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The Malacologist

The Bulletin of The Malacological Society of London

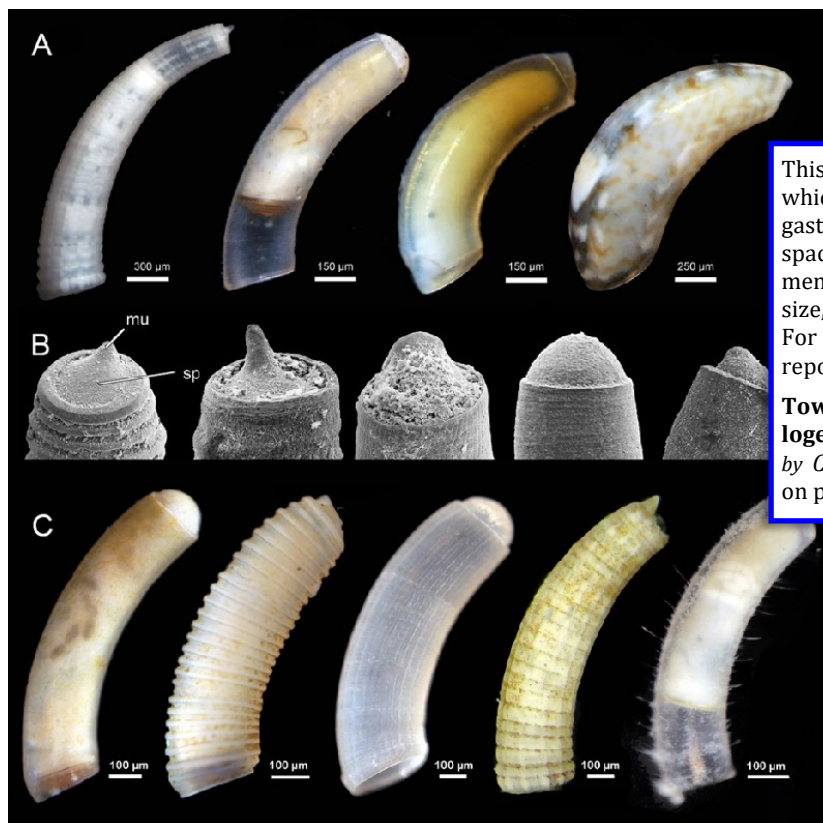
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AUGUST 2020

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This image is of some Caecidae which comprise a family of marine gastropods living in the interstitial spaces of algae, coral, and sediments. Most are less than 4 mm in size, with an uncoiled shell. For further information see the report entitled

Towards a first molecular phylogeny of Caecidae microsnails
by Christina Egger
on page 23

The Malacological Society of London was founded in 1893 and registered as a charity in 1978 (Charity Number 275980)

EDITORIAL

An old Chinese curse says “May you live in interesting times.” These are certainly interesting times for the Malacological Society of London (MSL). Because of Covid-19, the meeting on the *Biology of Limpets: evolution, adaptation, ecology and environmental impacts* which should have taken place at Plymouth on 17-19 March 2020 was cancelled. This created a huge headache for the organiser Prof Alan Hodgson, since invited speakers had been organised and travel grants had been given. Since the AGM was to accompany the conference, that, too, had to be cancelled. The AGM therefore took place together with a Council meeting on the 4 June 2020, virtually by Zoom. It was quorate and received the President’s report of Council, presented here on page 42.

In the light of the Black Lives Matter movement, the Council has been considering actions that might have a direct impact, including the possibility of dedicated travel/research awards for under-represented groups or ways to amplify the work of black and other non-white malacologists (in the journal, at meetings, on social media, etc).

The Council has had to take a seriously radical step in ceasing, at short notice, to print paper issues of the *Journal of Molluscan Studies* (JMS). The latter will now only appear in digital form only. This sad decision was forced on the Society by the economics of publishing and the turbulence in the academic publishing business. Some of the background to this is presented in three articles by Robert Cameron, Trevor Parry-Giles and Robert Harington. Covid-19 has made the situation even more difficult; thus “*Not only must learned societies reinforce their own mission focus, but they must also support their members as they confront significant challenges to their identities as scholars and teachers.*” says Trevor Parry-Giles (professor in the Department of Communication at the University of Maryland) in relation to the situation of learned societies in the time of the Covid-19 pandemic. He also says “*learned societies owe it to their members to affirm and enhance the academic enterprise, to support the scholarly identity in the face of budgetary, political, and social pressures, especially as those pressures are amplified by pandemic politics.*” Indeed.

On a happier note, it is always a pleasure to see the fruits of tangible support given by the Society to young and not-so-young researchers. Several reports are presented in this issue, as well as an invited article on Icelandic whelks.

TAXONOMIC/NOMENCLATURE DISCLAIMER

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

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NOTICES

Videos of *Conus* doing what *Conus* does

Dylan Taylor was a contributor at a recent Malacological Forum, where he presented a video on the work of Baldomera ‘Toto’ Olivera on *Conus* and its toxins. Dylan writes

“I’ve spent the last two years creating a mini-series all about Toto’s work. I’ve called it *Killer Cures*, and you can watch it online via my website, as I recently published it on YouTube.

<https://www.scarysnails.com/>

Toto asked that I aim to make it such a way that it engages high-school students, with a view to them considering science careers. As such I think you will find the format unconventional compared with much of the output in this sector...So far so good, I hope you find time to take a look at, and enjoy the films.”

Video titles include

- There are snails that can kill you
- The 700 million dollar snail
- Killer snails and the opioid crisis
- The quest for the holy snail
- Killer snail biotech
- Science careers
- Killer snails—the trailer

Dylan would like to increase the size of the audience for this material. “One idea I have is to present the films at ‘screenings’ with an interval and a Q and A session. I’ve tried this on a small scale here in Brighton and it went very well. I kicked off with a live aquarium feeding demonstration of a cone snail catching and eating a fish. Obviously there are some issues right away with perceptions and ethics at such an event (notwithstanding the fact that the snails in question are obligate piscivores). It really went very well on the first trial session, with an invited audience of friends and family of all ages.”

Please correspond directly with Dylan if you think you can help.

The contact is Dylan Taylor thefishstation@gmail.com



Engaging video of a snail eating a tomato

https://thumbs.gfycat.com/LikelyUnsilentlyDuckbillplatypus-size_restricted.gif



The Tony Whitten Conservation Prize 2020

Tony Whitten (1953-2017) was an inspirational conservationist who championed biodiversity across Asia and beyond, working as Senior Biodiversity Specialist at the World Bank and more recently as Director of Fauna and Flora International's Asia-Pacific programme.

This award is particularly relevant for malacologists - three of the six 2019 winners worked on molluscs, see the article in the 2020 issue of Tentacle:

https://www.hawaii.edu/cowielab/Tentacle/Tentacle_28.pdf

The application form is available at the link below.



Applications Open

Tony Whitten did world-class work on the discovery and conservation of limestone cave invertebrates, saving many species from obliteration by the region's rapidly expanding cement industry, and having no fewer than 11 new species named in his honour. Tony also established the IUCN Cave Invertebrate Specialist Group. As a tribute to Tony, the Cambridge Conservation Initiative is delighted to invite applications for the **2020 Tony Whitten Conservation Award** for early career conservationists and biodiversity researchers from East and Southeast Asia.

The prize is open to those under the age of 35 involved in any area of conservation or field biology within this region. Prizes will be awarded by a panel selected by Tony's family. The panel is especially interested in hearing about work on the overlooked species and habitats that Tony was most passionate about – such as caves and karst ecosystems, and understudied invertebrates and fishes – but all applications are welcome, regardless of where in the region and on what aspects of conservation or field biology the work is focussed.

The fund is able to provide five awards of GBP 2,000 each in late 2020, with a further round in 2021. Applicants should be nationals of Brunei, Cambodia, China, Indonesia, Laos, Malaysia, Mongolia, Myanmar, the Philippines, Singapore, Thailand, Timor Leste or Vietnam.

Application Form and Closing Date

An application form is available from:-

<https://www.cambridgeconservation.org/about/tony-whitten-conservation-award/>

The application deadline is midnight (GMT) on **1 November 2020**. Applicants will be notified of the outcome of their application by the end of 2020.

The contact is Kirsten Russell kt346@cam.ac.uk



Malacology publication initiative

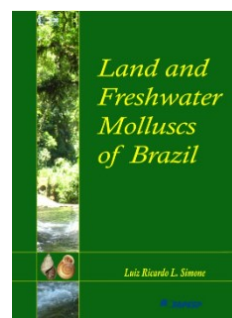
Luiz Ricardo L. Simone, highlighted his initiative to publicise interesting subjects on malacology, in popular scientific language and illustrations. Issues can be downloaded at :-

http://www.moluscos.org/malacopedia_previous.html

The contact is Luiz Ricardo L. Simone, Ph.D.

Museu de Zoologia da Universidade de São Paulo

lrsimone@usp.br



The Malacological Society of London's *Molluscan Forum*

Because of Covid-19, the Molluscan forum will take place in a different format this year. We still plan to hold the event and will do so via an online platform (probably Zoom) on **Thursday the 19th of November**.

As in previous years, for those wishing to offer a presentation, please fill out the attached registration form. For those just wanting to attend, please let me know so I can keep track of attendees. The deadline for registrations and talk applications is **Friday the 16th of October**, presenters will be informed of successful applications soon after.

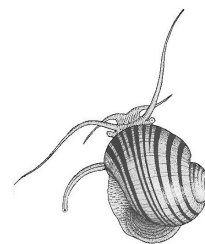
Registration is **free!**

In lieu of posters, we will instead have 5 minute (3 slide maximum) **quick-fire PowerPoint** presentations,

We hope these changes will still allow all those who wish to attend and present the chance to do so, even if we can't offer the customary wine reception!

For further details and an application form, see page 48.

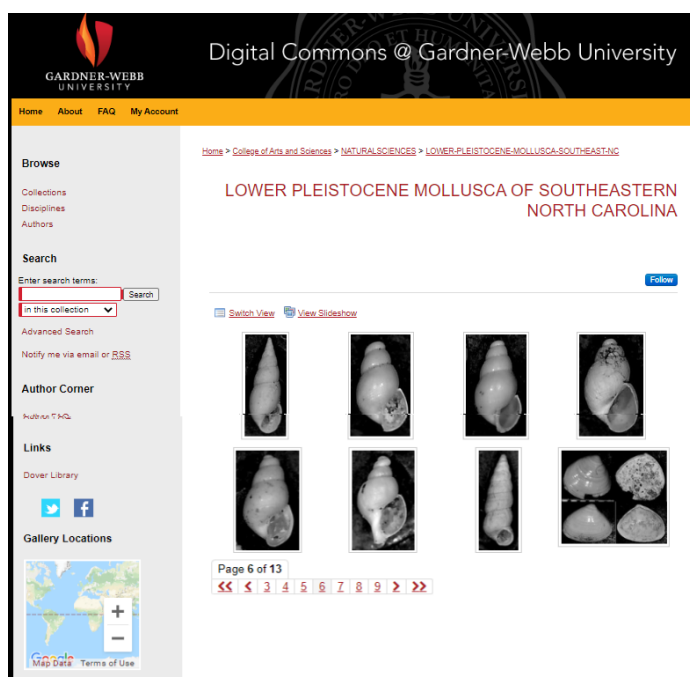
The contact is Dr Phil Hollyman
British Antarctic Survey, Cambridge CB3 0ET
Email: phyman@bas.ac.uk



Got the covid19 blues? Got nothing to do? Do some malacology!

If you need something to do during the quarantines, <https://digitalcommons.gardner-webb.edu/lower-pleistocene-mollusca-southeast-nc/> has photos of around 100 species (mostly micromollusks) from the Waccamaw Formation in southeastern North Carolina, for which the identification is somewhat uncertain. About 450 other species have been identified so far. Most have a genus, but a few are less certain. Any suggestions on identifications are welcome.

The contact is Dr. David Campbell
Associate Professor, Geology
Department of Natural Sciences
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Gardner-Webb University
Boiling Springs NC 28017



Argentine Malacological Association (ASAM)

The Argentine Malacological Association (ASAM) saluted all its colleagues on the occasion of celebrating, for the first time, Malacologists' Day in Argentina.

June 15 commemorates the date of the re-foundation of our association, which celebrates its 9th anniversary today. The ASAM was officially launched during the 8th Congreso Latinoamericano de Malacología (VIII CLAMA) held in Puerto Madryn, Argentina in 2011.

The contact is Javier H. Signorelli,
javierhsignorelli@gmail.com



Bailey-Matthews National Shell Museum

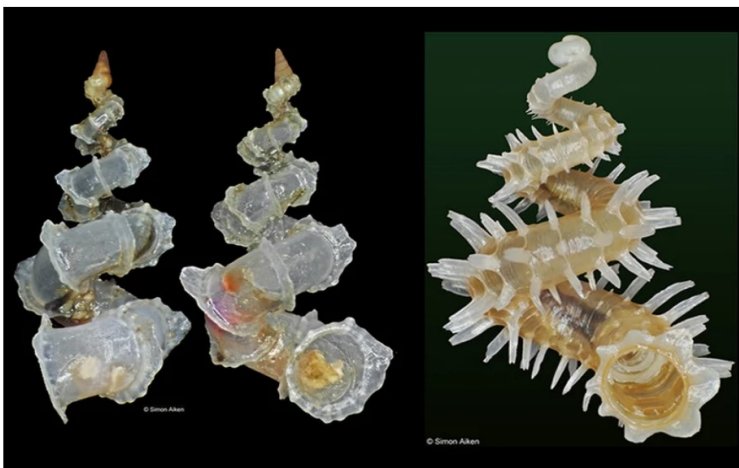
Shown here are examples of the gorgeous images to be seen on the website of the Bailey-Matthews Shell Museum website

<https://www.shellmuseum.org/>

The contact is José H Leal jleal@shellmuseum.org



Extractrix milleri, about 25 mm long.
Photo courtesy M.G. Harasewych



Cycloscala revoluta, 6.6 mm, Philippines;
Blaesospira echinus infernalis, Cuba, 9 mm.
Photos by Simon Aiken.



A Cepaea quiz

These *Cepaea* were found within 100m of each other. One was found on pasture, the other at the edge of an adjoining wood. They are approximately the same size. Which was found where? And what hypothesis might explain the difference in colour?

Posed by Dr Mike Nicholls

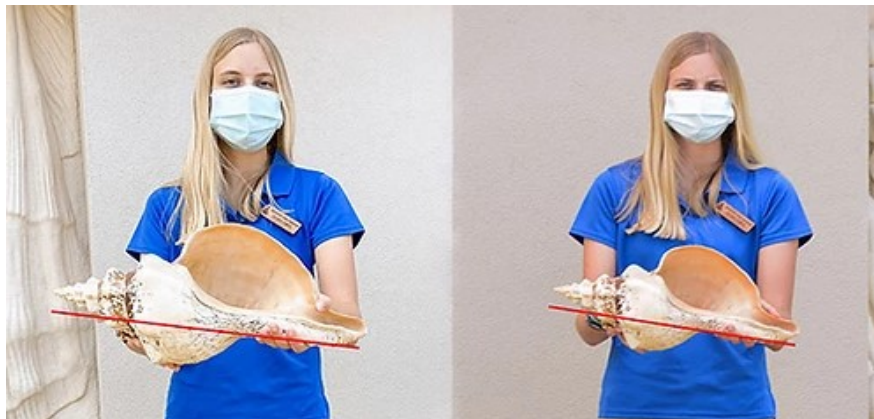
See the hypothesis at the bottom of page 7.



Be aware of relative size in photography

There is an interesting feature on the Shell Museum site about taking photos and being aware of relative size in the way the photo is taken. It is well worth a read, especially in relation to taking selfies. You can find it at :-

<https://www.shellmuseum.org/post/is-shell-size-relative>



This is the same shell, held away from, and close to, the body.

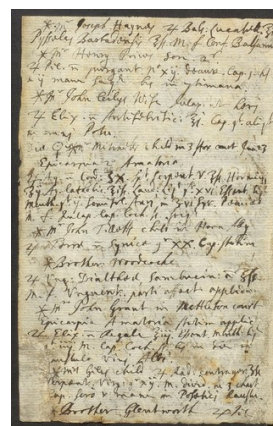


Remembering James Petiver

Royal Society Publishing has just published a special issue of *Notes and Records* - **Remembering James Petiver** organized and edited by Richard Coulton and Charles E Jarvis. This content is currently FREE to access at <https://royalsocietypublishing.org/toc/rsnr/2020/74/2> and there is also a blog post at <https://royalsociety.org/blog/2020/05/remembering-james-petiver/>

Petiver was mainly an apothecary and thereby a botanist. His taxonomic interests strayed a short way into malacology.

Contact is Felicity Davie
Royal Society Publishing, The Royal Society, 6-9 Carlton House Terrace
T +44 20 7451 2647



Covid19 Online exam question for malacologists

Is this an example of an obligate or facultative mutualism and is it likely to be a problem for malacology? Discuss.



Journal of Cephalopod Palaeontology (JCP)

Announcement of a new paleontology journal dedicated to fossil cephalopods, with a specialized dedicated editorial team: the *Journal of Cephalopod Palaeontology* (JCP). JCP is an international open access peer-reviewed online journal (using DOI) publishing original research articles with no restriction on geological time or palaeogeographic origin, as far as they are focused on fossil cephalopods, even as a model for theoretical issues. Its scope includes e.g. evolution, phylogenetics, systematic studies, stratigraphy, palaeobiogeography, palaeoecology, taxonomy, taphonomy, nomenclatural acts, heritage, field data, research methods. Taxonomy based research on or inspired by a population approach (taking into account intraspecific variability and evolutionary patterns and processes) is especially welcome. Submitted works can be discussions of broad interest, monographs, or more local descriptive research. JCP meets the requirements of the current version of the International Code of Zoological Nomenclature (ICZN, Art. 8). Articles are deposited in open online archives, without any embargo period, where they will be permanently and openly accessible. JCP is distributed under a Creative Commons BY licence, which means that all content is freely available without any charge to anyone, including the authors. More information at: <https://journals.opscidia.com/index.php/jcp/index>.

The contact is Didier BERT (didier.paleo@gmail.com)



Ming—The longest lived mollusc

The BBC notes that researchers from Bangor University in north Wales have found a marine clam which may be the oldest extant (or it was extant until they dredged it up) clam ever found. Its age was obtained by counting rings on its shell. The clam has been nicknamed Ming, after the Chinese dynasty in power when it was born. Unofficially, another clam - found in an Icelandic museum - was discovered to be 374-years-old, Bangor University said, making their clam at least 31 years older. Ming was aged between 405 and 410 years old.

Professor Chris Richardson (a past member of Council of the Malacological Society of London), from Bangor University's School of Ocean Sciences, told the BBC: "The growth-increments themselves provide a record of how the animal has varied in its growth-rate from year to year, and that varies according to climate, sea-water temperature and food supply. "And so by looking at these molluscs we can reconstruct the environment the animals grew in. They are like tiny tape-recorders, in effect, sitting on the sea-bed and integrating signals about water temperature and food over time."

Prof Richardson said the clam's discovery could help shed light on how some animals can live to extraordinary ages. "What's intriguing the Bangor group is how these animals have actually managed, in effect, to escape senescence " he said. The animals may have some difference in cell turnover rates that could be associated with similar processes in much shorter-lived animals. He noted that the university had received money from the UK charity Help The Aged to help fund its research.



Cepaea quiz—a hypothesis

One hypothesis is that bird predation has led to local cryptic colouration. The dark morphs were found in pasture land, where they were on, and adjacent to, sheep faeces. As can be seen from the photograph, they resemble sheep faeces. The brown morph was found at the woodland edge. It is possible that bird predation removes conspicuous light snails in the pasture and conspicuous dark snails near the woodland edge thereby maintaining a balanced polymorphism.

Discussion document

What is the future for the Malacological Society of London?

The Editor writes “The Council of the Society has been discussing the issue of what kind of society we should be in the future, given that we have had to terminate our production of a paper-based journal (after 150 years of paper print) and publish the journal in digital form only. Covid 19 has forced us into increasingly contorted thinking - for example, we had to hold a virtual/on-line Annual General Meeting. The following articles (reproduced here by permission of the authors) will hopefully encourage debate about our future as a specialised, academic society.”

The future of the Society and the *Journal of Molluscan Studies* in the age of Open (and digital) Access

Robert Cameron

Introduction and history

I assume that all members of Council will be aware of the increase in the number of Open Access (OA) journals: journals freely available digitally to all without payment. The contrast is with those like our *Journal of Molluscan Studies* (JMS) that are subscription journals; here, access depends on membership, or on access to a subscribing library or institution. Of course, access to papers in subscription journals is also available through the traditional means of asking authors for private copies (what we used to call reprints). Recently, JMS has carried some OA papers, either reviews agreed between OUP and the editor, or ones where the author has paid an Article Processing Charge (APC). Hence, to a limited extent, JMS can be thought of as a **Hybrid Journal** in which both routes to publication can be used. Quite a number of journals have gone down the hybrid route.

If you want to see what good OA journals look like, see any of the Public Library of Science (PLOS) journals.

At the moment, OA journals make up a small but rapidly increasing proportion of all scientific output, while subscription journals cover the whole range from say *Nature* to *Journal of Conchology*. Some subscription journals are published by a society itself; others are free-standing and owned by a commercial publisher, while many, like JMS, are published professionally under a contract with the Society concerned.

You may also be aware that this division between OA and subscription has become politicised. Some commercial publishers (notably Elsevier) have been accused of making excessive profits by increasing library subscriptions at a time when the latter's budgets are squeezed. Access to less-developed countries is seen as an equity issue. Finally, the case has been made, forcefully, that research funded by the taxpayer or by charities (e.g. Wellcome) should be freely available.

There are further complications, because the OA debate has coincided with debates about the validity of the traditional peer review process, and the custom of providing unreviewed preprints online. Further, it interacts with increasing concern that Citation Indices are misused and that there are “predatory journals” that operate in OA but have little or no quality control. Furthermore, there are sites like SciHub that download papers from subscription journals and make them freely available. It has proved hard for traditional publishers to counter this trend.

Varieties of Open Access

The key feature of OA is that reading/downloading academic research papers or monographs should be freely available to all. The most familiar form is **Gold OA**, where each paper published has been funded by an APC. It is available from the moment it is published. In addition, the publication is under a Creative Commons licence, which allows for a variety of uses within the public domain.

There is a less common variant of OA, **Diamond or Platinum OA**, in which publication is paid for by a government agency or other body and not by APCs. Otherwise, the access is the same. Our Polish sister journal, *Folia Malacologica*, is currently funded in this way. I see no prospect of this happening in the UK.

There is also **Green OA**, in which a paper is published in any journal, but the author deposits a copy in a free-access repository. There may be an embargo period before release, and there are copyright restrictions on use. Embargo periods vary among journals.

There are more complications than I have listed here. There is, for example, a category of **Bronze OA**, which resembles **Gold OA** except that there are more restrictions on use.

It is worth drawing the distinction between OA journals, and OA papers, as the latter may appear in the **Hybrid Journals** mentioned earlier. There is an additional trend, not as yet affecting malacology to any appreciable extent, where authors post preprints online, freely accessible but not reviewed; these attract comments (a kind of open review) and may later be accepted in a revised form by a normal journal.

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Plan S and the politics of OA

The increase in pressure for scientific research to become OA is particularly strong in Europe, and even more so in the UK (and it does not look as though this will be affected by the UK leaving the EU). Plan S (S was chosen to stand for shock) was introduced in September last year, but elements of it have already been implemented by the UK Research Councils and some major charities. It requires those getting funding from Research Councils or their analogues to publish only in journals that are completely OA (Gold or Platinum). In theory, it comes into force in 2020. Here are the underlying principles, taken from Wikipedia:

- authors should retain copyright on their publications, which must be published under an open license such as Creative Commons;
- the members of the coalition should establish robust criteria and requirements for compliant open access journals and platforms;
- they should also provide incentives for the creation of compliant open access journals and platforms if they do not yet exist;
- publication fees should be covered by the funders or universities, not individual researchers;
- such publication fees should be standardized and capped;
- universities, research organizations, and libraries should align their policies and strategies;
- for books and monographs, the timeline may be extended beyond 2020;
- open archives and repositories are acknowledged for their importance;

To appreciate the full scope of Plan S, and some of its political implications, I suggest you read the Wikipedia article on Plan S. I find some parts to be contradictory, particularly with respect to Green OA. Notice that APCs are not capped at present, and for some journals can run to \$2,000 or more per paper. Very low APCs (<\$ 100) are strongly associated with predatory journals.

The key point for *JMS* is that publishing OA papers in Hybrid Journals will not be regarded as meeting the criteria of Plan S unless there is an approved plan to move the journal to full OA over a limited time span.

General implications

If you read the Wikipedia article and some of its links, it will become apparent that there are a number of political agendas in play. You can get even more detail by going to "The Scholarly Kitchen" site, where publishers, librarians and researchers discuss the implications of Plan S for learned societies. It does not make comfortable reading. In what follows, I am expressing personal opinions, so this section is certainly less objective.

1. The obvious aim of this "movement" is to make publicly or charitably funded research freely available. In general, this is hardly something to object to!

2. There has been increasing anger at the rising costs of some commercially published subscription journals while profits remain buoyant. Elsevier has come in for particular animosity, but it is not alone. Library budgets have been declining, which adds to the pressure. Hybrid journals have been accused of "double dipping", receiving money both from APCs and subscriptions. Hence, the animosity towards such journals.

It is worth noting that some publishers have coped with this by offering libraries "big deals" in which subs to a number of journals are bundled together; cheaper than individual subs. OUP seem to have done this: hence I suddenly found that JMS was available in my library even though I may be the only malacologist in the place!

3. At the extreme, the activists in the OA movement want to eliminate subscription journals. There is a stream of thought that also wishes to use OA to break the influence of Citation Metrics. There is definitely an anti-elitist element present, but it is not necessarily the dominant thread.

4. Most of this pressure relates to fields with large numbers of researchers and with obvious practical and political implications, like biomedical sciences. The consequences for small specialist journals, and especially those run by societies are brushed aside. Indeed (again, I stress that this is not necessarily a majority view) there are claims that the fact that some societies use revenue from their journals to finance other activities is also a form of restrictive elitism.

5. Unsurprisingly, subscription publishers (including not-for-profit ones) have mounted some robust attacks on Plan S. But many societies are equally concerned, and not just for financial reasons. While Plan S claims to require OA journals to have robust reviewing and editorial policies, it is hard to see just how this will be policed, and with authors or their funders paying the costs, the temptation to turn scientific publication into vanity publishing will be strong. There are already many predatory journals whose standards are effectively non-existent.

At a personal level, this is very significant. I will not be unique in having no institutional support or Research Council grants. An APC of \$ 1,000 per paper could make a significant dent in my income from a pension. Almost certainly, I would effectively be frozen out. And any measures to assist people like me, or those from poor nations means higher charges for others.

6. I would draw attention to the coincidence of this enthusiasm for OA with a lot of doubts and anguish about the peer review system. You may have heard of spoof articles accepted by some journals, coupled with accusations of gender or

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institutional bias. At one extreme, we have calls for double-blind review, at the other, a completely open system where an unreviewed preprint is put up for public comment. Again, there is a degree of anti-elitist feeling here coupled with the sense that unconventional work is somehow censored.

Personally, as both reviewer and associate editor for JMS, I would plead not guilty to bias, though nobody can take my word for it. I think we carry out these duties in a very scrupulous way, and eliminate only the terminally unfit.

Implications for the Society and JMS

There is one immediate implication: at the time of writing (2019), our income from the journal was around ten times as much as from subscriptions. This disparity will have increased over the years, while our membership has declined (currently 160, I think, but it was more than 300 back at the turn of the millennium).

A while ago, there was an inconclusive debate in Council about the focus of the Society's activities. On one side, an argument for more public outreach, on the other a suggestion that the Society's main function was *JMS*, and that as long as there were enough members to sustain a Council and Editorial Board a reduced membership was not a problem. In practice, we have done both, and in particular we have used funds to aid students and those at the beginning of their career. While 2018 was a particularly heavy year for expenditure, even in 2017 our expenditure on non-JMS activities was about five times our subscription income. Clearly, institutional subscriptions via OUP are the foundation on which we operate.

Let us suppose that Plan S is fully and rigorously implemented. As a hybrid journal, *JMS* would lose submissions from authors who were mandated to use only true OA journals. I have no idea what proportion of submissions would be affected (the US has not appeared enthusiastic; I think Latin American countries have not signed up, and Asian countries vary). But we would certainly have fewer submissions, and possibly a decline in quality.

Further, as more OA outlets develop, libraries might start questioning the value of their subscriptions, whether individual or part of a big deal. At present, I think we get good submissions partly because if we accept, we publish without requiring APCs; I know of at least one case where the combination of no APC and a good Citation Index within the category of specialist biological journals led to a successful submission.

It is worth adding that for PhD students and others, the availability of *JMS* through their University Library, coupled with fact that they may not see themselves as permanent malacologists (rather than using molluscs as test beds for investigating more general problems) acts against paying a subscription to be members. This may give us a long-term problem.

I do not have some magic solution up my sleeve. My impression is that OUP is a very reliable partner with a mission that goes beyond merely making money. It would be good to see how they see the future for specialist journals like ours over the next decade. This would inform any discussion we have.

I do think that the future of specialist societies that form genuine communities of scholars is under some threat.

Robert Cameron
8 April 2019.



NCBI Resources How To Sign in to NCBI

PMCID: PMC6103326

PMID: 30133601

Rev Inst Med Trop São Paulo. 2018; 60: e41.
Published online 2018 Aug 20. doi: 10.1590/S1678-9946201860041

Identification of *Biomphalaria* sp. and other freshwater snails in the large-scale water transposition project in the Northeast of Brazil

Fernando Schemelzer de Moraes Bezerra,^{1, 2, 4} Marta Cristhiany Cunha Pinheiro,³ José Damião da Silva Filho,⁴ Jssis Maria Nogueira de Castro,¹ Roberta Lima Caldeira,⁵ Mariana Silva Sousa,² Albeniza Barbosa Cavalcante,⁶ and Alberto Novaes Ramos Júnior³

Formats:
Article | PubReader | ePub(beta) | PDF(2.0M) | Citation

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Similar articles in PubMed
Freshwater snails and Schistosomiasis mansoni in the state of Rio de Janeiro, Brazil. IV - Sul Fluminense (Mem Inst Oswaldo Cruz. 2004)
Freshwater snails and schistosomiasis mansoni in the State of Rio

Screenshot of the the PLoS website

“This post by Trevor Parry-Giles assimilates some of the issues raised by Robert Cameron, but extends into the effects of the Covid19 pandemic.”

Crafting a new normalcy

Trevor Parry-Giles.

Note from the editor of the Scholarly Kitchen.

Post by Trevor Parry-Giles. Trevor is the Executive Director of the National Communication Association (NCA) and a professor in the Department of Communication at the University of Maryland. He has served as editor of Communication Quarterly and is a Distinguished Research Fellow and a Distinguished Teaching Fellow of the Eastern Communication Association. Parry-Giles' research and teaching focus on the historical and contemporary relationships between rhetoric, politics, law, and popular culture.

In 1918, the still-new National Association of Academic Teachers of Public Speaking (now the National Communication Association) faced a very real problem — should it hold its annual convention when the nation was at war? For the first (and only) time in its history, the association's leaders cancelled its annual meeting, saying to the membership that everyone's first purpose in 1918 was to prevail in the Great War. The NCA convention bounced back in 1919, and the annual convention that winter in Chicago saw attendance growth of nearly 20%. NCA has held its annual convention every year since. Three weeks after the bombing of Pearl Harbor, members gathered for the 1941 convention in Detroit and thousands gathered two months after September 11, 2001 in Atlanta for NCA's 87th annual convention. Now, in the midst of the COVID-19 pandemic, I return to this history for lessons in resilience and for guides to the future of learned societies emerging from these challenging times.

Crafting a new normalcy

Communication scholar Patrice Buzzanell (2010) articulates five processes * that are useful as organizations seek to achieve adaptive-transformative resilience. The first of these is crafting a new normalcy; for the learned society, a new normalcy results from the moderated adjustments to mission and operations that productively emanate from the exigent context. The fear and uncertainty brought on by the COVID-19 pandemic is sweeping through all facets of the higher education sector; learned societies are not immune.

Our immediate task is to harness that fear as we progress to a new normalcy. Learned societies may, for example, make normal the generation and curation of advice on online teaching and learning as such advice emerged during the COVID-19 pandemic. Recognizing that the pre-pandemic university classroom is now an altogether different place, a new normal service for members may be webinars and podcasts about online instruction, regularly publishing materials and research about online teaching/learning, etc.

Importantly, as we craft the new normalcy for today's learned societies, we can't jettison all that has worked so well for decades. A new normalcy must find that balanced point where we retain programs and initiatives that have worked, reform those that need change, and reject those that aren't working for this new time.

For the new normalcy to be truly adaptive and transformative, learned societies must be flexible even as we conserve. The learned society must be self-reflective in its determination of the new normal — making long-term, programmatic decisions in the midst of a medium or short-term crisis is arguably not the wisest plan of action. Crafting a new normalcy must be deliberate, careful, and prudent.

Affirming Important Identities

Learned societies are, fundamentally, mission-driven institutions. In this respect, we differ from trade associations or for-profit corporations. Affirming this important identity and the important identities of our various members and staffs is the second process of organizational resilience. Difficult times, like during the COVID-19 pandemic, make this a challenging task. Responding to crises, reacting to ongoing, ever-pessimistic (and often highly speculative) news — all of this militates against care and thoughtfulness, especially as we stick to our inner sense of identity and purpose. The COVID-19 pandemic has the added dimension of putting into play an array of identity threats. Not only must learned societies reinforce their own mission focus, but they must also support their members as they confront significant challenges to their identities as scholars and teachers. Labs are closed, classrooms are shuttered, and we've all become masters of Zoom seminars and meetings. Academic identities were already under siege before COVID-19, especially in the humanities and humanistic social sciences; learned societies owe it to their members to affirm and enhance the academic enterprise, to support the scholarly identity in the face of budgetary, political, and social pressures, especially as those pressures are amplified by pandemic politics.

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Using and Maintaining Communication Networks

Like everyone else over the last few weeks, I've been inundated with countless emails, fliers, letters, television ads, all working very hard to convince me that this company or that organization is on my side while we confront COVID-19. It's hard to believe that a Communication scholar would ever say this, but there is definitely a danger of over-communicating in a crisis. Indeed, as Buzzanell's work suggests, the third process of resilience for a learned society facing the COVID-19 pandemic involves avoiding over-communication and instead using and maintaining salient communication networks strategically.

With over-communication comes over-emoting. A learned society's communications, particularly in a crisis situation, should always reflect the association's strategic plan and should avoid the heightened emotions of the moment.

Crisis communication should come from a place of calm, steady consideration and must emphasize the credibility of the learned society; our members deserve this care in our communications as they entrust us with their membership dollars. What's more, these resilience processes work symbiotically — careful communications with members and other publics work to construct a new normal as they also affirm membership and scholarly identity, all in the service of the learned society's mission.

Putting Alternative Logics to Work

A fourth process involved in building a resilient learned society is the delicate task of putting alternative logics to work in our operations and activities. Nowhere is this more challenging than with the learned societies' annual meetings and conventions.

The COVID-19 pandemic, along with its accompanying "social distancing" measures and other social, political, and economic dislocations, has given rise to numerous calls for learned societies and other groups to (re)assess the value and merit of an annual convention. Now is a good time, some believe, to determine if learned societies should even continue to host annual meetings. I might suggest that, against all conventional wisdom, this is precisely the worst time to consider, existentially and fundamentally, the value of an annual convention. Conditions surrounding the COVID-19 pandemic and the responses to the pandemic by local, state, and national political leaders have resulted in a highly charged, emotionally complicated context. A more prudent approach might be to use the pandemic and its consequences to assess operational readiness and associational flexibility and to put alternative logics to work. Exploring options for replacement virtual or hybrid conferences, rethinking fee structures and sponsorship opportunities, adjusting the amount and nature of submissions are all examples of putting alternative logics to work and assuring the resilience of our learned societies and our annual conferences.

Foregrounding Productive Action

Resilience requires strategy and patience — a resilient learned society seeks to transcend the anxiety and fear of the moment even as it deftly adapts to new, changing circumstances. Accompanying that deftness and that adaptability is an eye for the optimistic and productive. The final process of resilience calls on the learned society to foreground productive action while backgrounding the negative and the counterproductive. Learned society members are confronting a panoply of pessimism during this pandemic, from budget threats and hiring freezes on their home campuses to illness and disease in their homes, from forced online teaching to increases in mental health concerns among students and colleagues. Learned societies that reify and repeat that trauma and drama are not helping—our members are looking to us for productive action, for concrete ways that we can alleviate just a little of the anxiety shrouding their professional lives.

In short, resilient learned societies will understand how their operations and programs do (or do not) achieve the mission of the association and how operationally ready and flexible they are to make changes and/or accommodations in response to emergencies and contingencies. To do so from an alarmist or fatalistic perspective does a disservice to the learned society, its mission, and its members; a more resilient and somewhat more optimistic outlook comes from no less a leader than the ever-resilient Queen Elizabeth II: "We should take comfort that while we may have more still to endure, better days will return: we will be with our friends again; we will be with our families again; we will meet again."

*Buzzanell's five processes are (a) crafting normalcy, (b) affirming identity anchors, (c) maintaining and using communication networks, (d) putting alternative logics to work, and (e) downplaying negative feelings while foregrounding positive emotions, such as hopefulness and self-efficacy.

Patrice M. Buzzanell (2010) Resilience: talking, resisting, and imagining new normalcies into being. *Journal of Communication*, 60, (1) pp 1-14



“The argument is developed further by mathematician Robert Harington.....”

Why scholarly societies are vitally important to the academic ecosystem

Robert Harington (taken from the Scholarly Kitchen 3/10/19)

We live in a world where bigger is better, scale matters, and those with the largest coffers and most profitable businesses have an outsized influence on policy. Take, for example, the publishing trade organization, STM. STM presents itself as the leading global trade association for academic and professional publishers. In the STM 2018 Report, we learn that The Europa World of Learning has identified over 5000 scholarly societies globally. However, although STM’s members include learned societies, university presses, and for-profit publishers, there is relatively sparse representation in leadership, especially from smaller society members. The problem here is that STM is a commercial trade organization, and its activities are largely funded by the big commercial publishers who have the money to pay for initiatives – they get to call the shots. I will be attending the upcoming STM conference in Frankfurt, Germany in October – the wind-up to the Frankfurt Book Fair. I was somewhat dismayed this year to see that the program, while diverse in many ways, does not include a single speaker from a scholarly society, large or small – though I am sure it will be an enjoyable conference. It always is. Although I may be a wee bit biased (having worked for such societies for the past 10 years), I feel that this is a serious omission.

In this article I attempt to explain the critical role of scholarly societies, bearing in mind these societies vary enormously — in terms of the culture of the discipline and scale. I will argue that independent scholarly societies are vital to the academic ecosystem, and are the only community organizations whose sole reason for existence is to provide for the scholars in their academic community. The sad reality in publishing circles is that even with laudable initiatives such as the funder-driven [Plan S](#), which ostensibly aims for an open world of research and content, it is the big corporate publishers who win.

Let’s look at a “Life-in-the-day” of an independent scholarly society. The American Mathematical Society (AMS) is a fiercely independent society since 1888, with a mission to advance research and connect the diverse global mathematical community through publications, meetings and conferences, the discovery database MathSciNet, professional services, advocacy, and awareness programs. The AMS has 30,000 individual members in addition to 570 academic institutional members. The business reality is that sales of AMS publishing products account for 70% of the society’s annual operating revenues. There is an annual financial surplus, but it depends where you look as books, journals, and the MathSciNet database do not all contribute equally, and the AMS goes out of its way to be reasonably priced, frequently publishing content that perhaps would not be viable to publish if AMS were, like corporate publishers, purely serving the needs of shareholders. In fact, critics of publisher prices and unreasonable profit margins often lump societies and corporate publishers in the same pot. I am not going to share our financial details, but in essence, I find it remarkable that gross profit is almost always mistaken for net profit, and yet in reality the net is small and always reinvested by societies back into the academic community – indeed, that is their *raison d’être*.

Recently, Karen Saxe (AMS Associate Executive Director & Head of Government Relations) and I met by telephone with the new Director of the White House Office of Science and Technology Policy, Kelvin Droegemeier. It seemed clear to us that the OSTP does not want to burden authors with the complexities around open access policies, and is keen to take a completely different approach than Europe does in developing such policies. One critical point we aimed to communicate was that our services are not merely aimed at AMS members, but meant to benefit the field more generally. One could argue that any society purely providing benefits to its membership is not truly serving the wider academic community in the discipline. In fact, for the AMS, it is perhaps a strength and a weakness that the programs and services we provide are steered towards all mathematicians, not just members of the AMS. This of course raises a further problem – why would a mathematician join the AMS? In the end the value proposition is somewhat similar to belonging to a political party. You join to further policies you believe in, provide support for your community, knowing that in unity there is prosperity – a point that not everyone appreciates. The AMS is of course not alone in doing a terrible job of communicating our value to the world. If revenues evaporate, and the society withers, the mathematical community will notice — but by then it will be too late.

Let’s return to my claim that even initiatives such as Plan S are cementing the role of the corporate publisher, leaving societies to wonder whether they may survive unless they partner with a larger commercial organization. The Plan S transformative agreements have essentially created institutional lock-in businesses on a grand scale. Only publishers who have significant publishing scale may effectively form transformative Publish and Read agreements with institutions (a category that can include governments). This is a problem, not just for societies looking to be as open as possible, but even for fully open access publishers such as PLOS. As Alison Mudditt (CEO of PLOS) recently pointed out, if you are already in full compliance with Plan S you are essentially shut out of the monies attached to transformative deals as publishers move from subscription to gold open access. Where once the Big Deal created lock-in, leaving smaller publishers to scramble for remaining institutional funds, now there is the added realization that only through scale can open access be provided. Otherwise, where will the revenues come from?

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Add to this the cultural difference between fields and things look bleak for scholarly societies, especially when considering Gold open access. Where will authors without sources of funding find the money to pay for article processing charges? Gold open access works for well-funded fields and for principal investigators, but not for fields where research is not grant-driven and for those researchers who are not in charge of budgets, such as those starting out in their fields. An interesting recent development is the release of the report Society Publishers Accelerating Open Access and Plan S (SPA-OPS) Project. The report is encouraging in the sense that there is clearly a willingness from institutions and funders to at least consider how to help shift scholarly societies to open access. Yet, despite a plethora of general model suggestions, including discussion of Subscribe to Open, there is no clear path to sustainable revenues for many societies through open access, especially Plan S compliant open access. For me, the rather profound effect of discipline culture when considering a path to open access is missing from the report. I do also recommend reading Alison Mudditt's interesting article "Plan S and the Transformation of Scholarly Communication: Are we Missing the Woods?"

However, the future may not be as bleak as I have suggested so far.

It is a cliché to state that where there is a threat there is opportunity, but it really is true. If societies such as the AMS can communicate the value we bring to our communities effectively enough, help simplify a researcher's life so they may concentrate on research and teaching (which is what they signed up for), and provide a path for career success, tenure, and collaboration — then the value is clear. Most researchers do not want to be burdened with dissecting which open access policy they must follow, where they may and may not publish their articles, and where to find funds required to publish, when for most it is not a priority. In fact, what researchers really would like to see are publishers that make it easy to submit an article for consideration at a journal – why is it still so hard? If societies can demonstrate their value, then a financial model that allows subscriptions to thrive and promotes openness, such as *Subscribe to Open*, or joining initiatives such as *Research4Life* (as we at the AMS recently have) that are paired with subscriptions, societies will be stronger than ever before. The unity in collective action is what societies provide for their communities. This kind of unity is not achieved if the business of society publishing, and policy positions on openness are subsumed by a corporate partner with differing ideals from society governance.

Perhaps the next step is cross-discipline collective action between the many independent scholarly societies with missions and publishing programs globally. Indeed, there are seedlings of such an approach beginning to sprout. The *Scientific Society Publisher Alliance* (SSPA) is one such project.



"Harrington's 'next step' in his final paragraph might be a useful beginning to the process of re-realising the Malacological Society of London."

Invited article

Emerging from the shell: development of the common whelk as a novel model of phenotypic variation

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INTRODUCTION

For decades, the diversity of animal form has captivated both the public and scientific communities alike. The observable properties of an organism's appearance (typically referred to as a phenotype) and the degree to which such traits vary between individuals, populations, and species remain an area of intense scientific interest. Phenotypic variation can present as conceptually simple traits, such as variable hair or eye colour. However, it can also describe more complex morphological (e.g., height or limb length), behavioural (e.g., behavioural disorders), or developmental (e.g., body symmetry) variation. Phenotype manifestation is determined by an individual's genotype (which is shaped by selective forces imposed on the population in the past), as well as by the individual's environment during development.

Understanding the relative influence of genetic versus environmental variation on phenotype determination, and how these interactions create an impact on the evolution of novel phenotypes, presents a complex scientific task. Many significant advancements have been made by investigating various aspects of phenotypic variation in simplified model systems, of which molluscs represent one of the most notable. Molluscan shells are conspicuous, making the scoring of phenotypic variation highly tractable, while the molluscan shell is produced by a single conserved tissue (the mantle). Interactions between genetic and environmental factors on phenotype have been studied in various terrestrial and intertidal molluscs (e.g., in *Cepaea*, *Radix*, *Littorina* and *Nucella*), however assessments of subtidal species remain scarce.

Since 2007 our research group, based in Iceland, has been striving to address the knowledge gap in subtidal molluscs. By characterizing and documenting the phenotypic variation in the Common Whelk, *Bundatum*, we aim to provide critical insight into the prevalence, evolution, and regulation of polymorphism in subtidal gastropods. We share this overview of our works in the hopes it sparks further conversation and collaboration, as well as an opportunity to spotlight the various morphological and genetic datasets we wish to share with the broader scientific community in the future.



Example of the common whelk, *B. undatum*, a subtidal gastropod found across the North Atlantic.



Examples of phenotypic shell diversity in *B. undatum*. Note the variation in striping and ridges (top) as well as colour (bottom).

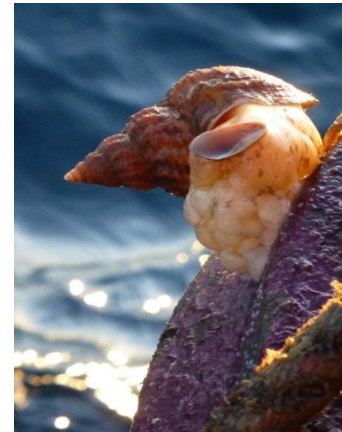
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BIOLOGY AND UTILIZATION OF THE COMMON WHELK

The common or waved whelk *Buccinum undatum* L. is a subtidal neogastropod found on both sides of the North Atlantic ⁽¹⁾. It can reach up to 150 mm in shell height and the age of ~13 years. *B. undatum* typically lives below the tidal zone down to a depth of 200 m but has been documented at even greater depths ^(1,2). The whelk is a commercially significant capture species across the North Atlantic, with the highest consumption markets being in Southeast Asia/South Europe. The species has historically been used for both human consumption and bait, and today it is fished with baited traps in Northwest Europe and North America. Given the ubiquity of *B. undatum* fisheries across the North Atlantic, various fisheries-focused surveys have been implemented, encompassing a diverse range of *B. undatum*'s habitat.



B.undatum are commonly fished for human consumption using baited traps.



A female *B.undatum* laying an egg mass on the outer edge of a whelk trap.

FISHERIES ENGAGEMENT BEGETS SCIENTIFIC DISCOVERY

Throughout the North Atlantic, fisheries surveys document a consistent trend of spatial variability in *B. undatum*. These trends can manifest as variations in life-history traits such as size at sexual maturity ⁽³⁾, size distribution ⁽⁴⁾, and timing of reproduction cycle ⁽⁵⁾, as well as spatial trends in shell morphology ^(1,6-8). *B. undatum* employs a sedentary life-history strategy, with internal fertilization, direct development, and low adult mobility life-history strategies. Therefore, signatures of population structuring following an isolation-by-distance model ^(6,9-11) are somewhat expected and are consistent with general expectations of sedentary marine species such as *B. undatum*. However, the scale of population structuring was significantly larger than anticipated, with spatial variation in shell morphology observed at distances as little as ~20 km ⁽¹²⁾.



Clear phenotypic divergence can be seen between sample sites in Breiðaffjörður. Note the primary red and orange colouration of individuals from Oddbjarnarsker (left) versus the green colouration of whelk from Brjánslækur (right). These two sample sites are approximately 21km apart.

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Example of fishing vessel and practices in Iceland. The Garpur SH-95 was the primary vessel used to collect whelk samples for fisheries surveys in Breiðafjörður.

ICELAND IN FOCUS: COMMON WHELK IN THE BAY OF BREIÐAFJÖRÐUR

The bay of Breiðafjörður, West Iceland, is a highly dynamic and diverse ecosystem, home to the most abundant whelk population in Iceland. Fishing of *B. undatum* began in 1996, with fishing intensities varying in the years that followed. At its maximum (in 2006), the industry stakeholders (i.e., fishers, vessel owners, factory processors) in Iceland and the Faroe Islands raised concerns over the sustainability of the fishery and potential for loss of biodiversity. In particular, the timing of the whelk's reproduction in Iceland was not known, and even though size at sexual maturity had been estimated in Iceland by Gunnarsson and Einarsson (¹³), it was not known for Breiðafjörður's primary fishing zones, at large. A collaborative project between Vör–Marine Research Centre at Breiðafjörður, Sægarpur Whelk Processing, Fiskirannsóknastovan and O.C. Joensen was initiated to address stakeholders concerns directly. Two key outputs resulting from this collaboration for Icelandic waters were (A) Icelandic whelk's reproductive period is analogous to European stocks, breeding from autumn to mid-winter; and (B) that a minimum landing size of 45 mm is too low, with Breiðafjörður's whelk reaching sexual maturity at shell heights ≥ 50 mm. Minimal landing size has since been raised to 50 mm in Breiðafjörður, while fishing quotas are reviewed annually, with the Northern and Southern regions of Breiðafjörður treated as separate fisheries.



Map of, and distribution of whelk sampled from Breiðafjörður during fisheries surveys. Ten sites were surveyed across Breiðafjörður (top), cataloguing a number of 'regional' variations in shell phenotype (bottom).

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Fisheries surveys were conducted across 10 different locations in Breiðafjörður, Iceland. Whelk were often stored in large sorting trays, and sampled on-boat during the drive from one sample site to the next.

CHARACTERIZING POLYMORPHISM IN BREIÐAFJÖRÐUR

In addition to fisheries-relevant datasets, the Breiðafjörður survey allowed us to accumulate an extensive catalogue of morphological and genetic data from whelk across the bay. This dataset serves as the perfect foil to validate a finding by Icelandic fishermen; that the size, shape, and colour of whelk varied across Breiðafjörður, with 'local ecotypes' being easily distinguishable based on morphology. In particular, shell colour was of great interest due to surveys describing multiple novel shell colour morphs that are not known to occur elsewhere across North Atlantic.

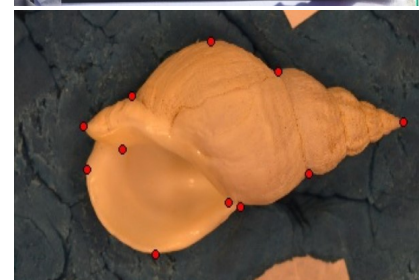
Morphometric analyses of Breiðafjörður's whelk concluded clear depth-associated trends in both shell shape, thickness, and colour. From the inner to the outer part of the bay ran a gradient of increasing roundness, shell colour diversity, the proportion of striped shells, and thinness of the shell (^{7,12}). Shape differentiation between sites increased with geographic distance and depth, suggesting limited population connectivity. Similarly, studies of molecular genetic variation ran in parallel to morphometric analyses concluded that population genetic structure was present within Breiðafjörður, with differentiation in microsatellite and mitochondrial markers also consistent with an isolation-by-distance model (^{10,11}). A secondary genetic study using a significantly expanded SNP dataset further confirmed the existence of population structure throughout Breiðafjörður, with genetic variation structured in concordance with the phenotypic variation (¹⁴).

In a bid to further delineate the relative influence of environmental versus genetic effects on the shell morphology, a common garden experiment was designed where juveniles from phenotypically different sites were raised in a controlled environment. Shell morphology and colour were scored throughout several years, and the juveniles mostly retained their parental phenotypes, indicating heritable variation, in particular with regard to shell colour (¹⁵). However, the green and red colours displayed by the wild-caught whelk were not present in the lab-raised juveniles. These colours have been hypothesized to be environmental colouration due to epibionts, algae, or cyanobacteria for the green colour (¹⁶) and coralline algae for the rosy colour (¹⁷).

Example of common garden experimental setup for rearing *B. undatum*.

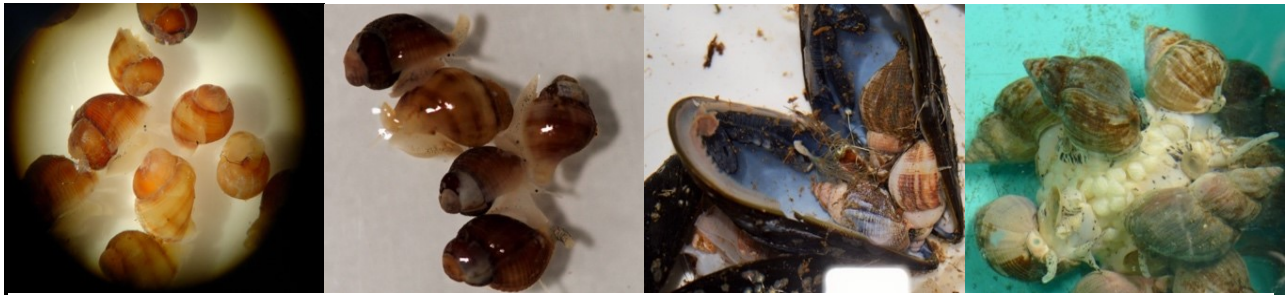
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Example of colour (top) and morphometric (bottom) analyses conducted on whelk sampled from Breiðafjörður.



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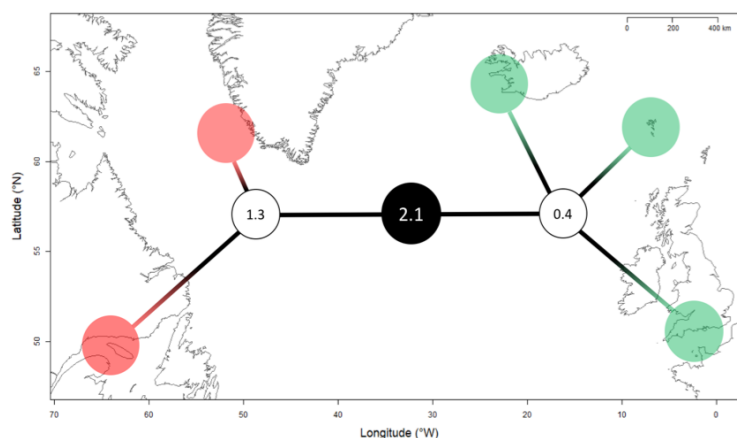
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Whelk were reared in a common garden experiment for approximately four years, from hatching (left), through juvenile (middle left), adolescent (middle right), and up until sexual maturity (right).

BIGGER QUESTIONS, BROADER HORIZONS

For our research group, Breiðafjörður continues to serve as a novel system for the analysis of phenotypic divergence across a relatively small geographical scale. It is well known that the topographic complexity of Breiðafjörður's various islands and fjords make the area unique amongst *B. undatum*'s broader Icelandic and North Atlantic distribution. Thus it is unclear whether the clines in colour, as well as genomic differentiation in association with depth observed for Breiðafjörður, are characteristic for the species more broadly. To complicate matters further, two distinct genetic lineages of *B. undatum* are evident within the North Atlantic based on mitochondrial, and RAD sequencing approaches (¹⁰, Goodall *et al.* under review, ¹¹). These distinct lineages occur across the Western (North America and Canada) and Eastern (Iceland, Faroe Islands, United Kingdom, and Europe) regions of the North Atlantic. The divergence between the two lineages probably takes place early in the last Ice Age (~2.1 mya), suggesting that the two lineages may represent cryptic species, which have diverged under allopatry (¹⁰). In general, the morphological variation across the North Atlantic agrees with the genetic split (^{8, 15}), as do spawning periods, with the timing of reproduction varying considerably between the two continental groups (or putative species) (⁵). Additionally, trends of depth-associated structuring have been reported for English populations (⁹), suggesting that some degree of congruence in population genetic structuring in association with depth may exist for the Eastern North Atlantic lineage.



Across the North Atlantic, mitochondrial markers (COI-1 and COI-2) indicate *B.undatum* constitutes two distinct genetic lineages, diverged ~2.1 million years ago (adapted from Magnúsdóttir H. *et al* (¹¹)). These two lineages comprise individuals from either the North Americas or Europe.

CONCLUSION—BUILDING TOOLS FOR A COLOURFUL FUTURE

Resolving trends in phenotypic variation across multiple geographic scales remains a difficult task. If progress is to be made, investment in genomic resources from a diverse array of species (such as subtidal molluscs) must be made. Our research team is working to build *B. undatum* as a robust model species for the ongoing study of molluscan evolution and adaptation. The first stage in this mission was the release of the *B. undatum* mitochondrial genome (18) last year. Moving forward, the three main goals of our current research are the generation of a draft genome assembly, an environment, and colour link transcriptome, and SNP profiling data sampled from whelk across the North Atlantic. We are working to release these resources publically, in the hopes they can be taken up and integrated into future scientific works. We hope these resources help to establish subtidal molluscs, alongside terrestrial and intertidal species, as critical models of phenotypic diversity.

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Current Common Whelk research team based in Iceland. From left to right, members include Erla Björk Örnólfssdóttir, Zophonías O. Jónsson, Hildur Magnúsdóttir, Snæbjörn Pálsson, and Jake Goodall.

REFERENCES

1. GOLIKOV, A.N. 1968. Distribution and variability of long-lived benthic animals as indicators of currents and hydrological conditions. *Sarsia* **34**(1):199-208.
2. ÓSKARSSON, I. 1982. Skeldýrafána Íslands. Reykjavík, Iceland.
3. HAIG, J.A., PANTIN, J.R., SALOMONSEN, H., MURRAY, L.G., & KAISER, M.J. 2015. Temporal and spatial variation in size at maturity of the common whelk (*Buccinum undatum*). *ICES Journal of Marine Science* **72**(9):2707-19.
4. EMMERSON, J.A., HOLLYMAN, P.R., BLOOR, I.S.M. & JENKINS, S.R. 2020. Effect of temperature on the growth of the commercially fished common whelk (*Buccinum undatum*, L.): A regional analysis within the Irish Sea. *Fisheries Research* **223**:105437.
5. BORSETTI, S., MUNROE, D., RUDDERS, D. & CHANG, J-H. 2020. Timing of the reproductive cycle of waved whelk, *Buccinum undatum* on the U.S. Mid-Atlantic Bight. *Helgoland Marine Research* **74**(1):5.
6. MARIANI, S., PEIJNENBURG, K. & WEETMAN, D. 2012. Independence of neutral and adaptive divergence in a low dispersal marine mollusc. *Marine Ecology Progress Series* **446**:173-87.
7. MAGNÚSDÓTTIR, H., PÁLSSON, S., WESTFALL, K.M., JÓNSSON, Z.O. & ÖRNÓLFSDÓTTIR, E.B. 2018. Shell morphology and color of the subtidal whelk *Buccinum undatum* exhibit fine-scaled spatial patterns. *Ecology and Evolution* **8**(9): 4552-63.
8. MAGNÚSDÓTTIR, H., PÁLSSON, S., WESTFALL, K.M., JÓNSSON, Z.O. & ÖRNÓLFSDÓTTIR, E.B. 2019. Morphological variation in genetically divergent populations of the common whelk, *Buccinum undatum* (Gastropoda: Buccinidae), across the North Atlantic. *Biological Journal of the Linnean Society* **128**(1):93-106.
9. WEETMAN, D., HAUSER, L., BAYES, M.K., ELLIS, J.R. & SHAW, P. 2006. Genetic population structure across a range of geographic scales in the commercially exploited marine gastropod *Buccinum undatum*. *Marine Ecology Progress Series* **317**:157-69.
10. PÁLSSON, S., MAGNÚSDÓTTIR, H., REYNISDÓTTIR, S., JÓNSSON, Z.O. & ÖRNÓLFSDÓTTIR, E.B. 2014. Divergence and molecular variation in common whelk *Buccinum undatum* (Gastropoda: Buccinidae) in Iceland: a trans-Atlantic comparison. *Biological Journal of the Linnean Society* **111**(1):145-59.
11. MAGNÚSDÓTTIR, H., PÁLSSON, S., WESTFALL, K.M., JÓNSSON, Z.O., GOODALL, J. & ÖRNÓLFSDÓTTIR, E.B. 2019. Revised phylogeography of the common whelk *Buccinum undatum* (Gastropoda: Buccinidae) across the North Atlantic. *Biological Journal of the Linnean Society* **127**(4):890-9.
12. MAGNÚSDÓTTIR, H., OLSEN, K., MATRAS, U. & ÖRNÓLFSDÓTTIR, E. 2010. Biology and distribution of the common whelk (*Buccinum undatum*) in Icelandic and Faroese waters/ Konksneglens (*Buccinum undatum*) biologi og udbredelse i farvandet ved Island og Faerøerne Project No. 282. VÖR Marine Research Institute. Contract No.: Project no. 282 NORA.
13. GUNNARSSON, K. & EINARSSON, S. 1995. Observations on whelk populations (*Buccinum undatum* L., Mollusca; Gastropoda) in Breiðafjörður, Western Iceland. International Council for the Exploration of the Sea. Available from http://www.ices.dk/sites/pub/CM%20Documents/1995/K/1995_K20.pdf.
14. GOODALL, J., WESTFALL, K.M., MAGNÚSDÓTTIR, H., PÁLSSON, S., ÖRNÓLFSDÓTTIR, E.B. & JÓNSSON, Z.O. RAD sequencing reveals fine-scale population structuring in European Common Whelk, *Buccinum undatum*, and confirms a genetic split across the North Atlantic. *Ecology and Evolution*. under review.
15. MAGNÚSDÓTTIR, H., PÁLSSON, S., WESTFALL, K.M., JÓNSSON, Z.O. & ÖRNÓLFSDÓTTIR, E.B. Assessment of morphological difference between distinct lineages of common whelk (*Buccinum undatum*) in a common garden experiment. *Journal of Experimental Marine Biology and Ecology* submitted.
16. HOLLYMAN, P.R. 2017. Age, growth and fecundity of the whelk, *Buccinum undatum*, in coastal shelf seas: Ph.D. Thesis, Bangor University.
17. GUNNARSSON, K. & EINARSSON, S.T. 2000. *Beitukóngur og hafkóngur*. In: Institute MR, editor. Reykjavík, Iceland.
18. JÓNSSON, Z.O., PÁLSSON, S., WESTFALL, K.M., MAGNÚSDÓTTIR, H., GOODALL, J. & ÖRNÓLFSDÓTTIR, E.B. 2019. The mitochondrial genome of common whelk *Buccinum undatum* (Neogastropoda: Buccinidae). *Mitochondrial DNA Part B* **4** (1):458-60.



Early Career Research Grant Reports

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Cryptic and invasive freshwater *Galba* snailsPilar Alda^{1,2,3}¹ Laboratorio de Zoología de Invertebrados I, Departamento de Biología, Bioquímica y Farmacia, Universidad Nacional del Sur. San Juan No. 670, B8000ICN Bahía Blanca, Buenos Aires, Argentina.² Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET), Argentina.³ MIVEGEC, University of Montpellier, CNRS, IRD, Montpellier, France.² Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET), Argentina.³ MIVEGEC, University of Montpellier, CNRS, IRD, Montpellier, France.

Morphological discrimination has proved to be difficult between certain species. In some cases, morphological variability can be higher *within* than *between* the species. When these cryptic species easily colonize environments beyond their native distribution, accurately identifying and tracking species becomes challenging. However, crypticity can be disclosed and species boundaries can be delimited by studying the genetic diversity and the phylogeography of the taxon of interest. Knowing the distribution of cryptic non-native species is essential to protect biodiversity, economy, and health⁽¹⁾.

Galba species are a group of small-shelled freshwater snails which distribution remains poorly known mainly due to the difficulty in morphologically differentiating them^(2,3). Most *Galba* species have a similar shell morphology (Fig. 1) and internal anatomy⁽³⁾. This is the reason why *Galba* species have been widely misidentified all over the world. For instance, *G. schirazensis* has often been confused with *G. truncatula* (Fig. 2) in Europe and Asia and with *G. truncatula* or *G. cubensis* in the Americas⁽²⁾. *Galba* species boundaries cannot be established by crossing experiments in the laboratory (as has been done, for instance, for snail species in the genus *Physa*) because *Galba* species reproduce mainly by self-fertilization⁽⁴⁾. Except for *G. cousini* that has a distinct morphology, *Galba* individuals can be accurately ascribed to one species or another only by DNA-based approaches.



Figure 1. Shell morphology of *Galba* species.
Pictures taken by Jean-Pierre Pointier.

Galba species can be dispersed for long distances thanks to their mode of reproduction⁽²⁾ and their capacity to withstand drought. One or a few individuals can settle and create a population because individuals are capable of (and mostly prefer) self-fertilization⁽⁴⁾. The great capacity for dispersal of *Galba* snails has facilitated the worldwide expansion of fasciolosis, the disease caused by the liver fluke *Fasciola hepatica* and transmitted by *Galba* snails to livestock and humans⁽⁵⁾. The absence of an accurate species identification and, hence, a lack of a well-known distribution can prevent us from correlating the arrival of an invading species with the (re)emergence of the disease. Despite the epidemiological relevance of *Galba* species, up to now most studies have focussed on one or a few species of *Galba* in specific localities or regions⁽⁴⁾.

I am a member of a group of malacologists and parasitologists⁽⁶⁾ who aimed to study the current distribution and the phylogenetic relationships of *Galba* species. We achieved this goal mainly thanks to a large-scale sampling mostly collected by Dr. Jean-Pierre Pointier in 13 countries (~200 sites) from the whole Americas—the largest and the most-covering geographical scale study done up to now (Fig. 3). We focussed this study in The Americas because it is the region of the world where these snail species originated and diversified and where fasciolosis represents a serious disease.

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Thanks to an Early Career Research Grant from the Malacological Society of London and other grants, we used an integrative approach combining morphological observations with molecular markers (microsatellites and DNA sequences for four genes) to analyze *Galba* samples taken from across the Americas⁽⁶⁾. Our American database was augmented with data retrieved from GenBank (including Old World samples; Fig. 3) and analyzed using species delimitation methods and Bayesian phylogenetic reconstruction. Our analysis suggest that the genus *Galba* evolved ca. 22 myr ago and today comprises six clusters of populations.



Figure 2. *Galba truncatula*.

We recommend redefining species boundaries such that three of these clusters are understood as one species each, and that the other three clusters correspond to two highly diverse species or species complexes⁽⁶⁾. We also conclude that crypsis in the genus *Galba* may best be explained by a 'shared morphological stasis'. *Galba* populations live in temporary habitats and are more amphibious than other freshwater snails, which may mitigate both predation and interspecific competition. Adaptation to such habitats may impose strong stabilizing selection for a shell morphology able to resist desiccation and concomitant morphological stasis⁽⁶⁾. We emphasize that cryptic *Galba* species must be accurately identified with molecular markers since these species demonstrate different patterns of invasiveness and susceptibility, host-parasite compatibility, and immunological resistance to *Fasciola hepatica*.

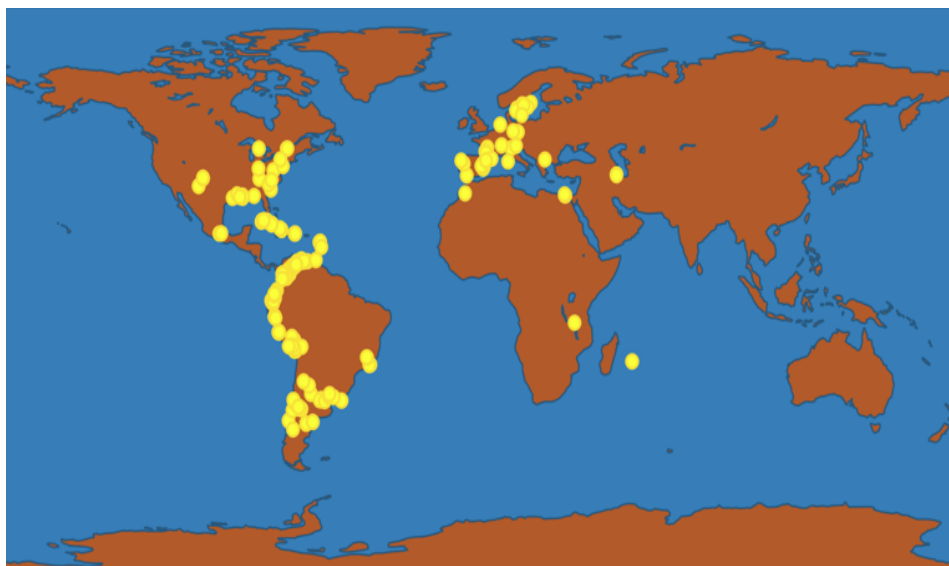


Figure 3. Worldwide records of *Galba* species based on DNA approaches.

REFERENCES

- 1 BICKFORD, D. *et al.* 2007. Cryptic species as a window on diversity and conservation. *Trends in Ecology & Evolution* **22**: 148–155.
- 2 CORREA, A. C. *et al.* 2010. Bridging gaps in the molecular phylogeny of the Lymnaeidae (Gastropoda: Pulmonata), vectors of Fascioliasis. *BMC Evolutionary Biology* **10**: 381
- 3 CORREA, A. C. *et al.* 2011. Morphological and molecular characterization of Neotropic Lymnaeidae (Gastropoda: Lymnaeoidea), vectors of fasciolosis. *Infection, Genetics and Evolution* **11**:1978–1988.
- 4 LOUNNAS, M. *et al.* 2018. Population structure and genetic diversity in the invasive freshwater snail *Galba schirazensis* (Lymnaeidae). *Canadian Journal of Zoology* **96**, 425–435.
- 5 MAS-COMA, S., FUNATSU, I. R. & BARGUES, M. D. 2001. *Fasciola hepatica* and lymnaeid snails occurring at very high altitude in South America. *Parasitology* **123**, S115–S123.
- 6 ALDA, P. *et al.* 2019. Systematics and geographical distribution of *Galba* species, a group of cryptic and worldwide freshwater snails. *PCI Evolutionary Biology*. <https://doi.org/10.1101/647867>



Towards a first molecular phylogeny of Caecidae micro snails (Truncatelloidea, Caenogastropoda)

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INTRODUCTION

Caecidae (Gray, 1850) form a species-rich family of marine gastropods with worldwide distribution that inhabit the interstitial spaces of algae, coral, and sediments. The majority of species are minute in size (i.e., < 4 mm), and caecids are unusual among gastropods in exhibiting different ontogenetic shell morphologies leading to an uncoiled, tubular shell in adult snails (see Fig. 1 for the typical caecid shell morphology). The intricate developmental patterns can vary among the different caecid genera (Bandel 1996), e.g., *Caecum* and *Meioceras* - which bear the highest known species diversity among Caecidae and comprise over 80% of described species - shed their coiled juvenile shell during the process of adolescence.

A molecular phylogenetic study by Criscione and Ponder (2013) places the family Caecidae within the Truncatelloidea (Caenogastropoda). However, until now, the phylogenetic relationships within Caecidae are poorly understood, and morphologically defined classification into genera and subgenera remains partially controversial. The present study is a first molecular approach to identify phylogenetic relationships among the Caecidae and species boundaries within the genus *Caecum*. It combines molecular phylogenetic analyses with microstructural (re-) investigation of shells to test the current taxonomy and to assess the validity of the established taxa. Within the framework of my master thesis, I plotted traditional shell characters used in caecid taxonomy onto the molecular phylogeny to gain insights into the evolution of the caecid shell and explore the range of the putative phylogenetic signal in the different characters.

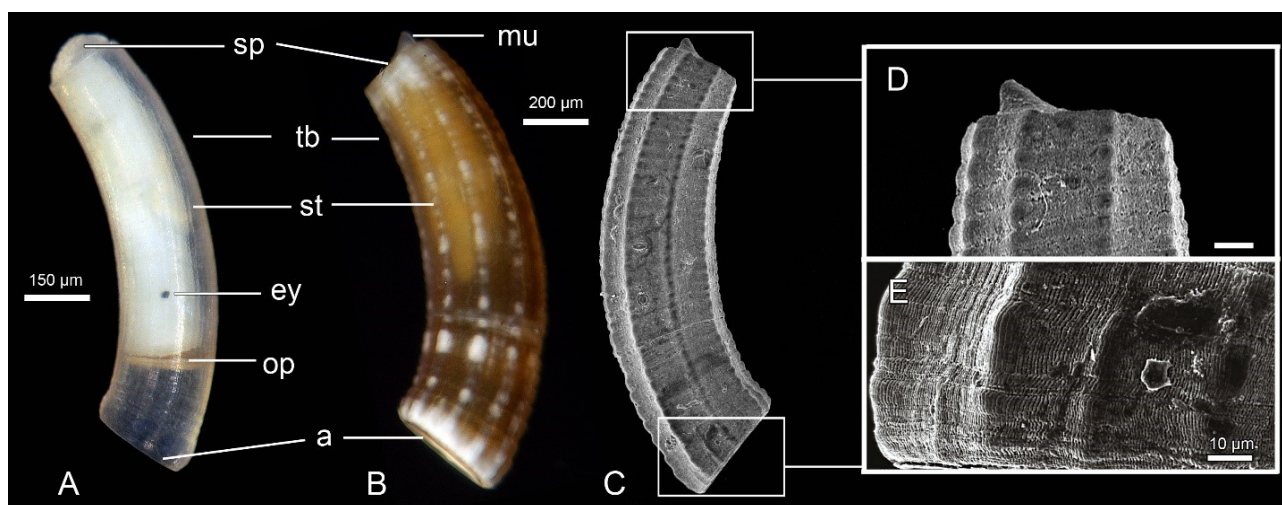


Figure 1. (A) *Caecum multicostatum* de Folin, 1867 and (B) *Caecum plicatum* Carpenter, 1858, showing important taxonomic characters traditionally used in species identification; (C) SEM scan of *Caecum plicatum*. SEM close-up of mucro (D) and septum (E) microstructure. *a*, aperture; *ey*, eye; *mu*, mucro; *op*, operculum; *se*, septum; *st*, shell structure (ornamentation); *tb*, tube.

MATERIAL AND METHODS

The present study comprises a worldwide sampling of Caecidae including species from all major biogeographic zones, which were kindly provided by different Natural History Collections.: The Bavarian State Collection of Zoology (ZSM), Germany granted access to material collected during recent expeditions (2008-2018) to Central and South America, Japan, Papua New Guinea and New Caledonia, the latter two organized by the Muséum National d'Histoire Naturelle (MNHN); the MNHN Paris, France to material from Madagascar (2010), Guadeloupe (2012) and Martinique (2016), and (3) the Smithsonian Institution, Washington, USA provided molecular sequences of Caecidae collected during meiofaunal sampling trips to Belize in 2010 and Panama in 2010 and 2016. My collecting events took place in 2018 and 2019 in Brazil, France, and Portugal. In total, 285 individuals were analyzed and assigned to morpho-species based on the traditional taxonomic characters of their shells.

One specimen of each morphospecies was further examined by Scanning Electron Microscopy (SEM) to document the microstructural pattern of the shell, that has shown to be taxonomically relevant (Figure 1, 2). DNA was extracted from 86 individuals (including the specimens previously investigated via SEM) using a CTAB-extraction protocol combined with spin-column based recovery of the DNA (see Doyle & Doyle, 1987 and Kneibelsberger & Stöger, 2012 for details).

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I amplified three molecular standard markers via polymerase chain reaction (PCR) using established primers and protocols for gastropods (see Jörger *et al.*, 2010; Klussmann-Kolb *et al.*, 2008): mitochondrial cytochrome *c* oxidase subunit I (COI) and 16S ribosomal RNA genes, and the nuclear 28S ribosomal RNA gene (partial). All sequences were screened for putative contaminations using the online web service BLAST of the public database NCBI GenBank. Single-gene alignments were generated using MAFFT (v. 7.419, Katoh *et al.* 2002) with default parameter settings. Further, a combined alignment of 79 taxa was generated, including all specimens of which at least two out of the three genetic markers were successfully sequenced.

Phylogenetic trees were inferred from the resulting sequence alignments using the Maximum Likelihood method (IQ-TREE, Nguyen *et al.* 2014 with the GTR+G4+FO model, equivalent to GTR+G in RAxML vers. 8.2, Stamatakis 2014) and Bayesian Inference (MrBayes, v.3.2.6; Huelsenbeck & Ronquist 2001) with a partition for genes and COI codon positions. Eight truncatelloid out-group taxa were selected based on previous phylogenetic analyses (Criscione & Ponder 2013; Golding 2014).

All resulting trees were critically compared and checked against each other for incongruences in the phylogenetic signal. Twelve shell characters that are traditionally used for caecid classification were scored to each of the specimens based on SEM scans, resulting in a character matrix which was then traced over the multi-marker phylogenetic tree using Mesquite (vers. 3.6; Maddison and Maddison 2018). Ancestral states were reconstructed from the observed terminal taxa according to the parsimony method for categorical data, and character state changes were highlighted on the tree (Fig. 3).

RESULTS AND DISCUSSION

Based on twelve distinct morphologic characters, and by comparison with published descriptions, 42 morphospecies were identified and illustrated with their light microscopic photographs as well as the SEM images and close-ups of the shell microstructures (see one example in Fig. 1). Several morphologically similar specimens with smooth and feature-poor shells that all closely resemble *Caecum glabrum* Montagu, 1803 from the Northern Atlantic but belong to different biogeographic zones were summarized as '*Caecum glabrum*-complex'.

For the first preliminary phylogeny on worldwide Caecidae (Fig. 3) we included 32 morphologically distinct species (79 specimens) which resulted in 38 genetically independent evolving lineages (Fig. 3) and thus confirmed the existence of at least six cryptic species among the '*Caecum glabrum*-complex' (one is currently being described based on genetic characters (manuscript submitted to Zookeys). All cryptic species inhabit the marine mesopsammon, and their smooth and feature-poor shells can be interpreted as an adaption to life between sand grains.

The phylogenetic analysis (Fig. 3) also revealed some unexpected results: the genera *Meioceras* (non-monophyletic) and *Parastrophia* (Clade A) cluster within *Caecum*. Further, the character tracing estimation over the phylogenetic tree shows that shell characters which were traditionally used for Caecidae internal classification into genera and subgenera have evolved at least two times independently. Examples are the bulbous shell for *Meioceras* and the retention of the partly straightened protoconch for *Parastrophia*, which in my analyses present a derived feature originating from non-retaining forms. Probably due to still-limited taxon sampling, deeper nodes of Caecid relationships, however, find no statistical support. Classificatory consequences for Caecidae need to be carefully reviewed, based on expanded taxon sampling. Within the genus *Caecum* some sister group relationships are well-supported in molecular analyses, and can be further associated with unique morphological character combinations (e.g., for clade C the axial microstructural threads, clade F the ribbed ornamentation with a small, pointed mucro, clade G the rhombic ornamentation or the cancellated longitudinal threads in clade H in Fig. 2), highlighting the value of the traditional shell characters at lower taxonomic levels.

CONCLUSION

These findings show that species diversity in Caecidae is still underestimated due to the presence of cryptic species and also highlights the need for an integrative taxonomic revision of Caecidae. In continuation of the present project, I aim to expand my taxon sampling especially targeting toward the addition of the missing caecid genera and adding further species within the problematic *Meioceras* and *Parastrophia* to test the validity of these taxa. I hope therefore to contribute to a better understanding of the evolution of this unique tubular shell.

ACKNOWLEDGMENTS

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The results of this study were presented on the 8th Evolutionary Biology Congress in Padua (SIBE, 1.-4. Sept. 2019).

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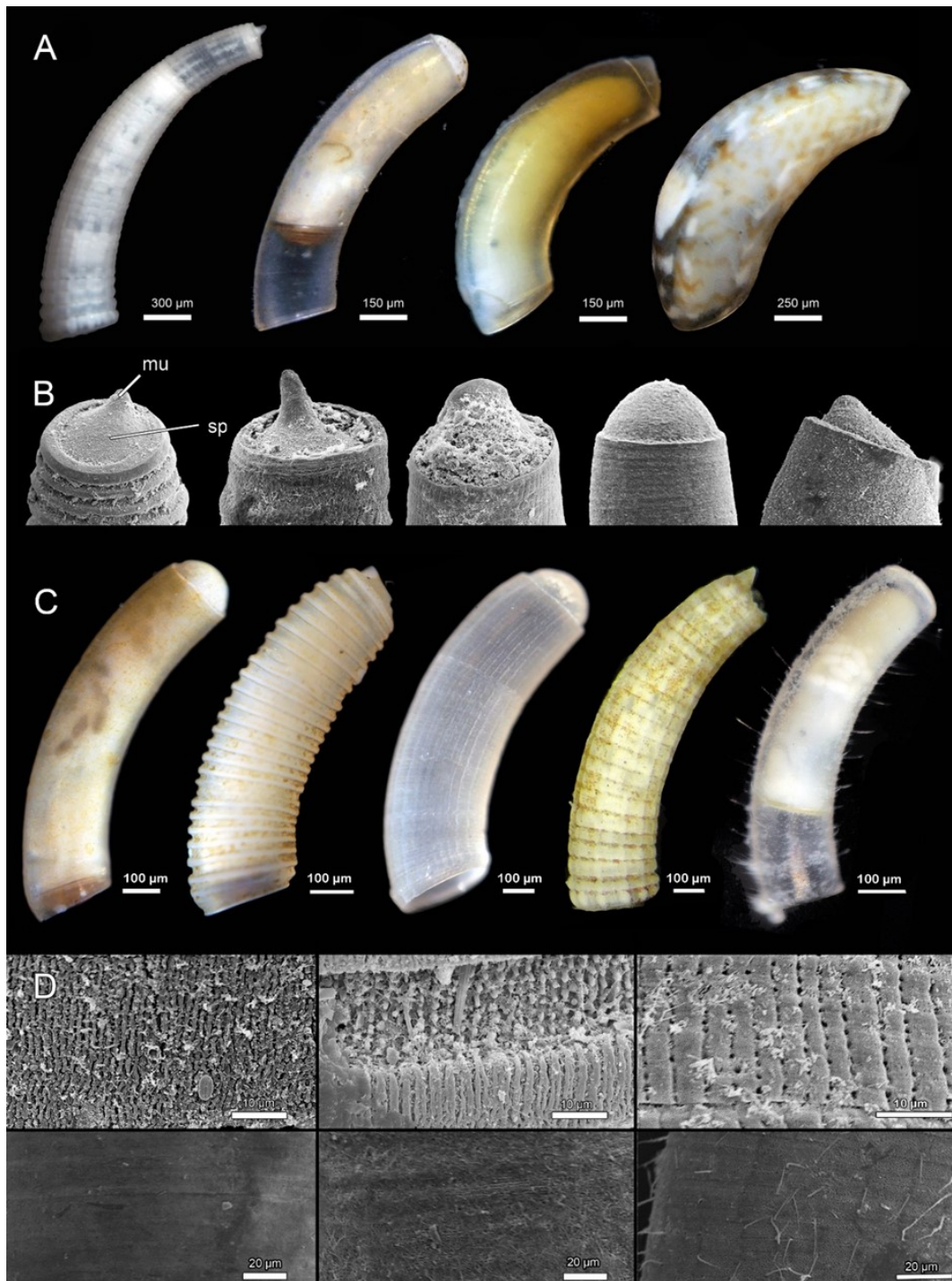


Figure 2 Shell morphological characters investigated and used for the character tracing estimation over the phylogenetic tree and ancestral state reconstruction. **A** Different shell tube shapes: *evenly widening tube*, *equally wide tube*, *compact restricted shell*, *bulbous shell* (from left to right). **B** SEM scans of different septum/mucro combinations: *flattish septum with distinct slim/pointed mucro*, *flat septum combined with strong slim/pointed mucro*, *concave septum with strong, wide/round mucro*, *strongly blistered septum with an absent mucro*, *concave septum with triangular mucro merging into each other* (from left to right, mu, mucro; sp, septum). **C** Ornamentations of different caecid shells: *smooth and lacking ornamentation*, *axial ribbed shell*, *shell with fine longitudinal striae*, *ribs crossing over longitudinal striae (forming a rhombic pattern)*, *smooth shell provided with fine spikes* (from left to right). **D** Microstructural patterns on caecid shells: *shell showing longitudinal threads*, *shell with ribbed ornamentation*, *longitudinal threads covering the ribs while the interspaces show a beaded pattern*, *cancellated longitudinal threads*, *smooth shell surface*, *axial threads*, *smooth appearance provided with fine spikes* (from left to right).

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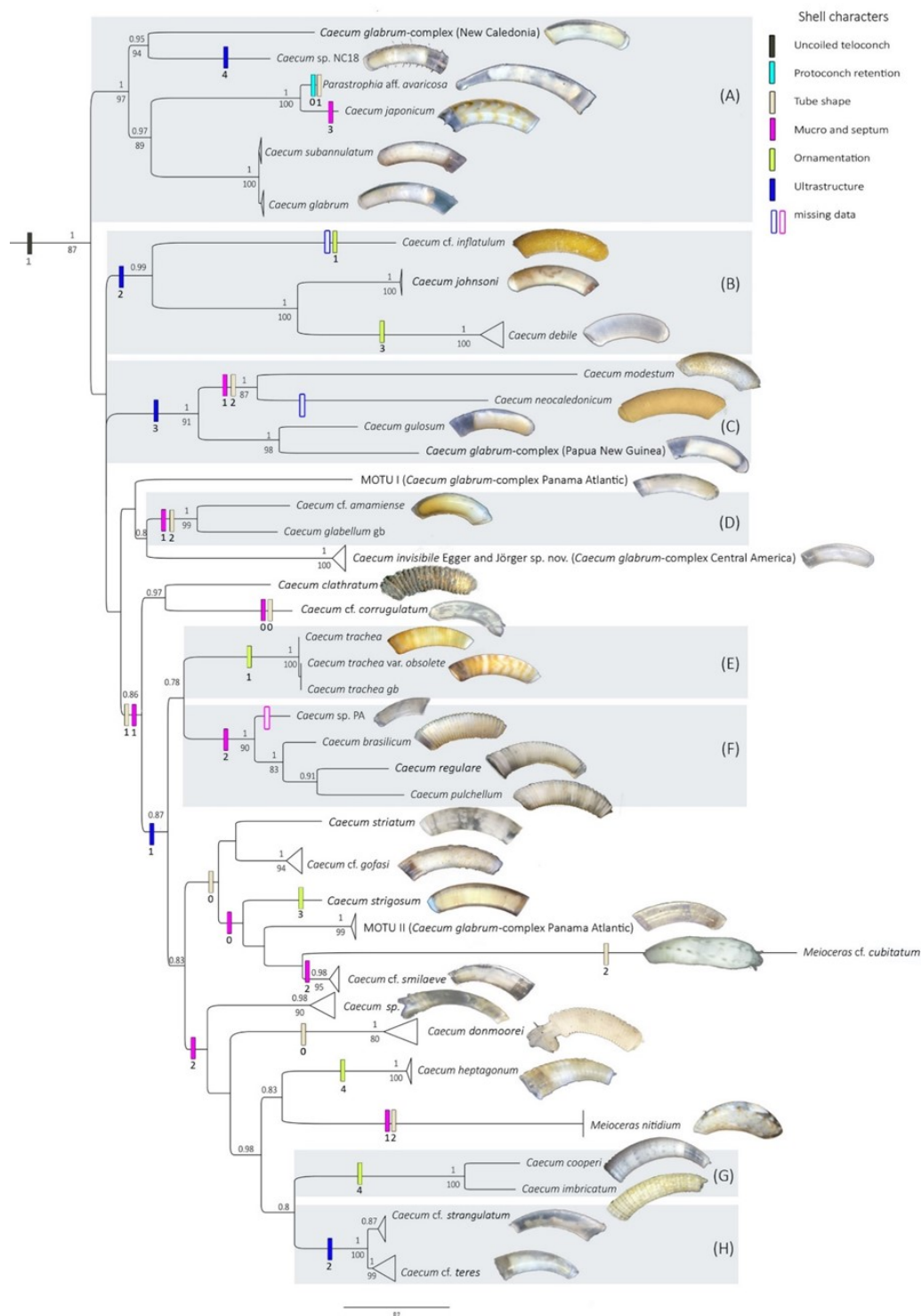


Figure 3 Maximum-likelihood tree of the in-group Caecidae based on the concatenated 28S rRNA, 16S rRNA and COI alignments partitioned by genetic markers and COI codon positions. Bootstrap proportions (below nodes) of the ML analysis are shown for values >50%, and Bayesian posterior probabilities (above nodes) of the corresponding BI analysis are shown for values > 0.75. Clades that are well supported highlighted in grey and labelled from A to H. Character changes obtained from the ancestral state reconstruction analysis based on the parsimony principle, plotted on the majority rule consensus tree. Colour bars indicate evolutionary shell character changes of 6 out of the 12 different shell characters that were traced over the tree, and numbers below indicate the change towards corresponding character state. *Uncoiled teloconch* (0) absent, (1) present. *Protoconch retention*, remaining only partly coiled: (0) absent, (1) present. *Tube shape* (0) equal, (1) increasing, (2) bulbous. *Mucro and septum* (0) blistered septum, no mucro, (1) flat septum, distinct mucro, (2) triangular septum and mucro, (3) flat septum, no mucro. *Ornamentation* (0) smooth, (1) axial rings, (2) axial ribs, (3) longitudinal striae, (4) rhombic pattern. *Microstructure* (0) smooth, (1) longitudinal threads, (2) cancellated longitudinal threads, (3) axial threads, (4) beaded pattern.

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REFERENCES

- BANDEL, K. 1996. Phylogeny of the Caecidae (Caenogastropoda). *Mitteilungen aus dem Geologisch-Paläontologischen Institut der Universität Hamburg* **79**: 53–115
- CRISCIONE, F. & PONDER, W.F. 2013. A phylogenetic analysis of rissooidean and cingulopsoidean families (Gastropoda: Caenogastropoda). *Molecular Phylogenetics and Evolution* **66**: 1075-1082. doi:<http://dx.doi.org/10.1016/j.ympev.2012.11.026>
- DOYLE, J. & DOYLE, J. 1987. A rapid DNA isolation procedure for small quantities of fresh leaf tissue. *Phytochemical Bulletin* **19**: 11-15
- GOLDING, R.E. 2014. Molecular phylogeny and systematics of Australian 'Iravadiidae' (Caenogastropoda: Truncatelloidea). *Molluscan Research* **34**: 222-257. doi:<https://doi.org/10.1080/13235818.2014.888971>
- HUELSENBECK, J.P. & RONQUIST, F. 2001. MRBAYES: Bayesian inference of phylogenetic trees. *Bioinformatics* **17**: 754-755
- JÖRGER, K.M., STÖGER, I., KANO, Y., FUKUDA, H., KNEBELSBERGER, T. & SCHRÖDL, M. 2010. On the origin of Acochlidia and other enigmatic euthyneuran gastropods, with implications for the systematics of Heterobranchia. *BMC Evolutionary Biology* **10**: 323. doi:<https://doi.org/10.1186/1471-2148-10-323>
- KATOH, K., MISAWA, K., KUMA, K. & MIYATA, T. 2002. MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. *Nucleic acids research* **30**: 3059-3066. doi: <https://doi.org/10.1093/nar/gkf436>
- KLUSSMANN-KOLB, A., DINAPOLI, A., KUHN, K., STREIT, B. & ALBRECHT, C. 2008. From sea to land and beyond – New insights into the evolution of euthyneuran Gastropoda (Mollusca). *BMC Evolutionary Biology* **8**: 57. doi:<http://dx.doi.org/10.1186/1471-2148-8-57>
- KNEBELSBERGER, T. & STÖGER, I. 2012. DNA Extraction, Preservation, and Amplification. In: Kress W, Erickson D (Eds) *DNA Barcodes Methods in Molecular Biology (Methods and Protocols)*. Humana Press, Totowa, NJ, 311-338. doi:https://doi.org/10.1007/978-1-61779-591-6_14
- MADDISON, W.P. & MADDISON, D.R. 2018. Mesquite: a modular system for evolutionary analysis. Version 3.51 <http://www.mesquiteproject.org>.
- NGUYEN, L-T., SCHMIDT, H.A., VON HAESELER, A. & MINH, B.Q. 2014. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Molecular Biology and Evolution* **32**: 268-274. doi:<https://doi.org/10.1093/molbev/msu300>



Preliminary data on the biodiversity of solenogasters (Mollusca, Aplacophora) in the China Sea (West Pacific): a step forward in knowledge of the Aplacophora

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INTRODUCTION

Aplacophora (Solenogastres + Caudofoveata) remains one of the least known molluscan groups (Todt, 2013). To date, 291 species of solenogasters are known, but many others are waiting to be formally described. New species are still found in relatively well-known areas (e.g. Kocot & Todt, 2014; Pedrouzo *et al.*, 2014), although the most recently discoveries come from remote localities (e.g. Todt & Kocot, 2014; Zamarro *et al.*, 2019; Cobo & Kocot, 2020). In these regions, where sometimes there is a complete gap in knowledge, it is estimated that most of the species will be new to science. This work aims to contribute to the knowledge on aplacophorans via a preliminary study of a collection from the China Sea where no solenogasters are known.

MATERIAL AND METHODS

Animals were collected during the DongSha 2014, and ZhongSha 2015 expeditions (Table 1) and preserved in 95% ethanol. Specimens were investigated using an integrative taxonomic approach that combines both traditional as well as modern morphological techniques in addition to DNA barcoding. Specimens were initially sorted into distinguishable morphospecies, through the study of habitus and mantle sclerites. At least one specimen from each group was selected for a complete



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Table 1. Studied specimens. (A) Anterior serial sections (P) Posterior serial sections (x) available data (-) no data (?) waiting for the results)

Expedition	Code	Station	Position	Depth (m)	SEM	Sections	16S	COI	Identifications
<u>DongSha</u>	MNHN-IM-2013-50092	CP4123	21°36'N 118°16'E	1612-1666	x	A P	x	-	<i>Dorymenia</i> sp1
	MNHN-IM-2013-66992	CP4123	21°36'N 118°16'E	1612-1666	x	A	?	?	<i>Dorymenia</i> sp1
<u>ZhoughSha</u>	MNHN-IM-2013-61611	CP4133	19°59'N 116°24'E	999-1071	x	AP	x	x	<i>Proneomenia</i> sp1
	MNHN-IM-2013-61905	CP4146	16°09'N 114°16'E	232-314	-	-	-	-	<i>Proneomenia</i> sp2
	MNHN-IM-2013-66991	CP4146	16°09'N 114°16'E	232-314	-	-	-	-	<i>Proneomenia</i> sp2
	MNHN-IM-2013-66993	CP4146	16°09'N 114°16'E	232-314	-	-	-	-	<i>Proneomenia</i> sp2
	MNHN-IM-2013-61955	CP4148	16°07'N 114°19'E	218-281	x	-	x	-	<i>Proneomenia</i> sp2
	MNHN-IM-2013-66989	CP4148	16°07'N 114°19'E	218-281	x	A P	x	x	<i>Proneomenia</i> sp2

study (Table 1) and sectioned into three regions: anterior and posterior parts were used for histology (following routine protocols; Cobo & Kocot, 2020) and the central part for low-vacuum, low accelerating voltage SEM; which allows us to obtain SEM data and high-quality DNA from the same fragment.

DNA was extracted from five specimens (at least one per morphospecies) using the EZNA MicroElute Genomic DNA Kit (Omega Bio-tek) following the manufacturer's protocol except that 20 µl of OB-Protease (Omega Bio-tek) was used. DNA concentration was measured using a NanoDrop Lite (Thermo). PCR amplification of a fragment of the mitochondrial 16S rDNA (SSU) and cytochrome c oxidase subunit I (COI) were attempted using Hot Start Taq 2X Master Mix (AmRESCO) following the manufacturer's instructions. For 16S, the solenogaster-specific primers 16Solenor and -f (Bergmeier *et al.*, 2017) were used with the following cycling parameters: 30 s at 98°C, 40 x (5 s at 98 °C, 5 s at 47–50 °C, 20 s at 72 °C) 60 s at 72 °C, and final cooling at 10 °C. For COI, the primers LCOApI (TTTCTACTAAYCATAARGATATTGG) and HCO (Folmer *et al.* 1994) were used with the following cycling parameters: 30 s at 95°C, 40 x (30 s at 95 °C, 15 s at 50 °C, 30 s at 72 °C) 7 min at 72 °C, and final cooling at 6 °C. Sequences of COI (two specimens) and 16S (four specimens) were obtained.

RESULTS

Specimens were grouped in three morphospecies and classified into the order Cavibelonia, Salvini-Plawen, 1978 and the family Proneomeniidae Simroth, 1893. A subsequent morphological study confirmed this decision, and it was determined that each morphospecies corresponds to a different species. Preliminary analyses of the COI and 16S sequences obtained confirmed the classification within Proneomeniidae.

Results available, so far, consist of a brief characterization classified as follows (taxonomy following García-Álvarez & Salvini-Plawen, 2007):

Proneomeniidae Simroth, 1893

***Dorymenia* Heath, 1911**

***Dorymenia* sp. 1**

Two specimens (MNHN-IM-2013- 50092; MNHN-IM-2013- 66992)

Animals with elongated rounded body (14 - 20 x 1 - 2 mm), and a rounded anterior end. One of the specimens has a posterior digitiform projection, while in the smaller one the posterior end was narrower than the anterior but without digitiform projection. Dark yellow in 95% ethanol. Slightly scaly appearance. Pedal groove, pedal pit and mantle cavity externally evident. Sclerites as hollow acicular sclerites with a wide range of sizes, although some are slightly curved, they are generally straight. With at least two types of knife-shaped scales of the pedal groove. Atrium with numerous digitiform papillae (more than 40). Ventrolateral foregut glands type C (García-Álvarez & Salvini-Plawen, 2007) *Epymenia*-type (Handl & Todt, 2005). The radular apparatus consists of a polystichous radula (12-14 teeth per row and 29 rows) and a radular sac. Foregut with a dorsal bag in the radular region. Midgut with caecum that projects far anterior. With rounded copulatory stylets, and without other accessory reproductive structures.

***Proneomenia* Hubrecht, 1880**

***Proneomenia* sp. 1**

One specimen (MNHN-IM-2013-61611).

Big and robust animal (80 x 3 - 5 mm) with the anterior end truncated and the posterior end narrower and with a digital projection. White in 95% ethanol. The sclerite cover is very compact and therefore the animal does not look scaly. The specimen had the foregut evaginated, where traces of a polyp (possibly gorgonian) were found, which suggests that it feeds on these animals. Pedal groove, pedal pit and mantle cavity externally evident. Externally, no grooves were observed that

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would suggest the presence of a dorsoterminal sense organ. Nor was this located in the study of the histological sections. Straight and curved hollow acicular sclerites, of similar size. Without scales of the pedal groove. Without copulatory stylets.

***Proneomenia* sp. 2**

Five specimens (MNHN-IM-2013-61905; MNHN-IM-2013-61955; MNHN-IM-2013-66991; MNHN-IM-2013-66993; MNHN-IM-2013-66989).

Elongate and straight animals (20 - 35 x 1.5 - 1.8 mm), with rounded anterior ends and posterior ends with digitiform projections, preceded by a slight ventral bulge. White in 95% ethanol. Pedal groove, pedal pit and mantle cavity externally evident. Sclerites as hollow straight acicular sclerites, some smoothed square and other elliptical in cross-section. With long knife-shaped scales, short knife-shaped scales and acicular sclerites around the pedal fold. Four pedal folds. Atrium with few big digitiform papillae. Ventrolateral foregut glands type C/ *Epymenia*-type. Polystichous radula (38-42 teeth per row and 40 rows). Big radular sac. Without copulatory stylets.

DISCUSSION

All the studied specimens have the defining characteristics of the family Proneomeniidae: thick cuticle, epidermal papillae, hollow acicular sclerites, polystichous radula, and the type C foregut glands (García-Álvarez & Salvini-Plawen, 2007). This family includes two genera: *Proneomenia* Hubrecht, 1880 and *Dorymenia* Heath, 1911, only distinguishable by the presence of copulatory stylets in *Dorymenia* (García-Álvarez et al., 2009). During the study of the habitus of one of the specimens (MNHN-IM-2013- 66992), these copulatory structures were observed. The serial sections revealed that the other specimen within this morphospecies also belongs to *Dorymenia* and that the remaining specimens (without copulatory stylets) belong to *Proneomenia*.

The sclerites in Proneomeniidae are mostly hollow needles without many differences between species. However, a good characterization and the occasional presence of other sclerites among them provides relevant information (Scheltema & Schander, 2000). In addition, SEM allows us to find useful particularities, such as the shape of the section. The external aspect of many solenogasters usually prevents specific differentiation but, in this case, it helps to delimit morphospecies (Fig. 1). We are still working on the study of the internal anatomy along with a thorough analysis of the molecular data. This will be based on a complete identification of the specimens. The available information suggests that the species included here are probably new. In addition to the morphological differences with the existing Proneomeniidae species, there are no known species of this family in the South Pacific (García-Álvarez & Salvini-Plawen, 2007).

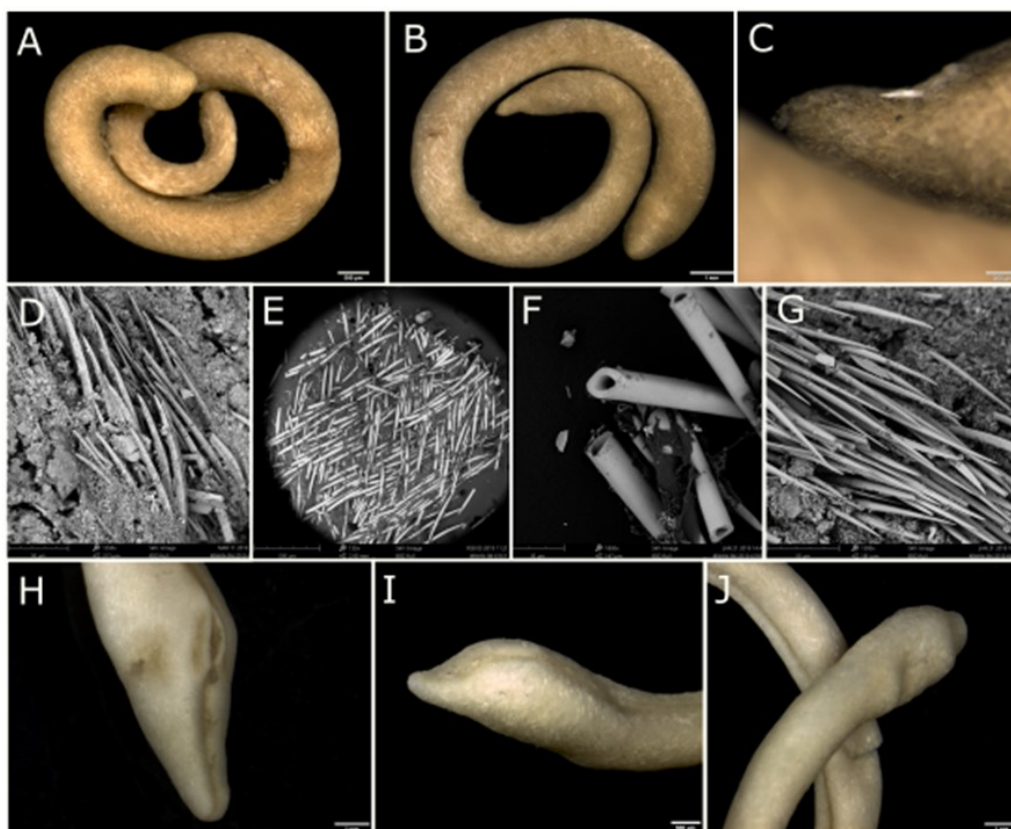


Figure 1. *Dorymenia* sp1. (A) Habitus: MNHN-IM-2013-50092) (B) Habitus: MNHN-IM-2013-6692 (C). Copulatory stylets (D) SEM image of the pedal groove region *Proneomenia* sp1. (E) SEM image of the sclerites. (H). Posterior digitiform projection. *Proneomenia* sp2. (F-G) SEM image of the sclerites (I-J) Habitus MNHN-IM-2013-61611.

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REFERENCES

- BERGMEIER, F. S., BRANDT, A., SCHWABE, E., & JÖRGER, K. M. (2017). Abyssal Solenogastres (Mollusca, Aplacophora) from the Northwest Pacific: scratching the surface of deep-sea diversity using integrative taxonomy. *Frontiers in Marine Science*, **4**, 410.
- COBO, M. C., & KOCOT, K. M. 2020. *Micromenia amphiatlantica* sp. nov.: First solenogaster (Mollusca, Aplacophora) with an ampho-Atlantic distribution and insight into abyssal solenogaster diversity. *Deep Sea Research Part I: Oceanographic Research Papers*, **157**, 103189.
- FOLMER, O., BLACK, M., HOEH, W., LUTZ, R. & VRIJENHOEK, R. 1994. DNA primers for amplification of mitochondrial cytochrome c oxidase subunit I from diverse metazoan invertebrates. *Molecular Marine Biology and Biotechnology*, **3**(5):294-9.
- GARCÍA-ÁLVAREZ, O., & SALVINI-PLAWEN, L. V. 2007. Species and diagnosis of the families and genera of Solenogastres (Mollusca). *Iberus*, **25**(2), 73-143.
- HANDL, C. H., & TODT, C. 2005. Foregut glands of Solenogastres (Mollusca): anatomy and revised terminology. *Journal of Morphology*, **265**(1), 28-42.
- KOCOT, K., & TODT, C. 2014. Three new meiofaunal solenogaster species (Mollusca: Aplacophora) from the north-east Pacific. *Journal of Natural History*, **48**(45-48), 3007-3031.
- PEDROUZO, L., COBO, M. C., GARCÍA-ÁLVAREZ, O., RUEDA, J. L., GOFAS, S., & URGORRI, V. 2014. Solenogastres (Mollusca) from expeditions off the South Iberian Peninsula, with the description of a new species. *Journal of Natural History*, **48**(45-48), 2985-3006.
- SALVINI-PLAWEN, L. 1978. Antarktische und Subantarktische Solenogastres-Eine monographie: 1898-1974. *Zoologica* **128**, 1-315.
- SCHELTEMA, A. H., & SCHANDER, C. 2000. Discrimination and phylogeny of solenogaster species through the morphology of hard parts (Mollusca, Aplacophora, Neomeniomorpha). *Biological Bulletin*, **198**(1), 121-151.
- TODT, C. 2013. Aplacophoran mollusks—still obscure and difficult? *American Malacological Bulletin*, **31**(1), 181-187.
- ZAMARRO, M., GARCÍA-ÁLVAREZ, O., & URGORRI, V. (2019). Biodiversity of the genus *Hemimenia* (Mollusca, Solenogastres, Neomeniomorpha) in Galician waters (NW Spain) with the description of three new species. *Iberus*, **37** (2): 177-20

As part of her report, M. Carmen Cobo Llovo also writes

“The project achieved its stated aim in identifying specimens in museum collection (several new species) and in the generation of DNA sequences. I am also happy to announce that Dr. Kocot was given a “National Science Foundation CAREER Award”. I will have the opportunity of continuing my research with aplacophorans, as a postdoctoral researcher in his group.

In addition to the report for *The Malacologist*, we are working in two scientific papers based on the project partially funded by the Malacological Society of London, and on which I will be the first author. Due to personal and job problems I have had to stay away from malacological research for a while, but I soon hope to meet all the expectations of this project. I again want to thank again the Malacological Society of London for the funds and for the good treatment and understanding. This project constituted an important training experience and it was the basis for the scientific relationships that will allow me to continue with my research career.”



BrdU-based sperm-labelling protocol in a hermaphroditic freshwater snail species

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INTRODUCTION

A method for following the fate of sperm can greatly expand the understanding of reproductive biology in hermaphroditic gastropods. The general pathway of sperm is as follows: sperm are produced in the ovotestis, where eggs are also produced (Tompá 1984; Davison 2006; Koene *et al.* 2009). Matured sperm cells are stored in the seminal vesicle, and when copulation occurs, spermatozoa are transferred through the vas deferens and mixed with accessory gland secretions to form an ejaculate or spermatophore. After transfer into a mating partner, most of sperm are digested in the bursa copulatrix and only a small amount of sperm is stored in the female sperm-storage organ for fertilization (0.025% in the garden snail *Helix aspersa*, Rogers & Chase 2001). Detailed knowledge for the fate of sperm is crucial for examining male fertility, sperm competition and even potential impacts of global warming (e.g., Manier *et al.* 2010; Kupfernagel *et al.* 2013; Giannakara *et al.* 2016; Sales *et al.* 2018).

In hermaphroditic gastropods, there are still plenty of knowledge gaps about the fate of sperm. For example, although it is known how gametes differentiate into either sperm or eggs (reviewed in Roosen-Runge, 1977), so far as I am aware, knowledge of the dynamics of spermatogenesis is quite limited. Previous studies showed that the spermatogenesis of *H. aspersa* takes 43.6 days on average (Bloch & Hew, 1960), depending on the day length (28 days under long day conditions, Medina *et al.*, 1988; Griffond & Medina, 1989). Also, it has been observed that spermatogenesis stops during the hibernation of *H. pomatia* (Lind, 1973). Freshwater snail species *Physa acuta* and *Bulinus tropicus* show increases in spermatogenesis under elevated temperature (Brackenbury & Appleton, 1991). For *L. stagnalis*, de Jong-Brink *et al.* (1985) reported a slight diurnal variation of spermatogenesis. Beeman (1970) reported that spermatogenesis takes 10-14 days in a sea hare *Phyllaplysia taylori*. Given the high bio- and reproductive diversity of this group (e.g., Jarne & Auld, 2006; Anthes & Michiels, 2007; Escobar *et al.*, 2011; Lodi & Koene, 2015; Swart *et al.*, 2019), knowledge of the fate of sperm is limited and sporadic. For example, in Hygrophila (i.e. Basommatophora), the female sperm storage organ remains unknown, despite their highly efficient sperm storage ability (Jordaens *et al.*, 2007; Koene *et al.*, 2009; Nakadera *et al.*, 2014). Therefore, conducting a systematic investigation on the fate of sperm could greatly expand the understanding of reproductive biology in hermaphroditic gastropods.

The major technical requirement for following the fate of sperm is sperm labelling and visualization. Labelling sperm allows us to measure the duration of spermatogenesis, and examine dynamics of spermatogenesis, e.g., under the prevailing sperm competition (Giannakara *et al.*, 2016). This method would also let us identify the female sperm storage organ, and which sperm are stored there, without needing to undertake long-term monitoring of offspring genotypes (Koene *et al.*, 2009; Nakadera *et al.*, 2014).

Here we aimed to develop a sperm-labelling method, incorporating a 5-bromo-2'-deoxyuridine (BrdU)-based immunocytochemical assay. BrdU is an analogue form of thymidine or uridine, so where new cells are actively synthesized, BrdU is incorporated into DNA molecule at the S-phase of cell division. Contrasting with radioactive isotope methods (e.g., Medina *et al.*, 1988), BrdU-based methods are more accessible and often used to examine cell proliferation (e.g., Zakharov *et al.*, 1998; Gorbushin & Iakovleva 2006; Giannakara *et al.*, 2016). Also, Kupfernagel *et al.*, (2013) used this method to successfully label 99.3% of sperm in the land snail *Arianta arbustorum*. Based on the protocols of these studies, we attempted to establish a BrdU-based sperm-labelling protocol for our model species, *L. stagnalis*.

L. stagnalis is a good model species for improving our understanding of spermatogenesis and its dynamics in hermaphroditic gastropods. This species is promiscuous in the laboratory and field (Nakadera *et al.*, 2017), and in the laboratory, they do not have distinct reproductive seasons; this contrasts with land snails which have hibernation seasons (Lind 1973; Griffond & Medina 1989). Thus, in *L. stagnalis*, the need for sperm is continuously high, since the snails repeatedly copulate after sexual maturation (Ramm & Schärer 2014). For example, the weight of seminal vesicle, where matured sperm are stored, increases after social isolation (De Boer *et al.*, 1997). Also, a previous study implied that spermatogenesis in this species takes 14 days under long-day condition (De Jong-Brink *et al.*, 1985), though the original data seem not to have been published.

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MATERIAL AND METHODS

L. stagnalis is a simultaneously hermaphroditic freshwater snail species. As other freshwater snail species, they sexually mature as male first (slight protandry, Jordaens *et al.* 2007). Once fully matured, the snails continuously copulate throughout their life in laboratory condition. They produce sperm in the ovotestis and stored matured sperm in the seminal vesicle. In this study, age-synchronized, fully matured snails were used.

BrdU incorporation

In order to insert BrdU into snails, we first anesthetized them by injecting approximately 1.5 ml of 50 mM MgCl₂ into the foot muscle using a syringe and thin needle (0.3 x 12 mm, FINE-JECT, Henke Sass Wolf). We then injected 150 μ l of 3.3 mM BrdU in *Lymnaea* saline solution (pH 8.1) via the pneumostome using 1ml syringe and thin needle (Gorbushin *et al.*, 2006; Kupfer-nagel *et al.*, 2013). After gently washing the snail with dionised water, we returned them into their container with mating partners. The snails usually recover from anesthetization several hours later.

Incubation

After the incorporation, we incubated the snails for 10, 12, 14, 16 and 18 days under a fume hood at room temperature. The light condition was 12L:12D. Each treatment consisted of two snails in each of five containers (N = 10 in total), so that every snail had the opportunity to use sperm produced before BrdU incorporation in a similar frequency (Koene & Ter Maat, 2007). During the incubation, we provided broad lettuce leaves *ad libitum*, and new water and a clean container every week.

Collecting sperm

After the designated length of incubation, we collected sperm by dissecting out the seminal vesicle. First, we anesthetized snails by injecting ca. 2 μ l of 50 mM MgCl₂. Next, we removed their shell from the soft body, and carefully transferred the seminal vesicle into a 1.5 ml tube with 300 μ l of phosphate-buffered saline (PBS). We broke and pulled apart the seminal vesicle. It was then vortexed for 30 sec to release sperm cells (Loose & Koene, 2008). The remaining tissue was transferred to a new tube containing 300 μ l of PBS, and vortexed for 30 sec again. After repeating the process, we collected the solution containing suspected sperm in 900 μ l of PBS. Next, we put 2 μ l of sperm suspension on a slide glass (HistoBond® adhesive microscope slides, Marienfeld, Kupfer-nagel *et al.*, 2013). After air-drying, we stored the slide glasses with sperm at -20°C until further processing.

Immunostaining

Lastly, we visualized the BrdU-labelled sperm with antibodies, using a modified protocol from Giannakara *et al.*, (2016). All the processing was conducted at room temperature unless noted otherwise. We first applied 4% paraformaldehyde for 45 min, then washed the slide glasses for 5 min with three separate aliquots of phosphate-buffered saline containing 1% Triton-X (Sigma, hereafter called PBS-T). After soaking the samples in PBS-T for 60 min, we applied 0.15 mg/ml of Protease XIV (Sigma) for 10 min at 37 °C. We monitored the digestion process under a microscope.

Next, we applied cooled 0.1N HCl to stop the reaction, then further applied 1N HCl for 60 min for DNA denaturation. After three washing steps using PBS-T, we blocked the unspecific binding sites with BSA-T [PBS-T with 1% albumin from bovine serum (Sigma)] for 15 min. We then applied primary rat anti-BrdU antibody (ab6326, Abcam Limited, diluted 1:400 in BSA-T), and incubated overnight at 4 °C. After four washing steps with PBS-T, we applied fluorescein isothiocyanate (FITC)-conjugated antibody (goat F (ab')₂ anti-rat IgG, ab6115, Abcam Limited, diluted 1:200 in BSA-T), and incubated for 60 min in the dark. After further washing three times with PBS-T and once with PBS, we mounted sperm samples on glass slides using a cover slip and Vectashield with DAPI (Vector Laboratories). Immediately after the mounting medium hardened, we observed the sperm samples under epifluorescence using a Nikon Ni-U microscope (Nikon GmbH, Germany).

RESULTS AND DISCUSSION

Through a FITC filter, we successfully detected fluorescent signals specifically from the sperm head pieces (Fig. 1a). The locations of signals corresponded exactly with the location of DAPI signals (Fig. 1b). This means that BrdU has been incorporated into the DNA molecules of the sperm, and the signal is detectable after the immunostaining processes described above. Although we are confident that the protocol for BrdU incorporation is reliable, the most challenging part was to figure out a reliable immunostaining protocol, and we feel that this part still requires further elaboration. For example, we attempted to quantify the number of BrdU labelled sperm cells, but decided not to do so, for the following reasons. Firstly, when we detected BrdU and DAPI signals, it seemed that every sperm contained BrdU. This could be because spermatogenesis was much faster than we expected (see below). Secondly, we examined four sperm droplets (2 μ l) from the same individual, and observed inconsistency of BrdU signals across, and in a few cases within, droplets. That is, even though we vortexed vigorously in order to make a sperm suspension, the distribution of BrdU signals seemed to be patchy. We suspect that this inconsistency is due to a technical issue (e.g., unequal degree of digestion across or within sperm droplets) rather than a biological reason (i.e., some sperm cells do not contain BrdU).

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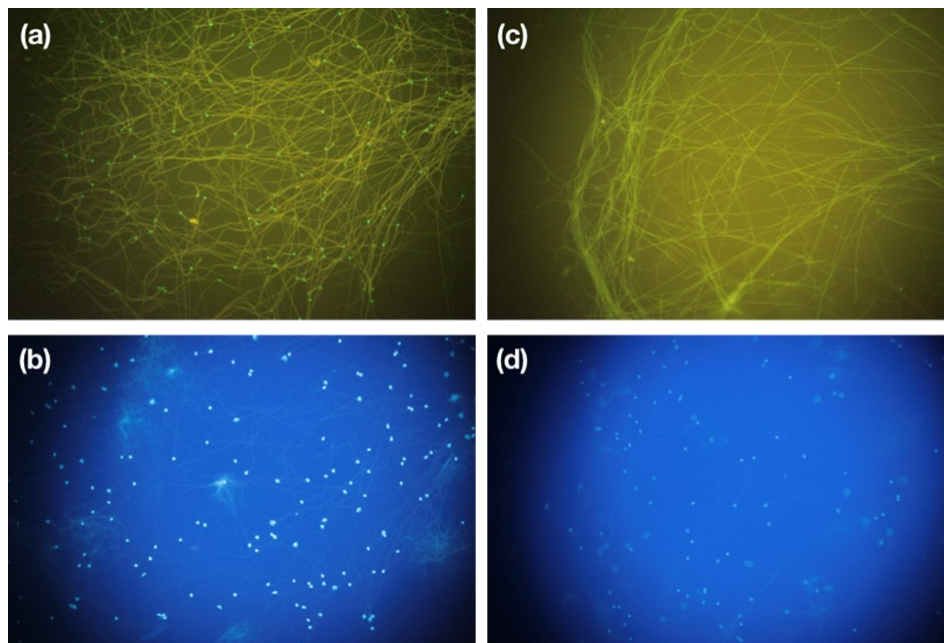


Fig. 1. We took photos of two samples under two different filters. In (a), we detected clear fluorescent signals specifically from sperm heads, indicating where BrdU has been incorporated. In (b) and (d), we can see all the sperm heads, due to the DAPI staining. (a) BrdU-labelled sperm under FITC filter. (b) BrdU-labelled sperm under DAPI filter. (c) non-BrdU-labelled sperm under FITC filter. (d) Non-BrdU-labelled sperm under DAPI filter.

We also found that the duration of spermatogenesis in this species is much shorter than previously expected. De Jong-Brink *et al.*, (1985) speculated that it takes 14 days under long day condition (L:D = 16:8), and that it would take longer under medium-day condition (L:D = 12:12). However, we observed BrdU-labelled sperm in the snails incubated 10 days after the incorporation (Fig. 2). Although we could not specify how many days, it is certain that spermatogenesis duration is shorter than 10 days under medium-day condition in the adult snails.

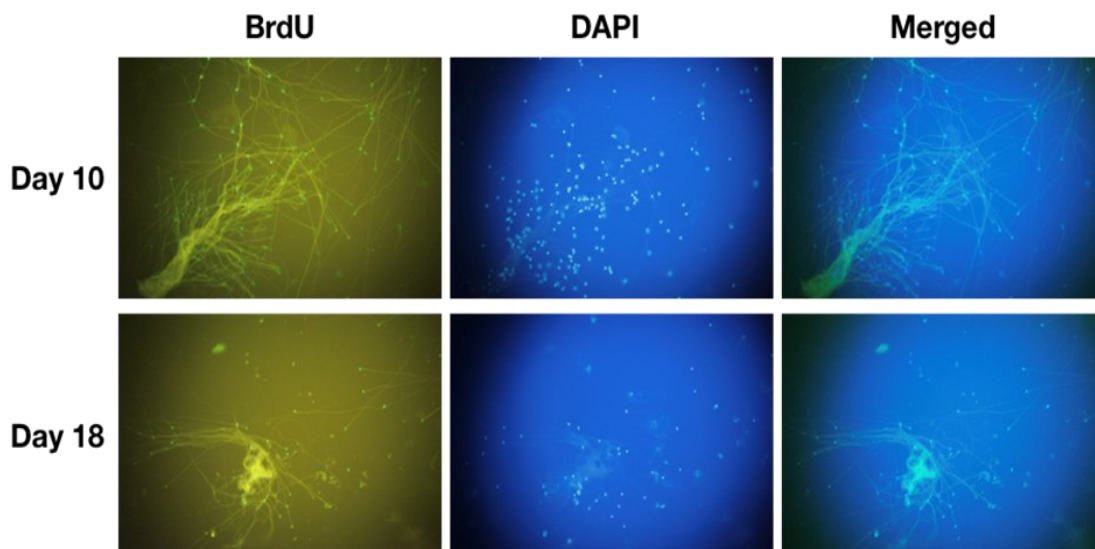


Figure 2. Spermatozoa with fluorescent signals. BrdU-containing sperm heads emit a green fluorescence under an FITC filter (right). Due to the application of DAPI, we can also see all the sperm heads on a glass slide, showing blue fluorescence (middle). The merged figures show that almost all the spermatozoa contain BrdU.

CONCLUSION

This method for following the fate of sperm could greatly expand the understating of reproductive biology in hermaphroditic gastropods. Here we report a BrdU-based sperm labelling protocol, adapted for a freshwater snail species *L. stagnalis*. Although the protocol still needs to be improved, this approach could prime future research to reveal various aspects of reproductive biology in a wide range of hermaphroditic gastropods.

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REFERENCES

- ANTHES, N. & MICHIELS, N. K. 2007. Reproductive morphology, mating behavior, and spawning ecology of cephalaspid sea slugs (Aglajidae and Gastropoteridae). *Invertebrate Biology* **126**: 335–365.
- BEEMAN, R. D. 1970. An autoradiographic study of sperm exchange and storage in a sea hare, *Phyllaplysia taylori*, a hermaphroditic gastropod (Opisthobranchia: Anaspidea). *Journal of Experimental Zoology* **175**: 125–132.
- BLOCH, D.P. & HEW, H. Y. C. 1960. Schedule of spermatogenesis in the pulmonate snail *Helix aspersa*, with special reference to histone transition. *The Journal of Biophysical and Biochemical Cytology* **7**: 515–531.
- BRACKENBURY, T. D. & APPLETON, C.C. 1991. Effect of controlled temperatures on gametogenesis in the gastropods *Physa acuta* (physidae) and *Bulinus tropicus* (planorbidae). *Journal of Molluscan Studies* **57**: 461–469.
- DAVISON, A. 2006. The ovotestis: An underdeveloped organ of evolution. *BioEssays* **28**: 642–650.
- ESCOBAR, J. S., AULD, J. R., CORREA, A. C., ALONSO, J. M., BONY, Y. K., COUTELLEC, M.-A., KOENE, J. M., POINTIER, J.-P., JARNE, P., & DAVID, P. 2011. Patterns of mating-system evolution in hermaphroditic animals: Correlations among selfing rate, inbreeding depression, and the timing of reproduction. *Evolution* **65**: 1233–1253.
- GIANNAKARA, A., SCHÄRER, L. & RAMM, S. A. 2016. Sperm competition-induced plasticity in the speed of spermatogenesis. *BMC Evolutionary Biology* **16**: 60.
- GORBUSHIN, A. M. & IAKOVLEVA, N. V. 2006. Haemogram of *Littorina littorea*. *Journal of the Marine Biological Association of the United Kingdom* **86**: 1175–1181.
- GRIFFOND, B. & MEDINA, A. 1989. Timing of spermatogenesis and spermiation in snails *Helix aspersa* bred under short photoperiods: A histologic and quantitative autoradiographic study. *Journal of Experimental Zoology* **250**: 87–92.
- JARNE, P. & AULD, J. R. 2006. Animals mix it up too: the distribution of self-fertilization among hermaphroditic animals. *Evolution* **60**: 1816–1824.
- JORDAENS, K., DILLEN, L. & BACKELJAU, T. 2007. Effects of mating, breeding system and parasites on reproduction in hermaphrodites: pulmonate gastropods (Mollusca). *Animal Biology* **57**: 137–195.
- KOENE, J. M., MONTAGNE-WAJER, K., ROELOFS, D. & TER MAAT, A. 2009. The fate of received sperm in the reproductive tract of a hermaphroditic snail and its implications for fertilization. *Evolutionary Ecology* **23**: 533–543.
- KOENE, J.M. & TER MAAT, A. 2007. Coolidge effect in pond snails: male motivation in a simultaneous hermaphrodite. *BMC Evolutionary Biology* **7**: 212.
- KUPFERNAGEL, S., BEIER, K., JANSSEN, R., RUSTERHOLZ, H.-P., BAUR, A. & BAUR, B. 2013. An immunolabelling technique to track sperm from different mates in the female reproductive organs of terrestrial gastropods. *Malacologia* **56**: 253–266.
- LIND, H. 1973. The functional significance of the spermatophore and the fate of spermatozoa in the genital tract of *Helix pomatia* (Gastropoda: Stylommatophora). *Journal of Zoology* **169**: 39–64.
- LODI, M. & KOENE, J.M. 2016. The love-darts of land snails: Integrating physiology, morphology and behaviour. *Journal of Molluscan Studies* **82**: 1–10.
- LOOSE, M. J. & KOENE, J. M. 2008. Sperm transfer is affected by mating history in the simultaneously hermaphroditic snail *Lymnaea stagnalis*. *Invertebrate Biology* **127**: 162–167.
- MANIER, M. K., BELOTE, J. M., BERBEN, K. S., NOVIKOV, D., STUART, W. T. & PITNICK S. 2010. Resolving mechanisms of competitive fertilization success in *Drosophila melanogaster*. *Science* **328**: 354–357.
- MEDINA, A., GRIFFOND, B. & GOMOT, P. 1988. Influence of photoperiod on differentiation of male cells in *Helix aspersa*. An autoradiographic study. *Reproduction Nutrition Développement* **28**: 617–623.
- NAKADERA, Y., BLOM, C. & KOENE, J. M. 2014. Duration of sperm storage in the simultaneous hermaphrodite *Lymnaea stagnalis*. *Journal of Molluscan Studies* **80**: 1–7.
- RAMM, S. A. & SCHÄRER, L. 2014. The evolutionary ecology of testicular function: Size isn't everything. *Biological Reviews* **89**: 874–888.
- ROGERS, D. & CHASE, R. 2001. Dart receipt promotes sperm storage in the garden snail *Helix aspersa*. *Behavioral Ecology and Sociobiology* **50**: 122–127.
- ROOSEN-RUNGE, E. C. 1977. *The process of spermatogenesis in animals*. CUP Archive.
- SALES, K., VASUDEVA, R., DICKINSON, M. E., GODWIN, J. L., LUMLEY, A. J., MICHALCZYK, Ł., HEBBERECHT, L., THOMAS, P., FRANCO, A. & GAGE, M. J. G. 2018. Experimental heatwaves compromise sperm function and cause transgenerational damage in a model insect. *Nature Communications* **9**: 4771.
- SWART, E. M., STARKLOFF, N. C., YPENBURG, S., ELLERS, J., STRAALLEN, N. M. & KOENE, J. M. 2020. The effect of mating on female reproduction across hermaphroditic freshwater snails. *Invertebrate Biology* **139**: e12275.
- TOMPA, A. S., VERDONK, N.H. & VAN DEN BIGGELAAR, J.A.M. 1984. *The Mollusca*. Elsevier.
- ZAKHAROV, I.S., HAYES, N. L., IERUSALIMSKY, V. N., NOWAKOWSKI, R. S. & BALABAN, P. M. L. 1998. Postembryonic neurogenesis in the procerebrum of the terrestrial snail, *Helix lucorum* L. *Journal of Neurobiology* **35**: 271–276.



Senior Research Grant Reports

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Physiological performance of an invasive freshwater gastropod under elevated CO₂-induced acidification

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INTRODUCTION

Biological invasions pose one of the greatest threats to global biodiversity (David and Janac 2018). While most biological introductions rarely result in full blown invasion events, those that do can severely disrupt ecological communities due to intense competition between native and non-native species (Simberloff *et al.* 2013). One issue of particular concern to invasion biologists is the synergistic effects that climate change and biological introductions may have on communities. (Hellmann *et al.* 2008). We can predict that some non-native species may be capable of shifting their ranges as environments begin to conform to their physiological limits while invasion potential may actual decrease for others.

In the aquatic environment, the two most important factors associated with climate change is carbon dioxide induced acidification and increasing water temperatures, both of which have been shown to negatively impact on species survivorship (Hoegh-Guldberg *et al.* 2007). While there have been numerous studies on the effects of increased water temperatures on both freshwater and marine fauna, CO₂-induced acidification research has mostly been limited to marine fauna. Prior to our study, there have been no published research on the effects of CO₂-induced acidification on freshwater molluscs, despite the fact that they are among the most threatened of all aquatic invertebrate fauna (Lydeard *et al.* 2004), while also being culprits in some of the most spectacular invasion events in recent history (Kappes & Haase *et al.* 2012). Therefore, the purpose of our study was to evaluate the physiological performance of the invasive freshwater gastropod *Viviparus georgianus* in its non-native habitat (northern New York, USA) under experimental CO₂-induced acidification.

METHODS

To carry out this study, we adopted the methodology of Cross *et al.* (2016) who used growth rates and shell repair – after a simulated predation event, as two measures of physiological performance. Preliminary work in 2015 and 2016 found that *V. georgianus*, also commonly known as the banded mystery snail can easily be cultured in a laboratory setting. Long term multi-generational cultures can be maintained through frequent water changes and providing the animals with freshwater algae *ad libitum*. Due to the ‘classical’ nature of this experiment, two undergraduate students were recruited to assist in this study, and are listed as co-authors in the forthcoming article in the *Journal of Molluscan Studies*. A total of 200 snails were collected from a river in northern New York, where they can be found littered on the shore from as early as May. The timing of the experiment was crucial as the rivers and lakes in the Adirondack region of New York are frozen for most of the year and *V. georgianus* begins migrating to deeper waters in early September to prepare for overwintering (Jokinen *et al.* 1982; David *et al.* 2017). Once animals were acclimated in the lab, carbon dioxide was bubbled into two aquaria for pH reductions of 0.3 and 0.5 resulting in a total of three experimental treatments: control (pH 7.31), pH 6.83 and pH 6.30. These reductions reflected the IPCC forecasted reduction in pH for the oceanic environment for the years 2050 and 2100 based on the ‘business as usual’ model. To investigate shell repair times at the different treatments, a 1-2 mm incision created on the shell margin of the largest snails in each tank. Photographs were taken of the shell margin at 6 and 12 weeks.

RESULTS AND DISCUSSION

After 12 weeks, our results showed that *V. georgianus* exhibited an impressive resilience to acidic conditions. None of the animals in the experimental treatments died and there were no significant differences in growth across all three treatments. Damaged snails in the control and pH 6.8 treatment also repaired their shells around the same time. The only evidence of stress was the damaged snails in the pH 6.3 treatment which required an additional 8-12 days post-experiment, to complete shell repair. Current studies are underway to compare the results with those of a native gastropod species that occurs sympatrically with *V. georgianus*. Such comparative experimental approaches are important as they provide clues to how native and non-native species will fare amid a changing environment.

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ACKNOWLEDGEMENTS

This project was partially funded by a Senior Research Grant from the Malacological Society of London, and the support of Clarkson University is greatly appreciated.

REFERENCES

- CROSS, E.L., PECK, L.S., LAMARE, M.D. & HARPER, E.M. 2016. No acidification effects on shell growth and repair in the New Zealand brachiopod *Calloria inconspicua* (Sowerby, 1846). *ICES Journal of Marine Science* **73**: 920-926.
- DAVID, A.A., ZHOU, H., LEWIS, A., YHANN, A. & VERRA, S. 2017. DNA barcoding of the banded mystery snail, *Viviparus georgianus* in the Adirondacks with quantification of parasitic infection in the species. *American Malacological Bulletin* **35**: 175-180.
- DAVID, A.A. & JANAC, M. 2018. Twenty-year anniversary of the ICAIS: progress and challenges towards a better understanding of aquatic invasions. *Aquatic Invasions* **13**: 433-437.
- HELLMANN, J.J., BYERS, J.E., BIERWAGEN, B.G. & DUKES, J.S. 2008. Five potential consequences of climate change for invasive species. *Conservation Biology* **22**: 534-543.
- HOEGH-GULDBERG, O., MUMBY, P.J., HOOTEN, A.J. & STENECK, R.S. *et al.* 2007. Coral reefs under rapid climate change and ocean acidification. *Science* **318** (5857): 1737-1742.
- JOKINEN, E.H., GUERETTE, J. & KORTMANN, R.W. 1982. The natural history of an ovoviviparous snail, *Viviparus georgianus* (Lea), in a soft-water eutrophic lake. *Freshwater Invertebrate Biology* **1**: 2-17.
- KAPPES, H. & HAASE, P. 2012. Slow, but steady: dispersal of freshwater molluscs. *Aquatic Sciences* **74**: 1-14.
- LYDEARD, C., COWIE, R.H., PONDER, W.F., BOGAN, A.E. & BOUCHET, P. *et al.* 2004. The global decline of nonmarine mollusks. *Bioscience* **54**: 321-330.
- SIMBERLOFF, D., MARTIN, J-L., GENOVESI, P. & MARIS, V. *et al.* 2013. Impacts of biological invasions: what's what and the way forward. *Trends in Ecology and Evolution* **28**: 58-66.



Meghan and Lily who worked with Drew (David Andrew) on the project



Annual Award winner's report

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.



Phylogenomics and comparative transcriptomics of West African cone snails

Samuel Abalde

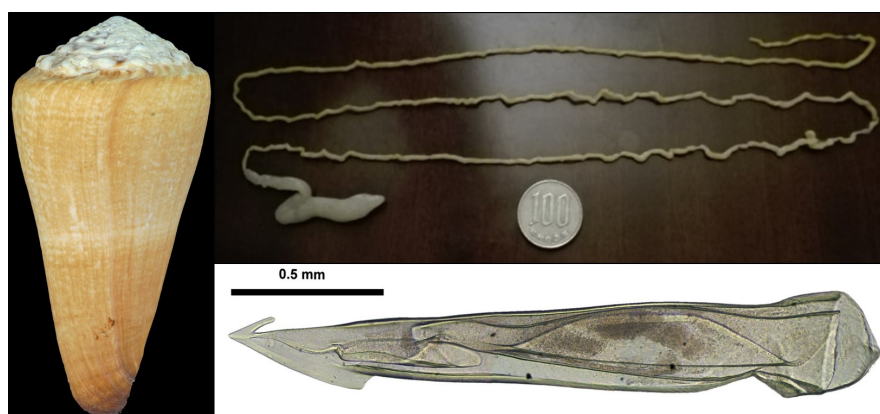
Departamento de Biodiversidad y Biología Evolutiva, Museo Nacional de Ciencias Naturales (MNCN-CSIC), Madrid, Spain
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The subject of this project is a fascinating group: cone snails (Gastropoda: Conidae). The family Conidae presents a striking diversity, including more than 900 species distributed in tropical and subtropical seas. Most species are concentrated in intertidal ecosystems, where they are a key ecological component, although they also inhabit deep waters. This species diversity is correlated with a high morphological diversity, which has attracted the attention of naturalists and shell collectors (Fig. 1). In fact, these two groups are often responsible for the description of new species, leading to a sharp increase in the number of species in the last years. One of the reasons that cones are known worldwide is their feeding behaviour, as they use a sophisticated venom system to hunt worms, other molluscs and even fish. This venom system includes a modified radular tooth in the shape of a harpoon, used to sting the prey, and a complex cocktail of hundreds of small peptides, named conotoxins, which trigger very different physiological responses: from sedation to tetanic paralysis (Fig. 2).



Figure 1 Small representation of the diversity of shapes and colours of cone snails. Shells from the malacology collection of the Museo Nacional de Ciencias Naturales, Madrid, Spain

Figure 2 Specimen of *Fraterconus distans* (left). In the right panel, pictures of its venom gland (top) and radular tooth (bottom). Pictures courtesy of Manuel J. Teno-río



Altogether, cones' species diversity, distribution, their ecological adaptations, diet specialization, and their complex venom have caught the attention of scientists from many different fields, such as taxonomists, evolutionary biologists, ecologists, neuroscientist, or physiologists. However, the Indo-Pacific region, where we can find a little more than half of the species diversity, has concentrated most of this scientific effort, thus neglecting other areas. That is the case, for example, of West Africa. This region extends from Angola to the north of Morocco, including the Macaronesian archipelagos. The cones living here present an invaluable opportunity for studying the evolution of this interesting group. Not only is this region a hotspot of biodiversity, including between 10 to 15% of the species, but also the West African cones present most of the characteristics present in the family, including the two modes of development (direct development and planktonic larva) and three out of four diet specializations (all but molluscivory).

The study of West African cones has been traditionally restricted to the morphological description of new species, and most of this work has been restricted to the Cabo Verde archipelago. These islands have been extensively sampled and studied since the 80s (e.g. Rockel *et al.*, 1980; Monteiro *et al.*, 2004). Before starting my thesis, there were almost 100 species, while the fauna of other regions has been limited to single comprehensive monographic studies. Interestingly, most of the few molecular studies focused on these cones were included in the doctoral thesis of Dr. Regina Cunha, receiver of the Annual Award of the Malacological Society of London in 2009 (Cunha, 2009). Moreover, the study of the venom from West African species is almost non-existent, as most of this effort has focused, again, in the Indo-Pacific species.

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The focus of this project was filling this gap in our knowledge about cone snails, and it could be divided into two main goals. On one hand, we used complete mitochondrial genomes and transcriptomes to infer the phylogenetic relationships within the family and, more specifically, among the West African species. On the other hand, we used transcriptomes to infer the venom composition of 15 species and to study the evolution of this system. The successful completion of this project was possible thanks to an exhaustive sampling campaign, spanning five years, collecting almost 100 out of the 145 species described to this area.

A robust phylogenetic framework is paramount for revealing the evolutionary polarity of important traits, and this was not available for the family Conidae. The only reference we had was a phylogeny based on three partial mitochondrial markers, which failed to resolve many of the nodes, probably due to the rapid diversification rate of this group (Puillandre *et al.*, 2014). Thus, using new and already published complete mitochondrial genomes and transcriptomes, we aimed to infer the phylogenetic relationships among genera of cones. This study revealed that five of the eight genera endemic to West Africa form a monophyletic lineage, while the genera *Chelyconus*, *Genuanoconus*, and *Monteiroconus* are more distantly related. Interestingly, the genus *Genuanoconus*, also endemic to West Africa, was closely related to the genus *Rhombiconus* from the Indo-Pacific Ocean. One of the main flaws of this study was the taxon sampling, as it only included about one third of all the genera. Yet, it has allowed us to infer the evolution of important traits in the family, such as the diet (Fig. 3). Our study suggests the ancestral diet of cone snails was vermivory, while the specialization to prey on worms of the family Amphinomididae and the diet shift to molluscivory happened as single evolutionary events. By contrast, the ability to prey on fish appeared at least in two independent events: once in the Indo-Pacific Ocean, and another time in the Atlantic Ocean.

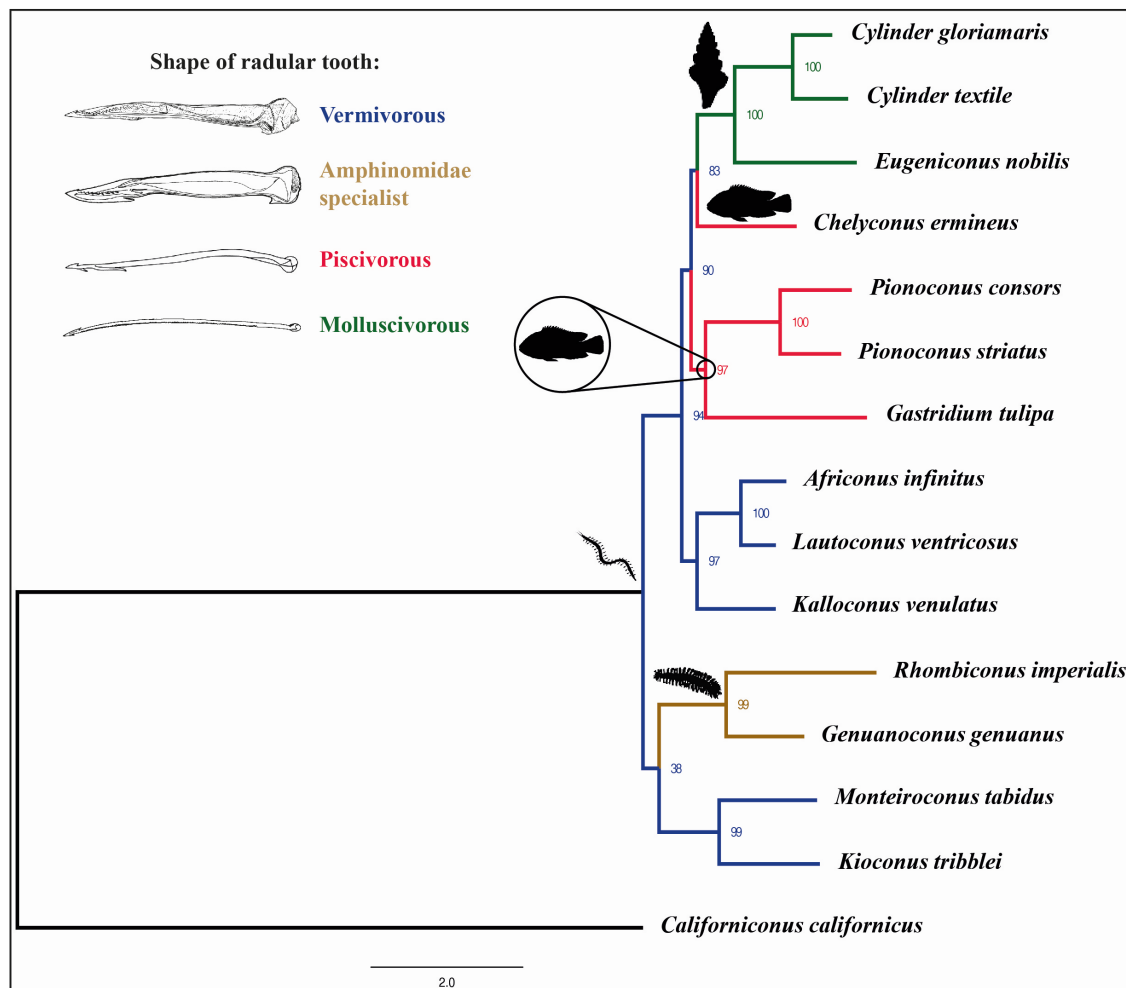


Fig. 3 – Simplified maximum likelihood phylogeny of cone snails based on complete mitochondrial genomes. The evolution of diet is mapped onto the phylogeny. The inset includes the typical radular shape for each diet and the corresponding colour code in the phylogeny. Bootstrap values are indicated aside each node

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Complete mitochondrial genomes have proved useful for inferring phylogenetic relationships among closely related genera and species. Here, we sequenced more than 120 mitogenomes from four of the five closely related genera endemic to West Africa: *Africonus*, *Kalloconus*, *Lautoconus*, and *Trovaconus* (only lacking the genus *Varioconus*, endemic to Angola). This analysis returned a fully supported phylogenetic tree, with most of the nodes presenting maximum statistical support. The particular results of species relationships can be consulted in the corresponding publications, but we can summarise here the three main conclusions of this work. Firstly, the clade including *Kalloconus* and *Trovaconus* is the sister group of the remaining genera. The genus *Lautoconus* was polyphyletic, separating the species endemic to Senegal and the Canary Islands from *Lautoconus ventricosus* from the Mediterranean Sea, the sister species of the genus *Africonus*. These results have led to the synonymization of *Trovaconus* to *Kalloconus* (given the relatively low level of divergence), and the assigning of the species from Senegal and the Canary Islands to the genus *Varioconus*. Secondly, we have proposed the synonymization of about half of the West African species, as they represent taxonomic artifacts. In recent years, the number of species described in this region has rapidly accumulated, mostly based on rather loose descriptions of homoplastic characters. Our molecular analyses reveal now this concerning situation, and call for caution in future descriptions. This systematic work has been recently summarised in a comprehensive open access monograph (Fig. 4; Tenorio *et al.*, 2020). Finally, we have inferred that main diversification events within these genera coincide with important eustatic sea-level changes which isolate or link populations.

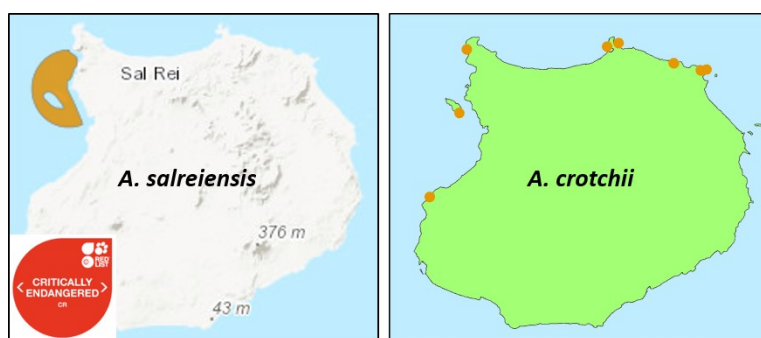


Figure 4 Implications for conservation: we proposed the synonymization of about one-half of the species, leading to important increases in distribution ranges and the consequent changes in their preservation status. In the figure the example of *Africonus salreiensis*, a critically endangered species restricted to Sal Rei Island that turned out to be a populational variant of the more widely distributed *Africonus crotchii*

The feeding habits of cone snails have been studied for decades, and their venom soon caught the attention of researchers. The pharmacological properties have been studied since the 60s (Endean & Izatt, 1965), eventually leading to the development of a powerful painkiller: Ziconotide. Since then, the pharmacological potential of conotoxins has driven most of the effort in cone snail venomics and the evolution of this interesting system has been limited to comparative studies among distantly related species. Here, we used transcriptomics, focused in West African species, to investigate a little better how this venom evolves (Fig. 5).



Fig. 5 *Africonus verdensis* (Santiago Island, Cabo Verde) and *Varioconus mercator* (Senegal), two of the species included in this study. Pictures courtesy of Manuel J. Tenorio and Carlos M.L. Afonso

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Diet might represent an important factor shaping venom composition. It has traditionally been described as quite specific. Since hunting performance relies in the specificity of the venom, changes in diet might be correlated with changes in venom composition. The double origin of piscivory offers an invaluable opportunity for understanding how much diet influences the evolution of venoms, as it allows comparative studies between both clades. We sequenced the venom gland transcriptome of *Chelyconus ermineus*, the only Atlantic fish-hunting cone, to compare its venom composition to that from the Indo-Pacific species. Among the more than 300 conotoxins identified in this species, we found that most of the expression was accumulated in the toxins belonging to the same superfamily (i.e. a conotoxin cluster based on the similarity of a conserved region): the superfamily A. This agreed with other studies focussed in Indo-Pacific fish-hunting cones, highlighting the importance in this particular superfamily of preying on fish. The relative importance of this superfamily has been strengthened by differential expression analyses against vermivorous species. More detailed comparisons have uncovered two subgroups of toxins, the so-called 4/4 and 3/5 conotoxins, exclusive to the Atlantic or Indo-Pacific species, respectively. Also, physiological analyses have proved that both groups trigger the same effect in the prey, as they target exactly the same channel. Altogether, these results suggest convergent evolution in the venom from both piscivorous clades, and the importance of diet as a selective force influencing the evolution of this complex system.

Finally, West African cones provide a good model for comparing, for the first time, the venom catalogues of closely related species. Based on our phylogenetic studies, we sequenced 15 venom gland transcriptomes from the genera *Africonus* and *Varioconus*, including at least one representative from each of the main lineages. Through pairwise comparisons of venom composition among species at different hierarchical levels, we found that individuals from the same species share 24-32% of the conotoxins, species within the same lineage 7%, species from different lineages 5%, and only 0.7 – 1.9% of the total sequences are shared between genera. In the same manner, PCA analyses comparing the presence and relative abundance of each superfamily in the 15 venoms cluster together the species from the same genus. Moreover, an ancestral reconstruction analysis showed several conotoxins in internal nodes and, even more, as the common ancestor of each genus. These results confirm that there is a certain phylogenetic signal for diet, although it is quickly eroded as species diverge.

CONCLUSION

This work provides important clues about the evolution of cone snails and their venoms. We have contributed to a better understanding of the phylogenetic relationships within the family and among West African species, which has important consequences in the systematic of this group. The results highlight the importance of performing comparative studies to understand the evolution of this system, and uncovering the selective forces shaping its composition.

New studies focussing in conoidean snails are steadily accumulating, with new phylogenies and venomous manuscripts being published every year. This growing collection of data provides valuable information and will make it possible to test more complex hypothesis in the future. Furthermore, technical developments will open new paths yet to be explored, such as the (still pending) first high-quality genome for a neogastropod. There is much left to do, and I am looking forward to learning what surprises are awaiting to be discovered.

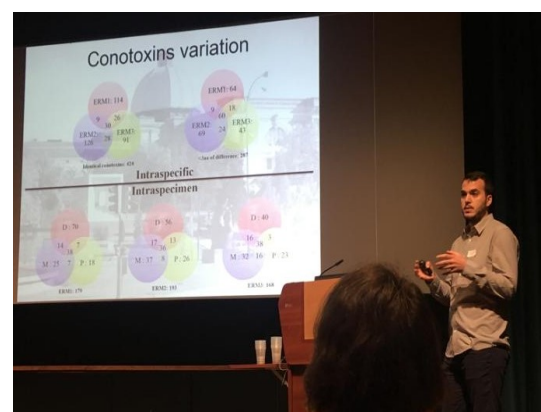
References

- CUNHA, REGINA L. 2010. Tempo and mode of evolution of the genus *Conus* in the Cape Verde islands. *The Malacologist* **54**: 5-7 (February).
- ENDEAN, R. & IZATT, J., 1965. Pharmacological study of the venom of the gastropod *Conus magus*. *Toxicon* **3**: 81-93.
- MONTEIRO, A., TENORIO, M.J. & POPPE, G.T. 2004. *A conchological iconography; the family Conidae: the West African and Mediterranean Species of Conus*. ConchBooks, Hackenheim.
- PUIILLANDRE, N., BOUCHET, P., DUDA, T.F., KAUFERSTEIN, S., KOHN, A.J., OLIVERA, B.M. & MEYER, C. 2014. Molecular phylogeny and evolution of the cone snails (Gastropoda, Conoidea). *Molecular Phylogenetics and Evolution* **78**: 290–303.
- RÖCKEL, D., ROLÁN, E. & MONTEIRO, A. 1980. Cone Shells from Cabo Verde Archipelago a difficult puzzle. Feito, Vigo, Spain.
- TENORIO, M.J., ABALDE, S., PARDOS-BLAS, J.R., & ZARDOYA, R. 2020. Taxonomic revision of West African cone snails (Gastropoda: Conidae) based upon mitogenomic studies: implications for conservation. *European Journal of Taxonomy*, **663**: 1-89.

In addition, Samuel writes....

"I would like to finish this brief report by expressing how happy I am about this award. Completing a PhD good enough to get it has been one of my goals since I first learned about it. I am very grateful to The Malacological Society of London for this recognition."

Samuel Abalde presenting part of his PhD at the Molluscan Forum at the NHM, London



Book review

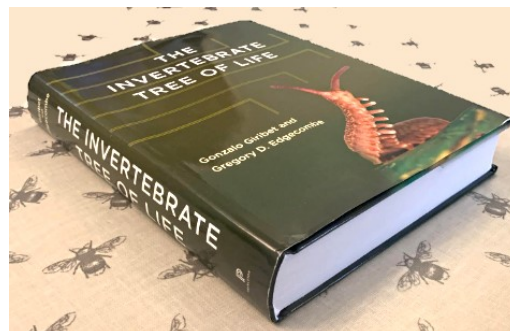
The Invertebrate Tree of Life

Gonzalo Giribet and Gregory D. Edgecombe

Princeton University Press

Systematics and phylogenetics are, like many other disciplines, in a state of constant and rapid transition. The writing of a book on modern phylogeny requires the energy and ability to rapidly assemble an enormous breadth and depth of information quickly and get it to press before it has become outdated. This book is an example of a generally successful attempt to keep up with and distill knowledge of these difficult fields.

The Invertebrate Tree of Life is a novel textbook that aims to act as an accessible source for some of the latest advances in systematics with respect to invertebrates. One of the authors' stated ambitions is to reconcile issues of phylogenetics and evolution using a multidisciplinary approach, for example, combining molecular tools with evidence from the fossil record.



The first of the authors, Gonzalo Giribet, is a Professor of Organismic and Evolutionary Biology, and an Alexander Agassiz Professor of Zoology in the Museum of Comparative Zoology, both at Harvard University. Professor Giribet heads a lab at Harvard that currently hosts 14 researchers who work on various aspects of evolution-focussed molecular biology and systematics. Gregg Edgecombe has been a merit researcher at the Natural History Museum in London since 2013, and is also an associate of the Museum of Comparative Anatomy at Harvard University. Dr Edgecombe has previously worked as Head of Division for Invertebrate and Plant Palaeobiology at the Natural History Museum, as well as holding both university and research posts in Canada, Australia, Thailand and China.

The book starts by neatly considering a number of the thorniest issues faced by the fields of evolution and systematics, and either reconciles these issues or clearly states the authors' approach to them, including any weaknesses of such an approach. The preface is well worth lingering over, as it sketches out the main challenges facing modern phylogenetics, such as the relative importance of genetic relationships versus morphological relationships, both in a purely academic and logistical context.

The introductory chapter takes the reader firmly in an evolutionary direction by considering the Metazoa in the context of all life, and then follows with a chapter that covers many of the issues that a reader would need to know to better understand evolution in a more systematic, or maybe taxonomic setting. This well-structured start to the book is followed by a traditional coverage of each individual phylum of invertebrates in separate chapters. Each chapter has a summary of some kind near the beginning that allows the reader to take in all the most important features of the subject phylum at a glance. The size of each section varies according to the state of knowledge of that phylum. The authors however, seem to have worked to prevent some of the larger phyla from dominating the smaller taxa. For example the Arthropoda, which is by far the most diverse grouping of invertebrates, is covered in less than 30 pages, whereas even the most obscure and enigmatic of phyla get a minimum of 3 pages of information. It is possible that in taking this approach, some information is overly summarised. For example, the whole diversity of arthropod mouthparts is summarised by a single picture of the mouthparts of a single crustacean species. However, the balance between the information in the book being accessible, and the information in the book being comprehensive seems to be generally well struck, certainly with regard to the space devoted to each taxonomic group that is covered.

The enthusiasm of the authors for their subject translates well onto paper. For example, within two paragraphs of the Introduction, they are delving into specific examples of the complexities of placing certain taxonomic groups in the context of all invertebrates, and you can imagine them regaling students and colleagues with similar stories. This feature could act as a weakness for some readers, as in places the anecdotal examples distract from the more universal points that the authors are working to convey. The obvious pay-off for this feature is a density of information that allows a committed reader to quickly assimilate a significant amount of knowledge in a short time.

For maximizing the accessibility to non-specialists and students, some of the excellent photographs and electron micrographs would benefit from more labelling in places. Overall though, the book is packed with a number of excellent illustrations and generalized diagrams of different groups.

In summary this book represents a useful and timely contribution to the field of invertebrate evolution and taxonomy. It is accessible at all levels, although it will be of most value to those who already have some established knowledge of invertebrate biology or taxonomy.

Reviewer - Dr P. Buckley



Annual report of Council for 2019/20

delivered by the President, John Grahame at a Virtual Annual General Meeting

Membership – no report.

Finance for the financial year ending 31st December 2019 (report by Katrin Linse)

The finances of the Malacological Society have been pleasing during 2019 with an overall gain of £65,997. This gain is explained by a gain in the Fixed Interest and Investment funds and lower awards and meeting expenditure. Our investments had an overall gain of £49,217 (comparing market value at 31 December 2019 with market value at 31 December 2018), with the COIF Investment Fund making a gain of £45,694 and the COIF Fixed Interest Fund a gain of £3,523. During 2019, no funds were transferred from the current account to savings accounts.

Separately, the profit-share from the publication of the Journal of Molluscan Studies in 2019 provided the Society with the majority of its income contributing £48,620. The Editors of the Journal, Dr David Reid (outgoing) and Dr Dinarzade Raheem (incoming), and the Assistant Editors are to be commended for their hard work contributing to the publication of our scientific journal. In addition, sales of the digital archives provided £1,351 of income.

In 2019, the year after celebrating 125 years of the Malacological Society of London and the 20th Malacological Forum, fewer funds were used for awards, being £15.2k in 2019 compared to £31.1k 2018, with research awards, travel awards decreased while the spending on Forum travel awards slightly increased. The Society (MSL) spent less money in 2019 compared with 2018, mainly based on less expenses paid for awards, for meeting charges, for JMS colour figures charged to MSL, and to the JMS editor, the latter including the attendance expenses for our new editor to the 3-yearly World Congress of Malacology.

Meetings

The AGM; and 'Molluscan Conservation'

The 126th AGM was held in the Neil Chalmers Theatre, The Natural History Museum, London. After the meeting two papers were presented by invited speakers, reflecting the theme of 'Molluscan Conservation' – Dr Eike Neubert (Natural History Museum of Berne) and Dr Paul Pearce-Kelly (Zoological Society of London; The Frozen Ark) (see *The Malacologist* issue 73, and Georges Dussart's report below).

Malacologists' Forum (report by Phil Hollyman).

The annual Molluscan forum was held on the 21st of November 2019, in the Flett Lecture theatre at the Natural History Museum, London. A total of 82 delegates registered to attend the event with several more arriving on the day. A total of 18 talks were presented during 4 sessions, along with 12 posters that were viewed during lunch break, coffee breaks and the social event in the evening. The Society provided lunch for all attendees which served to create a cohesive meeting, with excellent opportunity to network and discuss the posters. The Forum was again held consecutively with the Young Systematists' Forum, affording an opportunity for students to attend both meetings.

The Oxford prize for Malacology was awarded to Edgar Barajas Ledesma (Sheffield University) for his excellent talk titled "*Gastropod mucus: relating structure to function through protein hydration*". In total, 12 travel awards were granted to student attendees with a combined value of £1821. The forum was organised by Phil Hollyman with help from Katrin Linse, Andreia Salvador, Jon Ablett, Aidan Emery, Tom White and Fiona Allen, and also the President; a full report of the forum can be found in volume 74 of *The Malacologist*.

Publications.

The Malacologist (report by Georges Dussart)

In the 2019-2020 operating year, two issues of *The Malacologist* were posted to the website.

The August issue (73) of 35 pages included three research grant reports (*Geographical structure of cone snail species in a marine biodiversity hotspot* by Philip Vogt, *Population genetic diversity of invasive apple snails, in Malaysia* by Suganiya Rama Rao and *First survey of the terrestrial gastropods of Ulu Temburong, Darussalam* by Werner de Gier) and one travel grant report from Paula Ramos-Silva. There was one obituary (of Andrzej Wiktor), and an innovation in the form of invited articles. There were two of the latter. Cessa Rauch described the contribution of citizen scientists to an investigation of sea slugs in Southern Norway and Alex Ball (a past member of Council) described the development of imaging analysis over the past twenty years. Both these articles had originated as oral presentations at the previous November Forum. It is customary to report on the AGM and conference, so this issue included abstracts of two presentations on molluscan conservation (*Redlisting the non-marine molluscs of Europe* by Eike Neubert and *Partula snail conservation breeding and reintroduction* by Paul Pearce-Kelly), as well as the President's annual report of Council.

Comprising 32 pages, the February issue (74) reported on the Malacological Forum with sixteen pages of well-illustrated abstracts covering eighteen oral and twelve poster presentations. This issue also included three travel grant reports (Imogen Cavadino, Jenny Neuhaus, & Lauren Sumner-Rooney) and one research grant report (Joris Koene on *Mating behaviour and physiology of dart-possessing land snails*),

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The present report shows that *The Malacologist* presents a valuable snapshot of the malacological research activity in this part of the world, especially amongst young researchers. *The Malacologist* has an ISSN number (ISSN 1759-1406) and is therefore citable, so it is in the interest of awardees to present reports on their Society-funded research or travels.

***The Journal of Molluscan Studies* (report by Dinarzarde Raheem)**

The ISI impact factor for the Journal in 2018 decreased slightly to 1.345 (compared with 1.483 in 2017, 1.250 in 2016, 1.185 in 2015 and 1.326 in 2014). The Journal stands at number 65 in the ISI list of 163 zoological journals (it was 53 out of 166 in the previous year). Our chief competitor, *Malacologia*, had a higher and impressive impact factor of 3.250 in 2018. Note that this reflects only one particularly highly cited paper with 33 citations. The Journal continues to be truly international in terms of the geographical distribution of its authors; for volume 84 (2018) the corresponding authors represented 23 countries (of which the leaders were 13% USA and 13% Germany). The average publication time from receipt to Advance Access publication was 5.6 weeks (median 5.1 weeks) for 2018.

Circulation for the Journal in 2019 was 39 institutional (of which 18 were online-only and 12 print-only) and 157 membership subscriptions (compared with 44 and 157 respectively for 2018). In addition, a further 2,347 institutions have electronic access to the Journal through publishers' consortia (includes migrated figures; compared with 2,384 in 2018).

The new pricing structure has been fixed for 2020. The cost for a combined print plus online institutional subscription is £693; an online-only subscription is £539 and print-only subscription is £639.

Volume 85 (2019) contained 45 papers, research notes and review articles, totalling 452 pages (the preceding volume totalled 497 pages). In total, 117 manuscripts were submitted in 2019 (a decrease of 16% on the 139 in 2018) and the acceptance rate was 38%. The image of the stylommatophoran land snail *Indrella ampulla* on the cover of Volume 86 was kindly donated by Tarique Sani.

Our board of Associate Editors is now: Coenraad Adema (immunology, genomics, parasitology), Thierry Backeljau (molecular phylogenetics and genetics), Liz Boulding (population and reproductive biology), Robert Cameron (ecology and genetics of terrestrial gastropods), Richard Cook (agricultural malacology, physiology, feeding behaviour), Simon Cragg (life histories, sense organs), Mark Davies (marine ecology and behaviour), Dan Graf (freshwater bivalves), John Grahame (population genetics, morphometrics), Liz Harper (marine bivalves), Gerhard Haszprunar (microanatomy, 3D reconstruction, minor molluscan classes), Bernhard Hausdorf (terrestrial gastropods), Michal Horskák (ecology and biogeography of terrestrial gastropods), Yasunori Kano (systematics of vetigastropods, tropical ecology), Joris Koene (reproductive behaviour of gastropods), Manuel Malaquias (opisthobranchs), Peter Marko (marine biogeography and phylogenetics), Pablo Martín (freshwater ecology, life history), Ellinor Michel (ecology, freshwater gastropods), Jeff Nekola (community ecology of terrestrial gastropods), Nicolas Puillandre (neogastropods), Ellen Strong (freshwater and marine caenogastropods), Janet Voight (cephalopods), Janice Voltzow (microscopic anatomy), Heike Wägele (opisthobranch biology), Tony Walker (biochemistry, immunology, cytology), Suzanne Williams (molecular phylogenetics and genetics), Nerida Wilson (opisthobranchs, deep-sea and Antarctic molluscs) and Yoichi Yusa (general ecology and behaviour).

I would like to thank all the members of the editorial board, those members of the international malacological community who have contributed to the review process, the staff of Oxford University Press, particularly Cailin Deery and Jan Webster, and the typesetting teams at MPS Ltd, Chennai, India (led by Robin Raj) and SPi Ltd, Philippines (led initially by Mackie Fernandez and latterly by Ronel Mirano), for their work on behalf of the Journal.

Website – no report.

Facebook page (report by Chong Chen) <http://www.facebook.com/malacsoc>

The Society's Facebook page continues to perform well. We currently have 2,379 followers on the page, which is 150 more than the number we had last year. This means we have a direct outreach population of nearly 2,400 people/organisations who see our posts; the posts this year had an average confirmed view of over 1,200 people/organisations.

Again, although the Facebook page is doing well so far, it would benefit greatly from an increased number and variety of posts. If you come across items of potential interest for our Facebook audience, please e-mail me (cchen@jamstec.go.jp) with recommendations and I will generate posts. Also, if you have a Facebook account and would like to join the admin team with posting rights and see the performance stats, just let me know which e-mail address you used to register for Facebook, and I will add you as an admin.

If you have suggestions / comments on the Facebook page, please do not hesitate to contact me - Chong Chen, *Facebook Manager*

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Awards (report by Jonathan Ablett)

Overall, the Society is very pleased with the number of applications that it receives for Travel Awards and Research Grants. The schemes seem to be achieving their global aim to enable young scientists to engage in malacological research activity both in the laboratory/field and at meetings. Reports from researchers funded through both schemes appear in *The Malacologist*. The Society aims to make the following awards annually.

Travel Awards - at least 5 each of up to £500 for Society members, £300 for non-members

Research Grants - at least 5 each of up to £1500

Application forms and guidance notes for both schemes have been updated recently and can be downloaded from The Society's website.

Travel Awards

In 2019 there were 2 rounds of Travel Awards, June and December. The Society received 8 applications for awards to travel and was able to fund 5 of these requests. All Travel Award applications are reviewed by an Awards Committee. The Society is pleased to have announced the following awards.

June Travel Awards

- Hannah Parry-Wilson (University of Southampton) **£500** for the 'British Ecological Society Annual Meeting'. UK
- Halyna Morun (V.N. Karazin Kharkiv National University) **£250** for the 'The academic training upon the molecular taxonomy, genetic diversity and phylogeography of freshwater macroinvertebrates, University of Lodz'. Poland

December Travel Awards

- Diana Freitas (Porto University) **£300** for the 'Limpets 2020: Biology of Limpets: evolution, adaptation, ecology and environmental impacts'. UK
- Halyna Morun (V.N. Karazin Kharkiv National University) **£300** for the 'Physalia course upon a geometric morphometric analysis "Geometric Morphometrics" for intermediate users at the Department of Invertebrate Zoology and Hydrobiology, University of Lodz'. Poland
- Faith Jessica M. Paran (Kyoto University) **£300** for the 'Limpets 2020: Biology of Limpets: evolution, adaptation, ecology and environmental impacts'. UK

A total of **£1650** was allocated by The Society for Travel Awards. All applicants have been notified of the outcome. Note that this amount does not necessarily reflect actual 'spend' as occasionally students withdraw from the intended visit.

Research Grants for 2019 - Early Career Research Grants & Senior Research Grants

The Society awards both Senior Research Grants and Early Career Research Grant. Early Career Research Grants are conferred on students and researchers without professional positions, but without regard to nationality or membership of The Society. Senior Research Awards are aimed at established researchers in professional positions, but without regard to nationality. Applicants for Senior Research Awards must be members of The Society. Early Career Research Grants are reviewed by MSL council members and Senior Research Grants are reviewed by a Reviewers Panel including both council and non-council members invited for that purpose.

Early Career Research Grants

By the closing date of 15th December 2019, the Society had received 17 applications from workers from 16 institutions in 11 different countries. In general, the scientific quality of the research projects submitted was excellent. On behalf of the Society, I would like to formally thank the members of the Grants Review Panel for their hard work in reviewing all applications. The Panel has agreed the following awards, in alphabetical order.

- S. Abalde (University of Tokyo), **£1460** 'Using shotgun sequencing for disentangling a taxonomic jumble: the case of skeneimorph gastropods'
- P. Amodio (University of Cambridge), **£1500** 'Seeking the social octopus in the wild'
- Q. HUA (University of Adelaide), **£1457** 'Understanding population connectivity of two commercially harvested octopuses to assess vulnerability to fishing pressure'
- Irwin (Natural History Museum/University of Bristol), **£1500** 'Understanding the visual behaviour of strombid gastropods'
- H. Kostick (Academy of Natural Sciences of Philadelphia), **£1500** 'Vagility of Jamaican Terrestrial Mollusks'
- A. McNeal (University of Exeter), **£1401.83** 'How does ocean acidification alter the toxicity of marine contaminants to *Mytilus edulis*'
- M. Pembury-Smith (The University of St Andrews), **£1500** 'The use of lichen decoration by the snail *Napaeus barquini*'

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- J. Sakalauskaite (University of Turin), **£1500** 'Spondylus gaederopus: developing a new reference for amino acid racemisation dating using intra-crystalline proteins
- M. Williamson (The University of St Andrews), **£1420** 'Blurring the boundaries – are invasive slug 'species' hybrids? Integrating phenotypic and genotypic approaches to produce an objective definition of the boundaries between *Arion flagellus* and *Arion ater*'
- T. Yoshimura (Keio University), **£1100** 'Elucidation of Sulfur Detox Function in the Periostracum of Solemyid Chemo-synthetic Bivalve'

Therefore **10** Research Grants have been funded at a total cost of **£14,338.83**. The success rate was **59%**. The Grants Review Panel would like to emphasise that the quality of all applications was high and that it funded as many excellent projects as possible. Applicants have already been formally notified of the outcome of their application.

Senior Research Grants

By the closing date of 15th June 2019, the Society had received only 1 application for the Senior Research Grants. On behalf of the Society, I would again like to formally thank the members of the Grants Review Panel for their hard work in reviewing applications. The Panel has agreed the following award:-

- Dr Kiran Liversage (Estonian Marine Institute) **£1320** 'Tidal Pool Molluscs of NW India: Understanding seasonal population changes for conservation'

The Annual Award

The Society received two nominations for the 2019 Annual Award. The Judging Panel elected to offer the Annual Award to Samuel Abalde (University of Salamanca, Spain) for a thesis entitled *Phylogenomics and comparative transcriptomics of West African cone snails*. The Society sends its best wishes and congratulations to Dr Abalde. (A report on his thesis is given on page 37)

The Oxford Prize for Malacology

The Oxford Prize for Malacology is awarded annually for the best presentation at the Molluscan Forum, is generously supported by Oxford University Press, publisher of the Society's journal. The 2019 winner is Edgar Barajas Ledesma for his talk entitled *Gastropod mucus: relating structure to function through protein hydration*.

Officers and Council.

My second year as President has been marked by another extremely successful Forum, and I am very grateful to all who work so hard to make this the success it is. It has also been marked by difficulties attendant on typesetting problems concerning the *Journal*, and I am grateful for the patience and dedication with which Dinarzarde Raheem has continued to navigate the *Journal* as Editor in Chief. We believe that these difficulties may have been put behind us with the appointment by Oxford University Press of new typesetters.

John Grahame, President, MSL

Council elected for 2020-2021

Position	Name	years
President	John Grahame	3
Vice Presidents	Robert Cameron	3
	Phil Fenberg	2
Councillors	Debbie Wall Palmer	1
Councillors	Alan Hodgson	1
Councillors	Andreia Salvador	3
Councillors	Fiona Allen	3
Councillors	Lauren Sumner-Roone	2
Councillors	Phillip Hollyman	2
co opted	Aidan Emery	1
Journal Editor	Dinarzarde Raheem	
Bulletin Editor	Georges Dussart	
Hon. Treasurer	Katrin Linse	
Hon. Secretary	Rowan Whittle	
Awards Officer	Jon Ablett	
Memb Sec	Harriet Wood	
Web manager	Tom White/Chong Chen	

'Years' means 'years in post'.

These are limited as described in the objects of the Society

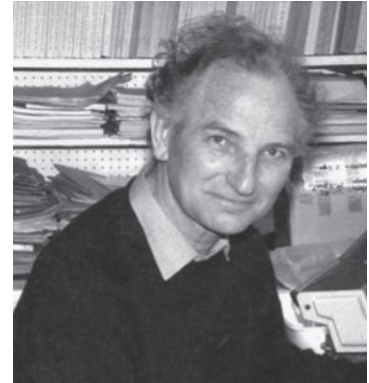
John Allen

We are sorry to record the death of Professor John Allen on June 6th. He was especially interested in bivalves and published extensively, most prominently on the systematics and ecology of deep-sea bivalves. He was director of the University Marine Biological Station Millport between 1976 and 1991, and served on several scientific boards and councils, including as President of the Malacological Society of London (1982-1984). An appreciation of his scientific life and work appears in the *Journal of Conchology*.

Oliver G. & Hannah, F. 2017. The publications and new nominal taxa introduced by John A. Allen. *Journal of Conchology* 42(5):257-266. *

John Grahame

(*As well as offering a biography of John Allen, this publication lists 76 articles and 135 new nominal taxa.)



And, from the website of the Deep Sea Biology Society
<https://dsbsoc.org/highlights/obituary-john-allen/>

John Allen made huge contributions to deep-sea biology through a monumental series of taxonomic monographs on deep-sea bivalves co-authored with his many graduate students and with Howard Sanders. These contributions culminated in the largest dataset available on the distribution of bivalves in major basins of the North and South Atlantic Oceans (Allen, 2008. Bivalvia of the deep Atlantic. *Malacologia* 50: 57-173). Bivalves are among the most abundant deep-sea macrofaunal animals, so the data have provided the foundation of many important ecological, evolutionary and biogeographic studies of the deep-sea benthos. Allen (2008) serves as an astonishing example of a publicly available dataset that allowed, and continues to allow, a wealth of recent studies that have built upon this original study. His studies of anatomy and feeding greatly advanced our understanding of adaptation to life in the deep ocean. John was also primarily responsible for the preservation of the vast amount of deep-sea bivalve material collected by British and WHOI deep-sea expeditions, and its incorporation into museum collections for study by future generations.

As well as his invaluable intellectual work, John was a delightful person to work with. His constant cheerfulness, kindness, and completely unselfish generosity will continue to inspire generations of deep-sea biologists.

Craig McClain,
Executive Director for the Louisiana Universities Marine Consortium



(Originally posted on the mollusca listserver).....

Ron O'Dor

Squid Biologist, Professor Emeritus Ron O'Dor died May 11, 2020 in Halifax, Nova Scotia of complications of COVID-19 and Alzheimer's disease. Ron spent most of his career at Dalhousie University after joining its Department of Biology in 1973. An ideas man, he always thought outside the box, planning and executing research, and mentoring students. He believed in discovery-oriented research, the bigger in scope a project, the more he enjoyed tackling it. Ron was a punster whose ready smile and laugh always lit up a room. His wry, and sometimes subtle sense of humour was particularly evident in dry academic meetings. Born in land-locked Kansas City, Missouri, on September 20, 1944, Ron was the only child of the late Claude Marvin O'Dor and Opal (Sears) O'Dor Mathes. His father died when he was ten and his mother later remarried. He grew up in Liberty, Missouri and after graduation from Liberty High School attended El Camino College in California and the University of California, Berkeley. Ron graduated in 1967 with an Honours degree in Biochemistry and as a member of Phi Beta Kappa.



In a physical chemistry class at Berkeley he met his future wife, Janet Spiller. The two travelled to Canada where Ron earned his doctorate in medical physiology at the University of British Columbia in 1971. His thesis topic was to sequence salmon calcitonin, a calcium-regulating hormone now used in the treatment of osteoporosis. During a two-year post-doctoral fellowship at Cambridge University in England and the Stazione Zoologica in Naples, Ron's research interests turned to octopus and squid, particularly their endocrinology, bioenergetics, life-history strategies and later their movement in the oceans.

When Ron arrived at Dalhousie he did not have to go far to study cephalopods. The short-finned squid was in abundance and the source of a lucrative fishery. Little was known about this oceanic squid but he quickly changed that with pioneering research on this species in the large and unique Aquatron seawater facility at Dal. Ron's large and active discovery-oriented research lab supported many students, studying not only squid but various other marine invertebrates, especially molluscs. He published frequently in scientific journals and supervised 40 graduate students and numerous honour students. At various times he was Chair of Biology, Director of Dal's Aquatron facility, and Associate Dean of the Faculty of Science. His international research career took him to all seven continents either as a visiting scientist or a participant in research projects at marine laboratories. In summers his family usually accompanied him to a marine laboratory somewhere in the world. On many occasions the family enjoyed a beach in the South of France while he enjoyed himself in the lab measuring some physiological aspect of an octopus or squid.

Often he would cobble together the experimental equipment himself by repurposing older equipment, because it didn't exist or there was no budget. Carrying all his gear on flights, he travelled to marine labs around the world. Ron's research was always interdisciplinary, blending his knowledge of chemistry, animal physiology, marine biology and animal migrations in the oceans. He was an ecophysiologicalist long before the term became popular. As his study on the bioenergetics of squid deepened he wondered what these animals were doing in the ocean when no one was looking, where did they go? So he partnered with a local electronics company to develop devices to monitor movements of small marine animals in their natural environment, especially his beloved squid. In 2001, he was appointed Senior Scientist with the Census of Marine Life, a ten-year, international program to assess and explain the diversity, distribution, and abundance of life in the ocean. He and Janet moved to Washington where he coordinated the scientific activity of this endeavour. Out of the CoML grew a dream of Ron's: the idea to build a global network of acoustic receivers and oceanographic sensors in all the oceans of the world to track keystone tagged animals along migratory routes. In 2006 Ron coordinated Dalhousie's successful application to the Canada Foundation for Innovation to establish the Ocean Tracking Network (OTN) to monitor and understand aquatic animal movements, habitats and survival for sustainable management in changing ocean environments. OTN is now a global research, conservation and infrastructure platform and one of Canada's National Research Facilities. Among his many awards are an honorary degree from Lakehead University (2011), Canadian Geographic's Environmental Scientist of the Year award (2009) and the Discovery Centre's award for Professional of Distinction (2012).

Ron will be sorely missed but always remembered for his big ideas on big science, use of cutting-edge technologies, for his ready smile and laugh, for his infectious enthusiasm associated with all things to do with cephalopods, for his scrappy inventiveness, and for his kindness and humanity. Most of all, he will be missed by his family. He is survived by his wife of 52 years, Janet; son, Matthew (Cathie Kessler), and grandchildren, Simon and Heather; and son, Stephen (Ayumu Ishii) and grandchildren, Korben and Alice. The family thanks the staff of 4C in Northwood for the kind and compassionate care Ron received in his year there. Donations in his memory may be made to the Ron O'Dor Memorial Fund at Dalhousie University to support a student prize in Marine Biology or to the Northwood Foundation.

Mike Vecchione



Forthcoming meetings

The Malacological Society of London

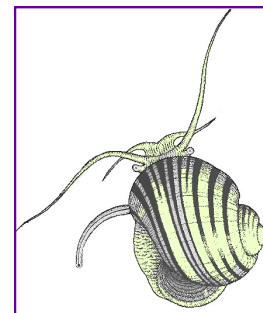
[HTTP://WWW.MALACSOC.ORG.UK](http://www.malacsoc.org.uk)

The VIRTUAL Molluscan Forum

Thursday 19^h November 2020
0945h – 1630h (to be confirmed)

CALL FOR REGISTRATIONS AND PAPERS DEADLINE 16 OCTOBER 2020

This informal, annual, and successful meeting is designed to bring together people starting their research on molluscs, to give them the opportunity to present and discuss their work and to compare notes on methods and problems. The deadline for registrations and talk applications is



Attendance to the Molluscan Forum is open to all, but preference is given to **research students, post-doctoral researchers, undergraduate students**, and **amateurs** engaged in substantial projects that have not yet been published. Any topic related to molluscs is acceptable: palaeontological, physiological, behavioural, ecological, systematic, morphological cellular or molecular.

Short talks (~15 min) or posters may be offered.

Instead of posters, we will have 5 minute (3 slide maximum) **quick-fire powerpoint** presentations,

They need not be polished accounts of completed work and can describe proposed studies at a later stage of preparation. .

There is **NO** registration fee

Enquiries and registrations to:

Phil Hollyman, Fisheries Ecologist, British Antarctic Survey (phyman@bas.ac.uk)

Non-presenters: please let us know you will be coming so that we can estimate numbers.

For more information see: <http://www.malacsoc.org.uk/MolluscanForum.htm>

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The Malacological Society of London

Molluscan Forum, Thursday 19^h November 2020
9:45 am – 4.30 pm

REGISTRATION FORM

Return before 16th October 2020, by email to:

Phil Hollyman, Fisheries Ecologist, British Antarctic Survey (phyman@bas.ac.uk)

Name.....

Address.....

.....

Tel. No.....

Email.....

Status: Research Student / Undergraduate / Post-doctoral researcher / amateur (delete as appropriate)

'Other' (please state)

Short talks (~15 min) or posters may be offered.

Instead of posters, we will have 5 minute (3 slide maximum) quick-fire powerpoint presentations,

I wish to give a talk / quick-fire talk (delete as appropriate) entitled:

.....

.....

Please attach, as a Microsoft Word attachment, an abstract of not more than 350 words, TOGETHER WITH TWO .JPG IMAGES IN SUPPORT OF THE ABSTRACT. Abstracts and images of accepted contributions will be published in the Society's on-line bulletin which is called *The Malacologist*. *The Malacologist* has an ISSN number and is published and archived on the website of the MSL.

Abstract submission

Abstracts submitted for the Molluscan Forum should be sent as Microsoft Word files.

Abstract submission

Please use the following format:

Title (12pt, left justified)

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Authors (10 pt, left justified, presenting author underlined; use superscript numbers to indicate institutional affiliation)

<blank line>

Institutions (10pt, left justified; in this order: Number (superscript), Department, Institution, City, Country)

Presenting Author email

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Abstract (11pt, no indentation, left justified, 350 words maximum)

EXAMPLE ABSTRACT**The geographic scale of speciation in *Stramonita* (Neogastropoda: Muricidae)**

Martine Claremont^{1,2}, Suzanne T. Williams¹, Timothy G. Barraclough², and David G. Reid¹

¹Department of Zoology, Natural History Museum, London, UK

²Department of Biology, Imperial College London, Berkshire, UK

Email: m.claremont@nhm.ac.uk

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

NOTE THAT ABSTRACTS ARE PUBLISHED IN *THE MALACOLOGIST* WHICH IS THE BULLETIN OF THE SOCIETY AND HAS AN ISSN NUMBER.

BEFORE THE FORUM, PLEASE EMAIL TO THE EDITOR TWO IMAGES TO ACCOMPANY YOUR ABSTRACT. TRY TO MAKE THESE IMAGES ONES THAT YOU WOULD NOT USE IN AN EVENTUAL FULL PAPER.

EDITOR georges.dussart@canterbury.ac.uk



Forthcoming meetings

Genomic Perspectives in Comparative Physiology of Molluscs: Integration across Disciplines

Dr. Maurine Neiman (University of Iowa) and Dr Omera B. Matoo, are organizing a symposium “**Genomic Perspectives in Comparative Physiology of Mollusks: Integration across Disciplines**” to take place at The Society of Integrative and Comparative Biology (SICB) annual meeting on January 4, 2021 (<http://burkclients.com/sicb/meetings/2021/site/index.html>). The symposium is co-sponsored by four SICB Divisions, including Division of Comparative Physiology and Biochemistry (DCPB), Division of Ecology and Evolution (DEE), Division of Evolutionary Developmental Biology (DEDB), Division of Invertebrate Zoology (DIZ) and Division of Phylogenetics and Comparative Biology (DPCB).

The program consists of 11 presentations representing a broad range of efforts to integrate large datasets across levels of biological organization in molluscs, towards the larger goal of linking genomes to phenomes - one of the Grand Challenges identified by the National Science Foundation (NSF). The symposium will be live-streamed and there will be additional opportunities for networking. In addition to the main symposium, there will be both oral and poster complementary sessions with speakers selected from submitted abstracts. Participants across disciplines will discuss major gaps, key barriers and leading edges in elucidating mollusk biology.

Abstract submission for the meeting is now open! Please share widely.

The Contributed Talks and Posters submission site: <http://sicb.burkclients.com/meetings/2021/abstracts/index.php>.

We are funded by The American Genetics Association, The Company of Biologists and the National Science Foundation. We have some student and trainee (undergrad/graduate/postdoc) funding support available to defray the cost of attending SICB meeting. Below is the link to our application. We will use this information to maximize inclusion from individuals from groups underrepresented in STEM fields. We will also make an effort to include individuals from a wide variety of laboratories, university settings, and across the range of topics.

Funding application for Mollusk Symposium:

https://docs.google.com/forms/d/1jWbGYcn07PXM0Ysdjwwk3YfpPNdmSGbtv_mQIBq4EGs/edit

Omera B. Matoo, PhD.

Res Assistant Professor, School of Biological Sciences,
University of Nebraska-Lincoln,
Lincoln, USA-68588



Grants and Awards

Malacological Society of London Awards and Grants

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

Early Career Research grants

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

Sir Charles Maurice Yonge Award

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

Senior Research Awards

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

Travel Grants

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

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

Annual Award

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

Applications

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



Malacological Society of London—Membership notices

Objects

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

Publications

The Society has a continuous record of publishing important scientific papers on molluscs in the *Proceedings*, which evolved with Volume 42 into the *Journal of Molluscan Studies*. The *Journal* is published in annual volumes consisting of four parts which are available on-line by members and student members. 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

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 fee structure

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

Methods of Payment

- (1) Sterling cheque to "The Malacological Society of London".
- (2) Banker's standing order to: HSBC (Sort code 40-16-08 Account no. 54268210) 63-64 St Andrew's Street, Cambridge CB2 3BZ
- (3) Overseas members wishing to pay electronically should use
IBAN GB54MIDL4016084268210
SWIFT/BIC MIDL GB22
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