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Molluscan Forum 2022

Last November an international group of young malacologists took part in the 23rd Malacological Forum at the Natural History Museum. The abstracts of the presentations start inside on page 7

Atlantic sea scallop fishery



These images are from an abstract entitled Spatial variation in food utilization by Atlantic Sea Scallops (*Placopecten magellanicus*) using stable isotope analysis by <u>Kait</u>lyn Clark, Roger Mann & David Rudders on on page 8

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EDITORIAL

Post-covid, it became possible to have hybrid meetings, meaning that there could be a mix of a digital, online presence as well as participation in-person. A consequence of this innovation was that more contributors could attend the Malacological Forum of the Malacological Society of London (MSL), and a further consequence is that this issue includes 37 abstracts of the presentations. A quick scan throught the provenances of the contributing authors shows that twenty four countries are represented, which shows a wide scientific reach for a small, specialist society such as the MSL. This issue of *The Malacologist* includes a research report from Dr Jose Fernández-Simón in Spain (*Barcoding the diversity of neglected meiofaunal molluscs in the western Mediterranean*), a malacological obituary from Dr. Joris M. Koene in the Netherlands (for Prof Ronals Chase in the USA) and an invited article (on the deep-sea Scaly Footed Snail) from Dr Chong Chen in Japan.

The MSL has a long and illustrious history but continues to innovate. For example the MSL is starting a Global Participation Postgraduate Student Scheme whereby students from developing economies can be awarded free membership of the MSL(see p34). The activities of the MSL invoke responsibilities too—for example on p30 there is an announcement for the AGM. The latter will include some proposed changes to the operating rules (p.31). The accompanying symposium links to the publication of a book entitled *William Benson and the golden age of malacology in British India*, though it should be noted that the role and administration of the British Empire is coming under increasingly critical and ethical scrutiny.

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 3^{rd} Edition (1985), edited by W.D. Ride *et al.*].

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News and notes

130th Malacological Society of London (MSL) AGM and Symposium

The **130th Malacological Society of London AGM and Symposium** which will take place in the afternoon, **Wednesday 29th March 2023** at the **Natural History Museum, London**. The symposium will be based around the launch of the new book '*William Benson and the golden age of malacology in British India*' and will feature talks from some of the authors along with research that has been inspired by Benson and the regions he studied.

At the accompanying AGM (see page 30), there will also be the usual annual elections to Council as well as proposals for changes to the MSL rules. See pages **31**-32 for further information



Meeting Date: Tuesday, September 5, 2023 to Friday, September 8, 2023 Location: University of Cambridge (UK) Organisers: Liz Harper (University of Cambridge), John Taylor, Emily Glover & Katie Collins (The Natural History Museum, London) Contact Email: emh21@cam.ac.uk

Description

We are pleased to announce the forthcoming conference focused solely on bivalved molluscs, to be held from 5th - 8th September, 2023, at the University of Cambridge (UK). This is intended as a successor to the previous bivalve meetings that took place in London (1977), Drumheller (1995), Cambridge (1999) and Barcelona (2006). Our aim is to host a relaxed, open in-person meeting to carry on this tradition of convivial review of all aspects of current bivalve research (living and fossil).

Changes to the Society's Travel Awards scheme

The Society is trialling upfront payments of travel awards to alleviate financial pressure on recipients. Recipients of Travel Awards will be asked to provide evidence of attendance at the event for which funding was sought, and if travel does not take place, recipients commit to repaying their award.

To better reflect the academic calendar, the deadlines for travel awards changed on January 2023. The new deadlines are 1st March, for travel scheduled between 1st June and 30th November, and 1st September for travel scheduled between 1st December and 31st May. Please note that the Society does not make awards in arrears.

We hope these changes will improve the scheme and the accessibility of conferences and workshops for our members. For further information, see page 33. Please get in touch with the Honorary Awards Secretary at <u>MSL awards@nhm.ac.uk</u> with any questions.



Some members of the Malacological Society of London make their own Christmas cards with molluscan themes. Here are a couple of examples from members of the Council. If you have your own examples, the Editor would be interested to see them for possible inclusion in a future issue of *The Malacologist*.





By Chong Chen



Malacological cartoons from the New Statesman 2022







Photo by Kateřina Kubíková: Faustina cinguella is a rock-dweling

species endemic to limestone areas of Slovakia with its centre of

distribution in the Malá and Veľká Fatra Mts

Molluscan Forum 2022

Natural History Museum, London took place on 17th November 2022

JONATHAN ABLETT, Organiser President of the Malacological Society of London Senior Curator in Charge, Mollusca, Natural History Museum (email: j.ablett@nhm.ac.uk)

PHIL HOLLYMAN, Organiser Vice President of the Malacological Society of London Fisheries Ecologist, British Antarctic Survey (email: phyman@bas.ac.uk)

LAUREN SUMNER ROONEY, Organiser Council member of the Malacological Society of London Junior Group Leader, Museum für Naturkunde Berlin (email: Lauren.Sumner-Rooney@mfn.berlin)

ANDREIA SALVADOR, Organiser Council member of the Malacological Society of London Senior Curator of Marine Gastropoda and Historical Mollusca Collections, Natural History Museum (email: a.salvador@nhm.ac.uk)

THOMAS GOULDING, Organiser

Early Career Representative of the Malacological Society of London PhD Candidate, Marine and Environmental Science Centre, Lisbon University (email: tgoulding@fc.ul.pt)

This year the Forum was a hybrid meeting, being both 'in-person' and on-line. In lieu of posters, there were 5 minute (3 slide maximum) **Quickfire PowerPoint** presentations,

Schedule

09.00 - 10.00 Registration, coffee & set up of posters

<u>10.00 - 10.15</u>

JONATHAN ABLETT: Welcome and introduction to the day

10.15-11.00 Session I (Hybrid)

- 10.15 YI-XUAN LI: Phylogenetic context of a deep-sea clam (Bivalvia: Vesicomyidae) revealed by ancient DNA from 1,500-year-old shells
- 10.30 HANNAN H. J. YEO: Grazing intensity of intertidal gastropods on tropical seawalls in Singapore
- 10.45 SOFIA HAZEL De GUZMAN: Cones and cobwebs:newly discovered cobweb-like excretion behaviour of *Conus geographus*.

11.00-11.20 Session II (Quick Fire Talks)

LAUREN COOK: Profiling disease and multi-trophic community dynamics through eDNA at the Solent Oyster Project, UK

FIONA WOODS: Ecosystem shifts associated with the restoration of native oyster (*Ostrea edulis*) reefs in the Solent, UK

LUCY MARTIN: Reducing successful shipworm larval settlement on wood that has been modified using furfurylation.



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11.45 - 13.00

Session III (Talks)

11.45 KATE DEY: Population dynamics and reproductive cycle of the invasive Asian date mussel in the UK and the potential for future spread.

12.00 MATTHEW KERR: Body size and abundance are decoupled from species richness in Australian marine bivalves

12.15 LUCY STEPHENSON: Studies on *Cadulus theilei* Plate, 1909: Distribution of a not so rare scaphopod and assessment of morphological diversity

12.30 LESLIE YOUTSEY: Comparing low salinity transcriptomic profiles and SNPs among Hard Clams, *Mercenaria mercenaria*, Lines

12.45 ANYA TOBER: The hidden parascape: digenean diversity in Kruger National Park

14.00 - 15.00

Session IV (Talks)

14.00 RACHEL FOSTER: The role of invasive bivalves on pathogen dynamics of invaded ecosystems

- 14.15 PETER ANDRUS: Seasonality infection rates of *Biomphalaria* (Gastropoda: Planorbidae) species found at the Great African Lakes in Uganda, East Africa
- 14.30 KATEŘINA KUBÍKOVÁ: Relationship between recent and Holocene mollusc fauna diversity of the Veľká Fatra Mts..
- 14.45 MARGARET JOHANSEN: A high-density linkage and binary trait map for shell-colour phenotypes in the grove snail (*Cepaea nemoralis*)

15.00-15.20

Session V (Quick Fire Talks)

YUMI NAKADERA: Discovery and inheritance of a new shell polymorphism in the great pond s nail *Lymnaea stagnalis*

MARK LASSNIG: Ocxplants: a novel technique to study octopus neurogenesis ex-vivo

15.20 - 16.00 Poster Session/ Coffee

16.00 - 16.45

Session VI (Hybrid)

- 16.00 MONICA FABRA: The plastic trojan horse: biofilms increase microplastic uptake in marine filter feeders impacting microbial transfer and organism health
- 16.15 CHRISTIAN DRERUP: Caustic flicker noise does not affect the hunting success and behaviour of cuttlefish
- 16.30 KAITLYN CLARK: Spatial variation in food utilization by Atlantic sea scallops (*Placopecten magellanicus*) using stable isotope analysis

^{13.00-14.00} Lunch break

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Poster presentations

CAVADINO I.C.N: Freshwater and terrestrial slug and snail species of potential threat to plant health in Britain

- YULIE FOKA-KAVALIERAKI: Cognitive enrichment suggestions for Octopus vulgaris in captivity
- VICTORIA GILLMAN: Integrating genomics and modelling to predict climate change response in the endangered freshwater pearl mussel (*Margaritifera margaritifera*)
- PARIN JIRAPATRASILP: Clarification on the name-bearing type designation of several cyclophorid land snail species by H. H. Godwin-Austen (1915).
- DANIELLE C. JORDAN: Deciphering calcium transport mechanisms in molluscan biomineralization using genome-editing.
- ZUZANNA KOWALESKA: Filter-feeders in "outside the box" strategies for water-borne disease control?
- LAURA E. MCBRIDE: Trophic ecology of *Moroteuthopsis ingens* from the Chatham Rise, Aotearoa New Zealand
- YUMI NAKADERA: Discovery and inheritance of a new shell polymorphism in the great pond snail *Lymnaea stagnalis*

AYANO OMURA: Ventral structure of Metasepia cuttlefish for walking on the sea floor

- KONSTANTINOS PANAGIOTIDISS: Quantitative gene expression analysis to shed light on the role of 5alpha-reductase in the development of a freshwater gastropod.
- LINA MARIE RAUBOLD: Less complex than expected? The controversial fate of four species from the genus *Phyllidia Cuvier*, 1797 (Mollusca, Gastropoda, Nudibranchia)
- MOLLY RIVERS: An evo-devo approach to invasive biology and resilience to climate change repaired shell in *Nucella lapillus* (Linnaeus, 1758)

JORUNE SAKALAUSKAITE: Molluscan shell bio - & archaeochromes: molecular archives for biomineralization and archaeology.

BO A. SCHOUTEN: An integrative taxonomic approach uncovers hidden diversity within the elusive *Peracle* genus (Pteropoda)

CORINNA SICKINGER: The microbiome of *Berghia stephanieae* (Valdés, 2005)

GIADA SPAGLIARDI: Species boundaries in the *Limacina* species complex

LUCY STEPHENSON: Equity, diversity, inclusion and accessibility in UK polar science and malacology

CHARITOS ZAPITIS: Oxygen consumption during digestion in *Anodonta anatina* and *Unio pictorum* in response to algal concentration

The President of the MSL Dr Jon Ablett welcomes participants (both in person and online) to the Forum



OLLUSCAN FORUM

Abstracts

Alphabetical by presenter

Seasonality infection rates of *Biomphalaria* (Gastropoda: Planorbidae) species found at the Great African Lakes in Uganda, East Africa

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Morphometric Analysis

A Canonical Variate Analysis plot of Landmark-based morphometric datasets of umbilical and apertural shell angles. Lake Victoria: (*B. choanomphala* | Two ecophenotypes)



The freshwater snail genus Biomphalaria is

the intermediate host of *Schistosoma mansoni*, the leading causative parasite of intestinal schistosomiasis. Identifying African *Biomphalaria* species using exclusively conchological characteristics is seen as unreliable, as many morphological features overlap between species. Similarly, the current phylogenetic structure of the African *Biomphalaria* species is still disputed, as many species are poorly differentiated from one another. Transmission rates of intestinal schistosomiasis are affected by many factors such as parasite-host compatibility and seasonality. This study investigated the morphological characteristics, the genetic diversity and the rates of *S. mansoni* infection present in the *Biomphalaria* species found at the shorelines of the Great African Lakes in Uganda. This was done by monthly collections of *Biomphalaria* from six sites along the Ugandan shorelines of Lake Albert (Bugoigo, Piida and Walukuba) and Lake Victoria (Bugoto, Bukoba and Lwanika) over the course of two years (2009-2010). *Biomphalaria* species collected were grouped together based on shell morphology and identified using rRNA 16S and mitochondrial COI genotyping, while the infection rate was measured using *S. mansoni* specific infection-detection primers. *Biomphalaria* infection rates were measured at a single point for each site, as well as for each wet and dry season that occurred over the course of the two-year period. We found (via 16S/COI genotyping) that Lake Albert had three species of *Biomphalaria* present (*B. pfeifferi, B. stanleyi and B. sudanica*), while only one species was present at Lake Victoria (*B. choanomphala*). All *Biomphalaria* species identified, exhibited unique shell morphological characteristics with minimal

overlap between species. Lake Albert had the highest mean infection rate of 12.5%, while Lake Victoria only had an infection rate of 6.7%. Of the species tested for infection, *B. stanleyi* had the highest rate of infection, followed by *B. sudanica*, then *B. pfeifferi* and lastly, *B. choanomphala*. When infection was measured for each season, infection was consistently higher in the wet seasons at both Lake Albert and Lake Victoria. When tested repeatedly over the two-year period, *B. pfeifferi* had the highest mean infection rate of 12.5%, followed by *B. sudanica* with 10.6% and *B. choanomphala* with 6.9%.



Freshwater and terrestrial slug and snail species of potential threat to plant health in Britain

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The non-marine molluscan fauna in Britain and Ireland contains a large proportion of established non-native species, with 80 out of 252 species (31.7%) considered non-native. The rate species are establishing in Britain appears to be increasing, with 23% of non-native terrestrial and freshwater molluscs added to the UK checklist since 2005. As the majority of terrestrial slug and snail species are polyphagous, they have the potential to pose a threat to plant health across a broad range of plant species. While many species of slug and snail pose a threat to plants though direct feeding damage, they can also act as vectors of plant pathogen transmission between plants, as well as being vectors of parasites and pathogens affecting humans and livestock. The globalisation of trade has allowed species of slug and snail to be transported from almost anywhere in the world to countries outside their natural range. The polyphagous nature of many species, combined with other life history traits, such as surviving long periods of aestivation, means that slug and snail species can be transported easily with many commodities, their associated conveyances, and packaging material. This deskbased study used available published data and literature to identify non-native species of slug and snail with high potential to arrive and possibly establish within Britain. Data on terrestrial and freshwater molluscs was extracted from the Global Register of Introduced and Invasive Species (GRIIS) country checklists to create ranked lists of the species commonly establishing globally. The Köppen-Geiger climate classification was used to re-examine the GRIIS dataset and create a frequency list of species introduced to countries with similar climates that are not established in Britain. This horizon scanning exercise yielded a total of 91 species of non-marine molluscs not yet present, but with the potential to be introduced to Britain.

Spatial variation in food utilization by Atlantic Sea Scallops (*Placopecten mag-ellanicus*) using stable isotope analysis

Kaitlyn R. Clark, Roger L. Mann & David B. Rudders

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The Atlantic sea scallop supports the largest wild scallop fishery in the world, with a range extending from Cape Hatteras to Labrador and major fisheries in the Mid-Atlantic Bight, Georges

Bank, Gulf of Maine, and Canadian Maritimes. Across the U.S. portion of the resource, growth, yield, and product quality vary widely, and food availability is being considered as a potential factor driving observed differences. Stable isotoperatios of carbon and nitrogen provide a useful metric for an initial resource-wide investigation of food resource utilization, as benthic producers are enriched in ¹³C compared to pelagic producers by an average of $\sim 7\%_0$ and anthropogenic wastewaters typically elevate ¹⁵N which then propagates through the food system. In 2021 and 2022, 454 sea scallop adductor muscle samples were collected from the Mid-Atlantic Bight and Georges Bank, with additional sampling by collaborates in the Gulf of Maine and Canadian Maritimes in 2022. Preliminary results from the first 129 scallop samples suggest that δ^{15} N generally follows the anticipated pattern, with elevated ¹⁵N in sea scallops collected from more near-shore stations and no difference between scallops collected from the Mid-Atlantic Bight and Georges Bank. However, preliminary δ^{13} C results show the opposite pattern to that predicted, with elevated ¹³C (increased trophic reliance on benthic

organic matter) in sea scallops collected at stations further offshore and a marked increase in ¹³C in Mid-Atlantic Bight sea scallops compared to Georges Bank. These trends will be investigated further as remaining samples are processed and generalized linear mixed models are developed to investigate the effects of latitude, depth, shell height, sex, reproductive stage, and product quality. Increasingly, habitat suitability is being considered as a driver of varying outcomes in the spatially-explicit management and assessment of the sea scallop resource and represents a key knowledge gap when considering how its productivity may change due to climate change and offshore wind development. This work will also help to characterize the relative importance of benthic primary production to a continental shelf bivalve, contributing to the burgeoning discussion of the food resources utilized by commercially important bivalves in the study region and on continental shelves globally.



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Profiling disease and multi-trophic community dynamics through eDNA at a site of native oyster reintroduction in the Solent, UK

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Oyster beds and oyster reef habitats are considered amongst the most threatened marine habitats globally, with an estimated 85% lost since the mid- 20th century as a result of coastal degradation, pollution, overfishing and disease outbreaks. One disease, bonamiosis caused by haplosporidian microeukaryotes, *Bonamiaostrea* and *B.exitiosa*, causes catastrophic mortalities and is estimated to be present throughout the natural range of the European flat oyster (*Ostrea edulis*). There is a growing effort now underway in Europe to restore populations of native flat oysters and the services they provide as ecosystem engineers, including enhancing biodiversity, acting as a natural erosion defence, improving water quality through filter-feeding behaviour, and as a food source. One such restoration site is the Solent, UK, where millions of oysters are being released, with the area closed to commercial fishing. At this site I will carry out two linked projects. The first examines the Solent as a *Bonamia*-positive area; for native oysters to be restored there, it is imperative that outbreaks of bonamiosis are controlled. Multiple co-inhabiting macroinvertebrate species could act as carriers of *Bonamia*, however, little is known about the occurrence or life history outside of the main host, particularly in the UK. This project aims to examine a range of invertebrate taxa associated with the native oyster, as well as plankton and environmental

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compartments for presence of *Bonamia* through highly sensitive and specific molecular screening. This will increase our understanding of disease transmission, routes of infection and life cycle stages. In a parallel study, I will investigate the impact of oyster reintroduction on the wider ecosystem by profiling the community change over time as the oyster reefs become established, using environmental DNA (eDNA). Environmental samples will be analysed across trophic levels by harnessing the DNA signal from micro- and macro- organisms present in environmental samples with metabarcoding and metagenomic analysis.

Population dynamics and reproductive cycle of the invasive Asian date mussel in the UK and the potential for future spread

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The Asian date mussel (*Arcuatula senhousia*) is one of the most globally widespread non-native marine species. Throughout much of its introduced range it is recorded as invasive, with the ability to form dense mussel mats and alter key ecosystem functions. *A. senhousia* recently arrived in the UK (first recorded in 2011) extending the known intro-



duced range of self-sustaining populations in Europe further north. However, there are significant knowledge gaps regarding A. senhousia's biology and ecology, and habitat suitability, in the UK. The aims of this study were to determine the population dynamics and reproductive cycle of A. senhousia and to understand its potential current and future distribution in the UK and across the globe. To address this, subtidal dredge surveys of an established A. senhousia population were undertaken for one year in an estuary on the South coast of England. Reproductive analyses were performed using histology and the gonadosomatic index, and cohort analysis was undertaken using shell length-frequency data. Additionally, present day (years 2010-14) and future (2090-2100) global species distribution models were created by in-putting presence data, sea surface temperature and salinity into the Maxent algorithm. The population consisted of two cohorts throughout much of the year, with individuals growing at approximately 2 mm per month, reaching the size of sexual maturity within 6-10 months. The main spawning period was from June to October, potentially followed by a second shorter spawning period from November to January, resulting in an extended larval recruitment (settlement) phase. The reproduction period is probably to overlap with other keystone bivalves, creating competition for substrate. More specifically, the spawning period overlaps with Mytilus edulis, posing a possible hybridisation threat and impact on aquaculture. According to the species distribution model, there will be a future shift of habitat suitability north and south of the globe, resulting in new areas that will be at risk from invasion, such as the East coast of the USA and the Black Sea. Furthermore, habitat suitability in the UK and much of Northern Europe is suboptimal but will increase in the future, highlighting the importance of continued monitoring and risk assessment.

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Caustic flicker noise does not affect the hunting success and behaviour of cuttlefish

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Many animals rely on their visual systems to perceive, localise or discriminate information from their habitat. However, information can be difficult to detect when other environmental stimuli (so- called 'visual noise') interfere with an animal's visual system. For example, an ubiquitous



form of visual noise in aquatic environments is caustic flicker, which comprises moving light patterns caused by the refraction of light through surface waves. Recent work on different fish species has shown that their ability to visually detect prey is impaired by caustic flicker. The impacts of caustics on the ability of non-vertebrates to target prey, however, remains untested. In the present study, we ask whether the hunting success of the European cuttlefish *Sepia officinalis* is impaired by the presence of caustic flicker. To do this, we introduced individuals of both *S. officinalis* and a common prey item, the brown shrimp *Crangon crangon*, into an experimental arena bathed with different computer- generated playbacks of caustic flicker. Playbacks varied in both the spatial (definition) and temporal (speed) components of caustic flicker. Regardless of the intensity of spatial or temporal component of the caustic flicker playbacks, neither the prey- detection latency nor the prey-capture time was significantly prolonged, indicating that caustic flicker, unlike in fishes, does not affect the hunting success of cuttlefish. We then tested whether cuttlefish display any behavioural adaptations to mitigate the effect of caustic flicker when hunting their prey. However, neither the approach speed and number of movement bouts towards the prey, nor the attack distance or angle changed with caustic flicker. As we can therefore exclude that cuttlefish adapt their behaviour to mitigate the effect of caustic noise, we discuss potential physiological mechanisms of the cuttlefish visual system that may provide a way to eliminate any potential impacts that such noise could have on their visual perception.

The plastic trojan horse: biofilms increase microplastic uptake in marine filter feeders impacting microbial transfer and organism health

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The ingestion of microplastics by biota poses a risk to wildlife and ecological processes, also having further impacts on food security, human health and socio- economic wellbeing when accumulated in aquatic organisms of commercial interest. However, the majority of studies to date investigating the impacts of microplastics ingestion by aquatic organisms have used virgin plastic particles, which do not reflect environmental microplastics. Once in the aquatic environment, microbeads are rapidly colonised by a wide variety of microorganisms. Ignoring the presence of biofilms may lead to underestimation of the real risks of microplastic pollution. The present study compared the uptake and bioaccumulation of virgin and *Escherichia coli* coated microbeads by the European flat oyster *Ostrea edulis*, while also assessing the physiological responses of oysters to both types of microplastics. The amount of microbeads ingested by oysters exposed to *E. coli* coated microplastics was found to be significantly higher than the ones exposed to virgin microplastics, suggesting that biofilms can make the surface of microplastics more attractive to benthic filter feeders. Contrary to virgin microplastics, which did not induce any physiological responses, the exposure to *E. coli* coated microplastics had clear effects on oyster respiration, with oxygen consumption and respiration rate increasing significantly over time. This may indicate an

immune response of oysters to either the presence of *E. coli* or the higher microbeads uptake. Less than 0.5% of the total amount of administered microbeads were retained by all oysters, suggesting a limited residence time within the organisms. However, whilst further research is needed to understand microplastic bioaccumulation and biomagnification pathways, microorganisms assimilated by the ingestion of coated microplastics may be transferred to higher trophic levels. The capacity to carry pathogens and expose a wide range of organisms to them means microplastics may have a crucial role as vectors for disease.



Cognitive enrichment suggestions for Octopus vulgaris in captivity

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Cephalopods have long been considered by experts to be sentient beings with cognitive abilities that can match those of many vertebrate species. Therefore, for cephalopods in captivity, whether they live in public aquaria for display purposes or are kept in scientific laboratories for research, there has always been a need for quantitative as well as qualitative knowledge of specific techniques that enrich the environment of these animals. Octopuses, in particular, seem to exhibit individual variations of personality and to require carefully designed cognitive and sensory stimulation in order to advance their healthy development and well-being. The provision of various puzzles, toys, materials for den construction (e.g., shelters, caves, tunnels), and opportunities for basic hunting activities, are considered to be appropriate stimuli, that enhance their problem solving, memory and learningabilities.We currently investigate which type of "toys" are more stimulating for Octopus vulgaris, by presenting our female, adult octopus with three novel objects. These simple objects are similar in size, colour and texture but differ in complexity, as per the number of moveable parts they have. Each toy will be alternatively presented five times, once every day, after feeding time, and we will measure the mean handling time of each toy. We expect that the amount of time during which the octopus engages with and explores each novel object should indicate the interest it shows in it. We also expect that more complex objects will challenge the octopus to spend more time exploring them. We anticipate our results will shed more light on the discussion about cephalopods' sentience and intelligence, as well as offering aquarists that accommodate octopuses further means for providing a cognitively rich environment to the captive animals, that will in turn enhance their health and welfare.

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The role of invasive bivalves on pathogen dynamics of invaded ecosystems

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Invasive non-native species have the potential to alter parasite dynamics within their invaded ecosystem. They can act as reservoirs causing parasite spillover and spillback, as well as co-transporting new and emerging pathogens to their invaded range. Some bivalves can act as so-called ecosystem engineers, attaining high densities and having a significant effect on aquatic ecosystems through filtration, bioturbation and excretion. Despite this, little is known about the effects on parasite dynamics of invasive bivalves and the pathogens they may be co-transporting. The potential effects invasive non-native bivalves can have on their invaded range are discussed, as well as two ongoing research studies from the UK.

The first study site is the freshwater upper tidal Thames at Richmond, where there are three established invasive bivalves; the Asian clam (*Corbicula fluminea*), zebra mussel (*Dreissena polymorpha*) and quagga mussel (*D. bugensis*), as well as declining populations of native mussels, namely the depressed river mussel, (*Pseudanodonta complanata*), duck mussel (*Anodonta anatina*), painter's mussel (*Unio pictorum*) and the swollen river mussel (*U. tumidus*). This site provides an ideal opportunity to compare parasite burdens between invasive and native bivalves, as well as increasing knowledge of pathogen and symbionts of freshwater bivalves, which are currently under-reported in the literature. The second project involves the marine Asian date mussel (*Arcuatula senhousia*), a recent invader that has formed self-sustaining populations, first recorded in the Solent in 2011 but not reported as "present" in scientific literature until 2018. Invasive elsewhere in Europe, they have been identified as a potential threat to functionally important habitats, fisheries and aquaculture in the UK. TheLittle is known about the pathogens they are associated with, both in the native and invaded range. Therefore a pathogen survey of the Solent population is being undertaken to inform risk assessments for this invasive bivalve in UK waters.



Integrating genomics and modelling to predict climate change response in the endangered freshwater pearl mussel (*Margaritifera margaritifera*)

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Given the rapid pace of climate change, there is an urgent need to understand adaptive capacity and how threatened species will respond to changes in their environment. Whole genome sequencing offers an opportunity to test for adaptation without prior functional knowledge, with genome scans and association analyses enabling the detection of adaptive variants across climate gradients. By integrating population genomics with ecological modelling, we can determine the mismatch between current adaptive variation and future climate, deemed 'genomic offset'. The freshwater pearlmussel (*Margaritifera margaritifera*) is a critically endangered, keystone species and while its decline has been linked to climate change impacts, this has never been investigated with genomic data. This project will use low-coverage, whole-genome sequencing data of mussels from 30 Scottish rivers to resolve fine-scale population structure, investigate climate-associated genomic variation along environmental gradients and identify populations at risk of loss under future climate change scenarios.



Cones and cobwebs: newly discovered cobweb-like secretion behaviour of *Conus geographus*

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Conus geographus is a specialized nocturnal cone snail, belonging to class Mollusca which has evolved the ability to engulf several target fish at once. *In-situ* observation of the species showed that cobweb like projections were utilized by the cone snail in order to descend from a rock. This study focusses on determining the rationale and to characterize this newly discovered behaviour as well as to identify the factors triggering the behaviour that distinguishes it from the other known behaviour of the species. The production of the cobweb-like secretions was recorded at night for comparison with normal feeding behaviour. The observations were then compared with previously published data and data from arachnids to determine similarities and to investigate their adaptive and evolutionary relationships. Comparisons revealed that the first factor was movement, such as the ability of the *C. geographus* to use cobweb-like secretions for vertical movement, similar to the secretions used by abseiling spiders of Theridiidae and Araneidae. Next was defense, whereby the use of the siphon was compared with spiders that have trichobothria which are both used for mechanoreception. The lastconsidered factor was an additional feeding strategy, wherein the *C. geographus* wrapped an a quarium aerator with its secretions, similar to the entangling mechanism for feeding used by certain species of spiders. The results showed similarities between the behaviours of cone snail and spiders , suggesting convergent evolution.

A high density linkage and binary trait map for shell-colour phenotypes in the grove snail (*Cepaea nemoralis*)

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The shell of the land snail *Cepaea nemoralis* has highly polymorphic colour and banding, varying between brown, pink and yellow, with anywhere between zero and five bands. Previous classical genetic studies have identified around nine loci controlling variation in colour and banding patterns, of which five are physically linked and inherited together as a so-called "supergene". The precise location and characteristics of the genes involved in the colour/ banding patterns are still unknown. As the first step to characterising the supergene, we have created a linkage map from pink x yellow cross and 79 offspring, using this linkage map to perform gene trait association for the colour loci. Markers were called for all individuals using a newly assembled reference genome. The final linkage map contains 216,411 markers representing the 3.5 Gb *C. nemoralis* genome, and consists of 22 linkage groups, corresponding to the haploid chromosome number of *C. nemoralis*. Gene-trait association analysis have localised the gene responsible for shell coloration to a 2 cM section in the middle of chromosome 11. Our results provide invaluable insight into the location of the colour locus in *Cepaea nemoralis*, an important step towards identifying the component parts and the evolutionary origins of the supergene.

Deciphering calcium transport mechanisms in molluscan biomineralization using genome- editing

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Biomineralization is the process that forms minerals on the interior of the organism (endoskeleton) or exterior of the organism (exoskeleton). Molluscs owe part of their evolutionary success to their ability to biomineralize, but little is known about the mechanisms for calcium transport to the shell secretion site in the mantle. Two possible mechanisms for calcium transport are supported in literature: paracellular (between cells) and transcellular (through cells). Prior research indicates that molluscs probably use a combination of both paracellular and transcellular pathways to transport calcium for shell deposition. Most of the evidence for calcium transport pathways however, come from a combination of pharmacological perturbation and microscopy but understanding of the genes regulating calcium transport pathways is less complete. We seek to understand the genes regulating calcium transport in molluscs using the slipper limpet, Crepidula fornicata, as a model organism. C. fornicata was chosen as a model for this study due to its long history as a molluscan model for developmental studies. RNA-sequencing data gathered from all developmental stages of *C. fornicata* will be screened for differentially expressed genes, with



a focus on shell developmental stages. *In-situ* hybridization (ISH) and hybridization chain reaction (HCR) will serve as a spatial analysis to confirm the precise cellular location of candidate genes. Once expression of the candidate genes has been confirmed in the shell gland or developing mantle tissue, CRISPR-cas9 will be used to knock-out the candidate genes via

microinjection and study the resulting phenotype in relation to calcium transport.



Clarification on the name-bearing type designation of several cyclophorid land snail species by H. H. Godwin-Austen (1915)

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The type series boundary and the name-bearing type designation of animal taxa are important in stabilizing the usage of each nominal name in zoological nomenclature. However, in some cases the type series boundary is not explicit in the original description, leading to some conflicts of subsequent name-bearing type designations. One example is the cyclophorid taxa originally described in the "Zoological Results of the Abor Expedition" by Godwin-Austen (1915). The original descriptions contain inconsistent patterns of the "Type" designation and specimen lot numbers corresponding to the registration numbers of the Natural History Museum, London (NHMUK) and the National Zoological Collection of the Zoological Survey of India (NZSI). The problem arises because the word "Type" was used only in the beginning of the first paragraph, but the original descriptions of some taxa contained more than one specimen lot number, either separated by a semicolon in the same paragraph or appearing in subsequent paragraphs. In addition, for some taxa Godwin-Austen (1915) provided figures of more than one specimen from different specimen lots, but associated the word "Type" in the plate caption to the figures of one specimen only. Consequently, the previous interpretation of Godwin-Austen's type series boundaries and the designation of the name- bearing type(s) is often contentious. In this study we clarify the boundaries of the type series and the name-bearing type designation of each cyclophorid taxon originally described by Godwin-Austen (1915) based on an interpretation that complies with the ICZN.We presume that the conflict between different interpretations of type series boundaries is rooted in the ambiguous usage of the "type" terminology in the 19th century, either as "hypodigm" or "onomatophore". We also posit that Godwin-Austen (1915) assigned specimens to the original hypodigm and onomatophore differently, illustrated by his writing structure of the original descriptions, plate captions, and the labels of the specimens.



Body size and abundance are decoupled from species richness in Australian marine bivalves

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The "more individuals hypothesis" suggests that increasing species abundances lead to increases in diversity. Abundance, biomass distributions and diversity do vary with latitude in several taxonomic groups. However, support for this hypothesis has otherwise been mixed. In this paper, we investigate latitudinal changes in all three variables for marine bivalves along the eastern coastline of Australia. We used a large, uniformly sampled field dataset of 5604 shells representing 156 species that spans 20° of latitude and crosses a major biogeographic transition. For each of 16 field sites, 10 quadrats were randomly placed and completely sampled, making it possible to quantify absolute abundance. Species richness was calculated using a new estimator based on the log series distribution. Body size was computed as the geometric mean of length and width. Despite uncovering a strong latitudinal gradient in species richness, we found no significant gradient in body size at any taxonomic level. This result contrasts with previous work, which found familylevel trends in bivalve size but was done at a larger spatial scale and therefore did not pertain to individual communities. Environmental variables do correlate with both abundance and richness; however, they are not related with each other. Because we find no gradient in abundance and no relationship between abundance and richness, we reject the "more individuals hypothesis" for our system. Instead, latitudinal richness trends in coastal Australia may result from an environmental gradient in dispersal constraint.



Filter-feeders in "outside the box" strategies for water-borne disease control?

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Water bodies are the source of numerous parasites and pathogens that have developed different ways of transmitting to their hosts. According to the WHO, water-borne diseases are a major global health threat, especially in developing countries. It should also be remembered that this problem also affects pets and farm animals, which can be both intermediate and final hosts. Numerous methods of prevention against water-borne diseases appear to be short-term or even harmful to the environment. "Outside the box" strategies such as repellants, traps, and natural enemies have generated intense debate recently. Among the natural enemies, we can mention the non-host species acting as physical barriers, predation, or decoys attracting the parasites. It seems that the importance of non-host filter-feeders, including mussels, is often overlooked in the discussions about the possibility of disrupting the transmission of free-living infectious agents despite their high potential. The main feature indicating their usefulness is that mussel filtration pumps are not limited by the nutritional needs of the individual. The aim of this investigation is to review literature reports on the possibility of using mussels in the fight against parasites and pathogens of vertebrates, including humans. Among others, two common species in Europe, the native duck mussel, Anodonta anatina (Linnaeus, 1758) (Unionidae), and the non-native zebra mussel, Dreissena polymorpha (Pallas, 1771) (Dreissenidae), will be compared as potential diluters of water-borne diseases. It is likely that the dilution effect caused by non-host species, including mussels, may be a good tool in "outside the box" strategies for water-borne disease control, but each parasite/pathogen-host-diluter system requires individual investigation, interpretation and careful cost-benefit analysis.

Relationship between recent and Holocene mollusc fauna diversity of the Veľká Fatra Mountains

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Quaternary molluscs assemblages are one of the most important sources of information used for palaeoecology and biogeography reconstructions, yet little attention has been paid to the informative value of quaternary profiles on a landscape spatial scale. In the area of Veľká Fatra Mts., a large number of existing records concerning both recent and quaternaryland snails enable us to compare Holocene and recent species diversity to estimate how many profiles are needed to evaluate species richness of such geomorphologically diverse area. In this study, available data are supplemented with samples from additional recent sites and quantitative analysis of material from quaternary profiles Stankovany and Skamenelá skala. Samples from seven Holocene profiles from the Veľká Fatra Mts. covered more than 85 % of recent land snails diversity. On the other hand, only about 50 % of recent land snail species were recorded in a single profile, thus highlighting the importance of multiple profiles for evaluation in palaeoecological studies.

Ocxplants: a novel technique to study octopus neurogenesis ex vivo

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Vertebrate nervous systems have been used quite often as a reference for correlates of intelligence, complex behaviour and high cognitive abilities. However, cephalopods diverged 580 million years ago from the vertebrate lineage and thus give important insights into the evolution and development of complex nervous systems. Known for their stunning behavioural repertoire, like tool-manipulating skills and millisecond camouflage, octopuses have evolved not only an interesting life history but also an underlying complex nervous system. Thus, we use *Octopus vulgaris* to investigate how complex brains develop and might have evolved. Previously, we described an embryonic neurogenic area surrounding the octopus eyes, termed lateral lips, expressing evolutionary conserved neurogenic transcription factors. Here, neurons originate and migrate into the brain, similar to vertebrate-like mechanisms seen during tangential or neural crest cell migration. In order to study the migration behaviour and influences of extrinsic factors on spatial and temporal patterning of lateral lipneurogenic cells, we established ocxplants, the first invertebrate neurogenic zone explants of *Octopus vulgaris.* We found cells in the explant that are neurogenic, based on expression of the achaete-scute orthologue Ov-ascl-1, an evolutionary conserved transcription factor found in almost all metazoan clades. Moreover, these neurogenic cells proliferate, possibly giving rise to cells migrating away from the explant. Strikingly, migratory cells are seen to proliferate and divide in the explant's periphery. Taken together, we can use ocxplants to study octopus neurogenesis, also by using evolutionary conserved marker genes



Trophic ecology of Moroteuthopsis ingens from the Chatham Rise, Aotearoa, New Zealand

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Cephalopods form important components of marine trophic systems worldwide, including those in the South Pacific. *Moroteuthopsis ingens* (Onychoteuthidae) is one of the most abundant deep-sea squids in the Aotearoa New Zealand region and is preyed upon by predators such as the sperm whale and orange roughy. However, despite many publications on the diet of *M. ingens*, knowledge on its feeding ecology remains limited. In this study, we analysed the prey of *M. ingens* from the Chatham Rise (an ecologically and economically important region east of Te Waipounamu/New Zealand's South Island) using DNA barcoding and otolith identification. Lanternfishes (*Myctophidae*) were the most frequently encountered prey item, but other teleost species, cephalopods and crustacean fragments were also found, indicating opportunistic and probable cannibalistic feeding behaviour. Five fish species (including a possibly undescribed species of *Gymnoscopelus*) and *Bathyteuthis abyssicola* are reported as prey items of *M. ingens* for the first time. *Moroteuthopsis ingens* appears to be a component of several dynamic food chains and probably plays an important role in the transfer of carbon throughout marine environments in the Southern Hemisphere.

Phylogenetic context of a deep-sea clam (Bivalvia: Vesicomyidae) revealed by ancient DNA from 1,500 -year-old shells

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Ancient DNA (aDNA) from mollusc shells has been recognized as an archive of historical biodiversity and evolution, but such information is currently lacking for mollusc shells from the deep ocean, especially those deposited in acidic chemosynthetic environments that are probably not ideal for long- term DNA preservation. Here, we report the recovery of mitochondrial and nuclear gene markers by Illumina sequencing of aDNA from three shells of *Archivesica nanshaensis* – a cold-seep vesicomyid clam previously known only from a pair of empty shells collected from 2,626 m water depth in the South China Sea. Our carbon¹⁴ analysis shows that the shells collected from 3,003 m water depth are ~1,500 years old, and sequence analysis indicates that *A. nanshaensis* is distinct from known vesicomyids with available molecular evidence, and it is sister to the congener *A. marissinica* with 3.4% K2P distance in mitochondrial cytochrome coxidase I gene. Fossil-calibrated dating indicates that *A. nanshaensis* and *A. marissinica* diverged approximately 8.5 Mya (4.8–13.1 Mya, 95% HPD) in the middle Miocene. Our study demonstrates the potential of high-throughput sequencing of aDNA in unlocking the evolution and historical diversification of deep-sea molluscs, especially for those species that are described solely on the basis of empty shells.



Reducing successful shipworm larval settlement on wood that has been modified using furfurylation

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Shipworms are Teredinid bivalves that have a highly modified shell for boring into wood and an elongated, vermiform shape. Teredinids are marine wood-borers, using timber as both shelter and a source of food. Wooden structures in the sea, such as piers and sea defences, can be severely damaged by these borers, costing billions per year for maintenance and replacement. Traditionally, broad-spectrum biocides have been used to protect timber, however, treatments like chromated copper arsenate and creosote are now restricted by legislation. In response, alternative methods to reduce marine borer attack have been explored, including chemical wood modifications. Furfurylation is a modification technique that uses furfuryl alcohol, derived from agricultural waste and high temperatures, for polymerisation. This technique is nonbiocidal and has been well proven for uses in terrestrial environments. However, products are continuously being tested for protecting wood against wood-borers. Changes to the exact mixes used, retention levels and curing procedures affect the service life of these materials so testing is performed to the European standard EN275. This standard however, currently involves only long-term marine field testing where products are rated based on the extent of damage by mature shipworm. More rapid testing provides a quicker insight into the efficacy of novel treatments and allows for flexibility to adjust mixes and procedures. Here, we evaluate small wood blocks after 5 and 10 weeks of deployment in Venice lagoon, where the most common species are Lyrodus pedicellatus and Teredo navalis. Under a stereomicroscope, hemispherical bore holes left by larval settlement attempts were counted and any successful metamorphosis was noted. After 5 weeks, control wood had a higher number of attempts but by 10 weeks, modified wood had significantly more attempts, as by then, successful settlement (metamorphosis) on the control was more common than failure. When compared to the longer-term trials as described in EN275, after several years of exposure, shipworm recruitment begins to increase on these treated woods and adults can be seen by x-ray imaging. Being able to disrupt settlement at this early stage of the life cycle will reduce recruitment and by consequence, damage by adult shipworm.

Discovery and inheritance of a new shell polymorphism in the great pond snail *Lymnaea stagnalis*

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Colour polymorphism is a classic study system for evolutionary genetics. One of the most colour-polymorphic animal taxa is molluscs, but the investigation to elucidate the genetic basis of determining shell colour is often hindered by their life history and limited availability of genetic resources. Here we propose a new model system to help expand the understanding of the genetic basis of shell colour polymorphisms in molluscs. We report on the discovery of shell colour polymorphism in a much-used model species, the great pond snail *Lymnaea stagnalis*. While the shell colour of this species is usually beige, some of the individuals that we collected from a Greek population showed a distinct red shell colour, which we nicknamed Ginger. In order to evaluate whether this shell colour polymorphism is useful for genomic research, we investigated its inheritance mode. In addition, we compared crucial life history traits (e.g., reproduction, behaviour) between Ginger and wild type individuals of the Greek parent population, to see if Gingers have any evolutionary (dis)advantages. We find that the life history traits of Gingers are similar to wild types, and that the mode of inheritance of the Ginger phenotype fits simple, single-locus Mendelian inheritance. We conclude that the relative simplicity of this polymorphism has the potential to provide a deeper understanding of the genetic basis of shell colour polymorphism and its evolutionary origin.

Ventral structure of Metasepia cuttlefish for walking on the sea floor

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The locomotion strategy of cephalopods is one of the important factors influencing their diversity in oceanic environments. Amongst cephalopods, *Metasepia* cuttlefish have a unique locomotion mode. They prefer walking, which is called ambling on the seafloor, as opposed to swimming. Their ambling manner resembles quadruped walking. They use their ventral arms (arm IV) as front legs and a pair of ambulatory flaps, which are along the margin of the ventrolateral mantle, as hind legs. For the walking, some mechanisms are needed to avoid slipping in the aquatic environment. However, the mechanism is not well understood. Here, to determine the structure for the walking, we observed the morphology of the ambulatory flaps and ventral arms and ambling behaviour of *Metasepia tullbergi*. We found that the ambulatory flaps and ventral side of the arm IV had structures to increase friction on the substrata. Morphological observations indicated that the surface of the ambulatory flap and the ventral side of arm IV had a rough structure. Histologically, the epithelium of the ambulatory flaps and the ventral side of the arm IV had neutral hexose sugar and acidic mucoprotein secreting cells, similar to the adhesive areas of other cuttlefish. Behavioural observations showed that sand (bottom sediment) with mucus was attached to the ambulatory flaps and the ventral side of arm IV, indicating that adhesive mechanisms are at play on the ventral surface. These rough surface structures and adhesive mucus may increase friction with the substratum. Our results improve the understanding of cephalopod locomotion strategies in distinct environments.



Quantitative gene expression analysis to shed light on the role of 5-alpha-reductase in the development of a freshwater gastropod

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In vertebrates, steroidogenic enzymes 5-alpha reductases (5α R) convert testosterone to its more potent 5α dihydrotestosterone. Despite a growing body of evidence indicating the absence of a nuclear androgen receptor and the inability of molluscs to biosynthesise testosterone *de novo*, homologues of 5-alpha reductase genes (5α R1 & 5α R2) have been identified in molluscan genomes. Consequently, the function of 5α R in molluscan tissues remains unknown. Pharmaceutical disruption of 5α R enzymes in the freshwater gastropod *Biomphalaria glabrata* was shown to disrupt normal embryo development causing the emergence of a "banana-shaped" shell. Expression of 5α R transcripts in the mantle tissues of *Biomphalaria glabrata* have also suggested a potential link with molluscan shell formation.

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These preliminary quantification data have confirmed the expression of both 5α R1 and 5α R2 transcripts in day 3-5 post oviposition embryos and the albumen gland. RNA isolation from day 1 and day 2 post-oviposition embryos is currently being optimised to confirm 5α R1 and 5α R2 expression in earlier stages of development. The data will be normalised against a set of endogenous control genes which are currently being tested, in the hopes of correcting for sample variation so that accurate comparison between expression levels and developmental stages can be achieved. Investigating those novel patterns of expression will shed some light on the role of 5α -reductases in gastropod snails and expand our understanding of molluscan endocrinology. Consequently, gene expression data will help to elucidate the link between molluscan endocrine system and shell formation. The optimisation of this assay will thus allow further investigation into the role of other gene targets involved in early gastropod development.



Less complex than expected? The controversial fate of four species from the genus *Phyllidia Cuvier* 1797 (Mollusca, Gastropoda, Nudibranchia)

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The genus *Phyllidia* Cuvier, 1797 (Mollusca, Gastropoda, Nudibranchia) comprises 29 accepted species and is the largest and most widespread genus within the Phyllidiidae Rafinesque, 1814. While these colourful and conspicuous nudibranchs have been studied for 225 years, the taxonomic order within this genus is still a matter of debate. As several species of the genus *Phyllidia* are subjects of pharmaceutical studies where their toxins are evaluated for pharmacological usability, knowledge of the evolutionary relationships within this genus and a coherent taxonomy of its species is crucial. A complex consisting of yellow species with a black and white pattern including *Phyllidia* ocellata Cuvier, 1804 as the centre of the complex, as well as the recently published *Phyllidia* cf. babai, *Phyllidia* multituberculata (Boettger 1918), *Phyllidia* undula (Yonow, 1986) and various undescribed species have sparked a decade-old but still unresolved discussion on the possible synonymisation of these species with *Phyllidia* ocellata. In a new study we want to shed light on the case of the *Phyllidia* ocellata complex using molecular as well as morphological data, trying to resolve whether these species remain to be separate described species or if they can, in fact, be synonymized as *Phyllidia* ocellata. In addition to the impact of this work on our understanding of the taxonomy and evolution of this genus, this species complex might be an interesting case of mimicry in Nudibranchia.



An evo-devo approach to invasive biology and resilience to climate change

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Mollusc shells have hugely diverse morphologies, despite being deeply homologous structures. The mechanisms controlling molluscan shell development, and thus the morphological evolution of shells, are still not well understood. Shell matrix proteins (SMPs) have been identified and genes that are expressed in the developing shell gland and adult mantle are known but no complete signalling pathway or gene regulatory network has been identified. Crepidula comprise a genus of intertidal gastropods that are well suited for developmental studies because their embryos are large and robust enough to be easily used for microinjection, they produce large broods, their embryos are accessible, they are easy to maintain in laboratory conditions, and there are good resources and knowledge available on their development (mostly for Crepidula fornicata). The study outlined here will use four closely related species of Crepidula (C. fornicata, C. atrasolea, C. plana and C. convexa) to investigate evolutionary differences in shell development, adult shell morphology and resilience to climate change. Studies into the evolution of shell development have found SMPs to rapidly evolve and thus be highly lineage specific, however, these studies have mainly focussed on distantly related species. Closely related species present an opportunity to better understand the microevolution of developmental shell genes and proteins by looking at more recent evolutionary differences. Stage matched RNA sequencing data across the development of the four species will be used to screen for genes differentially expressed during shell development. In situ hybridisations (ISHs) will be used to compare spatial expression of targeted shell development genes in the four species, to understand how the differential expression of these genes contribute to the variations in shell morphology seen across these four species. ISHs will also help clarify how these evolutionary differences in morphology contribute to discrepancies in climate change resilience between species. From this work we hope to begin to illuminate the evolutionary mechanisms involved in molluscan shell development and morphology, identify the level of conservation of these shell development mechanisms and to determine any phenotypic connotations of these findings.

Mollusc shell bio- & archaeochromes: molecular archives for biomineralization and archaeology

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Molluscs adorn their shells with a diversity of colours and patterns which have been highly appreciated since ancient times. Shell biochromes (pigments) encode important biological information which may play a role in immunity, shell strengthening, protection from thermal stress and UV radiation. They are also extremely durable in time - pigments can be found in fossil shells dating to thousands or millions of years. Could shell biochromes be among the most promising ancient biomolecules? Despite the great diversity and complexity of shell colours, there is limited understanding of shell pigmentation among many molluscan systems. Therefore, our knowledge how biochromes are mineralised (not to mention how they preserve) remains patchy. This research project on molluscan shell bio- & ancient biochromes (archaeochromes) is funded by an EMBO postdoctoral fellowship and launched recently at the Life Sciences Centre, Vilnius University (Lithuania). The project aims to investigate the colours of Littorina fabalis shells, commonly known as the flat periwinkles, which display colour polymorphism and are abundant in archaeological record. Littorina shells were widely used by prehistoric populations as symbolic objects and jewellery items. In fact, the colours may have had a special meaning in transmitting social or cultural messages. To study shell pigments, I will employ cutting-edge 'ShellOmic' techniques - transcriptomics and proteomics, coupled with the first application of CRISPR-Cas9 gene editing tools to elucidate the chemical nature of shell biochromes and associated proteins. If successful, gene editing will help to verify genes that are involved in shell coloration and perhaps, biomineralisation. Finally, the project will employ palaeoproteomics, the analysis of ancient proteins by mass spectrometric techniques, to investigate the preservation potential of archaeochromes. In the future, we could use these as biomolecular colour markers to study archaeological shells.

Integrative taxonomic approach uncovers hidden diversity within the elusive *Peracle* genus (Pteropoda)

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Pteropods are a group of holoplanktonic gastropods which are regarded as bioindicators of the effects of ocean acidification because of their delicate aragonite shells. However, identification of species based on their shell morphology alone can be problematic, particularly for lesser-known groups such as the deeper dwelling *Peracle* genus (Pseudothecosomata). Most species belonging to this genus are characterised by unique calcareous reticulate mesh patterns on the top coil of their shell, but their taxonomy is not well-resolved. The *Peracle* genus is circumglobally distributed. It can be locally abundant but it has been largely overlooked in ocean acidification research and is excluded from e.g. global estimates of CaCO₃ export to the deep sea. Currently, eight *Peracle* species are described across all oceans (World Register of Marine Species). We applied an integrative approach combining state-of-the-art imaging (including SEM, Micro-CT) and DNA barcoding (CO1, 28S) to assess species boundaries in 194 *Peracle* specienens sampled from the Atlantic and Pacific Oceans. Preliminary phylogenetic analyses uncovered multiple evolutionary independent groups, some of which could not be linked to existing species descriptions. However, most groups could be distinguished by distinctive shell characters such as the type of reticulate patterns or crests. Hence, the number of *Peracle* species in the world's oceans needs to be revised.

Microbiome of Berghia stephanieae (Valdés, 2005)

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With around 1000 described species, Cladobranchia (Nudibranchia, Gastropoda) is a highly diverse taxon of nudibranch gastropods. They are known for their striking coloration, effective defence mechanisms and their ability to establish a photosymbiosis with unicellular algae of the family Symbiodiniaceae. While a lot of studies in the past have focussed on the photosymbiosis of Cladobranchia, the bacterial community of these marine slugs has long been overlooked. Studies in other photosynthetically active marine animals such as corals and sponges, however show the importance of microorganisms for the host, for example regarding nitrogen fixation or antibiotic production. Here we characterised and analysed the microbiome of the stenophagous cladobranch species *Berghia stephanieae* (Valdés, 2005) and its food source *Exaiptasia diaphana* (Rapp, 1829), as well as *B. stephanieae* held under different one-week starvation conditions (normal light, high light and dark) by metabarcoding of the bacterial 16S rRNA gene. With our analyses we identified Bacilli, Proteobacteria and Bacteroidota as dominating bacterial strains in fed *B. stephanieae* while in starved *B. stephanieae*,

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independent of the light condition, the number of Bacteroidota decreased significantly and Bacilli became dominant. Furthermore, our results show that both organisms, slug and anemone, have distinct bacterial associations, and that starvation has a greater impact on the microbiome of the photosymbiotic slug than different light conditions. This study shows that starvation experiments induce a stress response not only in the animal host, but also in its microbiome, independent of the applied light stress.

Species boundaries in the Limacina species complex

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Holoplanktonic pteropods are widely regarded as bioindicators of ocean acidification due to their thin aragonitic shells vulnerable to dissolution. The *Limacina* genus is most frequently used for this purpose owing to its abundance and wide-spread distribution across all oceans. Different species and populations can exhibit different sensitivities to environmental stressors, depending on their genetic backgrounds and evolutionary histories. Therefore, a detailed assessment of the current species boundaries and distribution ranges is needed to better predict their species-specific potential to respond to ocean changes. Here, we assessed diversity across the five nominal species in the *Limacina* genus with an integrative approach combining morphology with DNA barcoding (cytochrome c oxidase subunit I, 28S rDNA). Shell shape was studied for 302 individuals based on linear and geometric morphometric analyses on stacking microscopy images and micro- CT scans. We found that shell thickness and volume varied significantly across species, and cold-water species were larger. All five extant species could be identified based on shell shape except for *L. lesueurii* and *L. helicina*, which showed overlapping shell shape distributions. There was evidence for unrecognized diversity in the Arctic and Antarctic populations of *L. helicina* and *L. retroversa*. Our analyses also suggest that there may be hidden diversity within the warm-water species, considering they occur in distinct ocean basins. The levels of divergence may imply substantial differences in physiology and adaptive potential in relation to climate change. We conclude that a taxonomic revision of the *Limacina* genus is a prerequisite to their use as bioindicators in acidification research.

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Studies on *Cadulus theilei* Plate, 1909: Distribution of a not so rare scaphopod and assessment of morphological diversity

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Prior to this study, *Cadulus thielei* Plate, 1909 was only known from its type locality in East Antarctica and 3 sites in the Bellingshausen and Ross seas from 157 to 438 m depth, with just 5 specimens known in the published literature. They are often present in epibenthic sledge (EBS) samples from the Southern Ocean, spanning from the Amundsen Sea (110 ° W) to the Lazarev Sea (9 °E), and from South Georgia (53°S) to the Filchner Trough (77 °S). Our EBS collections hold 11 782 scaphopods specimens morphologically assigned to *Cadulus thielei* collected in 161 to 5737 m depth. The aim of this study was to assess the shell morphometrics, to understand distributions, and to undertake an initial COI barcoding assessment of its genetic diversity. To date 360 specimens have been assessed for 10 morphometric parameters, using image analysis and SEM imagery, showing limited morphological diversity. Preliminary COI sequencing of 14 specimens from 4 areas has revealed 10 haplotypes and two genetic clusters (Amundsen Sea vs Lazarev Sea, Shag Rocks & South Georgia). This study has been able to significantly extend the known distribution ranges of *Cadulus thielei* vertically and spatially, confirming it as a circum-Antarctic species. Further investigations will include wider barcoding and multi-locus genetic studies and seek to understand the environmental drivers of this species' distribution and diversity patterns.

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The hidden parascape: digenean diversity in Kruger National Park

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Freshwater snails are intermediate hosts for digenean parasites of both veterinary and medical importance (e.g. fasciolids and schistosomes). These snails have been reported across southern Africa; however, little is known about their parasite diversity and distribution. Traditional methods of detecting digenean diversity in snail hosts

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have focused on light induced cercarial shedding or crushing and dissecting snails, followed by identification of individual cercariae using morphological keys. However, these methods are laborious and time consuming with a high likelihood of human error. This study used a novel metabarcoding approach to assess the distribution and diversity of parasitic digeneans and their intermediate freshwater snail host in the southern region of Kruger National Park. The metabarcoding approach highlighted large digenean diversity including species of medical and veterinary importance, across five snail genera. The invasive *Tarebia granifera* snail showed a significantly higher digenean alpha diversity compared to other snail genera, which contradicts the 'parasites lost' hypothesis for invasive species. Infection experiments are necessary to determine whether *Tarebia* snails can shed these parasites or whether they may cause a dilution effect on parasite transmission. Meta-barcoding is a promising tool for assessing the diversity of digenean parasites and within host communities



Equity, diversity, inclusion and accessibility in UK polar science and malacology

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The polar community has been historically dominated by white men, dating back to the "heroic age of Antarctic exploration". After the colonial discovery of the continent some 200 years ago, it wasn't until the 1980s that British female scientists were allowed to do fieldwork in Antarctica. The diversity of the UK Polar Science community, including that of malacological science, still does not reflect that of the wider UK Society. This under-represented talent includes women, Black, Asian and minority ethnic people, the LGBTQ+ community, people with disabilities, and those from a lower socioeconomic background. The continuing exclusion of these groups through systemic bias and under-representation (and the subsequent loss of diversity and innovation) confirms the need for targeted actions to improve equity and inclusion within the workplace. Whilst this is not an issue unique to polar or malacological science, it is one that we need to tackle for our research to remain relevant in society today. The desire for meaningful, proactive change has resulted in the 2019 establishment of the Diversity in UK Polar Science Initiative (DiPSI). The Initiative celebrates existing diversity, as well as enhancing further polar science opportunities for under-represented groups. Since DiPSI's formation, Equity, Diversity, Inclusion and Accessibility (EDIA) has increasingly grown in presence in UK Polar Science, with organisations and groups systematically including an EDIA voice in much of our

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work. We will introduce the recent work of committees and organisations, including the 2021/22 Natural Environment Research Council (NERC)- funded EDI internships. These have been timely, with the Covid-19 pandemic disproportionately affecting under-represented groups. The internships are an opportunity for such Early Career Researchers to address their experience and network gaps by providing lab-time and in-person working to help advance their careers. Two individuals undertaking malacological projects benefitted, resulting in publications and furthering malacological research interests. With alternative technologies and ways of working, malacological and polar science roles are evolving. It is imperative that there is a continued commitment to EDIA through processes, investment, listening and leadership to work towards a more inclusive and respectful culture across all areas of STEM and research.

Ecosystem shifts associated with restoration of native oyster (*Ostrea edulis*) reefs in the Solent, UK

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Whilst the native oyster Ostrea edulis is a commercially and ecologically important species which provides a spectrum of ecosystem functions and services, its role in the support of ecosystem biodiversity is less well established. Our limited understanding is primarily the result of substantial declines in oyster populations over the past century, rendering many populations functionally extinct. In the Solent, restoration efforts are focussed on creating self-sustaining reefs to re-establish wild populations. Baseline studies of reef sites in Langston Harbour and the River Hamble were completed prior to the creation of the reefs in the summers of 2021 and 2022 respectively. Low biodiversity was found at both sites, with annelid worms being the most prevalent group. At the Langstone reef site, cultch was deployed in September 2021, then populated with 35,000 commercially grown native oysters from the west coast of Scotland. The Hamble site is currently in the processes of getting licencing to lay cultch. As the reef matures, this project will quantify changes in the provisioning of ecosystem functions and services at installed reef sites as they mature. In particular, changes in species assemblage and trophic structure, juvenile ovster recruitment and reef growth and complexity will be determined. Species assemblages and trophic structure will be monitored using a combination of baited remote underwater video (BRUV), eDNA assays and stable isotope analysis. Juvenile recruitment will be monitored using a combination of in situ monitoring and lab-based experiments. Initial surveys, post-deployment, indicate a major shift in the benthic community, and an increase in pelagic fauna. Most notably, juveniles of commercially important species such as black bream (Spondyliosoma cantharus), bass (Dicentrarchus labrax) and cuttlefish (Sepia officinalis) have been recorded utilising the reef area.

Grazing intensity of intertidal gastropods on tropical seawalls in Singapore

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Accelerated human population growth, rising sea levels, and increased storm frequency due to climate change have driven the proliferation of artificial coastal structures such as seawalls worldwide. However, the ecology of these artificial structures remains understudied. Marine herbivorous gastropods are common rocky-shore animals and their role as topdown regulators of algal abundance, distribution, and community structure is well recognised in natural systems. In turn, algal cover influences intertidal assemblages by providing refuge from high temperatures and desiccation during low tides, and by restricting the recruitment of sessile organisms. Yet, no study has examined the grazing intensity of gastropods on artificial coastal defences. Here, we investigated grazing intensity of gastropods on tropical seawalls by examining species-specific radular scratches on wax discs deployed on seawalls. This method provides a direct quantitative measure of grazing intensity and can be used to measure grazing by co-occurring species, since species have different radular morphologies. A library of 15 species-specific radular marks was constructed ex situ using aquaria stocked with single species and granite boulders into which wax discs had been fitted. The wax discs were removed after seven days and grazing marks were examined under a light microscope and using scanning electron microscopy (SEM). Field experiments were later conducted at two islands in Singapore (Sentosa and Pulau Hantu) where replicate (n = 4) wax discs were deployed in a 3 by 3 grid (i.e., 9 disc per plot) for two weeks at two shore heights over three time points. A total of 432 wax discs were collected back from the field and the number of grazing marks per disc by the three most common species (i.e., Nerita spp., Monodonta labio, Patelloida saccharina) were enumerated. Counts of grazing marks on wax discs at both shore heights were not significantly different from each other. The majority were from *P. saccharina*, followed by *M. labio* and Nerita. In addition, certain species like M. labio prefer grazing at the lower shore height. Altogether, this study serves as a digital record/library of tropical gastropods radular morphology, and provides one of the first empirical evidence of gastropod grazing intensity on tropical seawalls.

Comparing low salinity transcriptomic profiles and SNPs among Hard Clam, Mercenaria mercenaria, Lines

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The hard clam is an important ecological and economic resource along the U.S. Eastern Seaboard and has been introduced to other areas of the globe for aquaculture. In Virginia alone, farm gate sales were estimated at \$38.8 million in 2018, making Virginia the largest producer of hard clams in the U.S. This industry is primarily limited to higher salinity habitats on the seaside of the Eastern Shore of Virginia or lower Chesapeake Bay. Although the hard clam can be found in lower salinity habitats, they do not grow or survive at rates that are practical for productive aquaculture. Even



in areas of higher salinity, hard clams are vulnerable to extreme precipitation events, which can lead to hyposaline stress and threaten natural and aquacultured populations. Transcriptomic analysis is a powerful tool for exploring the altered gene expression and cell cycle events that occur under osmotic stress. In the spring of 2019 and 2021, clam lines were created at the VIMS Eastern Shore Laboratory. Salinity exposures were conducted in the summer of 2021 and included replicates for two different salinities (35 and 15 ppt) and eight clam lines. RNASeq data from either the gill (2019) or pooled whole bodies (2021) of exposed clams were used to assess the transcriptomic response to salinity





stress. Using DESeq2, shrinkage estimator Apeglm, and thresholds of an absolute log fold change (LFC) > 1 and a false discovery rate (FDR) < 0.05, 545 genes in gills of adult hard clams and 465 genes in whole bodies of juvenile were significantly differentially expressed between 15 and 35ppt. Of the 545 differentially expressed genes (DEGs) in adults, 408 were upregulated in 15ppt, and of the 465 in juveniles, 303 were upregulated in 15ppt. Some of these genes belonged to important pathways like tight junction formation, protein processing in the endoplasmic reticulum, and apoptosis. The results from this study allow for a better understanding of how hard clams respond to low salinity stress and whether all populations of clams respond the same, which could benefit the aquaculture industry and lead to strategic breeding programmes.

Do eating habits affect oxygen consumption during digestion? The case of freshwater (unionid) mussels

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The metabolic activity of unionid mussels influences the oxygen fluxes and other physical and chemical characteristics in aquatic systems. Unionid oxygen consumption rate during digestion and its dependency on food availability is understudied. In laboratory conditions. We quantified the oxygen consumption rate of *Anodonta anatina* and *Unio pictorum* in response to algal concentration - 0.05, 6.0 and 12.0 mg of Ash Free Dry Mass of Chlorella vulgaris L⁻¹ and mussel dry soft-tissue mass at $19\pm 1^{\circ}$ C. Following a 5-h feeding-period, the oxygen consumption rate (mg O₂ h⁻¹) increased with algal concentration and mussel dry mass in both species during a 2-h digestion-period. The mean oxygen consumption per gram of dry mass (mg O₂ gDM-1 h⁻¹) increased with the algal concentration in both species. The oxygen consumption rate of *A. anatina* was significantly greater than that of *U. pictorum* at a given algal concentration. The *A. anatina* oxygen consumption per gram of dry mass decreased with increasing dry mass. Oxygen consumption rate during digestion shows inter-specific differences and is dependent on food availability. The findings inform the species-specific quantification of oxygen consumption. Validation is required in *in situ* conditions.

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Barcoding the diversity of neglected meiofaunal molluscs in the western Mediterranean (Gastropoda: Heterobranchia)

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Introduction

The mesopsammon is one of Earth's most ancient and widespread habitats. It is formed by interstices among the marine sediments. The meiofauna inhabiting here has been historically understudied due to its minute size, ranging generally from 60 μ m to 2 mm. Yet, despite its restrictive conditions, almost all major lineages of metazoans have meiofaunal representatives (Rundell & Leander, 2010) and one of the most common groups found are gastropods in the Heterobranchia . The interstitial habitat is characterized by some extreme environmental conditions such as faint light, the limited amount of space or the constant variation of temperature and salinity (Jörger et al., 2014). These factors have forced the fauna to an evolutionary convergence in what (Brenzinger et al., 2013) named the 'meiofaunal syndrome'. This set of typical characters comprises minute vermiform bodies, with adhesive structures to avoid being washed out, and body walls often reinforced by spicules or subepidermal cuticles. These facts have driven the meiofauna to be evasive and they are often distinguished by their high degree of cryptic speciation (Rundell & Leander, 2010; Jörger et al., 2014).

Molecular tools have shown the existence of species complexes in diverse heterobranchs lineages (e.g., Neusser *et al.*, 2011; Ornelas-Gatdula & Valdés, 2012). Although mesopsammic lineages represent key groups which can help resolve the inner relationship of Heterobranchia (Schrödl et al., 2011), studies on their diversity are scarce. Here, we explore the interstitial heterobranch diversity alongside the Spanish and Catalan coast (Western Mediterranean) to provide further insight into the group's systematics, taxonomy, diversity, and biogeography.

Material and methods

Coarse subtidal sand samples were collected in 12 localities along the North East Spanish Coast by diving and snorkelling. Extractions of the organisms from the sand were accomplished following the method described by Schrödl (2006), letting the specimens migrate to the surface for two days and using MgCl₂ to anaesthetize them. Specimens were photographed alive and preserved in molecular ethanol for molecular proposes that entailed DNA extraction and amplification of the marker cytochrome c oxidase I (COI). These new sequences were checked for contamination, edited, and aligned together with public sequences available on GenBank. Eventually, phylogenetic analyses were performed with a maximum likelihood (ML) approach and species delimitation tests (ASAP and PTP) were conducted to further investigate the identity of the specimens.

Results

In the present study, we collected more than 300 interstitial heterobranch specimens belonging to *ca.* 39 different species, providing high-quality images for most of them (Fig. 1 to 3). Out of the 17 families collected we amassed the following number of specimens: Omalogyridae (94), Acochlidiidae (76), Pyramidellidae (22), Rissoellidae (19), Philinoglossidae (17), Aglajidae (13), Rhodopidae (14), Murchisonellidae (12), Philinidae (10), Retusidae (9), Runcinidae (7), Embletoniidae (4), Haminoeidae (4), Laonidae (3), Akeridae (1), Acteonidae (1), Ringiculidae (1). A total of 27 of these elusive species have been barcoded. Phylogenetic analysis showed ten probably new species to be described, of which eight are sequenced here for the first time. Among our samples, we have contributed to expanding the geographical distribution of several species, including five new records from Spain (Ammonicera fischeriana, Rhodope cf. veranii, Rissoella inflata, Abavopsis latosoleata and Microhedyle glandulifera) and 12 for Catalonia (the above-mentioned and Hedylospis spiculifera, Retusa leptoeneilema, Rissoella diaphana, Parthenina emaciata, Philinoglossa helgolandica, Pontohedyle milaschewitchii and Omalogyra atomus). Regarding the groups with external shells, we may not provide first records, but we do provide live specimens, live photographs, and material to conduct molecular studies. This is particularly true for Omalogyra atomus, Ebala sp. or the several species of Retusa and pyramidellids from the genera Odostomia and Parthenina, many of which had not been sequenced to date.

Discussion

With the present study, we have contributed to increasing the knowledge of the fauna inhabiting the mesopsammon, one of the largest habitats but, at the same time, one of the least known. Sandy marine heterobranchs are minute, elusive, and hard to collect, so we deployed a specific protocol to be able to gather ca. 39 species, a relevant step forward to a better understanding of 30 of these rare taxa. We have provided new records and high-quality images, reporting five new records for Spain and 12 for Catalonia, barcoding many of these taxa and including them in a systematic context. The results show that at least eight of the species collected here are new species sequenced for the first time (Rhodope sp., Laona sp., Philine sp. 1,

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Philine sp. 2, *Philine* sp. 3, *Philine* sp. 4, *Aglaja* sp., and *Spinoaglaja* sp.) and two already sequenced nudibranch species of *Embletonia* are probably new species (also to be described) that will be assessed in future publications currently in preparation. The inclusion of new species in the phylogenetic analyses (in some cases the type species of some genera) has also revealed new sister relationships and the appearance of new clades, meaning the addition of these rare mesopsammic taxa is a significant step forward to a better understanding of the inner relationships of these lineages. For instance, the phylogenetic analysis for the cephalaspidean genus *Philine*, including here four probable new species, presenting a molecular intraspecific distance of up to 35% for the COI marker. This implies this is a 'wastebasket' taxon with many genera to be erected from it (Price *et al.*, 2011; Moles *et al.*, 2019). The complete results including the 13 phylogenetic trees constructed here will be available in a publication currently in preparation and the newly generated data will also be used elsewhere in different generarevisions (for instance *Rhodope* and *Embletonia*, in prep.).

Conclusion

In this exploratory study, we have revealed some cases of pseudo-cryptic speciation and shown that a comprehensive species and genera revision are needed for many of these neglected taxa. Thus, recalling what Rundell & Leander asserted, it is demonstrated that the study of these rare lineages is still an exciting frontier in malacology.

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Life photographs of 'lower heterobranchs' comprising the families Omalogyridae with (a) Ammonicera fischeriana and (b) Omalogyra atomus; Rhodopidae with (c) Rhodope cf. veranii and (d) Rhodope sp.; Murchisonellidae with (e) Ebala sp.; Rissoellidae with (f) Rissoella diaphana and (g) Rissoella inflata; Acteonidae with (h) Acteon tornatilis.

Invited article

The Scaly-foot Snail

Chrysomallon squamiferum Chen, Linse, Copley & Rogers, 2015 PELTOSPIRIDAE

The Scaly-foot Snail is an iconic gastropod known only from the Indian Ocean deep-sea hydrothermal vents, living in 'hot springs' of the deep – bathed in a mixture of warm hydrothermal fluid and cold bottom water. Its foot, uniquely among gastropods, carries numerous corneous dermal sclerites. Both its scales and shell are often mineralised with iron sulphide, making it the only extant metazoan known to use iron in the skeleton. With shell length averaging at around 35 mm and exceeding 50 mm in large individuals, it is large compared to most other members of the family Peltospiridae which are usually be-

low 10 mm in shell length. This species has established an obligate symbiotic relationship with sulphur-oxidising bacteria which live inside specialised cells inside its much enlarged oesophageal gland, probably contributing to its unusually large body size for the family. These bacteria are capable of making sugar from hydrogen sulphide (usually a toxic substance!), and hydrothermal vent fluid contains a high concentration of hydrogen sulphide. The snail extracts this and pumps it in its own blood to 'feed' the symbionts, and in turn receives energy and nutrition.

The Malacologist

Although discovered in 2001 and formally described in 2015, the Scaly-foot Snail has since captured the imaginations of scientists and the public alike. First discovered at Kairei vent field, Central Indian Ridge (CIR), the Scaly-foot Snail has sub-

sequently also been found in a few additional hydrothermal vent fields across the Indian Ocean. Individuals from different vent sites have distinct coloration of the scales ranging from white to metallic black, depending on their iron content, which is in turn influenced by the amount of iron in the vent fluid composition. The function of these scales was speculated to be protective, but a recent study revealed that their true function is detoxification. Since its symbionts produce toxic sulphur-rich waste products after using hydrogen sulphide to make sugar, the snail appears to secrete this sulphur into its scales as an additional way to remove it from the body. Most hydrothermal vent sites where the Scaly-foot Snail is found are unfortunately currently threatened by deep-sea mining, meaning this charismatic species is already listed as Endangered on the IUCN Red List. The ongoing campaigning against deep-sea mining may put a halt to this, however, and the

future of this fascinating animal (and many others that share its habitat!) is now in our hands







Chong Chen is a Senior Scientist with Tenure at the Japan Agency for Marine-Earth Science and Technology (JAMSTEC), the Japanese national research institute for marine sciences. He is also a member of the Queen's University Belfast Marine Laboratory and an Officer of the Malacological Society of London. He has dived up to >3,300 m deep in the manned submersibles DSV SHINKAI 6500 and TRITON 3300/3 Mk. II in person to explore hot vents and other deepsea environments, although he has also often worked with remotely operated submersibles. He is also a collector of molluscs ('shell collector')



Obituaries

Professor Ronald Chase 1940-2022

Professor Chase, Ron for some ...

How do I start the obituary about the passing of my PhD supervisor, colleague, friend and inspiration? Allow me to try to summarise him in a few sentences: Professor Emeritus Ronald Chase, who died on the 6th of September 2022, was a multifaceted person with a rich career. He was a neuroscientist, psychologist and malacologist, a talented writer and dedicated teacher, who also loved gardening, playing tennis and was clearly proud of his family. As will also be reflected in some of the alumni responses that I collected below, he had major impacts in different ways on people and fields of science.

"I first met him outside of class, playing squash at the old gym on Pine Avenue. After telling him of my interests in neurobiology one day after a match, we wrote an unsuccessful grant application to gain funding for me to join his lab over the summer. He was kind enough to take me on anyways giving me my first opportunity to work in the lab and introducing me to the molluscan nervous system." Dr. Benjamin Hall, Lundbeck (Denmark)

Ronald Chase was born in 1940 in Chicago and went to high school in Los Angeles. Only after his passing I learned that he set high school (running) track records that stood for decades and that he went to Stanford University on an athletic scholarship to study Psychology. Subsequently, after starting at Harvard Law School (HLS) he left to go to the Massachusetts Institute of Technology (MIT) for his PhD in Psychology, later called Brain and Cognitive Sciences. He did post-docs at the Max Planck Institute of Psychiatry in Munich and the Department of Zoology at the University of Washington in Seattle. Subsequently, he became professor at the Department of Biology at McGill University in Montreal in 1971, where he stayed until his retirement in 2008. During his career he worked on chemotaxis in octopus, the visual cortex in cats, and especially snail neurobiology and behaviour. On the latter topic, he wrote an influential and comprehensive book "Behavior and its Neural Control in Gastropod Molluscs" (2002).

"He was a gifted writer. I'm grateful for the careful editing he did on my first forays into scientific writing. My writing was improved by having him go through those early papers with his red pen." Prof. Dr. Shelley Adamo, Department of Psychology and Neuroscience, Dalhousie University, Halifax (Canada)

After his retirement, he kept writing and published several books on psychology, going back to the reason for why he turned to neuroscience in the first place: he wanted to understand his brother's mental illness. This was also his motivation to leave HLS and start at MIT at the time. He wrote an impressive book about this titled "*Schizophrenia: A Brother Finds Answers in Biological Science*" (2013). In this book he described his brother's schizophrenia from both a personal and scientific perspective, in alternating chapters. He clearly loved writing and was dedicated to it; several books on psychology followed. This did not go unnoticed, as he was proud to tell me at the time, since this led to a plenary lecture invitation to a major meeting on the topic.

"I always valued Ron as both a friend and an advisor. I hope that I have been able to convey some of the same wisdom and support to my own students. I appreciated great new insights into his background and motivation for studying neurobiology from reading his book a few years ago on his brother's struggles with schizophrenia." Prof. Dr. Roger P. Croll, Department of Physiology & Biophysics, Dalhousie University, Halifax (Canada)

Within the molluscan science community he will definitely be remembered for solving the question why land snails 'shoot' a love dart at their mating partner. As one of his alumni remembers:

"Dr. Chase generously introduced me to his work on snail mating behaviour and I was immediately hooked. Through his enthusiasm and curiosity, he showed me that serious science exists in all disciplines; the questions that leave you baffled, the ones that you can't get out of your mind, are the ones that most deserve to be answered." Dr. David W. Rogers, Max Planck Institute for Evolutionary Biology, Ploen (Germany)

I recognise this feeling. I came into his lab myself having been trained in neurobiology and behaviour and curious about the details of snail mating and left, after completing a PhD, with evolutionary questions that I needed to address about love darts. Thanks to Chase's persistent work on this topic together with (under)graduated and post-docs (including myself), we now know that these snails stab each other with a so-called 'love dart' in order to transfer accessory gland proteins that increase the proportion of the shooter's spermatozoa that gets stored by the recipient for later use in fertilisation. This was a question that could only be answered by integrating findings about these snails' behaviour, physiology, biochemistry, reproductive morphology and genetic diversity. In other words, by addressing proximate questions about how things work, he also answered ultimate questions about why they work the way they do. This integrative approach stuck with several of his alumni throughout their careers, including myself.

>CONTINUED

The above also illustrates that he had a broad interest for a range of biological fields and learned more about the ones he required to answer his questions. I think this is one of the reasons for why his former students found him inspiring and refer to him as a great teacher, mentor and inspiration:

"Ron gave me the opportunity to study in his lab in the 90s, I was young, a new immigrant to Canada and away from home for the first time. It was a difficult time for me, but this experience set me up for many future successes. I will always be thankful to Ron for giving me this first step in this right direction." Dr. Smriti Agrawal, Calgary (Canada).

Without putting any emphasis on it, he also showed how science does not always have to involve expensive, sophisticated, high-tech material and equipment. For example, he liked fixing things to be reused and he stimulated students to customise their recording equipment or setup to suit their specific needs. Likewise, rather than buying expensive, commercial snail feed, we made it ourselves in the lab from the raw ingredients, based on a recipe that he had optimised. In my lab we now refer to this as the Chase mix. Another trick-of-the-trade was harvesting spines from the cactus plants in the windows of the lab and using these, instead of stainless-steel micro-pins, to pin out the central nervous system of other organs of snails for (electro) physiological recordings. One downside to this clever method, as many of his alumni will remember, was that you would regularly get some of these small cactus spines stuck in your hand or arm if you were not careful.

"I had the pleasure to work in the lab of Dr. Ron Chase when I was an undergraduate student who knew next to nothing about fundamental research. My stint in his lab was instrumental with my decisions to get extra training in basic science research throughout my career. Without Ron as a supervisor and mentor early on, chances are I would not be the clinician-scientist that I have become." Mathieu Lemaire MSc MDCM PhD FRCP(C), Department of Pediatrics & Biochemistry, University of Toronto (Canada)

He always insisted on being called Dr. Chase by the people who started in his lab. You somehow had to earn calling him Ron over time. But he was a modest man and humble about the impact of his scientific contributions. Nevertheless, throughout his scientific career Ron wrote many research papers, reviews and several books that altogether made significant contributions to different fields of science. As he might have modestly concluded himself, with his disarming sense of humour: He nearly became a (rich and famous) lawyer but instead realised that he just (!) needed to understand how the brain worked. He certainly helped advance the field of neuroscience, and snail (neuro)physiology along the way, but by asking questions, debating and genuine curiosity he contributed so much more.

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Photo credit Dorothy Chase, with permission of the Chase family

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Obituary submitted by Dr. Joris M. Koene (joris.koene@vu.nl) Associate Professor Ecology & Evolution, Amsterdam Institute for Life and Environment (A-LIFE) Faculty of Science, Vrije Universiteit De Boelelaan 1085, 1081 HV Amsterdam, The Netherlands





130th Malacological Society of London AGM & Symposium

William Benson and the golden age of malacology in India

The Society's AGM & symposium will take place in the afternoon, Wednesday 29th March 2023 at the Natural History Museum, London.

The symposium will be based around the launch of the new book 'William Benson and the golden age of malacology in British India' and will feature talks from some of the authors along with research that has been inspired by Benson and the regions he studied

Confirmed speakers include:

- Dr Aravind Madhyastha (Ashoka Trust, India)
- Dr Richard Preece (Museum of Zoology, Cambridge)
- Dr Barna Pall-Gergely (Centre for Agricultural, Hungary)
- Dr Dinarzarde Raheem (Rajarata University of Sri Lanka)
- Dr Tom White (NHM, London)

Talk schedule and titles to follow

Talks can be viewed online for those unable to attend

The event is **free** to attend but registration is required non-members are welcome to attend the talks

Please register at <a href="mailto:president@mailto:presi



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Membership Notices

THE MALACOLOGICAL SOCIETY OF LONDON

Registered Charity No. 275980

Hon. Secretary - Debbie Wall Palmer

The 130th Annual General Meeting of the Malacological Society of London (MSL) will take place at 12.30h on Wednesday 29th March 2023 at the Natural History Museum, London. There will be an accompanying symposium be based around the launch of the new book '*William Benson and the golden age of malacology in British India*'

Agenda for the AGM

Apologies for absence Minutes of the last (129th) AGM Matters arising Financial report Annual report of Council (delivered by the President) Awards Changes to the rules Election of Council Any other business

Year of existence	2022–2023	2023–2024
	129	130
President	Jon Ablett (2)	Jon Ablett (3)
Vice Presidents	Fiona Allan (2)	Fiona Allan (3)
	Phillip Hollyman (1)	Phillip Hollyman (2)
Ex officio		
Councillors	Alan Hodgson (3)	Aidan Emery (3)
	Aidan Emery (2)	Robert Cameron (3)
	Robert Cameron (2)	Victoria Sleight (3)
	Victoria Sleight (2)	Katie Collins (3)
	Katie Collins (2)	Rowan Whittle (2)
	Rowan Whittle (1)	John Grahame (2)
	John Grahame (1)	
EC-Rep	Thomas Goulding (1)	Thomas Goulding (2)
Co-opted	Phil Fenburg (1)	Phil Fenburg (2)
	Crispin Little (1)	Crispin Little (2)
		Alan Hodgson (1)
Journal Editor	Dinazarde Raheem	Dinazarde Raheem
Bulletin Editor	Georges Dussart	Georges Dussart
Treasurer	Katrin Linse (final year)	Vacancy
Membership Secre- tary	Harriet Wood (2)	Harriet Wood (3)
Hon. Secretary	Debbie Wall-Palmer (2)	Debbie Wall-Palmer (3)
Web manager	John Grahame (web)/ Chong Chen (Facebook)	John Grahame (web)/ Victoria Sleight (Facebook)
Awards Officer	Lauren Sumner Rooney (2)	Lauren Sumner Rooney (3)
Archivist	Andreia Salvador (2)	Andreia Salvador (3)

Numbers indicate years in post; posts are usually for 3 years.

Proposed new Rules of the Society—to be validated at the AGM 2023

I. NAME

The Society shall be called The Malacological Society of London.

II. OBJECTS

The objects of the Society are to advance education, research and learning for the public benefit in the study of molluscs from both pure and applied aspects. In furtherance of these objects, but not further or otherwise, the Society shall have the following powers:

(a) To promote and co-ordinate meetings and symposia,

(b) To promote and co-ordinate research both pure and applied;

(c) To provide for the worldwide dissemination of the useful results of such research by publication of the *Journal of Mollus*can Studies;

(d) To award prizes to outstanding students in the field of molluscan biology;

(e) To award research grants to individuals which will advance the study of molluscan biology;

(f) To do all such things as will further the objects of the Society

(g) To award travel and membership support to students and early career scientists in the field of molluscan biology.

III. MEMBERSHIP

Membership will be open to all individuals who are interested in the study of molluscs, both from pure and applied aspects.

(a) There will be Student Members, Ordinary Members and Honorary Members. Honorary Members shall currently be limited to five; they shall be exempt from all payments and receive the same privileges as Ordinary Members. They shall be nominated by the Council and such nominations shall be confirmed at the ensuing Annual General Meeting.

(b) Members shall be entitled to online access the *Journal of Molluscan Studies* together with such circulars as may be issued during their membership.

(c) The Council has the discretion to remove any member that is considered to fall below a standard acceptable to the Society but shall not exercise these powers unreasonably.

IV. MANAGEMENT

The business of the Society shall be managed by a Council elected at Annual General Meetings of the Society. The Council shall comprise the Honorary Officers (President, Treasurer, Secretary, Membership Secretary, Editor of the Journal, Editor of *The Malacologist*, Archivist, Website Manager, Facebook Manager, Twitter Manager, Early Career Representative and Awards Officer), the immediate Past-President (ex-officio for one year), two Vice-Presidents and six Ordinary Members. One individual may hold more than one council position/role. In addition, Council may co-opt up to four members on an annual basis.

Vice-Presidents and Ordinary Members of Council are elected for three years and shall not be eligible for re-election in their respective offices for one year; the Officers of the Society shall be eligible for re-election each year, but the President shall normally serve for three years and upon retirement shall serve as a Vice-President (*ex officio*) for one year. Treasurer, Secretary and Membership Secretary shall normally serve for three years but shall be eligible for re-election after each three year period of service and can be re-elected indefinitely with agreement of the Council and the membership.

Nominations for Council from members must be proposed and seconded and in the hands of the Secretary by 31 December. It shall be the duty of Council to nominate members for election to the offices of President, Treasurer, Secretary, Membership Secretary, Editor of the Journal, Editor of *The Malacologist*, Archivist, Website Manager, Facebook Manager, Twitter Manager, Early Career Representative and Awards Officer, and for the vacancies in the Council caused by annual retirement. Nominations from the members and from Council shall be submitted to the Society with the notice convening the Annual General Meeting which shall be sent to every member of the Society not less than fourteen days before the Meeting

In the case of a vacancy arising in any office of the Society, or in the Council, the Council shall have power to fill up such vacancy until the next Annual General Meeting.

At Council Meetings any six members shall form a quorum.

NEW RULES CONTINUED>

V. FINANCE

(a) Admission fees and annual subscriptions shall be such sums as may be determined by a Special General Meeting convened under Rule VI(c), or at the Annual General Meeting.

(b) Subscriptions shall be due from the 1 January in each year; but in the case of a new member, immediately after election.

(c) Any member whose current subscription has not been received in full by 31 January shall be reminded of the arrears in subscription and be informed that online access of the Journal, and other membership benefits, are suspended until the arrears are paid.

(d) The Council shall revise and publicize the conditions of the Society's awards and grants from time to time.

(e) For the purpose of legal protection of the property of the Society, all funds, books and other property shall be declared vested in Council as the Society's Trustees.

(f) The Council shall cause to be kept Minutes of Council and Society Meetings and books of account in respect of all receipts, payments, assets and liabilities. Accounts shall be presented to each Annual General Meeting for approval by members and such accounts shall be independently examined.

VI. MEETINGS

(a) Council shall each year organize a programme of Ordinary Meetings of the Society, which may include meetings held in association with similar institutions.

(b) The Annual General Meeting shall be held at some time during the period February to April.

(c) The Council may, when they think fit, and shall upon a Requisition signed by not fewer than twelve members, convene a Special General Meeting of the Society. A notice of every Special General Meeting, stating the business, shall be sent to every Member of the Society not less than fourteen days before such meeting or announced in the Bulletin; no business shall be considered at such Meeting except that for which it was specially convened.

(d) Council shall meet regularly though out the year to discuss society business.

VII. RULES

Matters relating to the interpretation of the Rules shall be decided by the Council.

VII. AMENDMENT

No rule shall be altered except by a majority of votes of those present at a Special General Meeting called for the purpose, or at the Annual General Meeting. No change shall be made that would have the effect of causing the Society to cease to be a Charity in Law.

IX. WINDING UP

If upon winding up or dissolution of the Society there remains, after the satisfaction of all its debts and liabilities, any property whatsoever, the same shall not be paid or distributed among the members of the Society, as such, but shall be given or transferred to some other charitable institution or institutions having objects similar to the objects of the Society and which shall prohibit the distribution of its or their income and property among its or their members, such institution or institutions to be determined by the members of the Society at or before the time of dissolution, and if so far as effect cannot be given by such provisions, then to some charitable object.

(Adopted 17 May 1978, revised 25 March 1998, 19 March 2001, 28 April 2005. Proposed revision 29 March 2023)

Grants and Awards

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 probably 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. From December 2021, the Society also offers additional awards to a) applicants from developing and transition countries (as according to the UN), and b) UK/EU applicants from Black, Asian, or any other underrepresented ethnic background.

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. The award is to support attendance at 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

These 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 probably 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, The deadlines are 1st March, for travel scheduled between 1st June and 30th November, and 1st September for travel scheduled between 1st December and 31st May.

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 15th December. 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, Lauren Sumner-Rooney,** Museum für Naturkunde, Invalidenstrasse 43, Berlin 10115, Germany. For further information, guidance notes and to access the grant application form see http://malacsoc.org.uk/awards-andgrants/research-grants

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Global Participation Postgraduate Student Scheme.

This is a new MSL initiative to help support more students from across the world in their malacological studies.

The scheme will run every year, so each year ten new students will be given free membership for a 3 year period. So, in 2023 there will be 10 students, in 2024 there will be 20 and in 2025 and thereafter there will be 30.

We are offering 10 students each year free membership to *The Malacological Society of London* for a period of 3 years.

Students who are studying a postgraduate malacology-related course in countries designated 'developing economies' are invited to apply for this award with the support of their supervisor. Applications are open immediately and will close when all 10 memberships have been allocated. Membership of the first round starting on 1st January 2023 and ending on 31st December 2025.

The scheme will run on a yearly basis and applications will open again next autumn. Successful candidates will benefit from:

- online access to entire archive of Journal of Molluscan Studies (back to 1893)
- electronic delivery of Society's bulletin, *The Malacologist*
- access to a higher rate of travel grant
- regular communication from MSL about the Society's themed meetings and the annual Molluscan Forum

Application procedure:

Please send applications and proof of course registration to the Membership Secretary: membership@malacsoc.org.uk

Selection criteria:

Applicants must fulfil the conditions stated below and will be selected on a first-come basis.

Conditions:

- Students must be registered for their postgraduate course in a country designated as a 'developing economy'.
- The course must have a strong malacological focus.
- Students must have the support of their supervisor and must send proof of course registration with their application and for each membership year.



Council member Alan Hodgson found this in his coffee in South Africa



Malacological Society of London – Subscription and Membership

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 copy of the *Journal of Molluscan Studies* and such circulars as may be issued during their membership. The Society's website 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. The Society no longer produces paper copies of the Journal. Members also receive access to *The Malacologist*, which is the bulletin of the Society, issued twice a year, in February and August. *The Malacologist* is published on-line on the website of the Society.

Meetings and articles

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*.

Subscriptions

Membership subscriptions are valid from **1st January** for a single calendar year.

Membership fee structure

Ordinary Members: Journal on-line only £45 Student Members: Journal on-line only £25

Methods of Payment

New Members:

To join the Society for the first time please fill in the Membership Form on the MSL website and make your payment using a Credit or Debit Card (Mastercard, Visa, American Express):

https://malacsoc.org.uk/membership-form/

Existing Members:

If you already have an account on the MSL website please **login** to renew your membership and make your payment using a Credit or Debit Card (Mastercard, Visa, American Express).

OR

If you have already set up a standing order you may continue to pay in this way. We do not encourage members who have a MSL account on the website, or any new members, to set up a standing order.

Institutional Subscriptions to the Journal

Enquiries should be addressed directly to Oxford University Press, Walton Street, Oxford OX2 6DP, U.K.

For any membership queries please contact the Membership Secretary: membership@malacsoc.org.uk

*NEW * Broadening Access Membership Scheme

We are excited to launch a new initiative to help support more postgraduate students from countries listed as developing economies in their malacological studies.

We are offering **10** postgraduate students <u>each year</u> free membership to *The Malacological Society of London* for a period of 3 years under the new Broadening Access Membership Scheme (BAMS). Students who are studying a postgraduate malacology-related course in countries designated 'developing economies' are invited to apply for this award with the support of their supervisor. Applications open each autumn and will close when all 10 memberships have been allocated.

Successful candidates will benefit from:

- online access to entire archive of Journal of Molluscan Studies (back to 1893)
- electronic delivery of Society's bulletin, The Malacologist
- access to a higher rate of travel grant
- regular communication from MSL about the Society's themed meetings and the annual Molluscan Forum

Application procedure:

To find out more about the scheme, who is eligible and how to apply, please go to the following page on our website: <u>https://malacsoc.org.uk/developing-economies-membership-scheme/</u>