Coissac, Pompanon, Brochmann, & Willerslev, 2012). With these data we try to answer the question of whether the snail diet and/or microbiome influence the assembly of the species into communities. Or, are these traits that dictate assembly and sustain communities?

Fieldwork & Laboratory Procedures

With the financial aid of an MSL Early Career Research Grant (2017) and two others grants, K.B. and K.P. visited the Kinabatangan River floodplain in November 2017, together with another PhD student (F.J.R.M.) and three master students (J.C.K., H.H.K., and A.E.A.L.). Our goal was to resample plots from which K.P. had gathered community data (shells) during visits in 2015 and 2016, so that we could correlate newly gathered diet and microbiome data to previously gathered community data. A homestay in the small village of Sukau was our base for two weeks. From there, we visited seven different limestone outcrops (Figure 1) along the river, travelling by car, boat, and on foot. From each outcrop, samples were taken from three plots (four in a single outcrop, Keruak) along the base of the outcrop, with a between-plot distance of 50 m (sometimes more if the vegetation was too dense). Plots measured two by two metres (Figure 2). We focussed on three target species of unrelated gastropod: *Plectostoma concinnum* (Fulton, 1901), *Georissa similis* E. A. Smith, 1893 s.l., and *Alycaeus jagori* Von Martens, 1859. Studies using standardised plots along a transect that spans both limestone and non-limestone substrate have shown that the prosobranch microsnail genera *Plectostoma* and *Georissa* tend to be restricted to limestone (Schilthuizen, Chai, *et al.*, 2003), while *Alycaeus* was found away from limestone, but in very low numbers (personal observations).

Georissa similis E.A.Smith, 1893 was, until recently, considered a single species, endemic to the Kinabatangan River valley. Hendriks, Alciatore, Schilthuizen, & Etienne (in press), based on phylogeographic studies, suggested that the taxon could best be treated as a species-complex, characterized by high levels of endemism due to many long-distance colonization events. Recent taxonomic research by Khalik, Hendriks, Vermeulen, & Schilthuizen (2019), based on combined phylogenetic and conchological studies, also suggests that the taxon is, in fact, best treated as a complex of closely related species: *G. flavescens* (found along the Kinabatangan River at limestone outcrops Pangli, Keruak, Tomanggong Besar, and Tomanggong 2), *G. bangueyensis* (widely distributed over northern and eastern Sabah), *G. nephrostoma* (along the Kinabatangan River on outcrops Keruak and Tandu Batu), *G. xesta* (widely distributed over Sabah), and *G. similis* (widely distributed over eastern Sabah). The samples used in the current study were identified as general “*G. similis*” only. Because the species complex is composed of closely related, genetically nested species, evolutionarily (and probably ecologically) widely different from all other species in the region (Khalik *et al.*, 2019), we treat the taxon as a species complex here and refer to it simply as “*G. similis* s.l.”.

Figure 1. Sampling locations (in black and named) along the Kinabatangan River (in blue), Sabah, Malaysian Borneo. Other limestone outcrops in the region in grey. Each named outcrop was sampled from three different plots (four in Keruak). Inset map © Free Vector



We aimed to collect 40 individuals per target species per plot, with a minimum of 20, evenly distributed over the plot. To this end, we subdivided each plot into four quadrants of one by one metre (figure 2), each quadrant sampled for 30 minutes. In addition, we aimed to collect each individual snail from at least 10 cm distance from previous ones of the same species (not always possible for *G. similis* s.l. due to a combination of low numbers and our target number). All other snail species encountered within the plot were collected as well, with a maximum of 20 individuals per species per plot. We conserved samples in 96% ethanol and froze them directly in a styrofoam box filled with ice after the 30-minute search session had ended.

Figure 2. Sampling microsnails from limestone. Plots were defined by a grid (made of rope) of two by two metres, subdivided into four quadrants of one by one metre (highlighted in yellow). Each quadrant was sampled for 30 minutes. Researchers (from left to right): K.B., J.C.K., A.E.A.L., and H.H.K.



After registration of samples and deposition into the Borneensis collection of Universiti Malaysia Sabah (UMS), Kota Kinabalu, Malaysia, samples were exported to the Netherlands as a long-term loan. We performed our laboratory work at Naturalis Biodiversity Center, Leiden, the Netherlands, in January and February 2018. In short, we (1) double-checked identities, (2) performed genomic DNA-extractions on the snail gut contents (see Figure 3 for an example of how faecal pellets usually are visible when shells are translucent), (3) amplified and sequenced both plant and microbial DNA from the gut using metabarcoding, and (4) identified genetic read data by comparison with benchmark databases. We used general genetic markers that proved to work effectively in metabarcoding studies before: *rbcl* for the plant diet (Hofreiter et al., 2000) and 16S V3-4 region for the microbiome (Andersson et al., 2008; Liu, Lozupone, Hamady, Bushman, & Knight, 2007). Sequencing was performed on an Illumina MiSeq at BaseClear, Leiden, the Netherlands.

We filtered the resulting read data (removal of chimeras, too short reads, and reads with too low quality) and organized (grouping and counting of identical reads) using the software Qiime2 (Bolyen *et al.*, 2018) in combination with the dada2 tool (Callahan *et al.*, 2016). The identification of genetic read data, also performed in Qiime2, was based on the rbcL seed plant database by Bell, Loeffler & Brosi (2017) and the 97% 16S GreenGenes database v13.8 (DeSantis *et al.*, 2006). Subsequent analyses of the data are ongoing and performed in R v3.5.0 using package PhyloSeq v1.24.0 (McMurdie & Holmes, 2013).

Figure 3. Specimen of the euconulid snail *Kaliella calcuosa* (Gould, 1852) with faecal pellets in the gut clearly visible through the translucent shell. Such pellets were extracted from the snail in a sterile environment and used for genomic DNA-extraction. The white scale bar equals 1 mm. This is specimen BORMOL13455.01.



Preliminary results

We obtained an enormous dataset of both diet and gut microbiome data, which we are still studying at the time of writing. We plan to publish these data, along with analyses in which we correlate these data with community data, within the next few months. Here, we offer a glimpse of what the full output is like.

We collected a total of 1,712 individual snails (excluding empty shells) belonging to 31 different gastropod species (table 1). 893 samples were *P. concinnum*, 267 *G. similis* s.l., and 359 *A. jagori*. *Plectostoma concinnum* was particularly abundant in all but two plots. *Alycaeus jagori*, a rather conspicuous species due to its relatively large size, was usually common, too, but sometimes absent, such as from outcrop Batangan. *Georissa similis* s.l., at two millimetres the smallest of the three target species, was often difficult to locate, and in 11 out of 22 plots we found less than 10 individuals. It is clear that the three target species, as anticipated, were most abundant.

Sequence data for the diet, based on rbcL reads and after filtering, were obtained for 822 samples, covering 29 species. The full diet metabarcoding dataset consisted of a total of 6.55 million rbcL reads, with mean read number per sample $7,965 \pm 8,129$ (median 5,544). Sequence data for the gut microbiome, based on 16S V3-4 region reads and after filtering, were obtained for 823 samples, covering the same species as for the diet. The full microbiome metabarcoding dataset consisted of 7.47 million reads, with mean read number per sample $9,072 \pm 4,613$ (median 8,255). Most metabarcoding data could be classified down to at least the taxonomic level of the family (for plants) or phylum (for microbiome). Some preliminary results for randomly chosen specimens from six selected species, including our three target species, are given in figure 4. We see a diet consisting of multiple plant families for each individual, with a diet richness of up to six plant families for *A. jagori* (excluding the category “unassigned”, which is a bin category for all rbcL reads that could be identified as seed plant, but not specifically to a plant family; causes may vary). Not all plant families were retrieved from all specimens, although families like Brassicaceae and Fabaceae were identified in most samples. The microbiome for each specimen usually contains a large proportion of Proteobacteria, while 13 more bacterial phyla were found from the six example specimens.

Discussion

Our study demonstrates the potential of DNA metabarcoding techniques for the study of land snail community ecology and evolution. Direct observations of foraging snails, or a dissection of the gut and visual identification of its contents, are often hardly possible due to the small size of the many snail species in the communities we study. Visual identification of gut content is usually only possible down to broad categories. Instead, we reconstructed the diet using modern next generation sequencing techniques in combination with the latest genetic barcode reference databases for seed plants and bacteria. This allowed us to collect plant dietary and gut microbial overviews (both from a single individual) for many hundreds of snails in just several months of research (including preparations, fieldwork, laboratory work, and computational analyses). A study of similar size based solely on field observations would have taken tens of years and would likely be far less detailed.

We have created an overview of plant diet for 29 species of land snail, but it is important to be aware of the diet components that our technique cannot pick up, *viz.* all materials without chloroplast genes. Although data are sparse, Barker & Efford (2004) give a diet overview for various pulmonate families. At least for several families also encountered in our study (Ariophantidae, Euconulidae, Rathouisiidae, and Trochomorphidae), it is known that the diet includes also fungi and algae. Hence, to obtain a more complete diet overview, it is suggested to, in future studies, include genetic markers for these groups, too.

One sample worth mentioning specifically is that of the single individual of the rathouisiid *Atopos* sp. (Figure 4.1) we collected. This is a genus of carnivorous slugs, mainly preying on *P. concinnum* (Liew & Schilthuisen, 2014) in the region. We found its diet to include at least some different plants, which conforms to the description by Van Benthem Jutting (1953), who mentions fungi and plant materials in the diet of *Atopos* (Barker & Efford, 2004). Based on our dataset, though, we cannot know if the plants we encountered in the gut derive directly from a herbivorous or omnivorous diet, or indirectly from eating other, herbivorous animals.

Our study yielded much exciting new data. With new knowledge come new questions. The data we present here are just a starting point for looking for geographical and taxonomic patterns, and studying possible correlations with community data.

	<i>N</i>
NON-PULMONATE SNAILS	
Assimineidae	
<i>Acmella cyrtoglyphe</i> Vermeulen, Liew & Schilthuizen, 2015	5
<i>Acmella striata</i> Vermeulen, Liew & Schilthuizen, 2015	14
Cyclophoridae	
<i>Alycaeus jagori</i> Von Martens, 1859	359
<i>Chamalycaeus</i> sp.	4
<i>Japonia kinabaluensis</i> (E.A. Smith, 1895)	3
<i>Japonia</i> sp.	5
<i>Leptopoma pellucidum</i> (Grateloup, 1840)	1
<i>Leptopoma sericatum</i> (Pfeiffer, 1851)	15
<i>Pterocyclos</i> / <i>Opisthoporus</i> sp.	8
Diplommatinidae	
<i>Diplommatina asynaimos</i> Vermeulen, 1993	1
<i>Diplommatina calvula</i> Vermeulen, 1993	3
<i>Diplommatina gomantongensis</i> (E. A. Smith, 1894)	5
<i>Diplommatina rubicunda</i> (Von Martens, 1864)	6
<i>Plectostoma concinnum</i> (Fulton, 1901)	893
<i>Plectostoma simplex</i> (Fulton, 1901)	31
Helicinidae	
<i>Sulfurina</i> sp.	15
Hydrocenidae	
<i>Georissa kinabatanganensis</i> Khalik, Hendriks, Vermeulen & Schilthuizen, 2018	33
<i>Georissa similis</i> E. A. Smith, 1894 s.l.	267
<i>Georissa nephrostoma</i> Vermeulen, Liew & Schilthuizen, 2015	5
PULMONATE SNAILS	
Ariophantidae	
<i>Everettia</i> sp.	4
<i>Macrochlamys tersa</i> (Issel, 1874)	6
<i>Microcystina appendiculata</i> (Von Moellendorff, 1893)	2
Euconulidae	
<i>Kaliella accepta</i> (Smith, 1895)	7
<i>Kaliella barrakporensis</i> (Pfeiffer, 1852)	2
<i>Kaliella calculosa</i> (Gould, 1852)	4
<i>Kaliella scandens</i> (Cox, 1872)	5
Rathousiidae	
<i>Atopos</i> sp.	1
Trochomorphidae	
<i>Videna froggatti</i> (Iredale, 1941)	1
<i>Videna metcalfei</i> (Pfeiffer, 1845)	4
<i>Videna</i> sp.	2
Valloniidae	
<i>Ptychopatulula orcula</i> (Benson, 1850)	1
TOTAL	1,712

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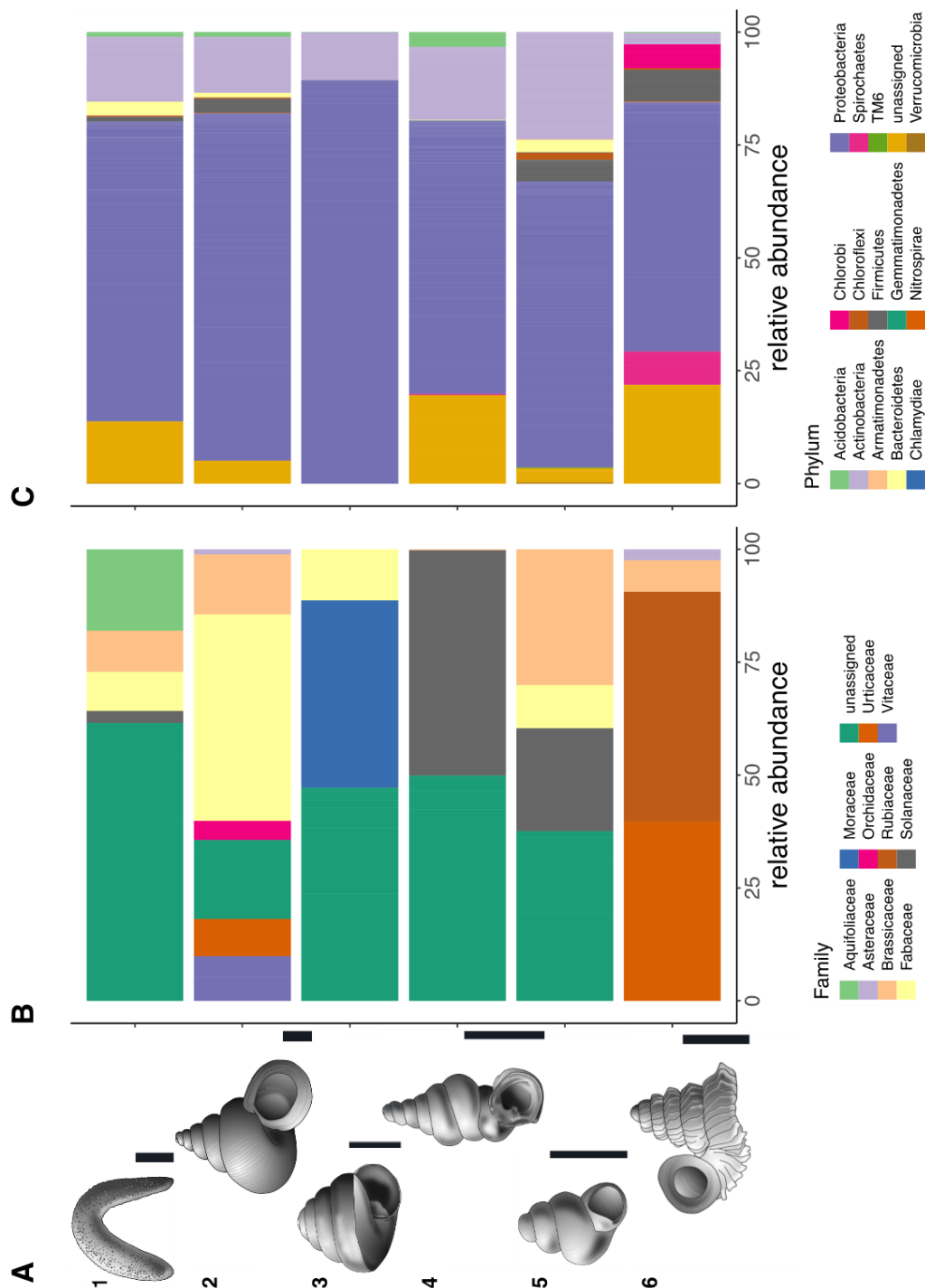


Figure 4. Preliminary results of diet and gut microbiome compositions for randomly chosen individuals from six different species. (A) Drawings of species' representatives of the six species: (1) *Atopos* sp. (data are for specimen BORMOL13662.01), (2) *Alycaeus jagori* Von Martens, 1859 (BORMOL13479.02), (3) *Kaliella accepta* (Smith, 1895) (BORMOL13455.01), (4) *Diplommatina calvula* Vermeulen, 1993 (BORMOL13425.01), (5) *Georissa similis* E. A. Smith, 1893 s.l. (BORMOL13410.01), and (6) *Plectostoma concinnum* (Fulton, 1901) (BORMOL13403.01). Drawings by Bas Blankevoort, Naturalis Biodiversity Center. Black scale bars equal 1 mm; (B) Relative distribution of seed plant families found from the diet, based on rbcL read numbers and normalized to 100%; (C) Relative distribution of microbial phyla found from the gut microbiome, based on 16S V3-4 region and normalized to 100%.

Acknowledgements

Supervisors Dries Bonte, Joana Falcão Salles, and Alex Pigot have been involved in setting up and review of the project. We thank Liew Thor-Seng of ITBC, UMS, Kota Kinabalu, Malaysia, for helping with access and export license applications. Arjen Speksnijder and Elza Duijm at Naturalis Biodiversity Center, the Netherlands, have been extremely supportive and helpful with our laboratory work. This research was funded by The Malacological Society of London (Early Career Research Grant, awarded to K.P.H.), as well as NWO (VICI grant, number 865.13.003, awarded to R.S.E.), KNAW (Fonds Ecologie Beurs, reference Eco/1711, awarded to K.P.H.), and the Leopold III-Fonds (awarded to K.B.). All samples were collected (permit numbers JKM/MBS.1000-2/2 JLD.6 (107, 112, 114, 116, and 118)) and exported (JKM/MBS.1000-2/3 JLD.3 (51)) under license of Sabah Biodiversity Council and have been deposited into the Borneensis collection of UMS. Sample numbers and details can be requested from the first author.

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The study area



Travel Grant Report

15th Deep-Sea Biology Symposium in Monterey Bay, California (USA)

Franziska Bergmeier, Dept. Biology II - Systematic Zoology, LMU Munich, Germany.
E-mail: franzi.bergmeier@gmail.com

The Deep-Sea Biology Symposium is the triennial conference of the Deep-Sea Biology Society, bringing together researchers working on different aspects of the deep oceans. For the 2018 symposium (9th to the 15th of September), more than 400 scientists from 33 nations gathered in sunny Monterey Bay (California, USA).

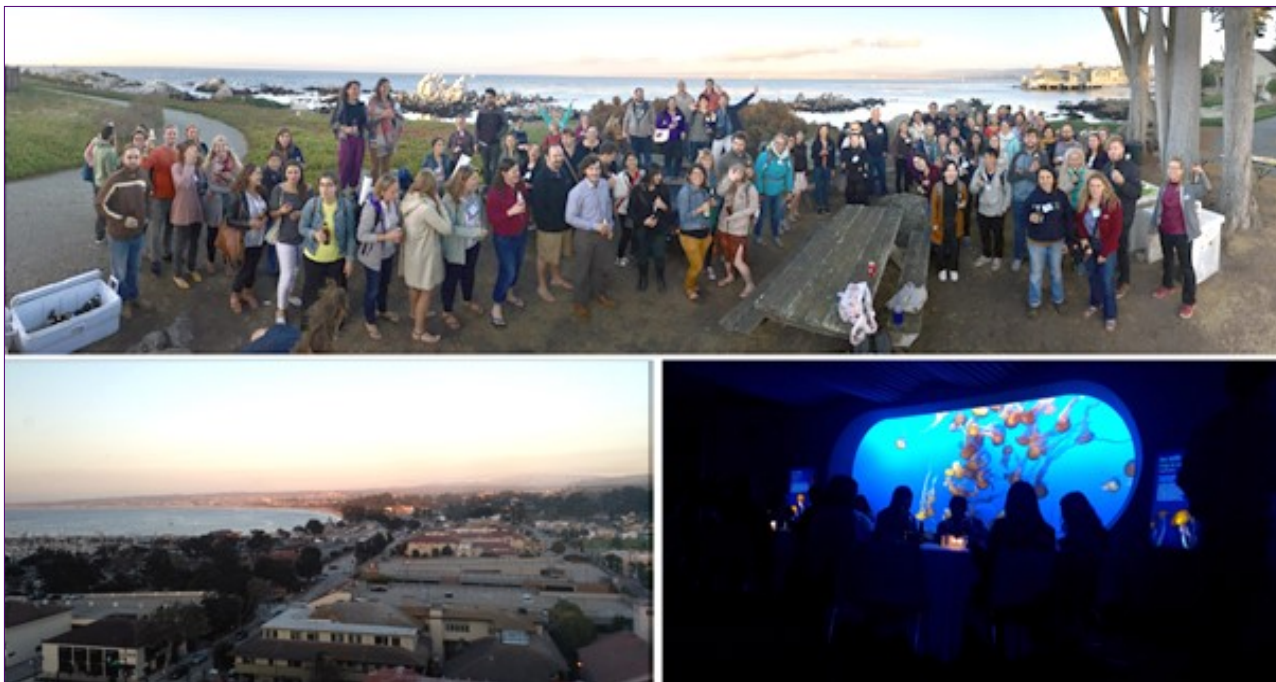
The symposium offered sessions covering a diverse range of topics, from different habitats (e.g. pelagic and chemo-synthetic systems, seamounts and canyons), to impacts of deep-sea mining and anthropogenic disturbances as well as advances in deep-sea “omics”, biogeography, connectivity, taxonomy and phylogenetics.

During the “Advances in Taxonomy and Phylogeny” session, I presented the current results of my PhD research on taxonomy and biogeography of deep-sea Solenogastres (Aplacophora, Mollusca). In addition, I presented a poster on behalf of master student Lukas Ostermair during the Trophic Ecology Session, giving new insights into the food-source diversity of Solenogastres.

Each day started with two plenary talks, all in all covering a wide range of deep-sea related research. On Tuesday morning, the day began with two hours of 90-seconds “lightning talks”: poster-presenters had the opportunity to advertise their research using only a single powerpoint slide. It was brilliant to see so many different topics covered by enthusiastic scientists, each and every one making the most out of their time slot! On Wednesday afternoon we were invited to enjoy the Monterey Bay Aquarium and on Thursday evening PhD students and early-career Postdocs met up at the Hopkins Marine Station for some socializing, networking, and BBQ.

The official part of the conference concluded with various announcements and awards. I felt much honored to receive the John Gage Prize for the best student talk. Overall, the symposium was a great success for me: I received a lot of useful feedback on my work, as well as suggestions for further research questions. Over coffee I exchanged new ideas and planned future collaborations.

The Travel Award from the Malacological Society was a substantial contribution to cover my travel expenses. Parts of my PhD-thesis as well as the presented poster by Lukas Ostermair were also financed through Early Career Research Grants by the MSL, and I am grateful for all this support I received from the Society!



Impressions from the DSBS: BBQ and student mixer (top, photo credit: Darrin Schultz), Monterey Bay at sunset (bottom left), conference banquet at the Monterey Bay Aquarium (bottom right).



Charles Sturm

Charles "Charlie" F. Sturm passed away yesterday. In his words, "If you are reading this, realize that while I fought the good fight, and ran the good race to the finish (2 Timothy 4:7-8), I have succumbed to my metastatic prostate cancer."

As many of us know, Charlie loved collecting fossils and seashells, especially scallops. He has been a highly valued research associate at Carnegie Museum of Natural History since 1992. In 2011, Charlie served as president of the American Malacological Society and hosted the annual meeting in Pittsburgh. As treasurer of that society for the past 5 years, he ably revived the financial records. In 2006, he published the book, *The Mollusks: A Guide to Their Study, Collection, and Preservation*. One of his proudest moments was describing a new genus and species of fossil scallop, which he named after his beloved wife: *Patriciapecten iona* (he has had a tattoo of it on his shoulder for over 15 years).

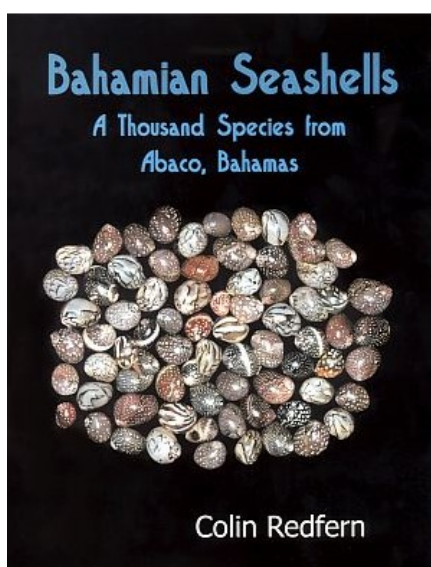
Vocationally a physician of family medicine, he practiced and taught medicine. His interest in geriatric medicine led him to serve as medical director of a rehabilitation and wellness center. His interest in wilderness medicine provided opportunities for hiking and backpacking.

Charlie's other passions included his decades-long affiliation with Boy Scouts of America, which he joined as a Cub Scout, rose through the ranks to Life Scout, and served in a leadership capacity as an adult.

More information can be found at <https://www.doc-fossil.com/> (and more in coming days).

Donations may be made to the Carnegie Institute - Mollusk Endowment, 4400 Forbes Avenue, Pittsburgh, PA 15213, or The Laurel Hills Council, Boy Scouts of America, Flag Plaza Scout Center, 1275 Bedford Avenue, Pittsburgh, PA 15219, or the Prostate Cancer Foundation, 1250 Fourth Street, Santa Monica, CA 90401.

Timothy A. Pearce, Ph.D., Curator of Collections & Head, Section of Mollusks
4400 Forbes Ave, Pittsburgh, PA 15213-4080, USA



Colin Redfern

It is with great sadness that I inform you that my great friend and collaborator Colin Redfern passed away this morning in a life-care facility in his hometown of Boca Raton, Florida. Born in Great Britain, Colin spent a big part of his life in Abaco, Bahamas. He was a classically trained professional pianist and productive citizen scientist who focused on collecting shells and mollusks in that Bahamian island, where he started to gather data and photographs for what eventually became the two editions of his well-respected "Bahamian Seashells" books. The first edition, from 2001, was subtitled "1000 species from Abaco, Bahamas," and the second (2013) was an entirely new book, subtitled "1161 species from Abaco, Bahamas." Colin's books are, in my opinion, among the best regional molluscan biodiversity guides ever produced. Colin was a member and strong supporter of the Bailey-Matthews National Shell Museum, and, in 2014, completed the donation of his 10,000-lots collection of Bahamian seashells and preserved mollusks to the organization. As part of his outstanding contribution to the Museum, Colin volunteered to enter the data for the entire collection in the Museum catalog. Colin's collection also includes literally thousands of specimens illustrated in his two magnificent reference works. He was a founding participant of Florida United Malacologists, and future FUM gatherings won't be the same without him. In 2014, Colin received the prestigious *Neptunea* award from Conchologists of America for his many contributions to the science of Malacology and the scientific interests of COA. Colin is survived by his wife Janet of Boca Raton.



José H. Leal, Ph.D. Science Director & Curator www.shellmuseum.org
Editor, *The Nautilus*
3075 Sanibel-Captiva Road
Sanibel, FL 33957 USA
25-01-2019





Limpets 2020: Biology of Limpets: evolution, adaptation, ecology and environmental impacts

(Meeting held in association with the Malacological Society of London and the Marine Biological Association UK)

First Announcement – 17th to 19th March 2020

Venue: Plymouth MBA, UK

Meeting Organisers

Professor Steve Hawkins (Plymouth MBA, UK), Professor Alan Hodgson (Rhodes University, South Africa), Dr Louise Firth (University of Plymouth, UK), Dr Phillip Fenberg (University of Southampton, UK)

In 1920 JH Orton published two important papers, one examining the importance of sea temperature on the breeding and distribution of marine animals, and the second on sex change in limpets. To mark the centenary of this work, Orton's contribution to marine biology in general and limpets in particular, as well as the work of the biologists who followed on from Orton including those in his student lineage, we are pleased to announce Limpets 2020. The aim of this meeting is to provide a forum for the discussion of recent findings on all aspects of the biology of limpets. Previous meetings, held in London (1993), Millport (2003) and Phuket (2010), were highly successful. It is hoped that the 2020 meeting will build on this success and stimulate more research on these ecologically important molluscs. A number of key-note speakers are being approached (names to be announced in 2019) and sessions will be available for contributed papers and posters.

Presentations of research in which limpets have been used as model animals in evolutionary, adaptational (morphology, physiology, reproductive biology, behaviour), ecological and environmental impact studies are especially encouraged. **There will also be a general session in celebrating Orton, in which papers on any aspect of molluscan or marine biology are welcome.**

Meeting duration – 2.5 days with no parallel sessions.

Day 1 – Arrival: 12h30-13h30 tea/coffee; 13h30 – 16h00 General Session ("*Orton and his legacy - molluscan and marine biological talks on any aspect that would have interested Orton*"); 16h00 tea followed by AGM of Malacological Society of London; Evening Free to explore Barbican pubs and restaurants.

Day 2 – Biology of Limpets – Evening Dinner at MBA

Day 3 – Biology of Limpets – Meeting ends at 16h00

To help plan the meeting, e-mail your expression of interest to Alan Hodgson (A.Hodgson@ru.ac.za) indicating type of presentation (platform paper or poster) and possible topic.

Details about registration, accommodation and transport will be announced in 2019 as plans for the meeting take shape.



Sponsored by University of Plymouth Marine Institute



Aspects of mollusc conservation

Wednesday 27 March 2019 1345h

126th AGM Malacological Society of London

Flett Theatre, Natural History Museum, London

In order to celebrate the 126th AGM of the Malacological Society of London, MSL together with the Natural History Museum are co-hosting a short symposium, on aspects of conservation of molluscs. When we have heard from our invited speakers, there will be a celebratory glass of wine. All are welcome.



Redlisting the non-marine molluscs of Europe

Eike Neubert

Department of Invertebrate Animals, Naturhistorisches Museum der Burgergemeinde Bern, Bernastrasse 15, CH-3005 Switzerland
eike.neubert@nmbe.ch

Terrestrial molluscs have been the target of red list activities for almost 3 decades, with sporadic and taxonomically scattered entries from the 1970's. Prerequisite to any redlisting, a scientifically well-tested and foreseeable stable taxonomic backbone was needed. Fortunately, this backbone for Europe was created in parallel through the MolluscaBase project, which was fed by fundamentally revised data retrieved from the Fauna Europaea list. The terrestrial gastropods are represented by 57 families, with the Clausiliidae being the largest group comprising 429 species. Since 2009, the complete non-marine malacofauna of Europe has been screened using the knowledge of almost 50 experts. The threat status was assessed against the standard categories and criteria of the IUCN Red List (IUCN version 3.1). Today, we can present data on the current conservation status of 3332 species of terrestrial and freshwater molluscs. These data were made visible through the IUCN Red List database in November 2017 (www.iucnredlist.org), presenting a lot of hitherto unpublished information on the species including as a novelty a distribution map for almost all species. For the terrestrial molluscs, there is good news: of the ca. 2.476 species, only 19.5% have a threatened category, and slightly more than 50% are considered Least Concern. Freshwater molluscs were assessed in 2011, and an update is urgently needed as recently described species are not assessed. So the latest numbers from 2011 stay with ca. 40% of the species having a threatened category, contrasted by only 22% of Least Concern species. As could be expected, the Balkans turned out to represent the area with the highest biodiversity. The Macaronesian Islands with all the small-range species show a very similar pattern in species richness. The major threats identified against terrestrial molluscs in Europe are grazing, increased incidence of fires, deforestation, agriculture and encroaching urbanisation.



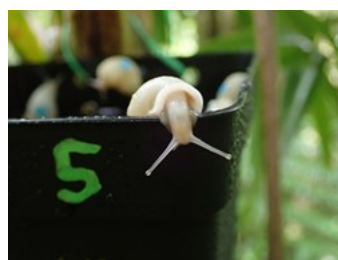
Partula snail conservation breeding and reintroduction and some wider species initiatives.

Paul Pearce-Kelly

Senior Curator, Ectotherms. Zoological Society of London
IUCN Climate Change Specialist Group Information Search and
 Synthesis work theme Leader
 Email: ppk@zsl.org



The *Partula* tree snail conservation breeding programme was established over 30 years ago in response to widespread *Partula* extinctions in the 1970s and 1980s from the introduced predator *Euglandina rosea*. The programme currently includes 15 species and sub-species (the majority of which have *Extinct in the Wild* Red List status). A long-term collaboration between the French Polynesian environment department and the zoo conservation breeding programme has enabled 10 species and 2 subspecies to be reintroduced. This presentation will update colleagues on progress to date, lessons learned and follow up initiatives. It will also summarise some future conservation environment considerations for this and wider species recovery efforts.



Membership Notices

THE MALACOLOGICAL SOCIETY OF LONDON

Registered Charity No. 275980

Hon. Secretary
Dr Rowan J. Whittle

The 126th Annual General Meeting of the Malacological Society of London (MSL) will take place at 12.10–13.30 on 27th March 2019 in the Flett Theatre, the Natural History Museum, London. The AGM will take place during a symposium organized jointly by the MSL and the NHM entitled *Aspects of conservation of molluscs*

Agenda for AGM

Apologies for absence
Minutes of the last (125th) AGM
Matters arising
Financial report
Annual report of Council (delivered by the President)
Awards
Election of Council
Any other business

Year of existence	2018-2019	2019-2020
	125	126
President	John Grahame (1)	John Grahame (2)
Vice Presidents	Richard Preece (3)	Robert Cameron (2)
	Robert Cameron (1)	Philip Fenburg (1)
Ex officio	Suzanne Williams	
Councillors	Aidan Emery (2)	Aidan Emery (3)
	Phil Fenberg (3)	Harriet Wood (3)
	Harriet Wood (2)	Andreia Salvador (2)
	Debbie Wall Palmer (3)	Fiona Allen (2)
	Andreia Salvador (1)	Philip Hollyman (1)
	Fiona Allen (1)	Lauren Sumner Rooney (1)
Co-opted		Debbie Wall Palmer
		Alan Hodgson
Journal Editor	Dinazarde Raheem/David Reid	Dinazarde Raheem
Bulletin Editor	Georges Dussart	Georges Dussart
Treasurer	Katrin Linse	Katrin Linse
Membership Secretary	Tom White	Tom White
Hon.Secretary	Rowan Whittle	Rowan Whittle
Web manager	Tom White/Chong Chen	Tom White/Chong Chen
Awards Officer	Jon Ablett	Jon Ablett



Grants and Awards

Malacological Society of London Awards and Grants

The Research Awards Scheme was established to commemorate the Society's Centenary in 1993. Under this scheme, the Society gives awards to support research on molluscs that is likely to lead to publication. The closing date for applications each year is 15th December. Grants are preferentially conferred on students and researchers without regard to nationality or membership of the Society. Preference is also given to discrete research projects that fall within the subject areas covered by the Society's *Journal of Molluscan Studies*. Applications will be assessed by scientific merit, value of the project and for student applicants, the extent to which the research will benefit the applicant's scientific aspirations. The successful applicants will be notified by 31st March and announced at the Annual General Meeting. Awardees are encouraged to publish their work in the *Journal of Molluscan Studies* (full papers) or *The Malacologist* (travel award reports, research award reports, news of ongoing research etc) as appropriate.

Early Career Research grants

Eligibility is restricted to those investigators at the outset of their independent scientific career. Applications must therefore be 1) postgraduate students, 2) within five years of being awarded their PhD (adjustable for career breaks), or 3) independent researchers not having a PhD. Early Career Research Grants will only be awarded to individuals twice, but not within 3 years of receiving a first award

Sir Charles Maurice Yonge Award

There is no application process for Sir Charles Maurice Yonge Awards. These awards are given for the best Travel Award application on bivalves, by a member of the Society to attend an international meeting (not including the Molluscan Forum). Authors of exceptional studies on bivalves in the *Journal of Molluscan Studies* may on occasion also be given this award. The Editor will nominate such papers as he/she sees fit. The award covers the costs requested in a Travel Award, or for open access publication of the paper. Members of the Society will also receive a personal cash prize of £300. Non-members will receive a personal cash prize of £250 plus one year's membership to the Society. If a paper is multi-authored, the award will be made to the corresponding author.

Senior Research Awards

are aimed at established researchers in professional positions, but without regard to nationality. Applicants for Senior Research Awards must be members of the Malacological Society of London. The Society currently awards up to five Senior Research Grants per year, each with a value of up to £1,500, to support research on molluscs that is likely to lead to publication. The maximum amount available should not be considered as a 'target'; rather requests should reflect the research that is proposed. The grants are reviewed by a Reviewers Panel including both Council and non-Council members invited for that purpose.

Travel Grants

Travel Awards are available as bursaries to support attendance at a conference or workshop relevant to malacology. Grants are preferentially conferred on students but researchers without professional positions may also apply. The maximum amount for one of these awards is £500 for Society members and £300 for non-members. Preference will be given to members of the Society. There are two closing dates each year, 30th June for travel starting between 1st September of the current year and 28th February of the following year, and 15th December for travel starting between 1st March and 31st August of the following year.

For further information, guidance notes and to access the application form see here - <http://malacsoc.org.uk/awards-and-grants/travel-grants>

Annual Award

This Award is made each year for an exceptionally promising initial contribution to the study of molluscs. This is often a thesis or collection of publications. The value of the Award is £500. Candidates need not be a member of the Society but must be nominated by a member. There is no application form: the nominating member should send the material for evaluation with a covering letter or letter of support to the Honorary Awards Secretary. The closing date each year is 1st November. The winner(s) will be notified by 31st March, and announced at the Annual General Meeting.

Applications

Applications for Research Awards and Travel Grants should be sent to the Honorary Awards Secretary, Jonathan Ablett, Division of Invertebrates, Department of Life Sciences, Natural History Museum, London, SW7 5BD. For further information, guidance notes and to access the grant application form see <http://malacsoc.org.uk/awards-and-grants/research-grants>. Please note that all applications must be sent by email to MSL_awards@nhm.ac.uk.



Malacological Society of London—Membership notices

Objects

The objects of the Society are to advance education and research for the public benefit by the study of molluscs from both pure and applied aspects. We welcome as members all who are interested in the scientific study of molluscs. There are Ordinary Members, Student Members and Honorary Members. Members are entitled to receive a digital &/or paper copies of the *Journal of Molluscan Studies* and such circulars as may be issued during their membership. The society's Web Site is at: <http://www.Malacsoc.org.uk>

Publications

The Society has a continuous record of publishing important scientific papers on molluscs in the *Proceedings*, which evolved with Volume 42 into the *Journal of Molluscan Studies*. The *Journal* is published in annual volumes consisting of four parts which are available on-line by members and student members. A paper copy of the *Journal* is available for ordinary members who are willing to pay a hard-copy premium. Members also receive access to *The Malacologist*, which is the bulletin of the Society, issued twice a year, in February and August.

Meetings

In addition to traditional research on molluscan biology, physiological, chemical, molecular techniques are amongst the topics considered for discussion meetings and papers for publication in future volumes of the *Journal*.

Personal Subscription

Personal subscribers gain access to the online archive of *Journal of Molluscan Studies* and receive *The Malacologist* twice a year; subscriptions including printed editions of *JMS* (four parts per year) are charged at a higher rate. Members are eligible to vote at the Annual General Meeting and to elect the Officers of The Society. The Annual Subscription for Ordinary Members and Student Members is due on 1st January each year.

From 2018 subscription rates are:

Ordinary Member (journal online and in print)	£90
Ordinary Member (journal online only)	£45
Student Member (journal online only)	£25

Membership subscriptions can be paid as instructed below and are valid from 1st January for a single calendar year.

Please remember that a subscription paid in December will therefore only be valid for one month and will have to be renewed the following January.

Application to join the Society

Please complete the application form below and send it to the Membership Secretary:

Dr Tom S. White, Membership Secretary, Malacological Society of London, Department of Life Sciences, Natural History Museum, London, SW7 5BD

Email: membership@malacsoc.org.uk

Membership Renewal

Existing members can renew their subscriptions from January 1st each year via online payment.

Methods of Payment

Payment may be made by:

Online payment using Credit or Debit Card (Mastercard, Visa, American Express)

Cheque (please fill in the Application Form above)

Changes of Address

Please use the address slip on the *Journal* wrapper to inform us, through Oxford University Press, of a change of address, or write to the Membership Secretary (see details above).

Institutional Subscriptions

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