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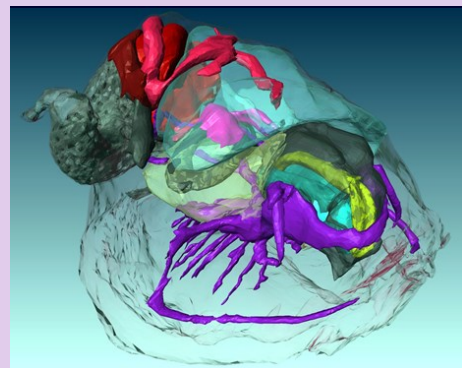
Includes abstracts of the ..

7TH CONGRESS OF THE EUROPEAN MALACOLOGICAL SOCIETIES
CAMBRIDGE, UK
7TH - 11TH SEPTEMBER 2014



Images from *The heart of a dragon: extraordinary circulatory system of the scaly-foot gastropod revealed*

Chong Chen, Jonathan Copley, Katrin Linse, Alex Rogers & Julia Sigwart
See Page 50



EDITORIAL

In the previous August issue of *The Malacologist* (Number 63), there were several research reports for projects supported by grants from the Malacological Society of London. The current issue however (Number 65), has relatively few such reports (two) but includes a summary of the thesis from Gregor Crista (page 10) which won the Annual Award of the Society. In a tradition established by previous editor Stuart 'Bill' Bailey some years ago, it has been customary to publish abstracts of our conference meetings in *The Malacologist*, hence the large number of pages in this issue (77p). It has been inflated into a bumper issue by (i) abstracts from the conference which accompanied the Annual General Meeting on April 1st 2015 entitled *Planktic Molluscs-Biology, Ecology, Palaeontology* organised by Deborah Wall-Palmer, Jon Ablett and retiring President, Prof. Tony Walker; (ii) abstracts of *Euromol- the Seventh Congress of the European Malacological Societies*. Digital preparation and publishing allows the abstracts to be complemented with illustrations which, I hope, lead to an interesting and attractive format. I endeavour to select images which will not compromise further publication in academic journals and which will also attract the reader into investigating the research of a particular author. For an example, see the image at the bottom of page 43.

I would like to take this opportunity on behalf of the Society to thank retiring President Professor Tony Walker for his sterling work for the Society over the past four years. He has been an efficient, firm and convivial leader who has had to deal with some tricky problems, doing so with a smiling and successful diplomacy. He handed the President's reins (and a secret piece of paper the contents of which are only known to Presidents) to Dr Suzanne Williams who has already shown herself to be a dedicated and good-natured advocate for the Malacological Society of London. We wish her an easy passage.

TAXONOMIC/NOMENCLATURAL DISCLAIMER

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

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NOTICES

The cost of membership of the Malacological Society of London

For some years, although membership was charged are £45, the Society has had to pay publishing costs of £92 to send each member a hard-copy of the *Journal of Molluscan Studies*. There was thus a strange situation whereby the members were costing the Society money. As announced at the 2015 AGM, in order to rectify the situation, the Council of the Malacological Society has therefore decided to move to offering a choice of an on-line journal, for members. The details are as follows:-

- Jan 2016 – Students £25 (on-line access only); full members £45 online; £70 with hard copy.
- Jan 2017 – Students £25 (on-line access only); full members £45 online; £80 with hard copy.
- Jan 2018 – Students £25 (on-line access only); full members £45 online; £90 with hard copy.
- Jan 2019 – Students £25 (on-line access only); full members £45 online; £90 with hard copy.
- Jan 2020 – to be revised as appropriate,



Cephalaspid Gastropods of Norway

Recently launched webpages dedicated to the diversity of the Cephalaspidea Gastropods of Norway: This results from ongoing work started 4-years ago and will be updated as we gather new relevant data.

<http://www.biodiversity.no/Pages/149434>

Manuel Malaquias, Associate Professor, Section of Taxonomy and Evolution, Department of Natural History, University Museum of Bergen, University of Bergen, PB7800 5020 Bergen, Norway



Compendium of Bivalves 2

Huber, M., 2015. *Compendium of Bivalves 2. A Full-Color Guide to the Remaining Seven Families. A Systematic Listing of 8,500 Bivalve Species and 10,500 Synonyms*. ConchBooks, Hackenheim, Germany. 907 pp., incl. numerous colour figs + CD-ROM. May.

This constitutes the conclusion of a bipartite work and is intended to be fully inclusive. <http://www.conchbooks.de/?t=53&u=36699> and <http://www.conchologistsofamerica.org/conventions/>.



Heroine for our time

Dr Rowan Whittle serves on the Council of the Malacological Society as Membership Secretary.



Katie Jane Rose: When did you know you wanted to work in this field?

Dr Rowan Whittle: I kind of always wanted to be a palaeontologist ever since I was a small child. I always loved collecting sea shells and aged six I found a coiled fossil on holiday with my parents. I became obsessed by it. My parents said "Oh, if you like that so much you should become a palaeontologist." I was obsessed with fossils and rocks and dinosaurs. I guess I went through that phase all children go through but I never grew out of it.

KJR: Did you feel like you had a good chance and support to enter this industry? Do you think enough is being done to get girls into science and engineering jobs?

DRW: I went to an all-girls grammar school where they encouraged us to do everything. No one ever said I couldn't do it; I felt very supported. No one ever said, "That's a boy's subject," it wasn't an issue. I probably would have just ignored it if anyone said anything back then! I've been very lucky - I was very focused from an early age.

KJR: So what path did you take?

DRW: I studied geography, biology and geology, as that's what you need to do to do a degree in geology



Flying snails seen in a supermarket in France.....

Research grant report

Molecular phylogeny of Chaetodermomorpha (=Caudofoveata) (Mollusca)

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INTRODUCTION

The shell-less, worm-shaped morphology of the Chaetodermomorpha (= Caudofoveata) and Neomeniomorpha (= Solenogastres) is unique among the Mollusca. The presumed plesiomorphic state of many morphological characters in these aplacophoran molluscs have led to them being regarded as early branching within the Mollusca, either as separate classes (e. g., Haszprunar 2000, Salvini-Plawen 2003), or grouped together in the clade Aplacophora (e. g., Scheltema 1993).

Recently, the aplacophoran molluscs have received much attention as part of the Aculifera, a clade grouping Neomeniomorpha and Chaetodermomorpha with Polyplacophora, which was first proposed based on morphology (see e.g., Scheltema 1993). Several studies employing molecular methods (Kocot *et al.* 2011, Osca *et al.* 2014, Smith *et al.* 2011, Vinther *et al.* 2011), as well as fossil evidence (Vinther *et al.* 2011, Sutton & Sigwart 2012, Sutton *et al.* 2012,) have provided strong support for the Aculifera hypothesis (but see review by Schrödl & Stöger 2014).

Despite of an increasing number of studies on the phylogenetic position of aplacophoran molluscs within Mollusca, many questions about relationships between and within the two aplacophoran groups remain (Todt *et al.* 2008, Todt 2013). Insight into the evolution of Chaetodermomorpha is important to understanding the relationships between aplacophoran molluscs and the evolution of characters within the Aculifera, and can thereby aid in understanding the direction of evolution within Mollusca as a whole. However, the internal relationships of the Chaetodermomorpha are not known, and the evolutionary relationships of the group have never been tested in a proper phylogenetic analysis, neither based on morphological nor molecular data. Besides a preliminary study using phylogenomic tools (Kocot *et al.* 2013), this study is the first attempt using molecular data to give insight into the relationships between the families of Chaetodermomorpha, using mitochondrial (COI, 16S) and nuclear ribosomal genes (18S, 28S).

Traditionally, the Chaetodermomorpha has been divided into three families, Prochaetodermatidae (Salvini-Plawen 1975), Chaetodermatidae (Théel 1875) and Limifossoridae (Salvini-Plawen 1970). A fourth family, Scutopidae, was suggested by Ivanov (1981), but has later been rejected (Salvini-Plawen 1992, Saito & Salvini-Plawen 2014). The validity of the families, and the relationships among the families are still debated (Todt *et al.* 2008).

The main characters defining the families of Chaetodermomorpha are the shape of the oral shield flanking the mouth, the general body shape, and most importantly the morphology of the radula. Both Prochaetodermatidae and Limifossoridae have a serial, distichous radula, setting apart the family Chaetodermatidae, which is defined by a radula reduced to a single pair of teeth supported by an unpaired cone. Prochaetodermatidae is in addition characterized by the presence of jaws and a middle row of central plates between the teeth, both unique among the Chaetodermomorpha (Salvini-Plawen 1975). The oral shield is divided in two paired lateral parts in Prochaetodermatidae. In Limifossoridae the oral shield is divided (in *Psilodens* and *Limifossor*) or circumoral (in *Scutopus*) and in Chaetodermatidae it is circumoral or horseshoe-shaped. Prochaetodermatidae have a cylindrical body with an abruptly tapering, tail-like posterior end, Chaetodermatidae have an elongated body clearly divided into three or four body regions, and Limifossoridae have a cylindrical body with externally scarcely pronounced body regions (Salvini-Plawen 1977).

In Chaetodermatidae and Limifossoridae, radular morphology is also used for defining the genera. Within Limifossoridae, species of *Limifossor* have paired teeth that consist of a plate with two pointed denticles: one larger lateral denticle and smaller median denticle. Species of *Psilodens* and *Scutopus*, in contrast, have simpler, hook-shaped radular teeth, in *Scutopus* bearing several small denticles (Salvini-Plawen 1977). In Chaetodermatidae, the two genera *Chaetoderma* and *Falcidens* both have radulas with a single pair of teeth, but the pincer-like *Falcidens* radula, with two teeth connected by a proximal symphysis and a central plate, differs from the simpler *Chaetoderma* radula, where the teeth have been reduced to a pair of denticles attached to the dome-shaped membrane which covers the distal end of the radula and is supported by two lateral projections. (Scheltema 1981).

Although Prochaetodermatidae have been thoroughly investigated and mapped in many areas (e. g., Ivanov & Scheltema 2001, 2008; Scheltema & Ivanov 2000), no hypotheses have been proposed for the internal relationships of this family. While the genera in the other families are defined based on radular morphology, the prochaetodermatid radula differs less between the genera, and so far no morphological pattern has been defined. The radulas are hypothesised to be more plastic than the shape and sculpture of the sclerites, which has been used as a primary character for the genera together with the number of rows of sclerites flanking the oral shield (e. g., Ivanov & Scheltema 2002, 2008; Scheltema & Ivanov 2000).

Morphology has traditionally led to Limifossoridae being regarded as first branching or most “basal” taxon, based on the presence of presumed plesiomorphic characters: the serial distichous radula and the simple body shape. Additionally, the ventral line found in several species of Limifossorids, has been interpreted as a vestige of a ventral furrow, homologous to the ventral foot groove in Solenogastres (Ivanov 1986, Salvini-Plawen 2003). Chaetodermatidae are assumed to be the most derived taxon because of the reduced radula and complex midgut (Salvini-Plawen 1975, Scheltema 1981).

MATERIAL & METHODS

For the present research, a systematic revision of the *A.papillosa* species complex was undertaken based on molecular data from two mitochondrial genes, cytochrome c oxidase I (COI) and 16S ribosomal RNA (16S), and from one nuclear gene, histone 3 (H3). Specimens covering a wide range of distribution of the target species were included, including specimens from both hemispheres. Additionally, morphological traits, such as external morphology, radula and reproductive system were examined to supplement the molecular results.

RaxML (Stamatakis 2006) was used for maximum likelihood analyses, applying the GTRGAMMA model and 500 bootstrap replicates, and Bayesian inference analyses were carried out in MrBayes (Huelsenbeck & Ronquist 2001) with 2 runs of 4 chains for 10 million generations, sampling every 1000 generations. For analyses in MrBayes, the data was partitioned according to gene, and appropriate evolutionary models based on the Akaike Information Criterion (AIC) computed by the program jModeltest (Posada 2008) were applied.

Specimens were fixed and stored in 96% ethanol, and DNA was extracted using the Qiagen DNEasy kit using the manufacturer’s instructions in the Blood & Tissue protocol.

The COI (Cytochrome c oxidase 1) and 16S genes were amplified with Takara Ex Taq HS. The 18S and 28S genes were amplified using Takara LA Taq. Primers used for COI were LCO1490/HCO21 (Folmer & Vrijenhoek 1994), for 18S 18e/18p (Hillis & Dixon 1991) for 28S F2-2/R2 (Passamaneck *et al.*, 2004) and 28Sa/28Sb (Whiting *et al.*, 1997), 16S 16LRN13398/16RHTB (Koufopanou *et al.* 1999).

RESULTS & DISCUSSION

We analysed sequences from twelve species, representing the three recognised families of Chaetodermomorpha (Figure 1). The same topology resulted from the Bayesian inference and maximum likelihood analyses. With the present taxon sampling, the data supports the monophyly of the three currently recognized families. All three families are recovered as monophyletic with strong support. Contrary to traditional views, the Prochaetodermatidae is the first branching taxon in our phylogeny, a surprising result, also found by Kocot *et al.* (2013). The Limifossoridae, the taxon traditionally viewed as “basal”, is recovered as sister to the Chaetodermatidae.

The simple, distichous radula of Limifossoridae has been viewed as the ancestral form in Chaetodermomorpha, in concurrence with a hypothetical ancestral aplacophoran radula of the distichous type (Scheltema 2003). A revision of the ancestral aplacophoran radula in the light of recent paleontological findings, however, supports the presence of a rhachidian tooth to represent the ancestral state in Mollusca, and probably also Aplacophora (Scheltema 2014). The more complex Prochaetodermatidae radula has a central plate, which has been assumed to be analogous to the rhachidian tooth found in the radulas in other mollusc groups and also in the ancestral molluscan radula (Scheltema 2014). If, however, the central plate of the prochaetodermatid radula is homologous to a rhachidian tooth, this would support our molecular data that show an early branching of Prochaetodermatidae within Chaetodermomorpha.

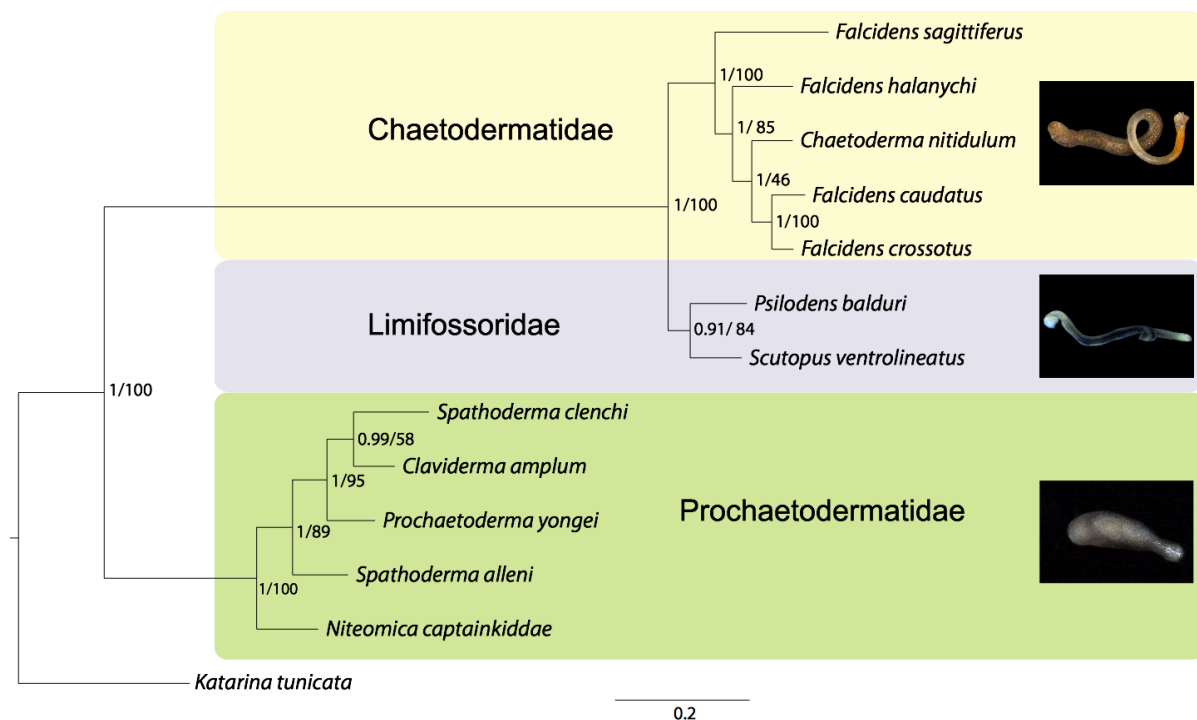


Figure 1 Phylogenetic tree of 12 caudofoveate species based on COI, 16S, 28S and 18S. Posterior probabilities from the Bayesian analyses and bootstrap support values are shown on the nodes. Sequences of the chiton *Katarina tunicata* were used as an outgroup; sequences from this species were downloaded from GenBank.

The relationships within each family are less convincingly resolved. Within the family Chaetodermatidae, *Falcidens* is paraphyletic as *Chaetoderma* is nested within this clade, however with very low bootstrap support for the clade including *Chaetoderma nitidulum*, mirroring the ambiguous placement of this species. *Falcidens sagittiferus* from the North Eastern Atlantic represents the first branch within Chaetodermatidae, showing a distinction between species of *Falcidens* with distinct morphologies: a tailed and a non-tailed body shape. The tailed *Falcidens* species included in the analyses, *F. crossotus* and *F. caudatus*, from European and North American waters, respectively, form a well-supported clade, and so our molecular results support monophyly of the tailed species of *Falcidens*. The non-tailed species (*F. sagittiferus* and *F. halanych*) are paraphyletic with respect to the tailed *Falcidens* and *Chaetoderma nitidulum*.

Sister to Chaetodermatidae is a clade comprising *Psilodens* and *Scutopus*. Thus, with the presently quite small taxon sampling, Limifossoridae form a monophyletic clade, although with modest support. Data from more species, including species of *Limifossor*, is necessary to further evaluate the relationships within the family Limifossoridae.

So far, no hypothesis has been put forward about the relationships between the genera within Prochaetodermatidae. Our analyses do not provide satisfying resolution within this group, either. The two species of *Spathoderma*, the only genus from which sequences from more than one species could be included, are not clustering together. The ambiguous placement of both species is poorly supported in the maximum likelihood analyses, and needs further investigation.

The initial results presented here provide support for the monophyly of the three currently recognized families of Chaetodermomorpha, and are consistent with some of the present theories about systematics based on morphology. On the other hand, they raise interesting questions about the relationships between the families, in particular the position of Prochaetodermatidae as the first branching taxon. This study indicates the usefulness of the sequenced genes to recover relationships within Chaetodermomorpha and provides a framework within which we can continue to investigate these relationships. We are now working on a dataset with increased gene and taxon sampling. The expanded dataset includes data from species from a larger part of the geographical range for each family and genus, and captures more of the existing taxonomic variation. The ongoing work will likely provide better resolution and give further clues about the systematics and evolution of Chaetodermomorpha.

ACKNOWLEDGEMENTS

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The Caribbean shipworm *Teredothyra dominicensis* (Bivalvia, Teredinidae) has invaded and established breeding populations in the Mediterranean Sea

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INTRODUCTION

The wood-eating bivalves of the Teredinidae, commonly referred to as shipworms, are a major economic pest of coastal and marine constructions, including ships, piers, jetties and fishing equipment. Indeed, recent estimates predict shipworm cause billions of dollars' worth of damage per annum around the world (Distel, 2011). Furthermore, historical artefacts such as shipwrecks, which are of considerable archaeological and cultural importance, are also at risk of destruction from these organisms (Bjordal & Gregory, 2011). The spread of teredinids into new regions is a cause for concern due the lack of effective measures protecting wooden structures from infestation (Cragg, 2007). Typically, these introductions lead to rapid and wide-spread destruction, as exemplified by the invasion of *Teredo navalis* in San Francisco Bay in 1912, estimated to have caused \$25 million worth of damage. As such, effective measures are required to monitor the distribution of teredinids, particularly the colonisation of new areas and the spread of invasive species, which are known to be more destructive (Hoagland & Turner, 1980). This investigation reports the invasion of the tropical teredinid, *Teredothyra dominicensis*, in the Mediterranean Sea, the first known report of this species in European waters. Furthermore, this research represents the only known case-study of a teredinid invasion.



Fig. 1. The invasive wood-eating bivalve, *Teredothyra dominicensis*, recovered from a shipwreck in the Mediterranean Sea. Scale bar equal to 1 cm.

MATERIALS & METHODS

Sample collection & rearing

Sample collection was carried out in Kaş in southern Turkey, during August 2010 and June 2011. Infested wood was recovered from the shipwreck, Uluburun III, located approximately 36 metres below mean sea level. Wooden panels of *Pinus sylvestris* (2.5 cm × 10 cm × 20 cm) were also attached to the mast of the wreck during August 2010 for retrieval and analysis the following year. Specimens of *T. dominicensis* were obtained from the Caribbean, the recorded native range of this species, for comparison with specimens sampled in the Mediterranean.

Molecular identification

DNA was extracted from siphonal tissue and associated musculature. Total genomic DNA was extracted using DNeasy Blood & Tissue kit (Qiagen), following the manufacturer’s protocol. Concentration, yield and purity of DNA were determined by UV spectrophotometry and DNA template was diluted using molecular grade water to a concentration of 10-20 ng/μL. A 658 bp fragment from the 5’ end of the cytochrome oxidase subunit I (COI-5P) was amplified using the primer pair LCO1490 (forward 5’ GGT CAA CAA ATC ATA AAG ATA TTG G 3’) and HCO2198 (reverse 5’ TAA ACT TCA GGG TGA CCA AAA AAT CA 3’) (Folmer *et al.*, 1994), following the protocol outlined by Borges *et al.* (2012). Amplifications were performed following the protocol outlined by Borges *et al.* (2012). A 6 μL aliquot of PCR product was then electrophoresed in a 2 % agarose gel. Amplified products were purified using a NucleoSpin Gel and PCR Clean-up kit (Macherey-Nagel, Duren, Germany) according to the manufacturer’s guidelines. All PCR products were sequenced by Source Bioscience.

Data Analysis

COI-5P sequences were edited and aligned using MEGA 6.1 (Tamura *et al.*, 2011). Edited sequences were compared with those on the GenBank database to confirm species identity and ensure that endosymbiont bacteria or other contaminant had not been co-amplified in error. Sequences were aligned using Clustal W (Tamura *et al.*, 2011) and COI sequences were translated to check for the presence of frameshift mutations, stop codons or unusually divergent amino acid profiles. Sequences consisting of 658bp were used for phylogenetic inference using Neighbour-joining (NJ). Neighbour joining trees were constructed using the Kimura 2-parameter model (K2P) with the programme MEGA 6.1. Selected GenBank sequences were used to compare with our data set and to be used as outgroups.

RESULTS

Collection

Specimens were acquired from a shipwreck off the coast of Kaş, southern Turkey, in which *T. dominicensis* (shown in Figure 1) was the dominant species present, representing 93 out of 104 specimens collected. Wooden panels placed at the wreck site and recovered the following year were colonised exclusively by *T. dominicensis* (Figure 2).

COI-5P Sequences of Sampled Teredinids

A total of eight COI-5P sequences were obtained for *T. dominicensis*. A BLAST comparison revealed ≥ 99 % maximum identity with existing COI-5P sequences of *T. dominicensis* by Borges *et al.* (2012). The neighbour-joining phylogenetic trees for COI-5P sequences are shown in Figure 3.

Fig.3 Molecular identification of *Teredothyra dominicensis* based on COI-5P sequences inferred by Neighbour-Joining. Asterisks denote sequences obtained from GenBank, including the shipworms *Bankia carinata*, *Lyrodus pedicellatus*, *Nototerodo norvagica*, *Lyrodus pedicellatus* and the bivalve *Corbicula leana* as an outgroup.

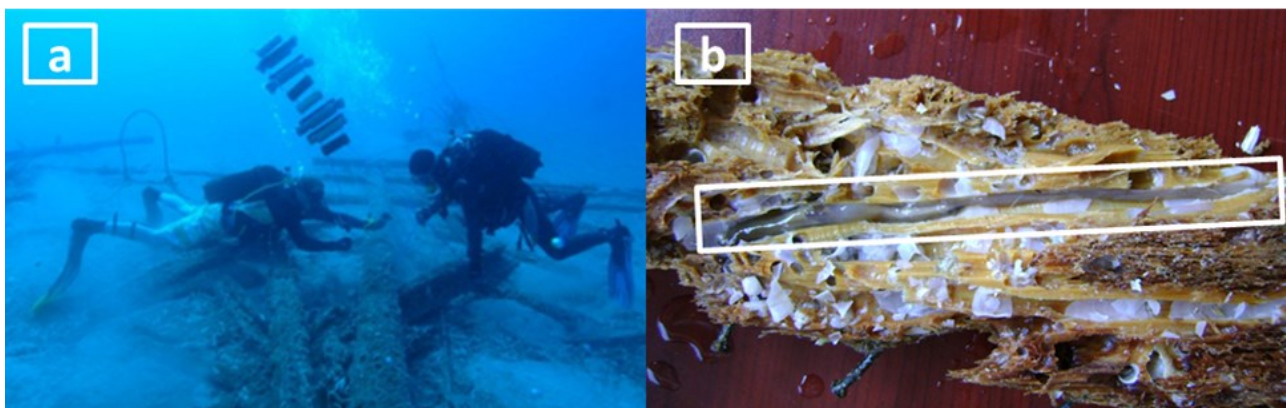
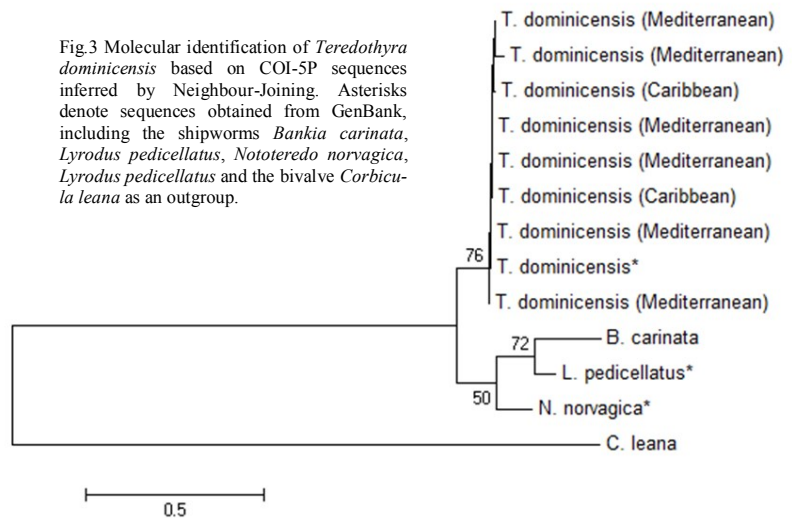


Fig. 2. a) The placement of wooden sampling panels in the Mediterranean. b) Collection of sample panels revealed exclusive infestation by the Caribbean shipworm *Teredothyra dominicensis*. The highlighted area indicates a single specimen, measuring approximated 25 cm in total length.

DISCUSSION

Molecular identification of *T. dominicensis* using COI-5P markers revealed a low interspecific divergence with known sequences on GenBank, as well as specimens of *T. dominicensis* collected from its native range in the Caribbean Sea, thus confirming the identity of the invasive species and ruling out the possibility of the Mediterranean population representing a cryptic species. This species was thought to be exclusively confined to the Gulf of Mexico and Caribbean Sea (Bartsch, 1922; Turner, 1966) and has never been documented in the Mediterranean, despite numerous and extensive surveys of the region (Roch, 1940; Turner, 1966).

T. dominicensis was confirmed by Shipway *et al.* (2014) as a broadcast spawning species, with larvae undergoing planktotrophic development lasting between three and four weeks. Wooden panels placed on the shipwreck where *T. dominicensis* was first discovered were subsequently infested by mature adult specimens. As the free-spawned larvae of this species must spend a number of weeks developing in the water column, recruitment is unlikely to have taken place directly from the population infesting the shipwreck as the larvae would disperse away from the site. Larval production is therefore most likely to have originated from other breeding populations of *T. dominicensis* in the Mediterranean. As larvae were capable of settlement, metamorphosis and growth to maturity, *T. dominicensis* must be considered an established species in the region. The appearance and establishment of a Caribbean shipworm in the Mediterranean is of concern, as tropical borers may grow to larger sizes than European borers (Castagna, 1961) and are known to be more destructive than their temperate counterparts (Edmondson, 1942; Southwell & Bultman, 1971). The impact of global warming, particularly the rise in temperature of the Mediterranean also needs to be considered in relation to teredinid activity. An increase in the temperature and salinity of the region has already been observed (Gibelin & Déqué, 2003; Sánchez *et al.*, 2004) and is expected to continue over the coming decades (Giorgi & Lionello, 2008; Giannakopoulos *et al.*, 2009). These increases are known to extend teredinid distribution ranges (Borges *et al.*, 2010; Paalvast & van der Velde, 2011), accelerate growth and increase boring activity (Eckelbarger & Reish, 1972). Introduced tropical shipworms have also been shown to out-compete native species as they respond more favourably to environmental change (Hoagland, 1983). Thus, the warming of the Mediterranean will increase the threat posed by all teredinids in the region, particularly that of the destructive Caribbean species, *Teredothyra dominicensis*.

ACKNOWLEDGEMENTS

I would like express my gratitude to the Malacological Society of London for a travel grant which funded the field work undertaken in this research. Without this grant, the research would not have been possible. I would also like to thank my Ph.D supervisor Dr Simon Cragg, whose advice helped facilitate this work.

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Evolution of chloroplast sequestration in Sacoglossa (Gastropoda, Heterobranchia)

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The Heterobranchia include various slug taxa such as Nudibranchia, Pulmonata and the Sacoglossa. The latter is a rather small taxon with about 300 described species and a worldwide distribution. They mostly inhabit the intertidal zone and feed mainly on algae of the taxon Ulvophyceae (Chlorophyta). The name Sacoglossa is derived from an autapomorphic structure called „saccus“ (von Ihring 1879), in which teeth of their radula are stored: the radula is reduced to a single tooth per row, and only the leading tooth is used for feeding. In the Sacoglossa two main groups are distinguished: the shelled Oxynoacea and the shell-less Plakobranchiacea. The latter unites the cerata-bearing Limapontioidea and the parapodia bearing Plakobranchiacea (Figure 1).

With the leading tooth, Sacoglossa cut a slit in the cell wall of their algal prey and subsequently suck out the cell content. Then specifically the plastids of the ingested cell sap are incorporated into the epithelial cells of the digestive gland at least in some sacoglossans (Figure 2). Intriguingly these „stolen“ plastids are kept photosynthetic active during times of food depletion. This, in a phenomenon unique in the Metazoa, is referred to as *functional kleptoplasty* and together with the gained green coloration gave the slugs botanical terms like „leaves that crawl“. We discriminate between different states of keeping the plastids photosynthetic active that mainly depends on the survival of starvation periods: species that are not able to maintain the plastids but digest them directly are called non-retention forms (NR), those that keep plastids active for up to 4 weeks of starvation are short-term retention forms (StR) and when they keep plastids active for more than several months we are talking about long-term retention forms (LtR). The majority of Sacoglossa is not able to maintain the plastids functional in the cytosol: out of the approximately 300 species, about 75 mainly belonging to the Plakobranchiacea are known for harboring functional plastids (Christa *et al.* 2015). Only one genus of the Limapontioidea, is now also well documented for functional kleptoplasty: *Costasiella* (Christa *et al.* 2014a), but none from the shelled Oxynoacea (Figure 1).

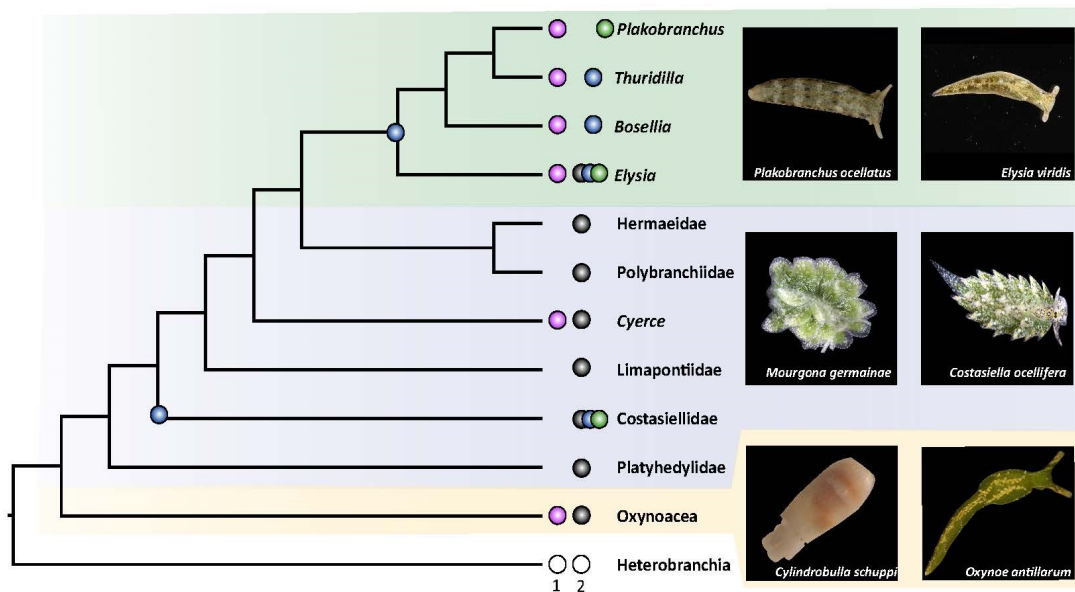
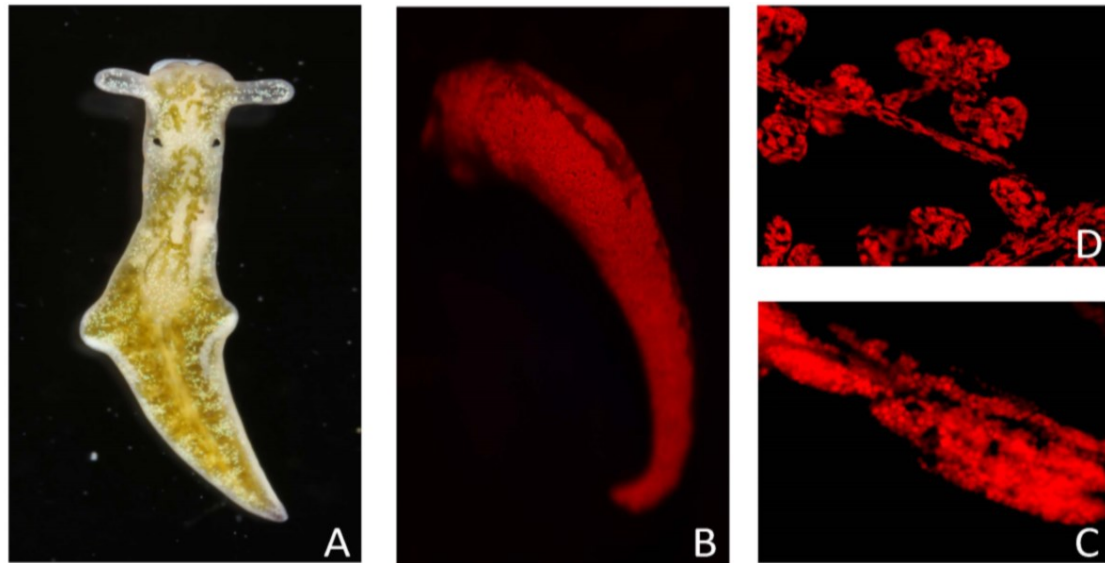


Figure 1 – The Sacoglossa unify the shelled Oxynoacea (yellow box) and the non-shelled Plakobranchiacea, the latter include the paraphyletic, cerate-bearing “Limapontioidea” (blue box) and the parapodia possessing Plakobranchiacea (green box). The ability to incorporate functional kleptoplasty evolved at least twice as short-term-retention, once in the Costasiellidae and once in the Plakobranchiacea (blue circles in the tree). Although there are some food sources that seem to be important for long-term-kleptoplasty, for example Halimeda (pink circle), these algae are also consumed by non-retention forms. 1. Food source 2. Retention form: **grey** NR, **blue** StR, **green** LtR.

When I started my PhD thesis, the phylogenetic relationships between the Limapontioidea and the Plakobranchiacea were uncertain, mainly due to unsettled relationships in the Limapontioidea. In my phylogenetic analyses, I could show that the Limapontioidea appear paraphyletic, in contrast to previous morphological analyses (Figure 1, Christa *et al.* 2015). The phylogenetic reconstruction set the base to analyse the evolution of functional kleptoplasty in Sacoglossa. This ability probably evolved multiple times, at least twice, independently: once in the Costasiellidae and once in the Plakobranchiacea (Figure 1, Christa *et al.* 2015).

We still do not know how slugs specifically embed specific plastids and what keeps the plastids active. Usually about 2000 proteins from the cytosol are needed to support plastids in an algal cell. Therefore it is quite astonishing that kleptoplastids survive for more than a few days outside their host cells - thus lacking any nuclear gene support. A putative transfer of photosynthesis related genes from the algal nucleus to the slugs' nucleus were investigated. However, based on detailed work on transcriptomes and on a genome we now know that no gene transfer could explain the plastids longevity in the foreign cytosol. I was interested in the role of the plastids in establishing functional kleptoplasty and if certain plastids have intrinsic factors (e.g., better protection with regard to photodamage) that make them more robust than plastids from land plants. In a first step I analysed the food sources of freshly collected Sacoglossa by DNA-barcoding or during various starvation periods. I then searched for a correlation of the food source and functional long-term kleptoplasty to get a list of plastids that might be more robust than others (Christa, 2014). Based on this work it seems that only a few plastids are apt for long-term kleptoplasty, but these are also consumed by NR and LtR form. The right slug needs to find the right plastid. The analyses of the food sources set the base for my current investigation on the photoprotection mechanisms of these plastids to verify whether such mechanisms are a major force in establishing functional kleptoplasty.

Figure 2 – *Elysia viridis* (a) possess functional plastids throughout its entire body (b) (in red the auto-fluorescence of the plastids) of *Codium*. These plastids are embedded in cells of their digestive gland (c and d) that branches throughout the animals' body.



Besides its evolution and mechanisms the benefit of functional kleptoplasty is not as obvious as it seems. One may assume that fixed inorganic carbon is made available as sugar and so may nourish the slugs. However, in starvation experiments the animals lost their weight not necessarily faster or died earlier when starved under non-photosynthetic condition compared with those starved under photosynthetic conditions (Christa *et al.* 2014b, 2013). But light intensities affect the functionality of the plastids: In darkness and in lower light conditions, the functionality declines less compared with specimens exposed to higher intensities (Christa *et al.* 2013, 2015).

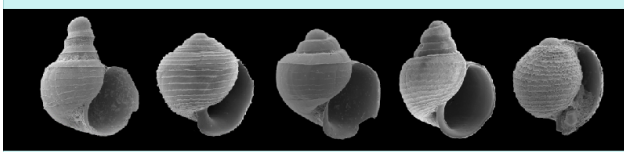
I want to especially thank my supervisor Prof. Dr. Heike Wägele for giving me the opportunity to do my PhD at her Lab and for four very special and great years. I feel very honored to be awarded by the Malacological Society of London for my research on Sacoglossa.

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Annual General Meeting April 2015



The Malacological Society of London Spring meeting and AGM

Planktic gastropods: biology, ecology and palaeontology

Organised by
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Images—juvenile specimens of Atlantidae. From left to right, *A. turriculata*, *A. helicinoidea*, *A. plana*, *A. brunnea*, *Oxygyrus inflatus*. D Wall-Palmer, Plymouth University.

AGM Conference Programme

09:30 COFFEE AND REGISTRATION

10:00 Welcome and introduction

TAXONOMY AND MOLECULAR RESEARCH

- 10:10 **Katja Peijnenburg** (Naturalis, Leiden) Keynote talk
Snails, Shells and Sequences: Adaptive Potential of Pteropods
- 11:00 **Peter Kohnert** (Bavarian State Collection of Zoology, Munich), **Christina Laibl** and **Michael Schrödl**
North vs. South: Who exactly is Limacina helicina? (Gastropoda, Euopisthobranchia, Pteropoda, Thecosomata)
- 11:20 **Alice Burridge** (Naturalis, Leiden), **Erica Goetze**, **Niels Raes**, **Jef Huisman** and **Katja Peijnenburg**
Global biogeography and evolution of Cuvierina pteropods
- 11:40 **María Moreno-Alcántara** (CICIMAR-IPN, México) and **Gerardo Aceves-Medina**
Ecological and taxonomic studies of holoplanktonic gastropods within the Mexican Pacific.
- 12:00 **Helen Scales**
Revealing hidden wonders: spreading the word about minute marine molluscs
- 12:20 LUNCH AND POSTERS
- 13:00 Annual General Meeting of the Malacological Society of London (MSL members only)
'Behind the scenes' tours for non-MSL members

PALAEONTOLOGY

- 13:40 **Malcolm Hart** (Plymouth University), **Christopher King** and **Christopher Smart**
Planktonic gastropods: survivors in a changing ocean
- 14:00 **Arie Janssen** and **Crispin Little** (University of Leeds)
Holoplanktonic gastropoda from the Miocene of Cyprus
- 14:20 **Deborah Wall-Palmer** (Plymouth University), **Christopher Smart**, **Richard Kirby** and **Malcolm Hart**
Palaeoceanography: clues from holoplanktic gastropods
- 14:40 TEA BREAK and *Frontiers in Science* informal meeting with Nina Keul

ENVIRONMENTAL CHANGE

- 15:10 **Silke Lischka** (GEOMAR, Kiel) Keynote talk
Pteropods – numerous, extraordinary, fragile, mysterious
- 16:00 **Clara Manno** (British Antarctic Survey), **Raul Primicerio**, **Victoria Peck** and **Geraint Tarling**
Pteropod race for life: swimming responses to anthropogenic climate change
- 16:20 **Antony Knights** (Plymouth University), **Jeff Polton** and **Tasman Crowe**
Predicting larval dispersal: The role of behaviour in minimising tidal transport
- 16:40 **Nina Keul** (Kiel University), **Peter de Menocal** and **Ralph Schneider**
Double trouble: Tracing the effect of ocean acidification and ocean warming in the shells of Arctic pteropods
- 17:00 Final remarks followed by a wine reception sponsored by the *Micropalaeontological Society of London*
- 18:00 CLOSE OF MEETING

Annual General Meeting - Conference Abstracts ... of oral presentations

Snails, shells and sequences: adaptive potential of Pteropods

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The oceans are changing on a global scale and, in some cases, at rates greatly exceeding those observed in the historical and recent geological record. Pteropods are a group of planktonic gastropods that have been identified as exceptionally vulnerable to rising CO2 due to their thin shells made of aragonite. Hence, interest in this group has grown considerably over recent years and pteropods have been used to explore the effects of ocean acidification. However, attention has focused on ecological responses and short-term experiments. In this talk, I ask 'what is the adaptive potential of pteropods?' I give an overview of the systematics and evolution of the group and present results from a recent study investigating intraspecific genetic and phenotypic variability along a latitudinal gradient of ocean acidification.

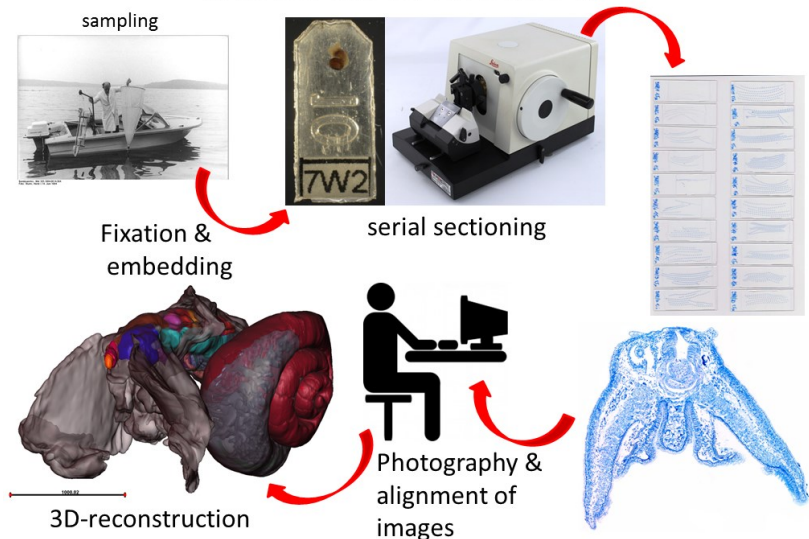


North vs. South: Who exactly is *Limacina helicina*? (Gastropoda, Eupisthobranchia, Pteropoda, Thecosomata)

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Pteropods form a clade of holopelagic eupisthobranch gastropods that includes shell-less Gymnosomata and shelled Thecosomata. The most famous thecosome "species" is probably *Limacina helicina*, which is widely distributed and increasingly used as a suitable indicator organism in polar regions, due to the high sensitivity of the delicate aragonitic shell for rising ocean acidification. Surprisingly, to date neither

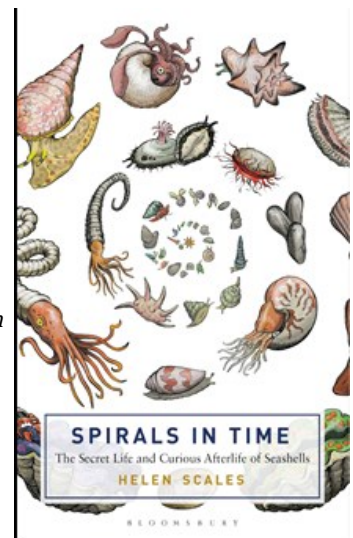
Material & Methods



Revealing hidden wonders: spreading the word about minute marine molluscs

Helen Scales
helenscales.com

Marine biologist, writer and broadcaster Helen Scales talks about her new book '*Spirals in Time*' and about communicating our science to a wider audience.



Global biogeography and evolution of *Cuvierina* pteropods

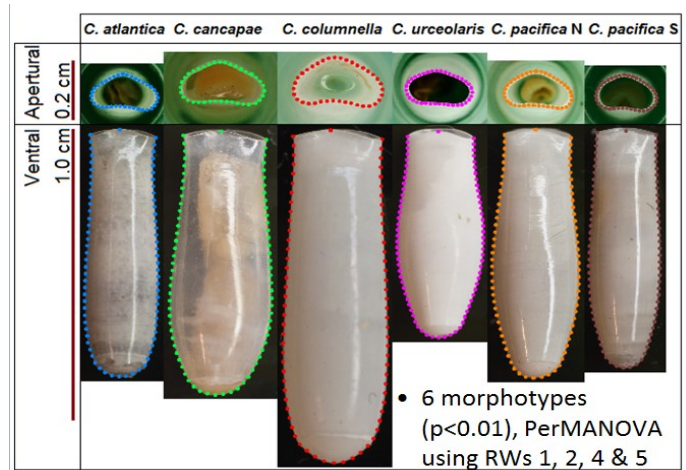
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Shelled pteropods are planktonic gastropods that are potentially good indicators of the effects of ocean acidification. They also have high potential for the study of zooplankton evolution because they are metazoan plankton with a good fossil record. We investigated phenotypic and genetic variation in pteropods belonging to the genus *Cuvierina* in relation to their biogeographical distribution across the world's oceans. We aimed to assess species boundaries and to reconstruct their evolutionary history. We distinguished six morphotypes based on geometric morphometric analyses of shells from 926 museum and 113 fresh specimens. These morphotypes have distinct geographic distributions across the Atlantic, Pacific and Indian oceans, and belong to three major genetic clades based on COI and 28S DNA sequence data. Using a fossil-calibrated phylogeny, we estimated that these clades separated in the Late Oligocene and Early to Middle Miocene. We found evidence for ecological differentiation among all morphotypes based on ecological niche modelling with sea surface temperature, salinity and phytoplankton biomass as primary determinants. Across all analyses, we found highly congruent patterns of differentiation suggesting species level divergences between morphotypes. However, we also found distinct morphotypes (e.g. in the Atlantic Ocean) that were ecologically, but not genetically differentiated. Given the distinct ecological and phenotypic specializations found among both described and undescribed *Cuvierina* taxa, they may not respond equally to future ocean changes and may not be equally sensitive to ocean acidification. Our findings support the view that ecological differentiation may be an important driving force in the speciation of zooplankton.



Ecological and taxonomic studies of holoplanktonic gastropods within the Mexican Pacific

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In the Eastern Pacific few studies involve the distribution and abundance of holoplanktonic gastropods. Nevertheless, there are records of 29 species of heteropods, 31 species of thecosomes and 13 species of gymnosomes between San Francisco, USA, and the Pacific coast of Costa Rica. Within the two most recent studies done in Mexico, there are 6 new records for the American Pacific, 41 range extension and 2 new species in process of description. However, certain taxonomic uncertainties, specifically within the Atlantidae, are being studied using morphological and genetic analyses. The morphological approach shows that Tokioka's whorl formula is not enough to separate species, but the morphometry can be combined with the eye type and numbers of spires in the protoconch to better identify species. Nevertheless, species like *Atlanta peronii* and *A. gaudichaudi* overlap, confirmed by genetic analysis. The taxonomic issue, among other things, complicates studies to understand basic

aspects of distribution and abundance. However it has been noticed that despite suggestions in earlier studies about their distribution being related with water temperature and salinity, additional factors are topography (coastal vs. oceanic environments) and hydrographic conditions of the area (concentration of organisms in anticyclonic eddies), as well as food availability.

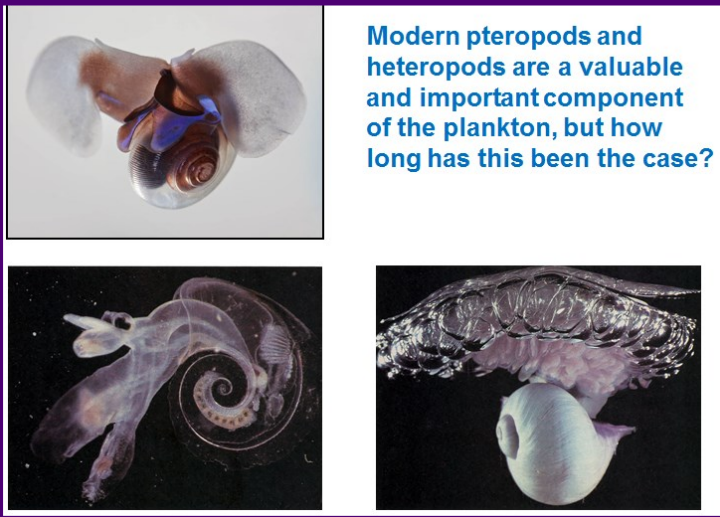


Planktonic gastropods: survivors in a changing ocean

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The geological record of the pteropods (Thecosomata) and heteropods (Pterotracheoidea) probably begins in the earliest Eocene (55 million years ago), although there are records – in the earliest Jurassic and mid-Cretaceous – of taxa that may be planktonic gastropods. In the early Paleogene there was the transition from a calcitic ocean to an aragonitic ocean and it seems logical that these aragonitic gastropods appeared at that time. While graphs of diversity or species richness are subject to taxonomic ‘distortion’, especially when comparing biological data with palaeobiological data, the heteropods appear to have been the product of our modern, thermohaline-driven ocean. The pteropods, with a potentially longer record, appeared during the hyperthermal events of the early to mid-Eocene surviving the transition to the modern, thermohaline-driven ocean and the onset of the present ‘icehouse world’. The fossil record of the planktonic gastropods can be used in biostratigraphy but, as their thin, fragile shells are composed of aragonite, their geological history is certainly incomplete. In some places they are preserved as phosphate, pyrite or limonite moulds, though such preservation often fails to retain some of their diagnostic characters, making species determination difficult.



Holoplanktonic Gastropoda from the Miocene of Cyprus: systematics and biostratigraphy

Arie Janssen¹ and Crispin Little²

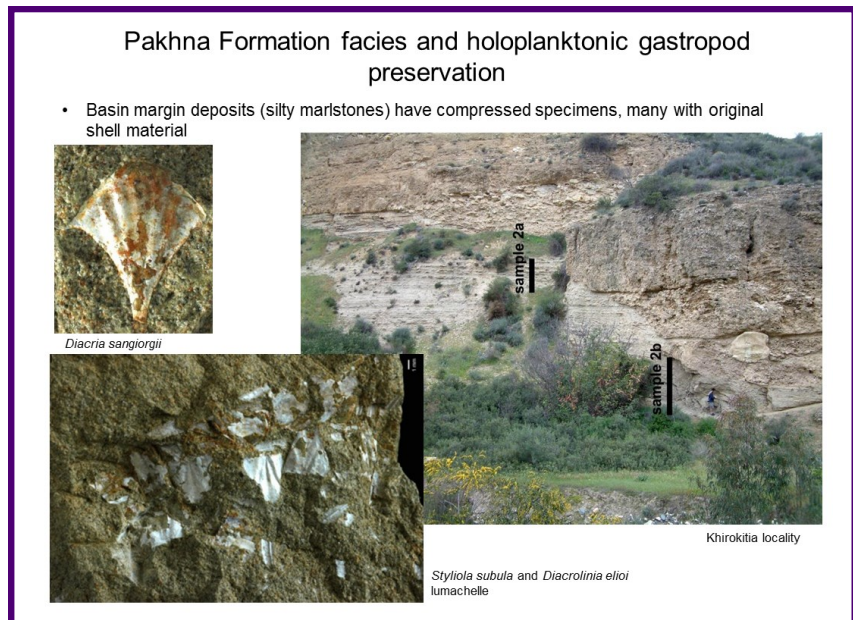
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Eleven randomly chosen outcrops in the Miocene Pakhna Formation of Cyprus were sampled for holoplanktonic Mollusca. Four species of Heteropoda were found and 24 of Pteropoda, a substantial increase from the two species recorded until now from the Miocene of Cyprus. One pteropod species, *Peracle charlotteae* sp. nov. (Pseudothecosomata), is introduced.

Age assignments based on holoplanktonic molluscs for the 11 localities are: Langhian (Alassa 1–4), (Serravallian?) Tortonian to Messinian (Episkopi 1), Tortonian (Agios Tychon, Tokhni and the Maroni Marlstone of Khirokitia 1–2) and Tortonian to Early Messinian (Episkopi 2). These age determinations in some cases are at odds with those from previous publications based on calcareous nanofossils and Foraminifera. At some localities, particularly in the Alassa area, pteropod assemblages are strongly variable on a bed by bed basis and this offers possibilities for future biostratigraphical interpretations. This is the first substantial holoplanktonic mollusc fauna described from the eastern Mediterranean basin and allows correlation with assemblages in the central Mediterranean and elsewhere. The Cyprus localities sit in the Mediterranean pteropod zonation (PZ) scheme of Janssen (2012) as follows: Alassa 1-4: PZ 18a (Alassa 1 and 4 agree with the Maltese zone 18a-2, but Alassa 2 and 3 might be slightly younger); Khirokita: PZ 20; Tokhni: PZ 20; Episkopi 1-2, PZ 20/21; Achios Tychon: ? upper part of PZ 20.



Palaeoceanography: clues from holoplanktic gastropods

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Living holoplanktic gastropods (pteropods and heteropods) are a common component of the zooplankton at all latitudes and highly sensitive indicators of surface ocean changes. Despite having a fossil record that extends from the Jurassic, there are very few detailed stratigraphic sequences of holoplanktic gastropods and consequently, they are rarely used in biostratigraphy. This is largely due to the susceptibility of their delicate aragonitic shells to dissolution. However, in well preserved sediments, fossil holoplanktic gastropods have the potential to contribute valuable information for paleoenvironmental reconstructions and stratigraphic correlation.

Here we demonstrate some of the stratigraphic and palaeoceanographic applications of fossil holoplanktic gastropods by presenting their distribution through a number of ~200–300 ka stratigraphic sequences from marine sediment cores. All cores have a stratigraphic framework, produced from a combination of AMS radiocarbon dating, oxygen isotope dating and biostratigraphy, against which the use of holoplanktic gastropods can be tested. Applications include detecting past ocean acidification and temperature of surface waters, use as stratigraphic markers in the Mediterranean Sea and as indicators of localised, strong bottom water currents in the Caribbean Sea.

More widespread study of holoplanktic gastropods in marine sediment cores is also likely to contribute new ecological information that can be applied to living populations. This is particularly important for the heteropods, whose abundances, distribution and environmental requirements in today's oceans are currently not well understood.

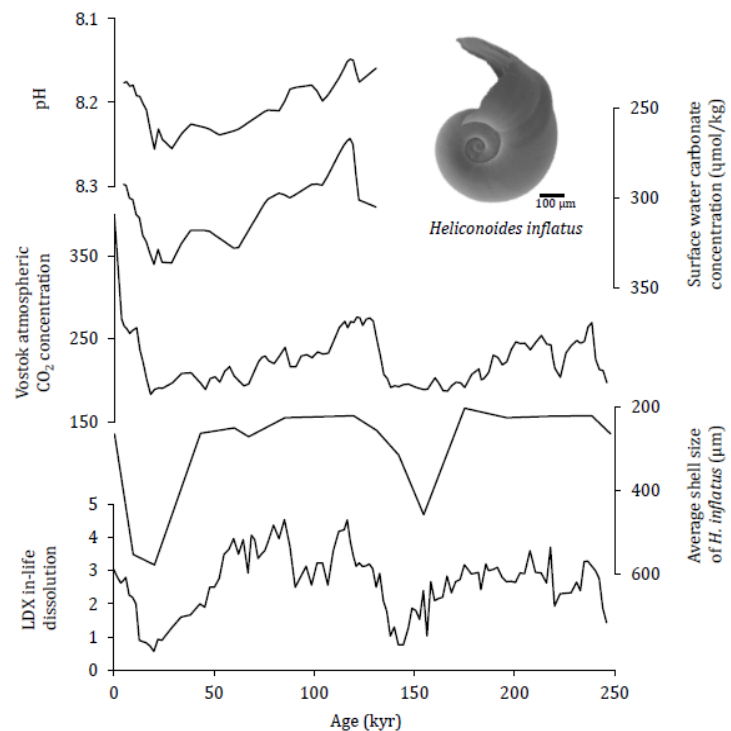


Figure: Detection of natural ocean acidification over the last ~250 ka using the shell size and condition of pteropod *Helicoinoides inflatus* from the Caribbean Sea (Site CAR-MON 2) modified from Wall-Palmer *et al.* (2013). The LDX is a simple scale of transparency and lustre which, in fossil records that have not been affected by post-depositional dissolution, represents the in-life shell dissolution caused by living in slightly acidic water. On the scale, 0 is a pristine shell and 5 is a corroded, weak shell. A significant relationship was found between atmospheric CO₂ concentration LDX in-life dissolution and average shell size, indicating that when living in more acidic waters (high atmospheric CO₂), *H. inflatus* produced smaller shells that were corroded by the water that they lived in.



Pteropods – numerous, extraordinary, fragile, mysterious

Silke Lischka

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Pteropods are amazing creatures. With their mollusk foot modified to a pair of wings, they 'fly' through almost all the worlds' oceans. These remarkable organisms exist in shelled (thecosome) and unshelled (gymnosome) forms that are tightly connected through their unique predator-prey relationship with the gymnosomes usually feeding exclusively on thecosomes. Pteropods can dominate zooplankton communities, particularly at higher latitudes, and are important food web components in the pelagic realm. Due to their calcium carbonate shell, thecosomes contribute significantly to the vertical flux of carbon in the oceans and constitute the main aragonite producers in the pelagic zone. Despite their presumed importance in the pelagic ecosystem, knowledge on their spatial and temporal abundance, stage distribution, ecology and life history traits is fragmentary. Furthermore, we do not know much about their resilience to temperature and $p\text{CO}_2$ rise from anthropogenic CO₂ emissions. Increased CO₂ emitted to the atmosphere goes hand in hand with changes in the seawater carbonate chemistry, i.e. lowered pH and carbonate ion concentrations, a phenomenon known as ocean acidification (OA), making it harder for shelled organisms to produce and maintain their calcium carbonate shells. After a period of more frequent studies on the biology, ecology and distribution of pteropods in the 60's, 70's and 80's of the last century, recently thecosome pteropods have again attracted increased attention in the science community because they are thought to be particularly vulnerable to OA due to their aragonitic shell. In my talk, I will give a broad overview on the current knowledge of the biology and ecology of pteropods with a focus on thecosomes: What do we know about their numbers, life cycles, spatial and temporal distributions as well as on their importance in marine food web of (key) species? What is so extraordinary about them? Where do we stand with regard to an evaluation of their fate in a high temperature and CO₂ ocean? Is the fuss about their possible fragility justified?

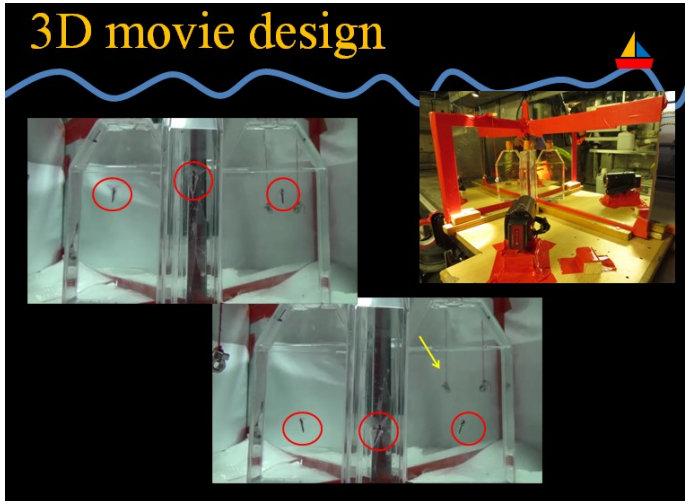


Pteropod race for life: behavioural responses to anthropogenic climate change

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Anthropogenic carbon dioxide emissions induce ocean acidification, thereby reducing carbonate ion concentration, which may affect the ability of calcifying organisms to build shells. Pteropods, the main planktonic producers of aragonite in the world's oceans, may be particularly vulnerable to changes in sea water chemistry. The negative effects are expected to be most severe at high-latitudes, where natural carbonate ion concentrations are low. In this study we investigated the combined effects of ocean acidification (OA) and freshening on the swimming behaviour of polar pteropods (*L. retroversa*). *Limacina* swim by means of paired muscular wings that extend upwards out of the shell aperture. Upward motion of the pteropods is a result of downward strokes of the wings. Living pteropods, collected in subarctic regions, were exposed to four different pH values ranging from the pre-industrial level to

that forecasted for the end of century. Since, over the past half-century, those regions have experienced a progressive freshening, each pH level was combined with a gradient in salinity (S) in two factorial, randomised experiments investigating swimming behaviour and survival. Swimming was monitored by a video camera for 15 min per treatment. We observed that OA affected the ability of pteropods to swim (changing in upward speed and wing beat frequency) only when freshening occurred at the same time. Furthermore, under the synergistic impact of reduced pH and S, survival was also affected. The pteropods were capable of counteracting OA and freshening when stress factors were not combined in the experiments. When stress factors occur concurrently, the extra energy required to avoid shell dissolution (reduced pH environment) and shell sinking (reduced S environment) probably exceeds the available energy budget, affecting first behavior and then survival. *L. retroversa* has a larger natural tolerance to variations in salinity and temperature than the polar species *L. helicina* which may make it more preadapted to the future changes in climate. Understanding whether or not polar pteropods will be replaced by sub-polar species is an important detail to be included in studies of polar food webs and carbon budgets.



Predicting larval dispersal: The role of behaviour in minimising tidal transport

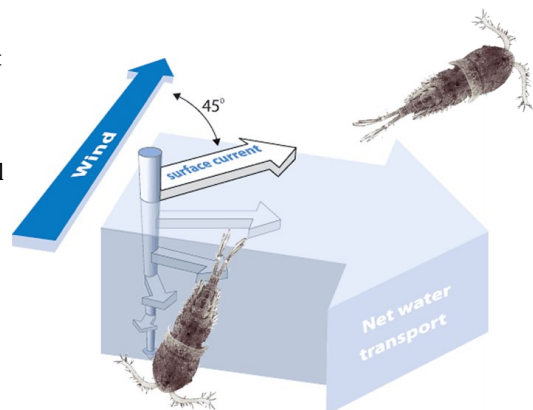
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Understanding the link between dispersal and demographic structure remains a fundamental challenge in population connectivity studies. Hydrodynamic models can be used to predict dispersal, but behaviour can decouple model estimates from patterns in nature for species. Behaviour can be responses to specific cues, but developing mechanistic descriptions that allow replication of observed distribution patterns remains a significant challenge. Here, we evaluate a novel approach that adopts a statistical likelihood approach based on observed vertical distribution profiles and predicted exposure of larvae to depth-specific current profiles to predict dispersal. Using two versions of a validated 3-dimensional hydrodynamic model of the Irish Sea, we show how larval behaviour greatly reduces tidal transport, retaining larvae close to natal patches. Dispersal is estimated for planktonic larval durations ranging from 4 to 42 days. Results indicate the presence of multiple dispersal strategies within a population but suggestion behaviour need not be incorporated in simulations for short PLD species.



Double trouble: tracing the effect of ocean acidification and ocean warming in the shells of Arctic pteropods

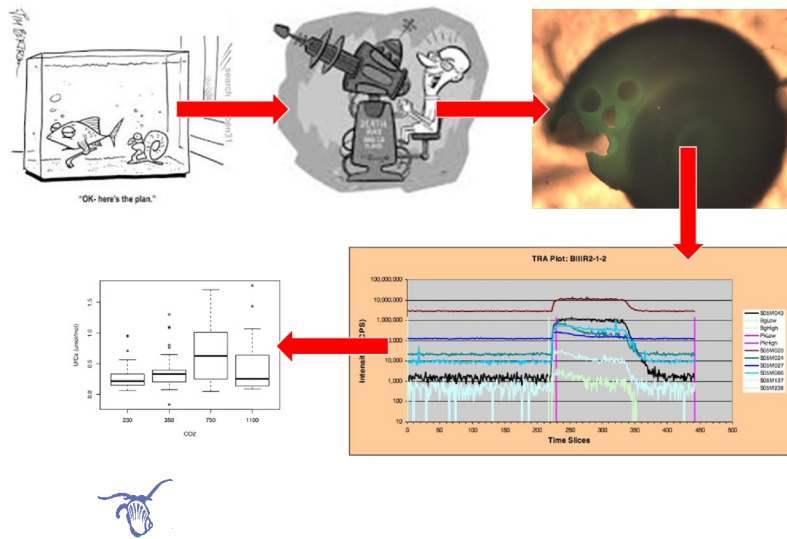
Nina Keul^{1,2}, Peter de Menocal² and Ralph Schneider¹

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Pteropods are pelagic molluscs, producing shells made out of aragonite, a metastable form of calcium carbonate. They are key components of high-latitude ecosystems, as they form a major dietary component for zooplankton and higher predators. Up to 70% of the total calcium carbonate flux in the Fram Strait is currently produced by pteropods, making them an important player in geochemical cycling in this region. The trace elemental composition of biogenically produced calcium carbonate serves as an excellent recorder of several ocean parameters, such as temperature and salinity (so called "proxy" relationships). Despite being present in high numbers in certain oceanographic settings, the potential use of pteropods as proxy carriers has not been fully explored. We present the correlation of trace elemental incorporation into pteropod shells with ocean warming/acidification as obtained from a culturing calibration study, where the arctic pteropod *Limacina helicina* has been cultured under a combination of different pCO₂ values and temperatures. Culture conditions ranged from present/preindustrial values to those projected for the Arctic Ocean by the end of this century (180, 380, 750, 1150 µatm pCO₂; temperature: 3, 5.5, 8 °C). Obtained proxy-relationships will be applied to pteropods from a 13-year sediment trap series located in the Eastern Fram Strait, allowing us to trace the effects of ocean warming and acidification during the last decade in the shells of arctic pteropods.



AGM Special Conference - Abstracts ... of poster presentations

Planktonic gastropods in the *continuous plankton recorder* survey

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The Continuous Plankton Recorder (CPR) survey, operated by the Sir Alister Hardy Foundation for Ocean Science, is the longest running, most geographically extensive marine ecological survey in the world. Beginning in 1931 in the North Atlantic, the survey today routinely collects and analyses plankton samples from the North Atlantic and North Pacific, and also operates in other major ocean basins including the South Atlantic, Southern Ocean and Indian Ocean, enabling multi-decadal data sets to be produced. The CPR survey regularly collects planktonic molluscs, particularly larval stages. However, due to the nature of the sampling technique, identification of these species is often challenging. More than 15 different genera are recorded in the survey, including *Oxygyrus*, *Atlanta*, *Clione* and *Cavolinia*, with higher taxonomic identification where possible. The recording of the distribution and abundance of this phylum is becoming ever more urgent in the face of changing environmental conditions, for example increasing temperatures and ocean acidification. Any change in the marine plankton has the potential to have serious negative ramifications: they are a life history stage for most benthic organisms, they form the base of the marine food web, provide the foundations of global food security for millions, and are responsible for approximately half of all carbon fixation. In the North East Atlantic, CPR data has revealed changes in the distribution and abundance of calcifying plankton, including molluscs, over the last fifty years, thought to be driven mainly by changes in ocean temperature. Sustained observations in the marine environment are rare, but essential in developing our understanding of the distribution and abundance of a myriad species, and by extension, the state of the marine ecosystem. Only by having a long-term time series can changes in the marine environment be detected and disentangled from longer frequency natural variation and trends.



EuroNads: the effect of recent warming and extreme weather events on limpet reproductive phenology across Atlantic Europe

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The climate-warming trend in northwest Europe has been punctuated by periods of extreme warming and cooling. Patellid limpets are key species on rocky shores controlling the distribution of macroalgae by their grazing activity. Recently, Moore *et al.* (2010) documented changes in the reproductive phenology of *Patella vulgata* and *Patella depressa* in relation to recent warming related to global climate change. Little is known about how phenology will change in response to extreme weather events, or how phenology varies throughout the geographic range. Using a combination of historic and contemporary data, collected from 15 locations across Atlantic Europe (Norway to Portugal), the EuroNads team investigated the effect of recent climate warming and extreme weather events on the reproductive phenology of four con-specific intertidal limpet grazers, with cool/boreal and warm/lusitanian centres of distribution. We present the preliminary data from a subset of the locations.



First record of *Opechona* sp. (Linton, 1900) (Trematoda: Lepocreadiidae) parasitising the pelagic gastropod *Firoloida desmarestia* Lesueur, 1817 (Gastropoda: Pterotracheoidea)

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Zooplankton communities include different trophic levels, which may have implications for transmission of parasites up the food chain. However, parasitic interactions have been scarcely studied at lower levels of the food web, making the recruitment process and ecological interaction between host populations and their parasites difficult to understand. Although there are few reports of helminth parasites occurring in heteropods of the genera *Atlanta* (parasitised by nematodes), *Cari-naria*, *Pterotrachea* or *Firoloida* (parasitised by trematodes in rediae stage), parasitic diversity is little known. In this work, we recorded occurrence of trematodes in the rediae stage and offer the first description of tailless cercariae parasitising the pelagic gastropod *Firoloida desmarestia*. Samples were obtained from a cruise belonging to the Mexican Investigation of the California Current program (IMECOCAL) carried out on March 2012, and from standard planktonic superficial sampling at La Sorpresa Beach, Gulf of California, Mexico during winter 2012. The rediae of an unidentified trematode occurred in the muscle layer of the host (prevalence of infection = 14 % and intensity = 9) recovered from the IMECOCAL cruise. The tailless cercariae identified as *Opechona* sp. (Family Lepocreadiidae) parasitised *F. desmarestia* at La Sorpresa Beach with high prevalence of infection (33 %) and mean intensity of 9 trematodes. *Opechona* sp. occurred in different microhabitats of the same host, for example - (a) cercariae, externally attached on the body (b) penetrating the epithelium; c) in the gelatinous substance between the epithelium and the muscle layer, and d) in the muscle layer. We suggest that infection of soft-bodied hosts such as *F. desmarestia* by active penetration represents an alternative in the life cycle for *Opechona* spp. Further ecological implications of heteropods as hosts harbouring different stages of digenean trematodes in the pelagic realm are commented upon and a conceptual model is proposed.



Will the gastropod *Crepidula fornicata* out-compete other molluscs under future ocean acidification?

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Whether they are brooders or broadcast-spawners, many benthic sessile or slow-moving molluscs rely on their pelagic phase to disperse and colonise new areas. Environmental conditions can have a critical impact on those pelagic early life stages and shape adult populations through the creation of bottlenecks. The current context of global changes in oceanic conditions, such as increased seawater temperature, increased hypoxia, and ocean acidification, is likely to affect marine molluscs during their pelagic phase (reviewed by Gibson *et al.*, 2011). Ocean acidification is of particular concern for calcifying species such as molluscs as waters become more corrosive and the necessary calcium carbonate becomes less available (Gazeau *et al.*, 2013). Early stages of molluscs are thought to be particularly vulnerable to ocean acidification, as they use more soluble forms of CaCO_3 (Kroeker *et al.*, 2013). How the effects of ocean acidification on the pelagic stages will transfer to the adult populations after settlement, and alter ecological relationships and ecosystem functions, remains largely unknown. My PhD will investigate the effects of climate change and ocean acidification on important species of molluscs including, but not limited to, the economically important bivalve *Crassostrea gigas* and the invasive gastropod *Crepidula fornicata*, thought to be its competitor (Decottignies *et al.*, 2007). A small number of studies have shown that the larvae of both species are negatively affected by ocean acidification, but that *C. fornicata* might be more tolerant. The project will assess how variations in recruitment and population size, from adverse effects on early stages during the pelagic phase, will impact on the broader ecosystem and the provision of ecosystem services. One of the aims is to evaluate the variations in ecological interactions, and particularly in competitive dominance, under future oceanic changes. One of the questions addressed is whether *C. fornicata* is more tolerant to future environmental changes than other species of molluscs, and if it is likely to out-compete *C. gigas*.



Changing the subject

from a retired hydrobiologist friend comes this:-

"I have a lidded water butt (fed from my house roof water) which I looked into today (for the first time in ages) during a torrential downpour to check that the downpipe diverter wasn't blocked by moss etc off the roof. I was very surprised to see a population of several dozen *Physa fontinalis* looking as happy as pigs in muck in the butt. Despite immediately thinking about possible unlikely aerial routes between my largish garden pond, which has a large population of said mollusc, and the house gutter, the probable truth eventually dawned. I got the water butt to minimise my financial support of our old friend United Utilities when we went onto water meter, and profligate use of mains water to keep the leaky garden pond topped up was contraindicated. The butt is now set to permanently discharge via a gravity fed *c. circa* 6 metre length of garden hosepipe into the pond which is lower down the gently sloping garden. It seems the answer is not like a rat up a drainpipe, but like a *Physa* up a hosepipe." Ray Prigg, Cumbria



Annual Report of Council for 2014

delivered by the President, Professor Tony Walker

The President thanked Deborah Wall-Palmer (Plymouth University) for her hard work in organising the meeting entitled “*Planktic Gastropods: biology, ecology and palaeontology*” at The Natural History Museum, London, on Wednesday 1st April 2015, during which the **122nd Annual General Meeting** of The Society was held.

Membership (reported by Rowan Whittle)

After the latest (January 2015) renewal round the society had 134 confirmed members, 27 of which were students. Fourteen members did not renew for 2015 from the January renewal period. Twenty-four new members joined in the 2014 – 2015 year, of which 12 were students. Ninety-seven members are due to renew on January 1st 2016, the distribution of renewal times of remaining members varies throughout the year. It would be important to synchronize renewals so that they all occur in January of a calendar year.

Finance, for the financial year ending 31 December 2014 (reported by Katrin Linse)

The finances of the Malacological Society of London have been more than satisfactory during 2014 with a gain of £42,466. Of our investments (comparing the position from 31 December 2013 to market value at 31 December 2014), the COIF Investment Fund made a gain of £12,317 while the COIF Fixed Interest Fund made a gain of £6,225. During the year 2014 no funds were transferred from the current accounts into the COIF Investment Fund or the COIF Fixed Interest Fund. However, the profit-share from the publication of the Journal provided the Society with the major proportion of its income. The Editor of the Journal, Dr David Reid, and the Associate Editors are to be commended for the hard work involved in the publishing our scientific journal. Sales of the digital archives provided over £7826 of income despite the fact that OUP started to sell the journal's digital archive in a subject package. Despite the main customers for this product have now purchased the archive and OUP has split archive sales into subjects, digital archive sales are still on-going but likely to be more modest in future.

The Society decreased the values of its various Awards in 2013. More funds were used for travel awards compared to 2013 while the research awards and the travel awards to the Forum decreased. The reduction in research awards was based on the quality of the submitted research award proposals.

The Society hosted EuroMal 2014 in Cambridge last September and the Organising committee of this successful event are to thank for their hard work. The surplus of EuroMal 2014 to the Society was £15,261 at the end of 2014; we had outstanding commitments and sponsorship at the end of 2014, which will alter the overall surplus of EuroMal 2014 to £14,505. The intention is to use this surplus for meetings and student travel awards etc.

The Society's independent examiner, Steven Ellis from Staffords Chartered Accountants, examined the Society's accounts following the Charity Commission and SOFA rules.

Meetings

It has been a busy year for meetings. On behalf of the Society, David Reid kindly organized a fascinating meeting on “*Sexual Selection in Snails*” at the Natural History Museum, London, on Thursday 6th March, 2014. This was also the place for the Society's 121st AGM. In September (7th – 11th), the Society hosted the 7th Congress of the European Malacological Societies (Euromal) 2014 at St Catherine's College University of Cambridge, for which David Aldridge was the Chair of the Organizing Committee. This was a big meeting to organize and based on feedback from delegates the congress was a huge success. The meeting started off on Sunday with an evening drinks reception in the Sedgwick Museum. There were 50 oral presentations, and a large number of posters that were presented in the Zoology laboratories. The Conference dinner was held in the spectacular Corpus Christie College and a wine reception was held on the lawn. Thursday, included tours of the botanic gardens and punting on the river Cam. A full report on the meeting will appear in the next edition of the *The Malacologist*. The 8th Euromal is scheduled to take place in Poland. On 20th November 2014, the 17th Annual Molluscan Forum was held in the Flett Lecture Theatre at the Natural History Museum, London, organized by Jon Ablett/Andriea Salvador and the President. There were 13 oral presentations and eight posters from UK and overseas participants. The Society provided lunch for all attendees and this served to create a cohesive meeting, with excellent opportunity to discuss the posters. The Forum was again held consecutively with the Young Systematists' Forum, affording an opportunity for students to attend both meetings. A full report of the Forum appears in number 64 of *The Malacologist*.

Publications

The Malacologist (reported by Georges Dussart)

The two issues of *The Malacologist* for August and February respectively are sent to members in digital form whereas paper copies are sent to the statutory bodies such as the British Library. Such a form of delivery saves the Society hundreds of pounds in postage and printing charges per annum. The August 2014 issue (34 pages) carried five research reports and two travel grant reports, plus a precis of the thesis of the annual award winner. The February 2015 issue (26 pages) focused on abstracts from the Molluscan Forum, which was held as usual at the Natural History Museum. Both issues also carried accounts of malacological meetings elsewhere, obituaries, news items, and notices of forthcoming events. Due to a lack of contributions, no updates were issued this year.

Journal of Molluscan Studies (reported by David Reid)

The ISI impact factor for the *Journal* in 2013 rose to 1.495 (compared with 1.358 in 2012, 1.227 in 2011, 0.969 in 2010, 1.074 in 2009 and 1.408 in 2008). The *Journal* stands at number 44 in the ISI list of 152 zoological journals (up from 55 of 149 in the previous year). These trends are in the right direction but, at relatively low values of the IF statistic, fluctuations are to be expected.

Circulation for the *Journal* in 2014 was 78 institutional (of which 33 were online-only and 28 print-only) and 135 membership subscriptions (compare 86 and 125 respectively for 2013). In addition a further 2,576 institutions have electronic access to the *Journal* through publishers' consortia (includes migrated figures; compare 2,473 in 2013) and 1,090 (compare 1,205 in 2013) have access through OUP's Developing Countries Offer (for details see http://www.oxfordjournals.org/access_purchase/developing_countries.html). This means that the *Journal* is now available to 3,879 member and institutional subscribers (compare 3,889 in 2013).

The new pricing structure has been fixed for 2015. The cost for a combined print plus online institutional subscription is £495 (\$940); online-only subscriptions are £395 and print-only subscriptions are £455.

Volume 80 (2014) contained 61 papers and research notes, totalling 472 pages (an increase on the 385–420 pages of recent volumes). Part 3 included eight papers from the symposium 'Tempo and mode in land snail evolution', part of the World Congress of Malacology (Azores, July 2013), edited by R.A.D. Cameron and B.M. Pokryszko. A second symposium from WCM 2013, 'There's something about Opisthobranchia', was edited by H. Wägele and published as Part 5, in an online-only, open-access issue of 13 papers. This model can potentially be used for future symposia and represents a welcome opportunity for increasing the scale of publication.

The delay between acceptance of a manuscript and electronic publication was 7.5 weeks. In total, 197 manuscripts were submitted in 2014 (an increase of 7% on the 184 in the previous year) and the acceptance rate was approximately 31%. In reply to a publishers' questionnaire, 97% of authors who responded rated their experience better than or equal to that with other publishers. The image of the *Spondylus* mantle edge on the cover of Volume 80 was kindly donated by Nicholas Hobgood.

Members are reminded that they can access the entire electronic archive of *Journal of Molluscan Studies* (and its precursor *Proceedings of the Malacological Society of London*). Full instructions describing how to access this archive were published in *The Malacologist* in August 2007.

Our board of Associate Editors is now: 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), John Davenport (marine ecology and physiology), Mark Davies (marine ecology and behaviour), Villie Flari (physiology and behaviour), Dan Graf (freshwater bivalves), John Grahame (population genetics, morphometrics), Liz Harper (marine bivalves), Bernhard Hausdorf (terrestrial gastropods), Robert Hershler (freshwater gastropods), Michal Horsák (ecology and biogeography of terrestrial gastropods), Kurt Jordaens (systematics, ecology and pest control of terrestrial gastropods), Yasunori Kano (systematics of vetigastropods, tropical ecology), Joris Koene (reproductive behaviour of gastropods), Anne Lockyer (genomics), Manuel Malaquias (opisthobranchs), Pablo Martín (freshwater ecology, life history), Ellinor Michel (ecology, freshwater gastropods), Fred Naggs (systematics and conservation of terrestrial gastropods), Jeff Nekola (community ecology of terrestrial gastropods), Nicolas Puillandre (neogastropods), Ellen Strong (freshwater and marine caenogastropods), Mikael Thollesson (opisthobranchs), Janet Voight (cephalopods), Janice Voltzow (microscopic anatomy), Heike Wägele (opisthobranch biology), Tony Walker (biochemistry, immunology, cytology), Suzanne Williams (molecular phylogenetics and genetics) and Nerida Wilson (opisthobranchs, deep-sea and Antarctic molluscs).

The 5-year publishing contract with Oxford University Press was due for renewal at the end of 2014 and has been renegotiated. Previously, a payment for editorial services of £2750 was paid annually to the Natural History Museum, employer of the Editor-in-Chief. The MSL Council decided that a more commercially appropriate rate should be paid, as a means of safeguarding the long-term future of the *Journal*. OUP agreed to increase the stipend to £7000 (which, as a production cost, is shared equally by OUP and MSL). The MSL will supplement this to make a total of £8489 (based on OUP salary scale for a Freelance Managing Editor working 45 hours per month). In addition, OUP has proposed to reduce the financial burden on the MSL of supplying all members with printed copies of the *Journal*, by offering either online-only or print-plus-online rates for members, with a considerable price differential between the two.

The Society's websites – www.malacsoc.org.uk and www.facebook.com/malacsoc (reported by Tom White)

Since the last AGM, the MSL website has been comprehensively updated and transferred to the Wordpress system. On behalf of the Society I would like to thank Stefan Senk, who built the new webpages, and Chong Chen, who created and continues to update the new MSL Facebook page. Their efforts have significantly improved the MSL webpages and brought them up to a modern standard. Problems with the old webpages reported last year, such as missing editions of *The Malacologist*, have now been corrected. There are two main advantages to the new website. Firstly, the process of editing and updating the basic information contained within key webpages, such as details of forthcoming meetings, is now much more straightforward. Secondly, the new pages are linked to the MSL Facebook page, which has made them accessible to a much wider audience. In August 2014 a meeting with Oxford University Press was arranged, attended by Chong Chen, Katrin Linse, Tom White and Alistair Shand (of OUP), at which potential support for a Facebook page dedicated to the *Journal of Molluscan Studies* was discussed.

The charges levied by our current Internet Service Provider (ISP) remain competitive and there is currently no reason to consider changing the current arrangements.

Awards (reported by Suzanne Williams)

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

The MSL hosted EuroMal 2014 in Cambridge and Council decided to have only one round of awards in 2014 to support attendance at this meeting. The Society received 21 applications for awards to travel to EuroMal and was able to fund the majority of these requests. All Travel Award applications are reviewed by an Awards Committee. The Society is pleased to have announced the following 16 awards.

To attend the European Malacological Congress 2014 at Cambridge, UK, 7-11 September, 2014

Carola Greve, **£250**, Zoologisches Forschungsmuseum Alexander Koenig, Germany
 Maria Carla de Aranzamendi, **£499.20**, Instituto de Diversidad y Ecología Animal, Spain
 Hanieh Saeedi, **£500**, University of Auckland, New Zealand
 Elisavet Georgopoulou, **£183.80**, University of Graz & Natural History Museum of Vienna
 Luis Javier Chueca, **£250**, University of the Basque Country, Spain
 Amaia Caro Aramendia, **£250**, University of the Basque Country, Spain
 Jazmín Deneb Ortigosa Gutiérrez, **£375**, Universidad de Cádiz, Spain
 Rebecca Kyle, **£494**, Queen's University Belfast, Northern Ireland
 Deborah Wall-Palmer, **£451**, Plymouth University, UK
 Chris Hughes, **£341.40**, Natural History Museum, London, UK
 Lucía Pedrouzo Regueiro, **£250**, Universidade de Santiago de Compostela, Spain
 Lucía Barrio González, **£250**, Universidade de Santiago de Compostela, Spain
 M. Carmen Cobo Llovo, **£250**, Universidade de Santiago de Compostela, Spain
 Oihana Razkin, **£250**, University of the Basque Country, Spain
 Trond R. Oskars, **£400**, University Museum of Bergen, Norway
 Lena Ohnheiser, **£400**, Ludwig-Maximilians University, Germany

A total of **£5,394.40** was therefore allocated by The Society for Travel Awards (more than double the funds allocated in the previous year). 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

By the closing date of 15th December 2014 the Society had received 35 applications from workers from 32 institutions in 19 different countries. In general, the scientific quality of the research projects submitted was excellent. One application was withdrawn prior to judging.

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.

Bergmeier, Franziska, **£684**, Ludwig-Maximilians-University, Germany
Challenge accepted! New approaches to Solenogastres taxonomy
 Coppock, Rachel, **£1500**, Plymouth University, UK,
The effects of parental exposure to stress on offspring behaviour and its molecular basis
 Foster, William, **£1500**, Plymouth University/NHM, UK
The recovery of benthic mollusc communities following a major climate change event
 Hale, Rachel, **£1467**, University of Southampton, UK
Habitat heterogeneity and burrowing behaviour in an intertidal gastropod
 Kohnert, Peter, **£1500**, Bavarian State Collection of Zoology, Germany
Who is Limacina helicina? Molecular and 3D-microanatomical taxonomy of a pelagic keystone species.
 Skála, Vladimír, **£1500**, Charles University in Prague, Czech Republic
Haemocyte extracellular traps as a defence response in the pond snail Lymnaea stagnalis (Lymnaeidae)
 Wort, Edward, **£1500**, University of Southampton, UK
Assessing the effect of habitat gaps on population connectivity: a phylogeographic study of a Trochidae species
 Zieritz, Alexandra, **£1500**, University of Nottingham Malaysia Campus, Malaysia
Ecosystem functions of freshwater mussels (Unionida) in Malaysian streams: the effects of land-use on unionoid health and functionality

Therefore eight Research Grants have been funded at a total cost of **£11,151**. The success rate was 24%. 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 will be formally notified of the outcome of their application within three weeks of the AGM.

The Annual Award

The Society received one nomination for the 2015 Annual Award. The Judging Panel elected to offer the Annual Award to Dr Gregor Christa (The University of Bonn) for a thesis entitled ‘*Evolution of chloroplast sequestration in Sacoglossa (Mollusca, Gastropoda)*’. The Society sends its best wishes and congratulations to Dr Christa.

Officers and Council

This is my third and last AGM as President of the Society and it has been an absolute pleasure to work with all Society Officers and Councillors during my three years in post. All Officers and Councillors have worked exceptionally hard towards the continued success of The Society. This is no small task; the Society is responsible for two excellent publications, maintains a healthy membership, has an active website, provides significant numbers of grants and awards, organizes stimulating scientific malacological meetings and has also managed to maintain good financial health. I therefore sincerely wish to thank all Officers and Councillors for their continued efforts, which is all the more notable given that each voluntarily gives their time and talents in support of The Society’s objectives. There have been some major achievements for the Society in the past year that have happened in addition to our usual annual operations and are a result of Council/Officer input; these include:

- Organization of the highly successful Euromal2014
- Establishment of a Facebook page
- Continued strength in the Journal of Molluscan Studies, enabling the Society’s financial position to remain healthy
- Renegotiation of the publishing contract with Oxford University Press that will help to safeguard the future of the Society.

There has been some shifting of roles and responsibilities during 2014, and from this AGM onwards: The position of Archivist is now not required as the Society’s archives are to be integrated into those at the Natural History Museum, London. Chong Chen, who did an excellent job of establishing the Society’s Facebook page, has kindly agreed to be nominated for Web Manager (in collaboration with Tom White).

Finally, as I step down from serving to Ex-Officio President, I am delighted that Suzanne Williams has agreed to be nominated for President of the Society. I would like to thank Suzanne for all of her hard work with the Society’s Grants and Awards, a role which Jon Ablett has very kindly agreed to be nominated for.

It has been a very busy year and much has been achieved. I am extremely proud of the work of the Officers and Councillors of the Society. It is through their hard work and dedication that the Society has continued to positively impact on malacology globally.

By election at the AGM, members of Council for 2015-2016

COUNCIL 2015-16	Elected
President	Suzanne Williams
Ex-officio	Tony Walker
Vice Presidents	Fred Naggs John Grahame
Councillors	Mark Davies David Aldridge Andreia Salvador Robert Cameron Richard Preece Simon Cragg
Hon. Secretary	Tom White
Hon. Treasurer	Katrin Linse
Membership Secretary	Rowan Whittle
Editor <i>Journal of Molluscan Studies</i>	David Reid
Editor <i>The Malacologist</i>	Georges Dussart
Awards Officer	Jon Ablett
Web manager	Chong Chen/ Tom White



**ORGANISING COMMITTEE**

Jon Ablett <i>Natural History Museum, London</i>	David Aldridge (Chairman) <i>University of Cambridge</i>
Katrin Linse <i>British Antarctic Survey, Cambridge</i>	Richard C. Preece <i>University of Cambridge</i>
Tony Walker <i>Kingston University</i>	Tom S. White <i>University of Oxford</i>

The Malacological Society of London

in association with

Conchological Society of Great Britain and Ireland
Deutsche Malakozologische Gesellschaft
Instituto Português de Malacologia
Magyar Malakológiai Társaság
Malacological Society of Latvia
Nederlandse Malacologische Vereniging
Sociedad Española de Malacologia
Società Italiana di Malacologia
Société Belge de Malacologie
Stowarzyszenie Malakologów Polskich

Comprising 12 lecture sessions and a poster session incorporating the following themes:

- (Molecular) Taxonomy and Phylogenetics
- Molluscan Biology and Physiology
- Biogeography, Ecology and Conservation
- Climate, Palaeontology and Archaeology

Theme 1: Biogeography, Ecology & Conservation Part I**Session 1**

Chair: Jon Ablett, Natural History Museum, London

- 09.00 – 09.40 **KEYNOTE:**
Tom Wilke (Justus Liebig University, Giessen, Germany)
 Catastrophic events shape patterns of mollusc biodiversity in ancient lakes
- 09.40 – 10.00 **Robert Cameron** (University of Sheffield, UK)
 The fashion in traits: how to unpick land mollusc diversity
- 10.00 – 10.20 **Dinazarde Raheem** (Royal Belgian Institute of Natural Sciences)
 A systematic revision of the land snails of the Western Ghats of India
- 10.20 – 10.40 **Martina Ilarri** (University of Porto, Portugal)
 Empty bivalve shells as a physical substratum to the associated fauna: potential scenarios prior to and after *Corbicula fluminea* invasion

Session 2

- 11.10 – 11.30 **John Grahame** (University of Leeds, UK)
 Shell phenotypes, adaptation, and trade-offs in rough periwinkles
- 11.30 – 11.50 **Archer Tik Long Wong** (University of Hong Kong, China)
 A comprehensive biodiversity study on sub-tidal benthic molluscs in the marine environment of Hong Kong
- 11.50 – 12.10 **Hanieh Saeedi** (University of Auckland, New Zealand)
 Global biodiversity and biogeography of razor clams (*Bivalvia*: Solenidae)
- 12.10 – 12.30 **Jesús Troncoso** (University of Vigo, Spain)
 The molluscs of a tropical oceanic island (Isla del Coco, Costa Rica)
- 12.30 – 12.50 **Suzanne Williams** (Natural History Museum, London, UK)
 Diversification in the deep sea

Theme 2: (Molecular) Taxonomy and Phylogenetics**Session 3**

- 14.20 – 14.40 **Julia Sigwart** (Queen's University Belfast, UK)
Chiton phylogeny (Mollusca: Polyplacophora) and the placement of the enigmatic species *Chorioplax grayi* (H. Adams & Angas)
- 14.40 – 15.00 **Alexander Fedosov** (Severtsov Institute of Ecology & Evolution, Russia)
Phylogeny and relationships of mitriform gastropods (Gastropoda: Neogastropoda)
- 15.00 – 15.20 **Marina Panova** (Gothenburg University, Sweden)
Genome sequencing project for *Littorina saxatilis* (Gastropoda: Littorinidae)
- 15.20 – 15.40 **Pedro Romero** (Goethe University, Frankfurt am Main, Germany)
Molecular adaptations in Euthyneura mitogenomes: Possible clues to land colonization

Session 4

- 16.10 – 16.30 **António de Frias Martins** (University of the Azores)
Unravelling the taxonomy of *Myosotella* (Gastropoda: Ellobiidae): penial structure is the key
- 16.30 – 16.50 **Joanna Pienkowska** (University of Poznan, Poland)
Insight into water transport proteins of terrestrial and freshwater gastropods based on their transcriptome NGS-sequencing
- 16.50 – 17.10 **Inga Reich** (NUI Galway, Ireland)
The Lusitanian species *Geomalacus maculosus* - a 'native' Irish slug?
- 17.10 – 17.30 **Amaia Caro** (University of the Basque Country, Spain)
Molecular systematics and population structure in *Pyrenaearia* (Stylommatophora: Helicoidea)

Theme 3: Climate, Palaeontology and Archaeology**Session 5**

- 09.00 – 09.20 **Kirsty Penkman** (University of York, UK)
Marking time at a snail's pace: million year-old amino acids
- 09.20 – 09.40 **Paul Butler** (Bangor University, UK)
Malacology and marine climate: using mollusc shells to investigate the history of the marine environment during the past 1,000 years
- 09.40 – 10.00 **Alejandro Román-González** (Bangor University, UK)
Yoldia eightsi as a scleroclimatological proxy for Antarctic coastal waters
- 10.00 – 10.20 **James Scourse** (Bangor University, UK)
The marine radiocarbon bomb-pulse across the temperate North Atlantic
- 10.20 – 10.40 **Ricardo Fernandes** (University of Kiel, Germany)
Bivalves as an important source of isotopic and radiocarbon archaeological data

Session 6

- 11.10 – 11.30 **Frank Wesselingh** (Naturalis Biodiversity Centre, Leiden, Netherlands)
The rise and demise of the Ponto-Caspian biota
- 11.30 – 11.50 **Elisavet Georgopolou** (Natural History Museum Vienna, Austria)
Exploring patterns of freshwater gastropod diversity in European lakes
- 11.50 – 12.10 **Nicole Limondin-Lozouet** (CNRS-Université Paris I, France)
The Quaternary history of non-marine molluscs in the Somme valley, northern France, during the last 1 Myr
- 12.10 – 12.30 **Alistair Crame** (British Antarctic Survey, Cambridge, UK)
The origin of the Antarctic marine molluscan fauna
- 12.30 – 12.50 **Elizabeth Harper** (University of Cambridge, UK)
The drillers and the drilled: molluscan predator-prey interactions over the K-Pg mass extinction of Antarctica

Theme 4: Biogeography, Ecology & Conservation Part II**Session 7**

- 14.20 – 14.40 **Rosa Freitas** (University of Aveiro, Portugal)
Spatial distribution and bioaccumulation in three Veneridae clams from a contaminated ecosystem
- 14.40 – 15.00 **Alexandra Richter** (University of Oviedo, Spain)
The alien slipper limpet *Crepidatella dilatata* (Lamarck, 1822) in northern Spain: a multidisciplinary approach on its biodiversity and invasive biology
- 15.00 – 15.20 **Ronaldo Sousa** (University of Porto, Portugal)
Invasive bivalves as an unusual resource for terrestrial invertebrates
- 15.20 – 15.40 **Janhavi Marwaha** (University of Bergen, Norway)
Is juvenile mussel growth rate related to time on gills?

Session 8

- 16.10 – 16.30 **Kevin Cummings** (Illinois Natural History Survey, USA)
The freshwater mussels (Bivalvia: Unionoida) of Northern South America and the Amazon
- 16.30 – 16.50 **Iara Rocchetta** (University of Buenos Aires, Argentina)
Environmental conditions shape molluscan lifespan: comparing markers of cellular fitness and aging in two populations of the freshwater bivalve *Diplodon chilensis*
- 16.50 – 17.10 **Rebecca Kyle** (Queen's University Belfast, UK)
Conservation strategies for the Freshwater Pearl Mussel, *Margaritifera margaritifera*, involving habitat restoration and release of captive-bred juveniles
- 17.10 – 17.30 **Joaquim Reis** (Instituto Português de Malacologia, Albufeira, Portugal)
Restoration of an endangered *Unio tumidiformis* population

Theme 5: Molluscan Biology and Physiology**Session 9**

- 09.00 – 09.20 **Antonio Checa** (University of Granada, Spain)
Chamber formation and calcification in the cuttlebone of *Sepia officinalis*
- 09.20 – 09.40 **Katja Trübenbach** (University of Lisbon, Portugal)
Hypoxia-driven protein regulation in muscle tissue of jumbo squids during diel migration to the oxygen minimum zones
- 09.40 – 10.00 **Michael Vendrasco** (University of Granada, Spain)
Periostracum of the chiton *Lepidozona pectinulata* and homology with the Bivalvia
- 10.00 – 10.20 **Lauren Sumner-Rooney** (Queen's University Belfast, UK)
Chitons that live in the dark can see light (Polyplacophora: Lepidopleurida)
- 10.20 – 10.40 **Aleksandra Skawina** (University of Warsaw, Poland)
The probable circadian rhythms in serotonin levels in hemolymph of *Unio tumidus* and tissues of *Pisidium casertanum*

Session 10

- 11.10 – 11.30 **Alexandre Lobo-da-Cunha** (University of Porto, Portugal)
Comparative microscopy study of digestive gland in cephalaspideans (Gastropoda, Euopisthobranchia)
- 11.30 – 11.50 **Fathia Gawish** (Theodor Bilharz Research Institute, Giza, Egypt) Assessment of certain food preservatives on biological and biochemical parameters of *Biomphalaria alexandrina*, as a biological model
- 11.50 – 12.10 **Coen Adema** (University of New Mexico, USA)
Somatic diversification of immune factors in *Biomphalaria glabrata* (Hygrophila: Planorbidae), insights from targeted approaches and genome assembly
- 12.10 – 12.30 **Daniel Lawson** (European Bioinformatics Institute, Cambridge)
The genome of *Biomphalaria glabrata* (Gastropoda, Mollusca) and the data base VectorBase
- 12.30 – 12.50 **Tony Walker** (Kingston University, UK)
Modulation of *Biomphalaria glabrata* immunity by excretory-secretory products of *Schistosoma mansoni*

Theme 6: Miscellaneous Highlights

Session 11

- 14.20 – 14.40 **Chong Chen** (University of Oxford, UK)
The heart of a dragon: extraordinary circulatory system of the scaly-foot gastropod revealed
- 14.40 – 15.00 **Serge Gofas** (University of Málaga, Spain)
MolluscaBase – announcing a World Register of all Molluscs
- 15.00 – 15.20 **Manuel Lopes-Lima** (University of Porto, Portugal)
Conservation of European freshwater mussels: historical background, challenges and future perspectives
- 15.20 – 15.40 **Winfried Peters** (Indiana/Purdue University, USA)
Strange snails indeed: Swash-Surfers, Self-Mutilators, Wave-Combers and Cannibals that dominate Pan-amic sandy beaches

Session 12

- 16.10 – 16.50 **KEYNOTE:**
Lloyd Peck (British Antarctic Survey, Cambridge, UK)
Title tbc
- 16.50 – 17.10 Closing remarks and awarding of prizes
Tony Walker and David Aldridge

Malacological Society of London President Tony Walker makes the opening address and welcome



Catastrophic events shape patterns of mollusc biodiversity in ancient lakes

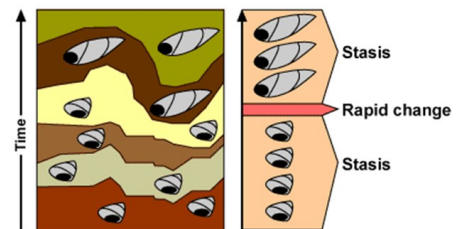
Thomas Wilke

Department of Animal Ecology and Systematics, Justus Liebig University, Giessen, Germany
tom.wilke@allzool.bio.uni-giessen.de

Ancient lakes (i.e. extant lakes that have existed since before the last glacial maximum) often contain a large number of endemic species. However, the evolutionary processes leading to this high degree of biodiversity are still not well understood. Two hypotheses have been proposed for ancient lakes: (1) that these waterbodies function as sinks for extralimital relic species, resulting in the accumulation of phylogenetically diverse assemblages (“reservoir function”), and (2) that ancient lakes serve as sites for intralacustrine speciation, resulting in species flocks (“cradle function”). Moreover, in the case of intralacustrine speciation it often remains unclear whether the extant endemic species evolved shortly after the respective lake came into existence or whether they are considerably younger than the lake.

Comparative phylogenetic, molecular clock and modelling approaches indicate that temporal patterns of endemic biodiversity largely differ between animal groups strongly affected by natural selection (such as molluscs) on the one side, and those subject to sexual selection such as cichlid fishes, on the other side. For mollusc faunas from African, Asian, European and South American ancient lakes it is demonstrated that the majority of taxa evolved through intralacustrine speciation. Moreover, many flocks are considerably younger than the actual lake as past catastrophic or near-catastrophic events are among the main drivers shaping patterns of extant biodiversity in these lakes. Although ancient lakes generally have a high buffer capacity for environmental fluctuations, global climate changes such as those during the Eemian (last interglacial) period (130,000-114,000 years ago) massively affected ancient lakes in Africa and South America. In contrast, higher-latitude lakes such as the Balkan Lake Ohrid are less affected. In fact, the recent SCOPSCO scientific deep drilling campaign in Lake Ohrid indicated that its extraordinary endemic mollusc biodiversity is largely driven by the lack of massive environmental fluctuations, resulting in reduced extinction rates and continuous speciation and radiation events.

These findings not only shed new light on the patterns and processes of mollusc evolution in ancient lakes, but may also serve as a working hypothesis for studying other highly isolated mollusc faunas, such as those on oceanic islands, in mountain refugia and in desert springs.



The fashion in traits: how to unpick land mollusc diversity

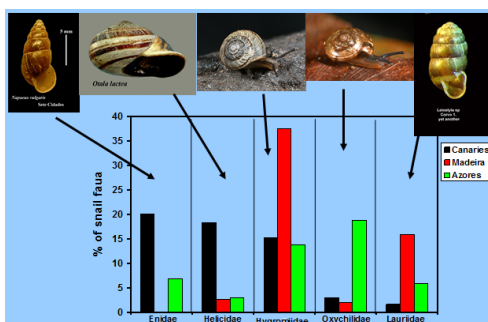
Robert A. D. Cameron^{1,2} and Beata M. Pokryszko³

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² Department of Zoology, the Natural History Museum, London SW7 5BD, UK

³ Museum of Natural History, Wrocław University, Sienkiewicza 21, 50-335 Wrocław, Poland

Studies on land mollusc diversity have shown a great variety of patterns varying with scale and with location. While assessments of species richness and species turnover are the predominant methods used in such studies, it is clear that we need more sophisticated approaches to understand some of the patterns found in nature. We consider here some possible approaches, starting with the well-attested analyses of size and shape spectra among faunas. Here, the evidence suggests that we are dealing with radically different sets of niches or ways of life in different regions. Information on other, potentially more directly functional, traits is less comprehensive, but the data we have also suggests that land mollusc faunas across the world do not represent simply different evolutionary responses to the same range of ways of life. Phylogenetic constraint is certainly a possible explanation for some differences among faunas, but it can be used too easily as a cover for ignorance about the forces that shape a fauna in ecological and evolutionary time.



A systematic revision of the land snails of the Western Ghats of India

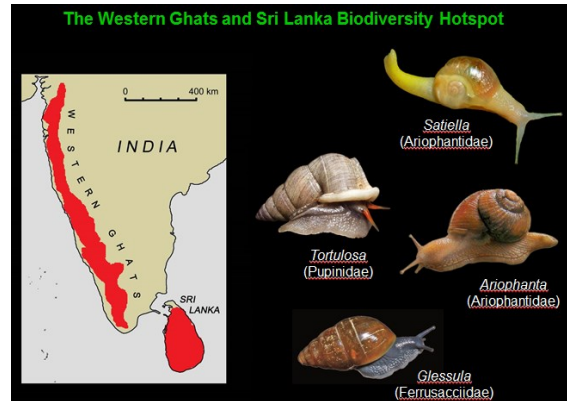
Dinarzarde C. Raheem^{1,2}, Harold Taylor², Jonathan Ablett², Richard C. Preece³, N. A. Aravind⁴ and Fred Naggs²

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⁴ Ashoka Trust for Research in Ecology and the Environment (ATREE), Royal Enclave, Srirampura, Jakkur Post, Bangalore 560 064, Karnataka, India



The Western Ghats, the mountain chain running along the western coastline of India, has a phylogenetically-diverse land-snail fauna dominated by endemic species. Although this fauna was well studied in British colonial times, little revisionary taxonomic research has been carried out since the publication of the three volumes of *The Fauna of British India (FBI)* series on land molluscs, between 1908 and 1921. The *FBI* is an essential work for anyone wishing to study the land snails of the Western Ghats, but is of limited use as a species-identification tool on its own. Access to type material, most of which is in the U.K., is essential. Furthermore, only a handful of species are illustrated in the *FBI*, many of the species descriptions are inadequate, and errors and inaccuracies abound. To address this issue, we here present a taxonomically-updated, fully-illustrated revision of the land-snail fauna of the Western Ghats. We use a broad definition of the Western Ghats, including the western coastline of the Indian peninsula and the lowlands and foothills surrounding the main mountain range. In total we consider 336 taxa (299 species and 37 so-called 'varieties'), and this consists largely of snails recorded from the Western Ghats (277 species and 28 'varieties' belonging to 64 genera in 23 families), but also includes 16 taxa (9 species and 7 'varieties') that may or probably occur in the Western Ghats (e.g. snails widespread elsewhere in the Indian peninsula). We critically evaluate and clarify the nomenclature and taxonomy of these snails within a modern systematic framework, designating lectotypes and neotypes where appropriate, and for the first time provide colour images and specimen data of type material for all the Western Ghats taxa, alongside distributional data from the original literature. Also included is a comprehensive geo-referenced index of localities for the taxa considered.



Empty bivalve shells as a physical substratum to the associated fauna: potential scenarios prior to and after *Corbicula fluminea* invasion

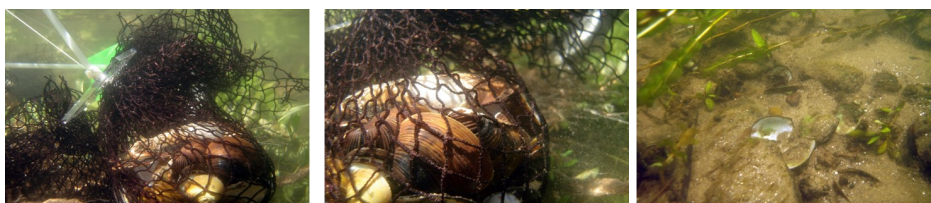
Martina I. Ilarri^{1,2}, Allan T. Souza¹, Vanessa Modesto¹, Lúcia Guilhermino^{1,2} and Ronaldo Sousa^{1,3}

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Bivalve shells can potentially alter the aquatic community, especially in the benthic domain. Until now, little is known about the influence of different shell morphologies and origins on the associated fauna. The present study aimed at understanding how empty shells of different freshwater bivalve species influence the macrozoobenthic community, using the Minho River (Iberian Peninsula) as a study area. Three native (*Anodonta anatina*, *Potomida littoralis*, *Unio delphinus*) and one invasive (*Corbicula fluminea*) species were used in this study. Comparisons among individual species and between different scenarios (before and after *C. fluminea* invasion) were performed. Our results indicate that the macrozoobenthic community structure did not vary among treatments (with the exception of species richness that was higher in the native species), and that almost no differences were detected when comparing the scenarios, despite the dissimilarities (size and morphology) between species. The empty shells of the invasive species *C. fluminea* partially (in terms of density and biomass but not in species richness) replace the empty shells of native species as a physical substratum for the associated macrozoobenthic community.



Shell phenotypes, adaptation, and trade-offs in rough periwinkles

John Watson Grahame^{*1}, Simon Robert Mace² and Thomas Norman Walker³

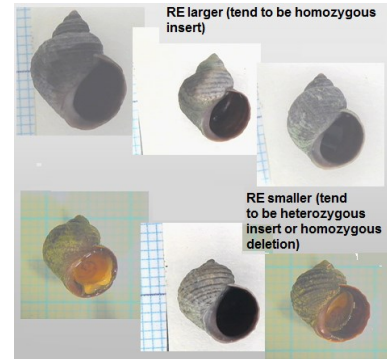
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Darwin was impressed that very small differences in features which fit organisms for survival - adaptive differences - could be the stuff of natural selection. At the same time, we are aware of the pitfalls of analysis of organisms as if they were a series of unconnected traits: the organism has to work as a unit. We analyse some of the features of the shape and strength of the shells of rough periwinkles to show how these may be related to important fitness attributes such as predator defence and reproductive capacity, and show evidence of trade-offs between some of the features.



A comprehensive biodiversity study on sub-tidal benthic molluscs in the marine environment of Hong Kong

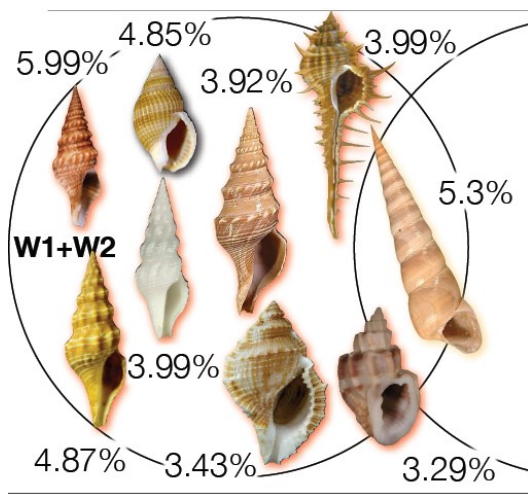
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Hong Kong has over 200 islands with a relatively long coastal line. As it is influenced by both the efflux from the Pearl River and various oceanic currents, it is enriched with various types of marine habitats and able to support a great diversity of marine organisms. Nevertheless, studies on the local diversity of sub-tidal benthic molluscan species were relatively limited. This study is designed to address the following questions: What are the molluscan species present in Hong Kong's benthic marine habitats? What are their abundance and biomass? What are the available commercially important species? What are spatiotemporal distribution patterns of the molluscan species?

Systematic, monthly-based surveys were conducted in eastern, western and southern waters, respectively, of Hong Kong between June 2013 and May 2014. We employed a shrimp trawler to sample benthic molluscs along four transects set within each of the three zone. In total, 133 species of molluscs from 55 families were cumulatively encountered during this 12-month survey. In the eastern waters, the Tolo Channel was dominated by the cockle, *Fulvia australis*, while the turrids shell, *Turritella nelliæ*, was dominant outside the Tolo Channel. In the southern waters, the scallop, *Minnivola pyxidata*, was the most abundant species along the four transects. In the western waters, the northern transects were dominated by another turret shell, *Turritella bacillum*, while the southern transects were dominant by *Turricula nelliæ*. All of these species are, however, not commercially important. Commercially important species only accounted for less than 5% of total catch per survey in terms of abundance and less than 18% of in terms of wet weight. Moreover, the size of specimens varied over time. For example, the turret shells collected in the wet season were generally larger than those in the dry season. Based on multivariate analyses, there were spatiotemporal patterns of the abundance, diversity and size of the molluscan species across Hong Kong waters. The current research will be continued until mid-2015 so as to investigate whether there is any progressive change in the community structure of benthic molluscs brought by the territory-wide ban on trawling in Hong Kong which has been implemented since 31 December 2012.



Global biodiversity and biogeography of razor clams (Bivalvia: Solenidae)

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Solenidae are deep-burrowing bivalves inhabiting from the intertidal to a depth of about 100 m. Razor clams are absent from Polar Regions and some oceanic islands such as New Zealand. Here we used data published in the literature, the Global Biodiversity Information Facility (GBIF), the Ocean Biogeographic Information System (OBIS), and museum collections to map the global geographic distribution of Solenidae species and study their latitudinal biodiversity gradients. We applied a species distribution modelling program 'Maximum Entropy' (Maxent) to predict the suitable environments for Solenidae species and determining the environmental factors which delimited the distribution of Solenidae species. Environmental data were obtained at a spatial resolution of 0.083° from the Global Marine Environment Datasets (<http://gmed.auckland.ac.nz>). The geographic distribution of species in 5° latitudinal bands showed a distinct bimodal pattern, and global patterns of richness decreased markedly from near the equator to the poles. The Indo-Pacific area exhibited the greatest species richness while the Philippines had a higher number of species (13) than any country in the whole of the Indo-Malayan realm. Model outputs also indicated that the majority of suitable Solenidae environments were likely to occur in the shallow waters of the Indo-Pacific area. The most important environmental factors in determining Solenidae environment suitability were distance to land, depth, wave height, and sea surface temperature.



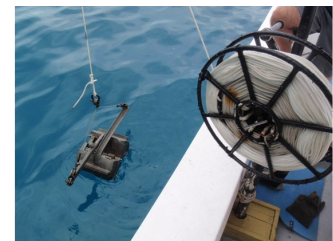
The molluscs of a tropical oceanic island (Isla del Coco, Costa Rica)

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We studied the mollusc assemblage present in the sand bottom of Isla del Coco (5°32'N-87°04'W), Pacific of Costa Rica. The island lies more than 500 km from the mainland, and the Galapagos. The number of species of molluscs reported is 545, with 180 species inhabiting sand bottoms. The malacofauna was sampled with five van Veen Dredges in 27 stations (3 to 75m depth) in April, 2010. A total number of 40 species and 434 individuals (density of 51 ind./m²) were found. The bivalves have 348 individuals, followed by gastropods (79), solenogasters (3), polyplacophorans (2), and 2 scaphopods (2). The most important molluscs were *Gouldia californica* Dall, 1917 (33 ind./m²), with more individuals outside the bays of the island. This species also increased in abundance with depth (Spearman $r=0.50$, $P<0.05$), carbonates ($r=0.58$, $P<0.05$), grain size ($r=0.60$, $P<0.05$), sorting of sediment ($r=0.60$, $P<0.05$), and increased at fine skewness of sediment ($r=-0.55$, $P<0.05$). The second in abundance was *Olivella (Olivella) cocosensis* Olsson, 1956 (3 ind./m²) occurring mainly in the exposed stations and outside of the bays; the main population in the Pacific occurs in Isla del Coco. This snail increased in abundance at lower organic matter % ($r=-0.36$, $P<0.10$), grain size ($r=0.45$, $P<0.05$), and at fine skewness ($r=-0.35$, $P<0.05$). The third most abundant was *Pristiterebra glauca* (Hinds, 1843), present near the shore and in the middle of the bays. Poor sediment sorting increase the size of interstices (facilitating excavation by bivalves), and ood availability is high in fine skewness (benefiting infaunal prey of *O. cocosensis* and *P. glauca*). The remaining species with few specimens were found randomly around the island, but followed a depth gradient (88% of change in their identity with the depth, $Z=-5.72$, $P<0.0001$), with few species common to several depths. The molluscs showed a high density between 40 to 50 m (χ^2 , $P<0.001$), although there were few species at this depth. It thus appears that deep sampling can result in new records for the Pacific.

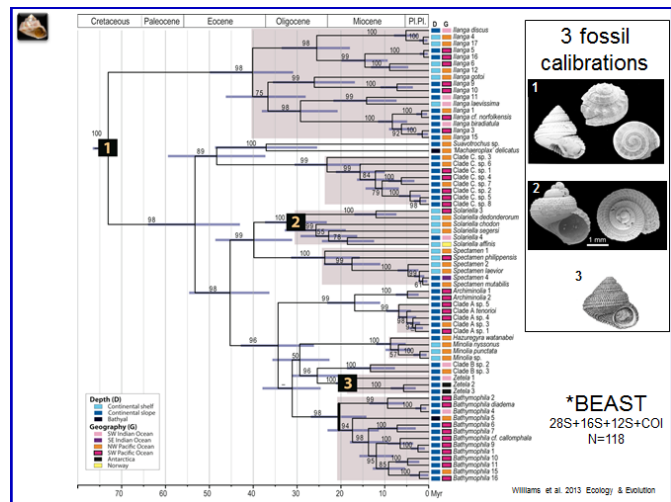


Diversification in the Deep Sea

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The deep sea is the largest and most enigmatic of the Earth's ecosystems. Covering almost two thirds of the planet's surface it was once thought to be devoid of life. Expeditions over the last hundred years, however, have shown that the deep sea is in fact rich in species, some with bizarre and unique adaptations to the challenges of living at great depth. I have been working the last few years (in collaboration with many others) to elucidate some of the factors driving diversification in the deep sea. In this talk I will show the results of a study where we found an increase in the rate of diversification of deep-sea solariellid gastropods approximately 33.7 Mya, coinciding with a period of global cooling at the Eocene-Oligocene transition. Increased nutrients made available by contemporaneous changes to erosion, ocean circulation, tectonic events and upwelling may explain increased rates of diversification, suggesting that food availability may have been a factor limiting exploitation of deep-sea habitats. I will also show that key innovations in trophic habits may explain four independent invasions of the predominantly shallow-water family Trochidae into the deep-sea. In these four lineages a small number of taxa have developed specialized xylophagous habits enabling them to make use of a new resource. Similarly, a shift to active carnivory has played an important role in the diversification of deep-sea anomalodesmatan bivalves. These examples in three different families emphasize the challenge the deep sea offers with respect to nutrient acquisition and iden-



Chiton phylogeny (Mollusca : Polyplacophora) and the placement of the enigmatic species *Chorioplax grayi* (H. Adams & Angas)

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Shallow marine chitons (Mollusca : Polyplacophora : Chitonida) are widespread and well described from established morpho-anatomical characters, yet key aspects of polyplacophoran phylogeny have remained unresolved. Several species, including *Hemiarthrum setulosum* Carpenter in Dall, 1876, and especially the rare and enigmatic *Chorioplax grayi* (Adams & Angas, 1864), defy systematic placement. *Chorioplax* is known from only a handful of specimens and its morphology is a mosaic of key taxonomic features from two different clades. Here, new molecular evidence provides robust support for its correct association with a third different clade: *Chorioplax* is placed in the superfamily Mopalioidea. *Hemiarthrum* is included in Cryptoplacoidea, as predicted from morphological evidence. Our multigene analysis of standard nuclear and mitochondrial markers demonstrates that the topology of the order Chitonida is divided into four clades, which have also been recovered in previous studies: Mopalioidea is sister to Cryptoplacoidea, forming a clade Acanthochitonina. The family Callochitonidae is sister to Acanthochitonina. Chitonoidea is resolved as the earliest diverging group within Chitonida. Consideration of this unexpected result for *Chorioplax* and our well-supported phylogeny has revealed differing patterns of shell reduction separating the two superfamilies within Acanthochitonina. As in many molluscs, shell reduction as well as the de novo development of key shell features has occurred using different mechanisms, in multiple lineages of chitons.



Phylogeny and relationships of mitriform gastropods (Gastropoda: Neogastropoda)

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The hyperdiverse order Neogastropoda encompasses over 12,000 Recent species, about quarter of the total species diversity of marine molluscs. One of the most diverse neogastropod groups to date completely ignored by molecular studies is the so called "Miters". This informal name refers to the total of about 800 Recent species in two families, Mitridae and Costellariidae, both widely distributed in tropical waters and most diverse in the central Indo-Pacific. Mitridae and Costellariidae are similar in external morphology and are traditionally treated as close relatives. Some genera of deep water families Ptychatractidae and Volutomitridae are close to miters in shell morphology. The term "mitriform gastropods" has been introduced to refer to Mitridae, Costellariidae and a variety of convergent forms. We studied over 90 species from 20 genera of Costellariidae, Mitridae, Ptychatractidae and Volutomitridae. Striking differences in anatomy were shown for different families of mitriform gastropods, contradicting their close relationship. Four genetic markers (COI, 16S rRNA, 12S rRNA and H3) were sequenced; the molecular dataset was complemented by the data on anatomy of alimentary system and radular morphology. Our analysis recovered Mitridae as a monophyletic group. Of 42 mitrid species, 37 formed a well supported "core Mitridae" clade, which includes Cylindromitrinae and Imbricariinae (both well supported), and a third clade, which, along with others, includes type species of the genus *Mitra* (which was found to be polyphyletic). Basal to the "core Mitridae" are four minor lineages with the genus *Charitodoron* recognized as a sister group to all other Mitridae. Our results support monophyly of the Costellariidae and confirm its close affinity to some ptychatractid genera (*Ceratoxancus* and *Latiromitra*), but not to Mitridae. Most advanced and diverse among Costellariidae are species of *Vexillum*, characterized by multicuspidate rachidian. Several previously unknown deep water costellariid lineages are revealed, their members retaining some plesiomorphies (in particular tricuspidate rachidian) and are morphologically intermediate between Ptychatractidae and *Vexillum*. In our analysis the our studied ptychatractid genera did not cluster together and were all found to be unrelated to Pseudolividae, suggesting 1) paraphyly of the Ptychatractidae and 2) its exclusion from Pseudolivoidea. Volutomitridae was found to be monophyletic, though we failed to resolve its relationships with certainty.



Genome sequencing project for *Littorina saxatilis* (Gastropoda: Littorinidae)

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New sequencing techniques made it feasible to produce genome sequence data for any species. The challenge of genome projects for molluscs, as well as for other invertebrate groups, lies instead in *de novo* assembly of short sequence reads into the genome draft. Recently genomes have been published for several species (*Aplysia*, *Lottia*, *Crassostrea*, *Conus*, *Pinctada*). Still, given the size and diversity of the phylum, Mollusca are poorly represented in genome databases. Emerging features of mollusc genomes are large size, complexity, common repetitive elements and high level of heterozygosity. Intertidal snails of genus *Littorina* have been model for ecological and evolutionary studies for a century yet the genetic resources for this group of snails were very limited. In particular, *L. saxatilis* provides ample opportunity to study evolution of natural adaptation and speciation. The *Littorina* genome sequencing project was started in 2011 by the Centre for Marine Evolutionary Biology (<http://www.cemeb.science.gu.se>) in collaboration with other research groups working on littorinid genomics (R. Butlin, R. Faria, A. Sá Pinto). I present our genome sequencing strategy, current status of the *Littorina* genome assembly, challenges of *de novo* sequencing large and complex non-vertebrate genome and possible ways to overcome these challenges. Even though the genome assembly draft at the current stage is very fragmented, it is already being helpful in several ongoing projects, and I will give a few examples. Finally, several genome re-sequencing projects for other individuals of *L. saxatilis* and other *Littorina* species have been initiated.

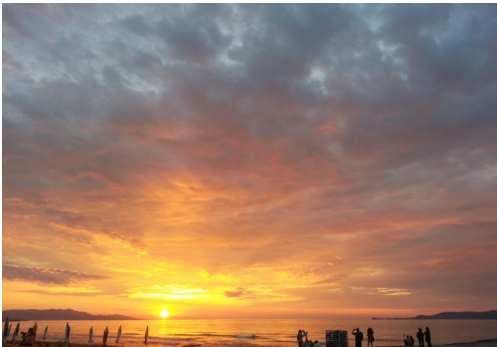


Molecular adaptations in Euthyneura mitogenomes: possible clues to land colonization

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Euthyneura is one of the most diverse groups of gastropods regarding ecological adaptations and species richness. One of the key innovations within this group has been the evolution of air-breathing in pulmonate snails and slugs which triggered the radiation into terrestrial and freshwater niches. We hypothesize that the adaptations to these new niches left traces in the euthyneuran genomes. Thus, our main objective was to find possible signs of selection at the molecular level related to land transitions. We used data from mitochondrial genomes to test this hypothesis. We sequenced three new mitogenomes from eupulmonates (two from Stylommatophora: *Arion* and *Helicella*, and one from an Ellobiidae: *Carychium*). We annotated each mitochondrial genome using the MITOS web server, and then performed phylogenetic analyses using the thirteen mitochondrial coding sequences: *cox1*, *cox2*, *cox3*, *cytb*, *nad1*, *nad2*, *nad3*, *nad4*, *nad4l*, *nad5*, *nad6*, *atp6*, and *atp8*. Then, we used the tree topology as a framework to test positive selection (PS) events using site or branch models. Tests of PS were performed in PAML 4.7, models M1a vs. M2a (sites) and Model A vs. Model A1 (branches) were compared using the Likelihood Ratio Test (LRT). Our results support the Panpulmonata/Euopisthobranchia hypotheses in concordance with previous multi-loci topologies. The comparison of site-specific models showed that *nad2*, *nad5*, and *nad6* presented positions affected by PS, these proteins belong to the OXPHOS Complex I. Aminoacid changes in these proteins related to proton pump could have influenced the fitness during the radiation to land. For branch-specific models, we found PS comparing Stylommatophora (land snails) with other marine and intertidal taxa. Finally, we found PS in mutations in the *cox3* gene, for Stylommatophora and other fully terrestrial adapted snails (*Carychium*, Ellobiidae) and slugs (*Rhopalocaulis*, Veronicellidae). Future analyses considering complete transcriptome data would shed light into other regions related to the land transition.

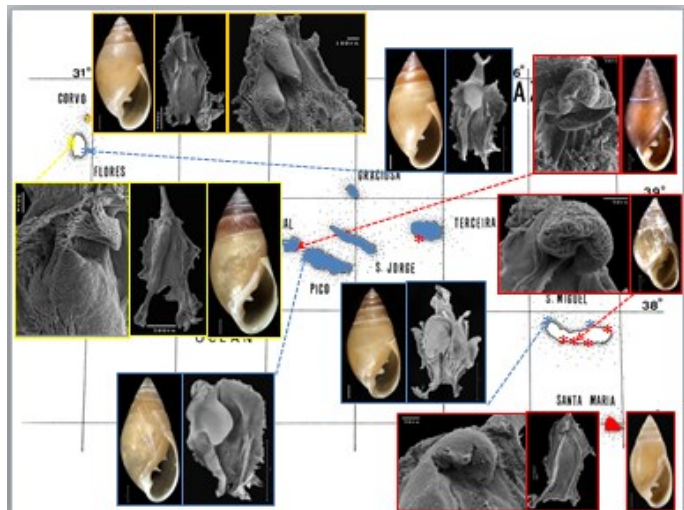


Unravelling the taxonomy of *Myosotella* (Gastropoda: Ellobiidae): penial structure is the key

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The taxonomy of *Myosotella* Monterosato, 1906, has relied mainly on conchological characters, the apertural dentition of the shell providing most of the diagnostic features. However, the apertural aspect of the shell varies greatly even within the same population, thus becoming an unreliable character. For that reason, the 40+ nominal species were synonymized into *Myosotella myosotis* (Draparnaud, 1801). Attention has been given lately to aspects of the anatomy, namely the internal morphology of the penial complex, revealing consistent patterns of the shape of the penial papilla: 1) *flap*, leaf-like with the pore opening at the base of the right margin (*M. myosotis* from Southern France and continental Mediterranean Europe, Azores, South Africa, Peru); 2) *hood*, with retractile papilla at the center of a protective cover (*M. denticulata* from non-Mediterranean continental Europe and eventually British Isles); 3) *club*, with papilla solid, thick and long, bifid at the tip, the pore opening on the right branch (various species in the eastern Mediterranean islands, Azores, Madeira, California); 4) *twins*, with two papillae, the distal one resulting from the main pilaster and bearing the pore (two new species from the Azores islands). Preliminary molecular research supports the taxonomic relevance of the anatomical patterns presented here. The NMNH / Naturalis (Leiden) kindly provided specimens from around Europe and the Mediterranean.



Insight into water transport proteins of terrestrial and freshwater gastropods based on their transcriptome NGS-sequencing

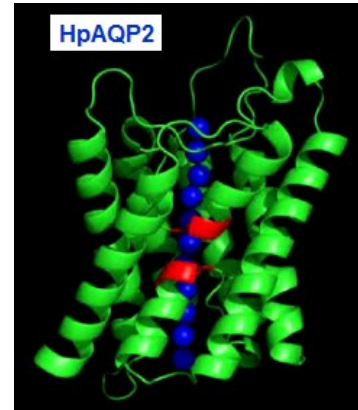
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Aquaporins, proteins forming tetrameric water channels in biological membranes, have been identified and characterized in many organisms of all kingdoms of life as the main way of fast water movement through membranes. Water channels can increase the rate of water transport and regulate this process as well. Thus aquaporins are thought to be responsible for maintaining the water homeostasis of cells and even entire organisms. It is also assumed that in animals control of body hydration is linked to a regulation of cell membrane permeability to water. These ubiquitous proteins share overall 3D structure but are different in the amino acid sequence and in transport features. Generally, they are divided into two subfamilies: 'orthodox' aquaporins (AQP) transporting mainly water, and aquaglyceroporins (AQGP) permeating also larger uncharged molecules, like glycerol. The best described water channel proteins are vertebrate AQPs. Among invertebrates the most studied ones are insect AQPs while molluscan AQPs are the least studied. However, the manner, in which molluscs deal with water management, is extremely interesting, especially when it comes to the type of environment in which they live. Therefore, we selected four snail species, two freshwater (*Lymnaea stagnalis* and *Planorbarius corneus*) and two terrestrial (*Helix pomatia* and *Arion vulgaris*), for AQP identification and analysis. *De novo* transcriptome assembly of the snail species based on Illumina next-generation sequencing data allowed us to identify and analyze ORFs encoding AQPs. We compared predicted sequences with identified AQPs, performed studies of organ-specific expression and estimated their functionality by complementation assay in yeast cells. Financial support for this work was provided by the National Science Centre grant NN 2011/01/B/NZ4/00630.



The Lusitanian species *Geomalacus maculosus* - a 'native' Irish slug?

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The EU – protected slug *Geomalacus maculosus* belongs to the Lusitanian fauna and occurs only in the West of Ireland and in Northern Portugal and Spain. To determine whether this species is a 'native' Irish species or has been introduced from Iberia after the last glacial maximum, we assessed the population structure and genetic variability of Irish and Iberian slug populations. Partial sequences of the mitochondrial 16S rRNA and COI genes and from the nuclear ITS-1 region were compared from 78 specimens collected from 12 locations within Ireland and 10 locations within Spain. Only one 16S rRNA haplotype and two COI haplotypes were found in Ireland, while in Iberia, 23 haplotypes were discovered for COI and 22 for 16S rRNA, which clustered into several regional clades. All of the four ITS-1 haplotypes that were found in Ireland were also identified in Iberia, where a total of ten ITS-1 haplotypes were discovered. The reduced genetic diversity of Irish populations compared to Iberia suggests the presence of a population bottleneck, probably due to a founder effect: the lack of a unique ITS-1 haplotype highlights the strong link between Irish and Iberian populations, as do the results of our phylogenetic analyses. Possible modes of introduction for this Lusitanian species and implications for its conservation are discussed.



Molecular systematics and population structure of the genus *Pyrenaearia* (Stylommatophora: Helicoidea)

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Pyrenaearia is a genus of terrestrial gastropods endemic to the north of the Iberian Peninsula where it inhabits mainly the northern slopes of limestone mountains. The genus comprises taxa confined to high altitudes as well as some species living at high altitudes in close vicinity to others restricted to the valleys so it is a good model to study both parapatric and allopatric speciation. Nevertheless, its phylogeny and taxonomy remains unclear with difficult evolutionary inferences. Here



Habitat of *P. oberthueri*



Habitat of *P. navasi*

we use new molecular species delimitation methods together with molecular dating techniques to investigate species boundaries and the process that generate them based on the phylogeny constructed for 2 mitochondrial genes (COI & 16S rRNA) and 1 nuclear gene (ITS1) of 124 specimens representing all genus species. We extended the dataset with AFLP markers and compare its phylogenetic signal with the sequences signal looking for inconsistencies. AFLP markers were obtained for almost 700 samples belonging to 35 populations. Then, the population structure and gene flow of the obtained species were analysed. The AFLP dataset was also explored in order to detect candidate loci for adaptation to altitude.



Marking time at a snail's pace: million year-old amino acids

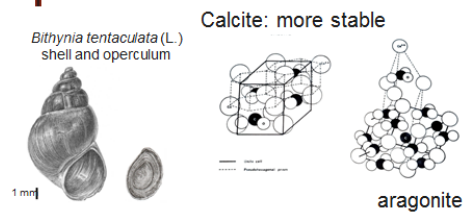
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First used for dating in the late 1970s, amino acid racemization (AAR) dating of fossil mollusc shells has helped develop our understanding of Quaternary stratigraphy, Palaeolithic archaeology and their links to the climatic record. However, problems of analysing open-system biominerals have dogged the technique. Recent studies have shown that a very small fraction of 'intra-crystalline' protein forms a closed system, and if this is targeted, the difficulties caused by leaching, contamination and environmental factors are removed. The analysis of a coherent calcite intra-crystalline system in *Bithynia* opercula has enabled the development of an AAR chronology spanning at least the last 2.8 Ma. Our research has focused on building chronological frameworks on a wide spatial and temporal scale. However, it's not like waving a magic wand - there are still several important factors that need to be taken into account (such as species effects, the importance of the calcium carbonate matrix, and responses to temperature) and it is clear that we need to interpret the data in the light of these considerations. Although the limits of dating using solely racemization is reached within the Pliocene, the isolation of an intact closed-system of amino acids from Miocene and Eocene fossils opens up a world of other amino acid degradation reactions with potential for use as a dating tool.

Not all shells are equal...



Malacology and marine climate: using mollusc shells to investigate the history of the marine environment during the past 1,000 years

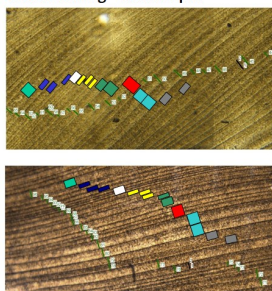
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Crossmatching – an example



It is now possible to use the annual banding patterns in the shells of some long-lived marine bivalve species (in particular *Arctica islandica* and *Glycymeris glycymeris*) to create chronologies of annually-resolved and absolutely-dated shell material for hundreds or even (potentially) thousands of years. The increment widths and the geochemistry of the shell material are unique high-resolution proxy archives for high latitude marine environments. In particular, the north Atlantic shelf seas, home to some of the longest-lived bivalve species, are also close to locations of convective overturning that are a key contributor to the global ocean circulation. Significant research has recently been published using shell-ring chronologies to investigate changes in the Atlantic Meridional Overturning Circulation (AMOC) over the past millennium. Other work has focused on seawater temperature reconstruction and the stable carbon isotope signature of seawater. This has been achieved by applying techniques of pattern matching and crossdating derived from tree-ring research.

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In this presentation, I will describe these techniques as they are applied to growth increments in shells, and highlight some of the challenges we face when interpreting growth marks in different species. I also discuss some of the specific questions that are being raised as we seek a much fuller understanding of the drivers and variability of shell growth. How does the growth rate vary through the growing season? What morphological, structural and geochemical differences are there between the increments and the growth lines (or growth checks) that separate them? How and when does the growth check form? Do the answers to these questions vary among species and among different populations of the same species? These issues bring into play the complex relationships between the environment, molluscan biology and the shell formation pro-



Yoldia eightsi as a scleroclimatological proxy for Antarctic coastal waters

Alejandro Román-González¹, Ian Hall¹, Caroline Lear¹, James Scourse²,
Paul Butler², Lloyd Peck³ and Martin Ziegler⁴

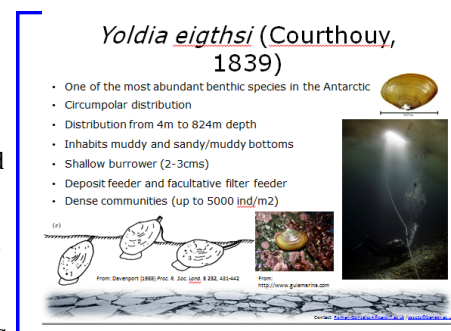
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The ice loss in the West Antarctic Peninsula (WAP) is undergoing a dramatic change as the climatic changes reported in the Arctic. Although Antarctic ice trend have strong regional variability with a net increase of 1.5% decade⁻¹ for the past 34 years, the WAP is the region that has warmed the most in the southern hemisphere since the 1950s when the records begun. In order to understand the ongoing changes in the Antarctic it is necessary to comprehend its natural variability and the key climatological feedbacks acting in the region. Due to the scarcity of long-term instrumental records interpretations of current climatic trends remains speculative. Here is where the use of sclerochronological techniques based on absolute dated growth increments present in the shell of marine bivalves can help us to develop environmental proxies for Antarctic coastal waters. Results based on a chronology developed out of 47 *Yoldia eightsi* specimens suggest that there is a negative relationship between shell growth and fast ice duration. In addition a positive relationship between shell growth and winter sea surface temperatures (wSST) was found. As the mean regional wSST has not varied for the time studied this indicates that winter duration is the parameter modulating shell growth. These findings provide an example of the potential use of sclerochronological proxies for Antarctic coastal waters.



The marine radiocarbon bomb-pulse across the temperate North Atlantic

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Radiocarbon measurements from known-age annual increments in recent (last 50 years) long-lived bivalve shells contain bomb-pulse time histories. These data constitute calibration series for the use of the bomb-pulse as a high-resolution dating tool in the marine environment for the last 50 years and as a tracer of coastal ocean water masses. We present series of $\Delta^{14}\text{C}$ excess from known-age annual increments of the long-lived bivalve mollusc *Arctica islandica* from four sites across the coastal North Atlantic (German Bight, North Sea; Tromsø, north Norway; Siglufjordur, north Icelandic shelf; Grimsey, north Icelandic shelf) combined with two previously published. The atmospheric bomb-pulse is a step-function whose response in the marine environment is immediate but of smaller amplitude and which has a longer decay time as a result of the much larger marine carbon reservoir. Attenuation is determined by the regional hydrographic setting of the sites, vertical mixing, processes controlling the isotopic exchange of ^{14}C at the air-sea boundary, ^{14}C content of the freshwater flux, primary productivity and the residence time of organic matter in the sediment mixed layer. The inventories form a sequence from high magnitude-early peak (German Bight) to low magnitude-late peak (Grimsey). All series show a rapid response to the increase in atmospheric $\Delta^{14}\text{C}$ excess but a slow response to the subsequent decline resulting from the succession of rapid isotopic air-sea exchange followed by the more gradual isotopic equilibration in the mixed layer due to the variable marine carbon reservoir and incorporation of organic carbon from the sediment mixed layer.



Bivalves as an important source of isotopic and radiocarbon archaeological data

Ricardo Fernandes^{1,2,3} and Alexander Dreves²

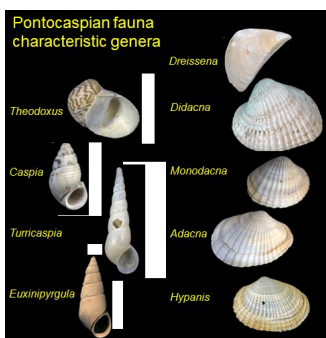
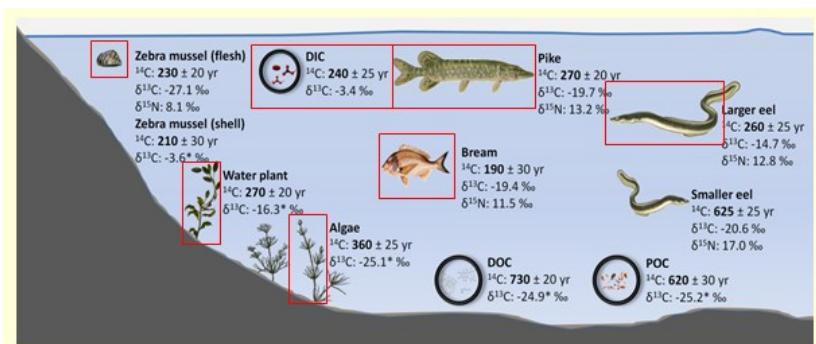
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Bivalve shells are found in diverse archaeological contexts and are indicative of their varying contribution to past human diet. Radiocarbon and isotopic analysis of often well-preserved bivalve shells can provide important information on past environmental conditions, site's chronology, and on the isotopic baseline relevant in human paleodiet studies. As part of ongoing research, modern and archaeological bivalve samples of different species have been recovered from marine and freshwater locations within Germany. Different bivalve fractions (soft tissues, shell carbonate, and shell conchiolin) were physically/chemically pre-treated and targeted for radiocarbon and isotopic analysis ($\delta^{13}\text{C}$, $\delta^{15}\text{N}$, and $\delta^{34}\text{S}$).

Our results show that bivalve specimens from different locations have a highly variable but significantly lower ^{14}C content compared with the contemporary atmosphere, i.e. they show a radiocarbon reservoir effect. Furthermore, in some instances, significant differences were observed between radiocarbon measurements in different bivalve fractions (shell carbonate vs. soft tissues). These were linked to species, growth stage, and variations in ^{14}C concentrations of the water carbon pools (dissolved inorganic carbon, dissolved organic carbon, and particulate organic carbon). The variability in local radiocarbon reservoir effects and potential differences in ^{14}C concentration between edible (soft tissues) and preserved (shell carbonate) bivalve fractions constitute a potential challenge in the establishment of accurate chronologies. However, large local radiocarbon reservoir effects also provide a novel dietary proxy that can be used in the detection of past human consumption of aquatic resources when other isotopic proxies provide ambiguous results.



The rise and demise of the Ponto-Caspian biota

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The Ponto-Caspian fauna is an anomalohaline fauna dominated by endemic neritid and hydrobiid gastropod species and lymnocyprid and dreissenid bivalve species that live in the Black Sea, Caspian Sea and formerly in the Aral Sea Basin, but it is also known from lakes in Anatolia and the Balkans. The fauna has furnished several freshwater and brackish-water species, such as Caspian mudshrimps and Zebra mussels, which have invaded western Europe and North America. The Ponto-Caspian fauna, however, includes a large number of endemic species, several with very restricted distributional ranges. The distribution and conservation status of many of these species is unknown, but it is clear that significant elements of the Ponto-Caspian fauna are severely threatened. In the Black Sea basin, the development of coastal wetlands and pollution may have played a role, in the Caspian Sea a severe faunal turnover has resulted from introduced species since the 1930s, whereas desiccation of the Aral Sea has severely impacted the Ponto-Caspian biota. Satellite lake systems in Anatolia and the Balkans are also severely impacted by human activities resulting in desiccation and eutrophication.

The modern Ponto-Caspian fauna came into existence during the middle Quaternary in the Black Sea and Caspian Sea basins. Several of the taxa (mostly genera) that now typify the Ponto-Caspian fauna were derived from areas such as the Pontian-Dacian system, from rivers in the Ponto-Caspian drainage basin, but several were derived from Neogene Anatolian lake systems. Throughout the Quaternary faunal exchange existed between the Ponto-Caspian domain and the Anatolian lake systems. By documenting successive Ponto-Caspian faunas in the different areas, and by studying component processes of the faunas, we aim to elucidate the resilience of the fauna during adverse conditions in the past and to compare these situations with the modern, human-mediated Ponto-Caspian biodiversity crisis.

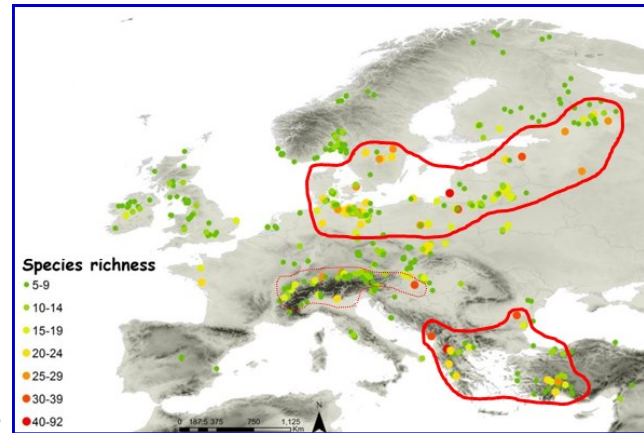


Exploring patterns of freshwater gastropod diversity in European lakes

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We investigate the biogeography of freshwater gastropods of European lakes. We have compiled the first occurrence records concerning more than 300 gastropod species, as well as data on the limnological and geographical parameters (e.g. latitude, longitude, altitude, lake size and shoreline) for 1050 lakes across Europe. Our objectives were to identify biogeographical regions, document the patterns of freshwater gastropod species richness and reveal possible causes of their distribution. To identify the regions, cluster analyses were applied on multiple subsets of the data in order to estimate the similarity of lake faunas, while Simpson's diversity index was used as a distance metric. Moreover, correlation analyses and regression models were applied to explore the relationships between species richness and lakes' characteristics. Preliminary results show that species richness increases to the south (e.g. Balkans, Turkey) and north-east (e.g. Poland, European part of Russia) of Europe. An increase of endemic species is observed in southern Europe, while central and north European lake faunas are rather homogenous with a clear absence of endemic species. Dendrograms reveal well-defined units for the Turkish, central and north eastern European lake groups. The main factors explaining species richness of different lake groups are area and shoreline length.

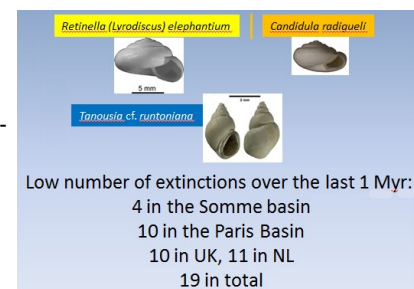


Quaternary history of non-marine molluscs in the Somme valley, Northern France, during the last 1 Myr

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The Somme valley is a key area for the Human occupation of NW Europe. At the end of the 19th century, the contemporaneity of Man and extinct mammal faunas during Prehistoric times was first recognized by French and British scientists in a quarry at Abbeville. In this region, Quaternary deposits comprise a terrace system including ten alluvial sequences covered by slope deposits which formed over the last million years. Geomorphology and dating have been intensively studied and provide a consistent view of geometrical evolution of the landscape together with a solid chronological frame of events. Many sites have been excavated within these formations and have given opportunities to report on changes of climate and environment through time. Non-marine molluscs, which are a good proxy for palaeoenvironmental reconstructions, are regularly preserved in these deposits. In 1952, Breuil published a detailed report of the non-marine molluscan faunas known from Quaternary deposits of the Somme and the Seine valleys which had been identified by A.S. Kennard. Sixty years later, after a lot of supplementary analysis, the present contribution intends to provide a new synthesis of the history of malacological assemblages over the last 1 Myr. How have climatic cycles influenced the composition of snail communities? Is there a model of malacological evolution vs climatic and environmental changes? What evolution of biodiversity can be reported? Change in number of species? Extinction of taxa? Evolution of geographical distribution of species?

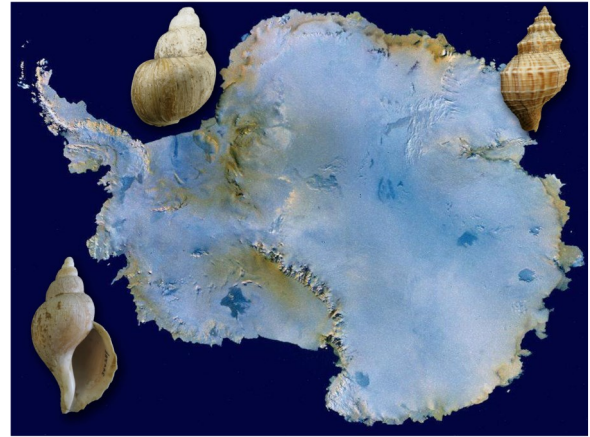


The origin of the Antarctic marine molluscan fauna

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Some 38 modern Southern Ocean molluscan genera, representing ~18% of the total fauna, can now be traced back through at least part of the Early Cenozoic fossil record of Antarctica. Of these 38 taxa only five can be extended even further back across the Cretaceous/Paleogene boundary, and these are all bivalves. The Early Cenozoic fossil record of Antarctica is in fact marked by a substantial radiation of gastropods, with the large neogastropod clade being particularly prominent. Some of the first modern taxa occur in the Early Paleocene (~63 Ma) and are linked to the recovery fauna following the mass extinction event. However, the most significant evolutionary expansion occurs in the Early – Middle Eocene (~45–50 Ma) and is associated with a distinct pulse of global warming. With the Buccinoidea comprising 47% and the Conoidea 25% of the neogastropods, this Eocene fauna already bears a striking compositional similarity to the modern one. A prominent extinction event in the late Middle Eocene is provisionally dated at ~42 Ma and linked to the early onset of global cooling. Thereafter the fossil record is very incomplete but there are no indications that it was ever again as rich as in the Early – Middle Eocene. Thus the evolutionary roots of the modern Antarctic marine fauna appear to lie within the Eocene greenhouse world. This means that a number of taxa must have subsequently adapted to much colder water conditions, presumably doing so slowly over very long periods of time. There is growing evidence to suggest that this Early Cenozoic radiation of gastropods seeded not only the modern Antarctic marine fauna but also the modern deep-sea fauna too.



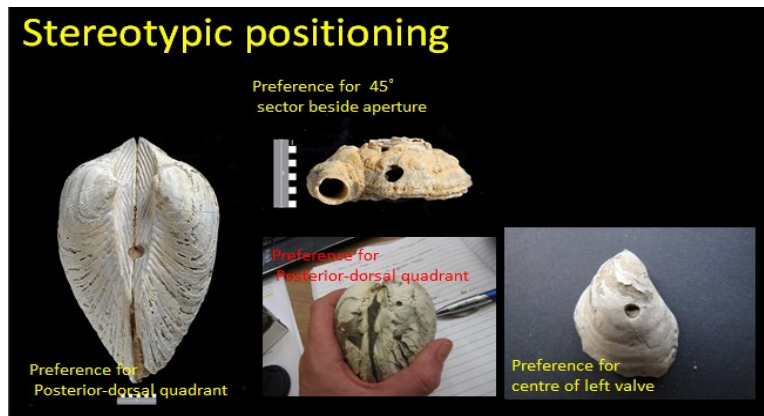
The drillers and the drilled: molluscan predator-prey interactions over the K-Pg mass extinction of Antarctica

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Molluscan interactions have played a central role in attempts to unravel the evolutionary importance of predator-prey dynamics. Some of the persistent questions asked in these studies involve whether there has been escalation in predator and prey efficiencies over time and what, if any, influence mass extinctions have had on such systems. In this study, we examine the record of predatory drill holes over the K-Pg boundary section at Seymour Island, Antarctic Peninsula. This section is one of the best exposed and most complete Late Cretaceous–early Paleogene sedimentary sections anywhere in the world and the invertebrate fauna of these predominantly near-shore clastic sediments is extremely well preserved. In this study we have used material collected in a recent detailed sampling over the K-Pg boundary by the PALAEOPOLAR project. The Late Cretaceous shelly fauna contains abundant gastropods, bivalves and rotulariid worms, all of which are potential prey items. Bivalves are the commonest benthic group, with large numbers of relatively large ‘meaty’ taxa such as oysters, cucullaeids, trioniids, and the enigmatic ‘cockle’, *Lahillia*. Although gastropods are less common, there are large numbers of aporrhoids, amberleyids, pleurotomariids, naticids and cerithiids. By contrast, the Paleogene recovery fauna has a much diminished diversity, with key taxa such as the trioniid bivalves and most rotulariids notably absent, whilst the *Lahillia* is particularly abundant. Our investigations have revealed the activities of large drilling predators, most likely naticid gastropods, throughout the Late Cretaceous – early Palaeogene sequence. We have used a large data of drill holes to test hypotheses relating to the selective removal of escalated prey and the subsequent ‘improvement’ in predator success, paying particular attention to changes in potential prey morphologies and to behavioural patterns shown by the predators over the interval.

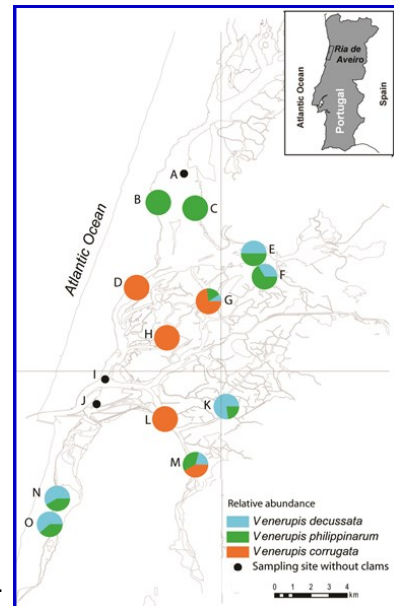


Spatial distribution and bioaccumulation patterns in three Veneridae clams from a low-contaminated ecosystem

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The introduction and spread of invasive species has been identified as a major ecological threat in coastal marine communities that, in most cases, can negatively affect native species leading, in extreme situations, to their replacement. Thus, the study of interactions between non-indigenous and native marine species has become a focus of interest, especially when dealing with economically relevant species. In this regard, different bivalve species have been intentionally introduced in several coastal ecosystems, such as the case of the Manila clam *Venerupis philippinarum* (Adams and Reeve, 1850). In Portugal, *V. philippinarum* was recently introduced, living in sympatry with the native clams *Venerupis decussata* (Linnaeus, 1758) and *Venerupis corrugata* (Gmelin, 1791). For Portugal, the most updated information shows that the national annual production of clams represents 42% of the total shellfish production and is fundamental to the national socioeconomic framework involving, directly or indirectly, thousands of employees. When consuming bivalves, special concern should be taken in relation to the total element burden. In order to assess this issue, this study aimed to measure the element levels in the sediments of different harvesting areas and relate them to the accumulation in clams; assess the element body burdens available for assimilation and relate these to the total accumulation in clams, compare the native (*Venerupis decussata* and *V. corrugata*) and the invasive (*V. philippinarum*) species and finally evaluate the human risk associated with the consumption of different clam species. The results showed that the element burden in clams does not reflect the sediment contamination and BAF values were higher in the less contaminated areas. Comparison of MLs from international organizations with the concentration of elements in clams showed that As exceeded standard levels. For As, the ingestion of less than 1 Kg of clams exceed the PTWI threshold. Furthermore, the results showed that As and Hg are more easily available to be transferred trophically.



The alien slipper limpet *Crepipatella dilatata* (Lamarck, 1822) in Northern Spain: a multidisciplinary approach on its biodiversity and invasive biology

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Species introduced through human activities to new territories outside their native ranges may cause negative impacts to the receiving environment at various levels. These impacts may have ecological and evolutionary consequences and in extreme cases lead to economic

losses. Among the most sensitive systems to biological invasion are the marine coastal and estuarine ecosystems. Since it is usually difficult to control and prevent the potential negative effects of introduced species once they have become established, their early detection and identification as well as the tracing of their origin and introduction vector are imperative, in order to develop effective preventive and control strategies. Among marine alien species that have become invasive and are currently pests are slipper limpets. In the present study, we focus on a slipper limpet attributed to the South American species *Crepipatella dilatata* (Lamarck, 1822), recently detected in central Northern Spain. The present work undertakes a multidisciplinary study of two geographically distant newly-detected populations of these individuals attributed to *C. dilatata* in order to verify their taxonomic status, determine their source of introduction and the most plausible introduction pathway, assess their variability in size, anatomical and reproductive characters and evaluate their invasive potential. For this purpose, species identification by shell morphology has been complemented via anatomical, reproductive, larval and molecular characterisation. Genetic analyses with the COI gene, life history and anatomical traits have confirmed that individuals of both populations pertain to the mentioned slipper limpet. One locality in the Chiloé Island at Southern Chile, a major site of *Mytilus* mariculture and export, has been identified as the most likely site of origin. Besides, comparisons between both populations revealed differences in the sexual strategy, gregariousness, reproductive output and size-gender distribution. Further results indicated that in one of the populations, sex change was socially controlled, which contrasts with previous findings in the native range of distribution. This raises the question of whether protandric species exhibiting low gregariousness and a narrow plasticity in size at sex change may have the capacity to respond also to social clues under particular environmental conditions. It is possible that this kind of social plastic responses of *C. dilatata* may improve the invasion capacity of this species and may partially explain its invasion success.



Invasive bivalves as an unusual resource for terrestrial invertebrates

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Resource pulses are episodes of low frequency (rarity), large magnitude (intensity) and short duration (brevity) that result in increased resource availability in space and time. Recent studies in food web dynamics highlight the importance of resource pulses at the individual, population, community and ecosystem levels. However, the number of studies in freshwater ecosystems assessing their importance, mainly in the direction of water to land, is rare. Even rarer are studies addressing this topic using invasive species. In this study, we assessed the importance of massive die-offs of the Asian clam *Corbicula fluminea* as a resource pulse to the terrestrial macroinvertebrate community after extreme climatic events (floods). We manipulated *C. fluminea* density (0, 100, 500, 1000 and 2000 ind./m²) and collected samples 7, 30 and 90 days after the beginning of the experiment. Clear differences were detected in abundance, biomass, richness and diversity of terrestrial macroinvertebrates regarding *C. fluminea* density and time. This study highlights invasive bivalves as a major resource subsidy after massive die-offs, possibly contributing with remarkable amounts of nutrients and energy to the adjacent terrestrial ecosystem. Part of this bivalve carrion can be consumed directly by a great number of macroinvertebrate species (but possibly by other organisms such as birds and mammals) and other part can enter the detritus food-web.

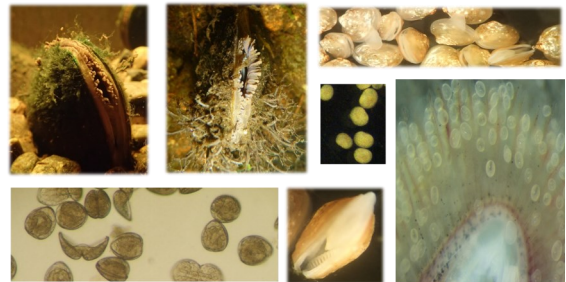


Is juvenile mussel growth rate related to time on gills?

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The unusual life cycle of the endangered freshwater pearl mussel *Margaritifera margaritifera* involves an obligate parasitic stage. The parasitic glochidia remain attached to the salmon (*Salmo salar*) or trout (*Salmo trutta*) host for one year. The glochidia grow on the host fish up to 500 times larger than their initial size. Once they excyst they remain buried in the river sediment for about five years and depend on a stable substratum with good sediment quality and exchange of free-flowing and interstitial water. This post-parasitic stage (juvenile mussels) is the most critical stage of the life cycle and a bottleneck in conservation projects. Juvenile mussels excyst over a period of 40 days during May to July. To gain a better understanding of juvenile mussel fitness (mean size and growth rate) we measured the mean size and growth rate of mussels from seven rivers from southern Norway. A relation between growth rate and time on gills was observed. We also observed that the mussels that fell earlier in the season were smaller and had poor survival compared to the late fallers.



The Freshwater Mussels (Bivalvia: Unionoida) of Northern South America and the Amazon

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The river basins of Northern South America (NSA) (including the Rios, Magdalena, Sinu, Orinoco, Essequibo, as well as smaller systems of Guyana, French Guiana and Surinam) and the Amazon are inhabited by three families of freshwater mussels: Etheriidae, Hyriidae, and Mycetopodidae. Our systematic re-evaluation of the species and genera of the region is based on fieldwork conducted by KSC in collaboration with Christine A. Mayer (1986-1995), collections-based research in 17 major

“Combine their efforts to maintain an efficient malacological strike force equally capable of working in remote collection localities or urban mollusk collections “



research collections, and a comprehensive literature review. Digital photographs of specimen lots and geo-referenced localities were integrated into a comprehensive database of freshwater mussel taxonomy, literature records, and museum specimens. To-date, we have nearly 30,000 specimen lots: 6800 from South America, about 650 from NSA, and 1130 lots from the Amazon basin. These data are publicly available via the MUSSEL Project Web Site (<http://www.mussel-project.net/>). We currently recognize 37 species in 12 genera in NSA, including at least one species new to science and approximately 50 species in 14 genera in the Amazon. Of these species, 20 are endemic to NSA and about 16 in the Amazon. A few species are shared between northern South America and the Amazon through connections between the Orinoco and Amazon through the Casiquiare Canal and the Essequibo and Amazon via the upper Rio Branco. We present our results on patterns of species richness and taxonomic diversity in these Neotropical basins and summarise the known deficiencies in our understanding of the biogeography and evolution of these taxa.



Environmental conditions shape molluscan lifespan: comparing markers of cellular fitness and aging in two populations of the freshwater bivalve *Diplodon chilensis*

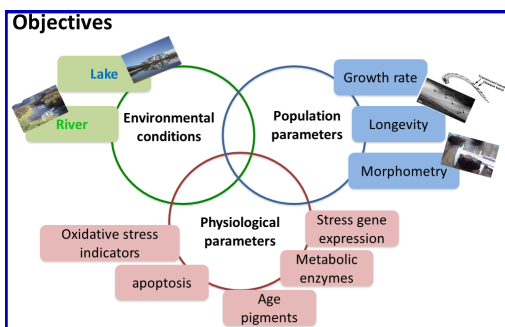
Iara Rocchetta^{1,2}, María S. Yusseppone¹, Cora Albrecht², Carlos M. Luquet³, Thomas Brey², Stephan Frickenhaus⁴, Christoph Held² and Doris Abele²

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Bivalves can be aged by counting the growth rings in their shells and are emerging as new models in aging studies. The unionid *Diplodon chilensis* is abundant in rivers and lakes of Andean Patagonia and can exceed 100 years old. Two natural populations from a river and a lake in Patagonia (Argentina) were studied to analyse the effects of abiotic and biotic environment factors on fitness and senescence. Oxidative stress (malondialdehyde (MDA), protein carbonyls) and apoptosis markers (caspase3-7 activities) in mantle tissue, antioxidant enzymes (catalase (CAT) and superoxide dismutase) and metabolic enzyme activities in gills (citrate synthase (CS) and cytochrome oxidase) were analysed over age. Maximum population lifespan was 120 years in the lake and only 40 years in the river. When comparing the same age at

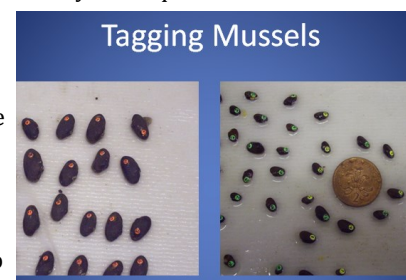
both sites, individuals from the river had higher CAT activities and lower lipid oxidation levels (MDA). Furthermore, apoptosis and protein oxidation intensities were higher in bivalves of river than lake individuals, which could mean that protein turnover is faster in the river bivalves. Even more, stress gene expression (SOD, HSP70-90, GST, GPX, apoptosis) was higher in river individuals compared with the same age group from the lake. Plotted over lake population lifetime, a similar pattern was observed for of river bivalves. CAT activity was increased and MDA levels in individuals diminished with age, while the age pigment lipofuscin, protein carbonyls and caspase activity increased over age. Metabolism activity would seem to be slower in the older bivalves, deduced from lower CS. In conclusion, compared with the lake, the river represents a more stressful (variable) environment in which bivalves invest more energy into stress defence and tissue maintenance (apoptosis). This contributes to the 3-fold higher population specific life expectancy in the lake.



Conservation strategies for the Freshwater Pearl Mussel, *Margaritifera margaritifera*, involving habitat restoration and release of captive-bred juveniles

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The Freshwater Pearl Mussel, *Margaritifera margaritifera*, is an endangered species with limited recruitment in global populations. Northern Ireland has six populations, none of which are recruiting. Collaborative work between Queen's University and the Ballinderry Fish Hatchery has created a successful captive rearing facility and has now begun trials to release juveniles into the river. Current work, reported here, tests mussel silos (Barnhart, Missouri State University) as an intermediate culture system for juvenile mussels prior to their release in the catchment. Silos containing three size classes (range: 4-21 mm) of captive-bred juveniles have been placed in two



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locations within the catchment. This study is ongoing but results to-date suggest differences in growth and survival between different size classes over a one year period. Possible reasons for these differences are considered in this presentation. Catchment restoration work by the Ballinderry Rivers Trust, aimed at reducing siltation has been ongoing in parallel with these experimental studies. It is necessary to reduce the levels of silt entering the river to increase the chances of success of releases and ultimately create a naturally recruiting population. Habitat restoration, which complements experimental releases, involves identifying key pressures and impacts in the catchment and addresses them using a combination of hard- and soft-engineering techniques involving the participation of riparian land owners and volunteers.



Restoration of an endangered *Unio tumidiformis* population

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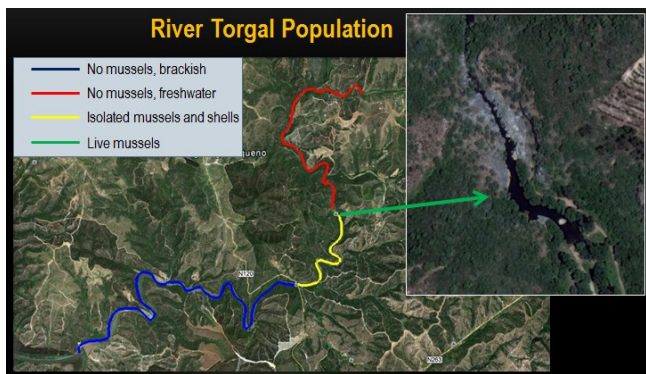
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The freshwater mussel *Unio tumidiformis* is an endangered Iberian species protected under the Habitats Directive. Under the scope of the Life+ project "ECOTONE - Management of riparian habitats towards the conservation of endangered invertebrates (LIFE10 NAT/PT/000073)", a population of this species located at the river Torgal, was targeted for restoration. The river Torgal (Mira basin, south-western Portugal) is a temporary Mediterranean-type stream, alder lined for much of its extent. A much localised community of unionids (*A. anatina*, *Potomida littoralis*, *U. delphinus* and *U. tumidiformis*) lives in the best preserved 750 m long reach of this river. Restoration of the river bed and banks has been performed during the course of the project, re-instating suitable habitat for freshwater mussels. At the same time, captive reared fish specimens belonging to the species *Squalius torgalensis*, the host for *Unio tumidiformis* glochidia, were used to reinforce the natural population. Likewise, captive reared juvenile mussels were introduced in the river to enhance its population abundance and range. It is expected that the actions taken will lead to a gradual expansion of the mussel species, ensuring the population's long term viability.



Chamber formation and calcification in the cuttlebone of *Sepia officinalis*

Antonio G. Checa¹, Julyan H.E. Cartwright², Francisco Ruiz Raya³ & Isabel Sánchez Almazo⁴

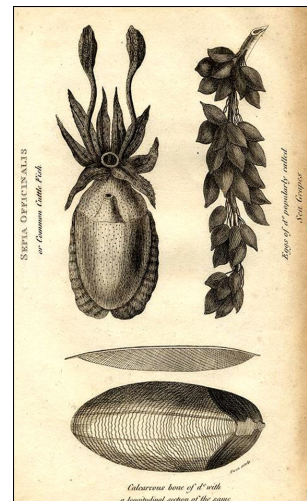
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The cuttlebone of the cephalopod genus *Sepia* is a notable buoyancy device with a complex structure. It is made of extensive superposed chambers limited by dorsal (roof) and ventral (floor) walls and with a complex internal arrangement of calcified pillars, and horizontal and vertical organic membranes. Current models of chamber formation imply that both the pillars and the membranes are accreted progressively with chamber growth. Our SEM and TEM data imply that: 1) the horizontal membranes usually observed are produced by the stacking of miriads of minor membranes filling in the whole chamber; each membrane is made of evenly oriented nanofibres, which are slightly rotated with respect to those of the preceding plane in the same direction, such that a spiral 3D arrangement is finally obtained; this pattern is consistent with the cholesteric phase of a liquid crystal. The same material composes the chamber floor, although fibres are much thicker here. 2) The horizontal membranes go uninterrupted across the pillars, which implies that membranes predate calcification. 3) Pillars and septa in the most recently formed chambers have been observed in different states of calcification, from almost fully organic (in juvenile specimens) to moderately calcified (in larger specimens). We propose a model for chamber formation in which the mantle secretes a chamber consisting on a mixture of chitin nanofibers and a viscous gel. At the same time, the organic precursors of the pillars are secreted. Immediately after, calcification of the chamber roof, pillars and floor proceeds, except at the siphonal area of the chamber. In summary, the whole structure is formed from an organic precursor via a liquid-crystalline phase.



Hypoxia-driven protein regulation in muscle tissue of jumbo squids during diel migration to the oxygen minimum zones

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The jumbo squid, *Dosidicus gigas*, an oceanic top predator in the eastern tropical Pacific undertakes diel vertical migrations into mesopelagic oxygen minimum zones (OMZs) using metabolic suppression. The underlying mechanisms of these migrations are poorly understood, as squid glycogen storage capacity is greatly limited and their diet is highly protein-dominated at well-oxygenated depths. Here, we exposed juvenile *D. gigas* to oxygen levels typically found in the OMZ off the Gulf of California (1 kPa at 10°C, 3h) to unravel potential energy sources and pathways via proteomic tools. In our study, concentration of transcription factor BTF3 was significantly decreased ($P < 0.05$) at hypoxia indicating reduced transcriptional initiation and protein synthesis - a strategy of metabolic suppression. Total protein concentration did not change under hypoxia ($P > 0.05$), meaning protein decomposition was blocked to retain structural integrity and ensure instantaneous recovery when O₂ becomes available again. Although some proteins were significantly less abundant ($P < 0.05$), namely: (1) heat-shock protein (Hsp) 90, (2) α -actinin, and (3) unidentified ($n = 6$), we suggest that α -actinin and other specific proteins might be degraded under hypoxia to support anaerobic ATP production via the ubiquitin-proteasome system - a process initiated by decreased protection of the Hsp90 chaperon machinery. Conversely, key metabolic enzymes involved or closely linked to glycolysis were significantly elevated ($P < 0.05$) (i.e. glyceraldehyde-3-phosphate dehydrogenase (GAPD), triosephosphate isomerase (TPI), octopine dehydrogenase, adenylate kinase isoenzyme) or developed hypoxia-induced isoforms (i.e. GAPD, TPI). These findings strongly suggest that under hypoxia, glycogen is the major energy provider of jumbo squids. However, the contribution of anaerobic protein degradation might increase under progressing hypoxia due to fast glycogen storage limitation and depletion. Moreover, reduction of locomotory performance is another well-known strategy of metabolic suppression to conserve energy. In *D. gigas* tropomyosin content was significantly elevated ($P < 0.05$) at hypoxia, resulting in reduced myosin binding sites (muscle contraction frequency) and therefore might favour its lethargic behavior under prolonged periods in OMZs. Our data suggest the presence of more hypoxia-regulated proteins but the current lack of database entries for cephalopods strongly limits protein identification and mapping.



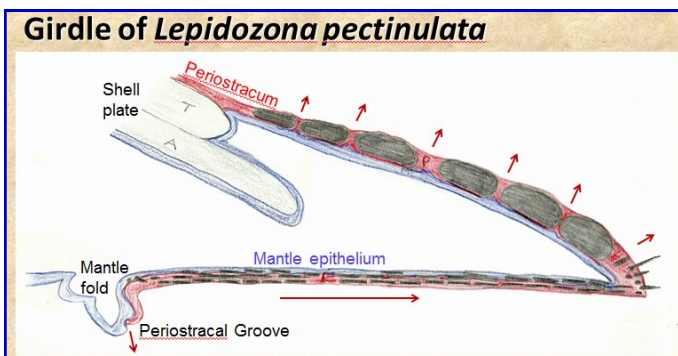
Periostracum of the chiton *Lepidozona pectinulata* and homology with the Bivalvia

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The extent of homology between polyplacophoran and conchiferan molluscs in the fine morphology and mineralisation of the periostracum is not well known. To obtain evidence useful in testing hypotheses of homology, we examined the periostracum and embedded aragonitic spines and scales in the chiton *Lepidozona pectinulata* from California, USA. The periostracal groove was unexpectedly found on the ventral side of the animal, near the mantle cavity, not dorsal as suggested by previous authors. The fine-scale structure of the periostracum and location of the periostracal groove relative to the scleritome in *L. pectinulata* are similar to what occur in the Bivalvia: the periostracum in both contains a thin dark layer and thick, laminated translucent layer; and all the calcareous elements are dorsal with respect to the direction of extrusion of the periostracum.



But there are also apparent differences in the periostracum of *L. pectinulata* and bivalves: the embedded calcareous structures are more diverse in morphology and mode of formation in chitons than in bivalves; and the chiton periostracum lacks a tough outer pellicle. Plus we have yet to find in *L. pectinulata* any bivalve-like infolded basal cell at the point of origin of the periostracum, although additional thin sections are needed to confirm this preliminary conclusion. Gastropods likewise seem to lack a basal cell. Future tasks include TEM observations of representatives of the other two chiton suborders, with an eventual goal of determining common features of the periostracum throughout the Class Polyplacophora.

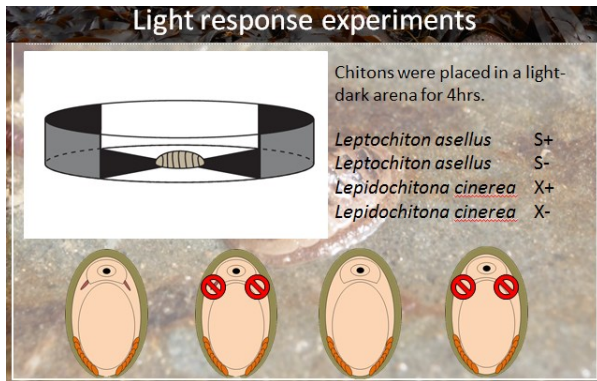


Chitons (Polyplacophora: Lepidopleurida) that live in the dark can see light

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Chitons are benthic marine molluscs which are found globally from the shore to the abyss. There are two living orders of chitons, Chitonida and Lepidopleurida, of which the former is considered to be the more derived. A new sensory structure, the "Schwabe organ", has recently been discovered in some species. It is clearly visible in living animals as a pair of brownish pigmented streaks either side of the mouth. The Schwabe organ is found throughout Lepidopleurida but entirely absent in Chitonida, representing a novel synapomorphy for this clade. Species within Lepidopleurida are largely found in deep sea habitats, with only a few shallow water species. Anatomical studies of the Schwabe organ using histology and electron microscopy have confirmed the sensory nature of the epithelium in this region. Of particular interest is a concentrated dot of

pigment within the Schwabe organ. This dot is positionally homologous to the larval eye, a photoreceptive structure present in all chiton larvae. Using species from the two clades, one with and one without a Schwabe organ, we studied phototactic behaviour in both intact specimens and those with the Schwabe organ (or corresponding region) ablated. Subjects were placed in an arena with two quarters exposed to upwelling light and two quarters in darkness, and their movements were recorded over four hours. Lepidopleurida with an intact Schwabe organ actively avoided upwelling light, spending a significantly higher proportion of their time in darkness, whereas Chitonida and ablated Lepidopleurida did not. Similarly, those with an intact Schwabe organ were significantly more likely than the other three groups to settle in a dark area for an hour or more. These results suggest that the Schwabe organ plays a role in light response behaviours, which is particularly curious given the general deep-sea habitat of lepidopleurans. Electrophysiological work and a pigment characterisation study are also ongoing to complement and confirm our behavioural experiments, and some preliminary results are reported here. Discovering the role of the Schwabe organ will help us understand how these ancient organisms see their world, and why a group of deep-sea chitons should need to see at all.



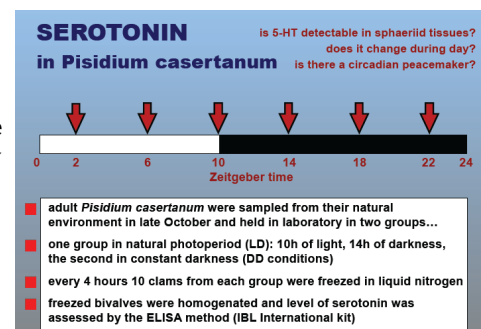
The probable circadian rhythms in serotonin levels in hemolymph of *Unio tumidus* and tissues of *Pisidium casertanum*

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Light is regarded as the strongest zeitgeber for biological rhythms in organisms. Body of bivalves is usually light protected by their shell; furthermore, semi burrowing bivalves live buried within the deposits, nevertheless they may have a simple photoreceptors (nerve endings) within their tentacles on incurrent aperture. Photoreceptors of organisms drive the light information to the nervous system, eg. by the serotonergic nerves. Serotonin levels in hemolymph of the marine gastropod *Aplysia* are regulated by light-dark conditions. Little is known if unionoids or sphaerids do recognize the light signals and have a light-depending rhythmicity in serotonin levels. We conducted two preliminary experiments: 1) *Unio tumidus* were kept in situ in lake littoral in natural photoperiod, LD conditions (12h of light and 12h of darkness); every 4 hours hemolymph was isolated from 5 adults. 2) *Pisidium casertanum* were sampled from their natural environment and held in laboratory, in natural photoperiod in LD conditions (10h of light and 14h of darkness) or in constant darkness (DD conditions). Every 4 hours 10 bivalves from each group were frozen in liquid nitrogen, then tissues were homogenated. The level of serotonin was assessed by the ELISA method. For the first time we demonstrate a possible circadian rhythm of serotonin level in hemolymph in *U. tumidus*. We observe lower levels of serotonin during the light phase of the day, and about double higher levels in the darkness. We can't recognize if the changes of serotonin level were driven by the light/dark cycles, or are the effect of biological clock. We demonstrate circadian rhythms in serotonin levels in tissues of *P. casertanum*. In LD conditions we show the highest levels of serotonin during late light phase of the day, and low during darkness and beginning of light phase. Furthermore in DD conditions we observe a 4 hours shift of the maximum serotonin level - highest levels of serotonin are at the beginning of subjective darkness and low during subjective darkness and subjective light phase. We believe rhythms in serotonin levels in *P. casertanum* are regulated by the endogenous biological clock as they are sustained in the constant darkness.



Comparative microscopy study of the digestive gland in cephalaspideans (Gastropoda, Euopisthobranchia)

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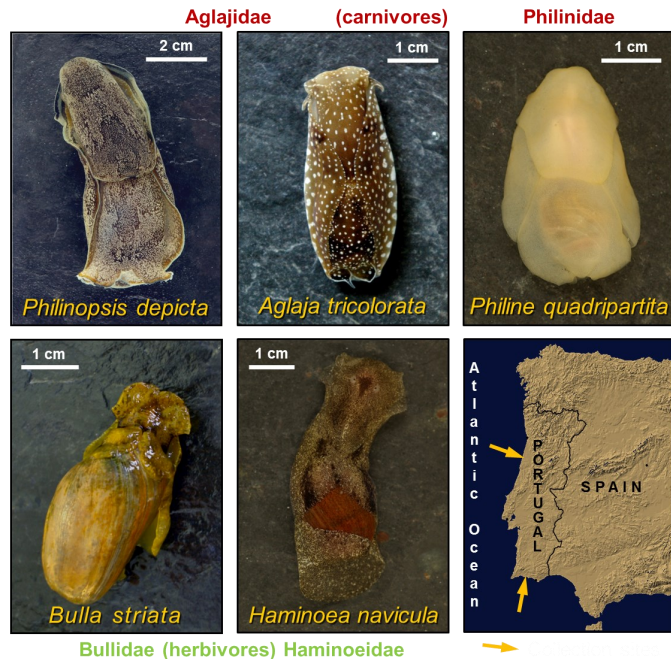
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The digestive gland is a major organ of the digestive system of molluscs, consisting of blind ending tubules formed by digestive and basophilic cells, with additional cell types in some gastropods. The digestive gland of cephalaspideans was investigated with light and electron microscopy methods in two herbivores (*Bulla striata* and *Haminoea navicula*) and three carnivores (*Philine quadripartita*, *Aglaja tricolorata* and *Philinopsis depicta*). Digestive cells presented an intense endocytic activity, revealed by cell membrane pits, many vesicles and endosomes at the cell apex. With the pyroantimonate method, calcium was detected in endocytic vesicles and in endosomes, but not in lysosomes. In these cells, very large lysosomes seem to result from the fusion of smaller ones. Arylsulphatase activity was detected in smaller electron-dense lysosomes and in the large vacuole-like ones. Basophilic cells are typical protein secreting cells, but contained many vacuoles with electron-dense inclusions. Calcium was also detected in these vacuoles using the pyroantimonate method. Peroxisomes are abundant in basophilic cells, and in *P. depicta* these organelles reached about 5µm being among the biggest ever reported. The digestive gland of *P. depicta* and *A. tricolorata* contained mucous cells. Differences between herbivores and carnivores were not evident in the digestive gland of cephalaspideans.

Samples

Digestive gland samples were fixed with glutaraldehyde and formaldehyde, postfixed with OsO₄, dehydrated and embedded in Epon.



Assessment of certain food preservatives on biological and biochemical parameters of *Biomphalaria alexandrina* snails, as a biological model

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The present investigation was designed to evaluate the effect of food preservatives sodium metabisulphate (SMS) and potassium metabisulphate (KMS) on biological and biochemical activity of the medically important snails *Biomphalaria alexandrina* as a biological model. The activities of four vital enzymes, the total protein (TP) and albumin were laboratory tested; the four vital enzymes were alkaline phosphates, acid phosphates, aspartate amino transaminase and alkaline amino transaminase. Results showed that the survival rate of *B. alexandrina* snails exposed to concentrations of LC₁₀ and LC₂₅ of KMS was 24% and 4% respectively at the 4th week of exposure compared with controls (90%). A marked increase of deposited eggs (32, 18.7eggs/snail/week) was recorded at the 3rd and 4th weeks of exposure to KMS LC₁₀ compared with the control (4.27, 4.7 eggs/snail/week). The egg production of snails exposed to LC₂₅ of KMS completely inhibited. The infection rate of *B. alexandrina* snails exposed to KMS LC₂₅ concentrations for four weeks was significantly lower than that of control group being 11.8 % and 58%, respectively. Cercarial production increased significantly, being 5199 and 5183 cercariae/snail exposed to LC₁₀ and LC₂₅ of SMS compared with 1921 cercariae/control infected snail. The results also revealed that all the tested chemicals increased the activity of alkaline phosphates and decreased the activity of aspartate amino transaminase in both tissue and haemolymph of tested snails. On the other hand, the level of total protein and albumin decreased after treatment with the test chemicals. In general, the two chemicals significantly affected the activities of enzymes, total lipids and total protein compared with control treatment.



Somatic diversification of immune factors in *Biomphalaria glabrata* (Hydrophila: Planorbidae), insights from targeted approaches and genome assembly

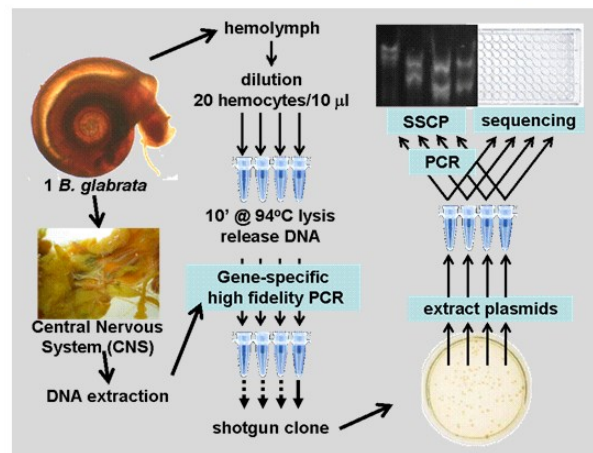
Coen M Adema¹, Christoph Grunau² and Milind Misra¹

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²CNRS Ecologie et Evolution des Interactions (2EI), University Perpignan, France

Fibrinogen-related proteins (FREPs) are prominent components of anti-parasite responses in the fresh water gastropod *Biomphalaria glabrata*. Somatic diversification generates extensive diversity of FREP sequences among and within individual *B. glabrata*. FREPs complex with polymorphic antigens from intramolluscan larval parasites in a manner thought to facilitate non-self recognition. RNAi knockdown alters *B. glabrata* resistance phenotypes. Investigations of mechanisms for FREP diversification benefit increasingly from next generation sequence (NGS) data, including the genome sequence from *B. glabrata*. The genome assembly reveals abundant FREP sequences, with intact genes and gene fragments, often arranged in tandem. Mapping of RNAseq-reads to the assembly provides indication of further sequence diversification. Targeted PCR and amplicon sequencing from hemocyte subsets reveals sequence diversity among some immune factors (lectins, FREPs) relative to others (PGRP, GNBP) and housekeeping genes (CO1 and eIF2alpha) in each of four *B. glabrata* strains tested. Specific targeting of diversification suggests possible involvement of cytidine deaminase-like enzymes to effect somatic mutation. Alternatively, diversification may be regulated epigenetically: some affected genes have high CpG content and DNA methylation (present in *B. glabrata*) marks cytosines of CpG dinucleotides for spontaneous mutation. Genome analysis identifies potential candidate genes for study of mechanisms for somatic diversification and the role of diversification in immunity of *B. glabrata*.

DETECTION OF SEQUENCE DIVERSITY WITHIN HEMOCYTE SUBSETS AND CNS OF *B. glabrata*



The genome of *Biomphalaria glabrata* (Gastropoda, Mollusca) and the data base VectorBase

Daniel Lawson¹, Gloria I. Giraldo-Calderón², Coenraad M. Adema³, Patrick Minx⁴, Scott J. Emrich², Frank H. Collins² and the members of the VectorBase consortium and the international *Biomphalaria glabrata* Genome Initiative

¹European Molecular Biology Laboratory (EMBL) - European Bioinformatics Institute (EBI), Hinxton, Cambridge, United Kingdom

²Department of Biological Sciences, University of Notre Dame, Notre Dame, Indiana, USA

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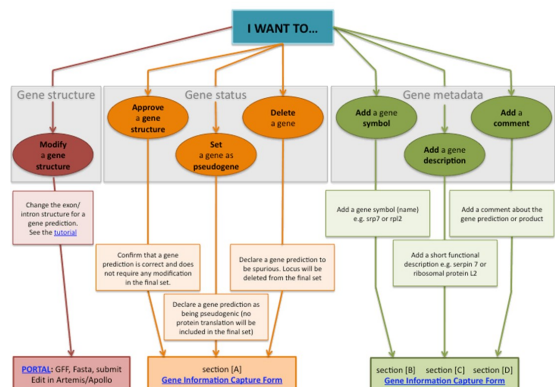
⁴The Genome Institute at Washington University, Washington University School of Medicine, Saint Louis, Missouri, USA



VectorBase is a Bioinformatics Resource Centre that hosts the genomes of invertebrates that transmit human parasites and pathogens, such as the malaria mosquito *Anopheles gambiae* and the snail *Biomphalaria glabrata*, a major intermediate host of *Schistosoma mansoni*. VectorBase data, tools and resources are updated and expanded every two months. The tools include VectorBase Blast, ClustalW, Hmmer, BioMart, Galaxy, Web Apollo and the Genome, Ontology, Expression and Population Biology browsers. In 2013, while increasing the number of hosted genomes from 11 to 30, VectorBase made available the genome assembly of BB02 strain *B. glabrata*, providing an the updated BglaB1.1 predicted gene set in February 2014. For details of this resource for study of molluscan biology please follow this link:

www.vectorbase.org/organisms/biomphalaria-glabrata

You are very welcome to submit sequence data for any field or laboratory study related to this or any other genome hosted at VectorBase. Once you have deposited your data in public repositories such as EMBL/EBI, GenBank/NCBI or the DDBJ, please let us know to make it also available in VectorBase. For submission of non-sequence data please contact us. If you have any questions or were not able to meet with us for a demo, or need more help please send us your questions, comments or feedback to info@vectorbase.org



Modulation of *Biomphalaria glabrata* immunity by excretory-secretory products of invading *Schistosoma mansoni*

Zahida Zahoor^{1,2}, Anne E Lockyer^{2,3}, Angela J Davies¹, Ruth S Kirk¹, Aidan M Emery², David Rollinson², Catherine S Jones³, Leslie R Noble³ and Anthony J Walker¹

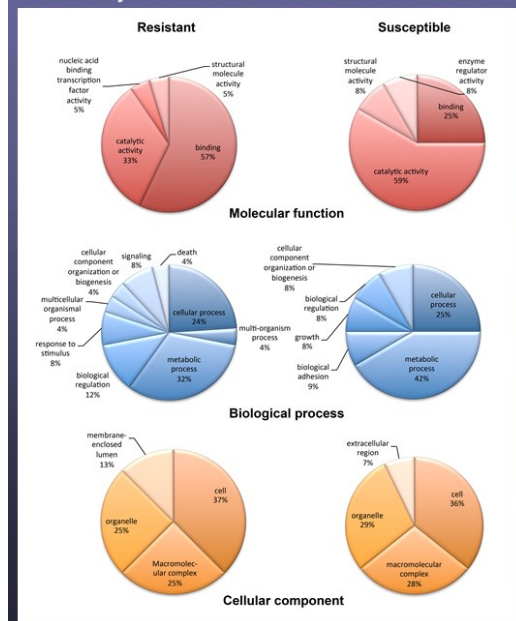
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The freshwater gastropod, *Biomphalaria glabrata*, is intermediate host to *Schistosoma mansoni* an important intravascular parasite of humans. Upon penetration of *B. glabrata*, the schistosome parasite transforms from a miracidium to a mother sporocyst. During this early post-embryonic larval development, excretory-secretory products (ESPs) are produced by the parasite that interact with host defence cells (haemocytes) and modulate their physiology and behavior. Using *B. glabrata* strains that are either resistant or susceptible to *S. mansoni* it has been possible to unravel some of the molecular interactions and responses to ESPs in the context of snail host phenotype. Thus, ESPs have been found to differentially influence the activities of the extracellular signal-regulated kinase pathway, nitric oxide output, and heat shock protein 70 levels in haemocytes from the resistant and susceptible strains. Here we further demonstrate using a 5K *B. glabrata* cDNA microarray that 98 genes were differentially expressed between haemocytes of these snail strains when exposed to 20 mg/ml ESPs for 1 hour *in vitro*; these comprised 57 resistant-specific and 41 susceptible-specific genes. Comparative analyses with other gene expression studies revealed 38 of the 98 genes to be uniquely differentially expressed in haemocytes in the presence of ESPs thus identifying ESPs as important molecules that influence global host snail haemocyte gene expression profiles. Such effects might influence the outcome of infection by the schistosome parasite enabling it to survive and reproduce asexually in the snail.

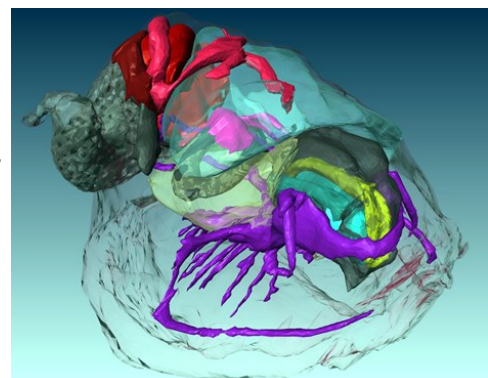
Gene Ontologies for Differentially Expressed Haemocyte Genes that Possessed GO Matches



The heart of a dragon: extraordinary circulatory system of the scaly-foot gastropod revealed

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The scaly-foot gastropod, endemic to deep-sea hydrothermal vents in the Indian Ocean, is famous and unique among gastropods for its numerous dermal sclerites, which are often mineralised with iron sulphide. It inhabits a harsh environment, living close to highly acidic hydrothermal vent effluents on diffuse-flow sites and on the walls of "black smoker" vent chimneys. This study investigated the anatomical adaptations of these animals to life in an extreme environment. One of the smallest specimens ever collected (juvenile, shell length: 3 mm) was embedded whole and serially sectioned into 1.5 µm semi-thin slices. A tomographic model was reconstructed with the specialist 3-D modelling software AMIRA, to visualise whole organ systems and anatomical structures. This revealed a large nervous system without distinct ganglia, and a simple and reduced digestive system, but of particular interest is the circulatory system. The animal has a large ctenidium supported by extensive blood sinuses filled with haemocoel, posterior to which is a remarkably large and well-developed heart (approx. 0.5 x 0.5 x 0.4 mm). Based on the volume of the auricle and ventricle, the heart complex represents approximately 4% of the body mass. For nutrition, these animals are known to rely primarily on endosymbiotic bacteria housed in a greatly enlarged oesophageal gland (over 9% body mass in the specimen investigated). New insights from this juvenile specimen indicate this is true throughout post-settlement life. The oesophageal gland is highly vascularised, and thus we infer the elaborate cardiovascular system most likely evolved to oxygenate the endosymbionts in an oxygen poor environment and to provide the animal with nutrition to survive in its extreme conditions. As a result, this dramatic dragon-like animal has become a simple carrying vessel for its bacteria.



MolluscaBase – announcing a World Register of all Molluscs

Ruud A. Bank¹, Rüdiger Bieler², Phillipe Bouchet³, Wim Decock⁴, Stefanie Dekeyzer⁴, **Serge Gofas**⁵, Andreas Kroh⁶, Bruce Marshall⁷, Thomas A. Neubauer⁶, Eike Neubert⁸, Gary Rosenberg⁹, André F. Sartori³, Simon Schneider¹⁰, Aina Trias-Verbeek⁴, Leen Vandepitte⁴ and Bart Vanhoorne⁴

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The Mollusca, second largest phylum on Earth, lacks a global listing of valid names or even precise figures for the number of Recent species. The launching of MolluscaBase is intended to fill this gap, expanding the contents of the World Register of Marine Species (WoRMS) to include all marine, freshwater and terrestrial molluscs, recent and fossil. The WoRMS database, hosted at the Flanders Marine Institute (VLIZ) at Oostende, had more than 1,000,000 unique visitors in 2013 and provides the taxonomic backbone for initiatives such as Encyclopedia of Life, Catalogue of Life, and others. It currently contains more than 44,000 valid species names of Recent marine Mollusca, which are estimated to represent approximately 95% of all valid species. There is no similar global list of the freshwater and terrestrial Mollusca. It is estimated that there are about 23,000 species of land snails/slugs and about 5,000 freshwater gastropods and bivalves. The number of named fossil Mollusca is not known, but is in the same order of magni-

tude as that of Recent species. MolluscaBase is intended as an authoritative taxonomic database, relying only on published sources and built by taxonomic editors who are active malacologists and respond to feedback from users. As in WoRMS, the content should include Taxonomic hierarchy, Current name and synonymy, Literature sources, Distributions (using countries as the basic unit for land-based distributions), Fossil range (expressed in terms of the international chronostratigraphic chart) and other taxon attributes. This initiative is supported by LifeWatch, the E-Science European Infrastructure for Biodiversity and Ecosystem Research. In a first move, MolluscaBase will build on the existing WoRMS contents incorporating the contents of existing initiatives like CLEMAM (Checklist of European Marine Mollusca), FreshGEN (Freshwater Gastropods of the European Neogene) and Fauna Europaea. The long term goal of filling the gaps in non-marine and fossil components of MolluscaBase needs your support! If you are a taxonomist, specialising in any group of non-marine or extinct molluscs, and wish to become a contributor to MolluscaBase, please let us know and contact the WoRMS team at info@marinespecies.org, or the corresponding author, to find your possible role in MolluscaBase!



Conservation of European Freshwater Mussels: Historical Background, Challenges and Future Perspectives

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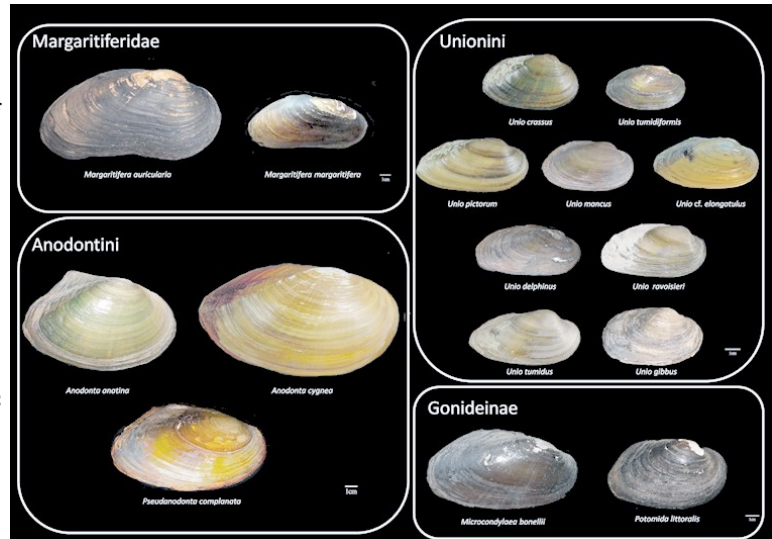
David C. Aldridge; Rafael Araujo; Jakob Bergengren; Yulia Beshpalaja; Erika Bódis; Lyubov Burlakova; Dirk Van Damme; Karel Douda; Elsa Froufe; Dilian Georgiev; Clemens Gumpinger; Alexander Karatayev; Ümit Kebapçı; Ian Killeen; Jasna Lajtner; Bjørn M. Larsen; Rosaria Lauceri; Anastasios Legakis; Sabela Lois; Stefan Lundberg; Evelyn Moorkens; Gregory Motte; Karl-Otto Nagel; Paz Ondina; Adolfo Outeiro; Momir Paunovic; Vincent Prié; Ted von Proschwitz; Nicoletta Riccardi; Mudite Rudzite; Māris Rudzītis; Christian SCHEDER; Mary Seddon; Hülya Şereflifşan; Vladica Simić; Svetlana Sokolova; Katharina Stoeckl; Jouni Taskinen; Amílcar Teixeira; Frankie Thielen; Teodora Trichkova; Simone Varandas; Heinrich Vicentini; Katarzyna Zajac; Tadeusz Zajac; Stamatis Zogaris

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Freshwater bivalves of the Superfamily Unionoidea provide important ecosystem functions and services, yet many of their populations are in decline. Here, we comprehensively review the status of all of the currently described species in Europe, collating for the first time their life history traits, distribution, conservation status, habitat preferences and main threats in order to suggest future management actions. Sixteen species are presently described in Europe. In northern, central and eastern Europe a relatively homogeneous species composition is found in most basins. In southern Europe, despite of the

lower species richness per basin, distinct and spatially restricted species occur which make them a high conservation priority. Information on the current status and habitat requirements of unionoids in Europe is very unevenly distributed with considerable differences in data quality and quantity across countries and between species. Rather detailed information is available for flagship species such as the freshwater pearl mussel (*Margaritifera margaritifera*) while much less is known of other species such as *Unio gibbus* and *Microcondylaea bonellii*, where even the host fishes remain unclear. Conservation efforts need to address declines of widespread species such as *M. margaritifera* and *Unio crassus*, as well as the maintenance and restoration of habitats of spatially restricted species such as several *Unio* spp. in southern Europe. In order to make conservation more effective in the future, we suggest a more standardized approach, with higher international co-operation using similar protocols and methods, to monitor and manage European freshwater bivalve diversity. Such an approach will not only help conserve this vulnerable taxon but also, through the protection of these important ecosystem engineers, will offer wider benefits to freshwater ecosystems.



Strange snails indeed: Swash-Surfers, Self-Mutilators, Wave-Combers and Cannibals that dominate Panamic sandy beaches

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The intertidal macrofauna of many sandy beaches in the Panamic faunal province (American west coast from Baja California to North Peru) is numerically dominated by a small number of olivid species (families Olividae and Olivellidae, Caenogastropoda) which exhibit a fascinating multitude of unique behavioural and morphological adaptations to their demanding habitat. *Olivella semistriata* and *O. columellaris*, sister species that have been confused in all (!) papers addressing their ecology so far, have powerful appendages of the propodium which deploy and suspend mucus sheets to capture particles from the backwash. As the backwash zone moves with the tides, so do the snails, using parts of their body as underwater sails. *O. semistriata* is the main prey of *Agaronia propatula* which is aptly described as an *Oliva* adapted to life in the intertidal. Being a swash-surfer itself, *A. propatula* leaves its intertidal hunting grounds with sunset, probably to avoid a yet unidentified predator that also may be the evolutionary driving force behind the snail's habit of shedding parts of its foot when irritated (autotomy). *A. propatula* is the quintessential opportunistic predator, and is not shy of attacking artificial objects or human fingers. It will happily prey on conspecifics; since the success of cannibalistic attacks strictly depends on the size ratio between cannibal and conspecific prey, *A. propatula* forms size-structured populations in which size classes function as 'ecological species' with distinct trophic roles. On the other hand, *O. semistriata* applies various unusual modes of locomotion to escape aggressive *A. propatula*, including serial jumps on exposed sediment and active swimming when submerged. We will present the various types of behaviour - most of them for the first time - in movies taken in the wild, and discuss their evolution and ecological function. As a result, we will criticize and question established wisdom about swash-surfing snails, specifically the notions (1) that tidal migration is the main purpose of and context in which swash-surfing evolved, (2) that swash-surfers steer towards resources guided by olfactory clues, and (3) that swash-surfers would benefit and therefore can be expected to possess biological clocks aligned with the tidal cycle.



Closing lecture

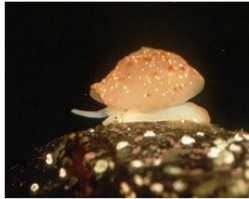
Marine molluscs at high latitude

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High latitude marine environments pose a range of challenges and possibilities for marine organisms. The primary factors studied are low temperature and seasonality, although acidification has received significant attention in recent years. The low temperature and highly seasonal environment, with the presence of ice in various forms, low carbonate saturation compared to other latitudes, and higher viscosity constrains organisms in many ways, but also has some advantages over warmer, temperate and tropical habitats. These constraints and opportunities are discussed in this lecture, using molluscs as the group to highlight adaptations and limitations.



Abstracts

... of poster presentations

Distribution and morphological variation of *Thalessa savignyi* and *Ergalatax junionae* (Gastropoda: Muricidae) from rocky shores of Kuwait

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Thalessa savignyi and *Ergalatax junionae* are two predatory gastropods common along the intertidal rocky shores of the state of Kuwait. Little is known about the factors affecting their distribution in the region. This study investigates whether the variation in abiotic factors affects the population distribution, abundance and morphological differences in both species latitudinally, seasonally and intertidally across the shore. Three different areas (Ra's Ajūzah, Ra's Eqaila and Ra's al Qulay'ah (about 30 Km apart)) were chosen and surveyed at three different shore heights. Sampling was carried every three months between May 2012 to January 2013 to cover the various periods of warm and cooler seawater temperature of the four seasons. At each time, quadrats (25×25cm) and timed searches were used to estimate the density and abundance of each species. The pattern of distribution and abundance were examined in relation to season, topography of the substratum and time of exposure. Morphometric measurements also were taken to observe allometric variation. Shell length, width and aperture length were obtained to examine the allometric relationships. There were little geographic and local fluctuations in the abundance and distribution for both species. There was however, a dramatic seasonal variation. The presence of large boulders and associated fissures in the southern sites were more suitable to occupy by *T. savignyi* populations while small boulders and crevices in the northern sites were preferred by *E. junionae*. The relationship between shells dimensions in *T. savignyi* was isometric except for Ra's al Qulay'ah where negative allometry was observed. Also, *E. junionae* shells showed isometric relationships for all studied sites except for Ra's Eqaila. The evidence presented in this study suggests that variations in both species are directly related to environmental causes.



Genetic population structure in *Nacella magellanica*: evidence of rapid range expansion throughout its entire species range on the Atlantic coast

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Nacella magellanica is the most abundant limpet in the biogeographic Magellanic Province of Argentina and Chile; it is characterised by a noticeable variability in shell morphology and color patterns. Ecological as well as evolutionary features make this limpet an interesting species for evolutionary and population genetic studies. Here, arbitrary nuclear molecular markers, Inter-Simple Sequence Repeat-PCR, are used to analyze the population genetic structure in 14 localities of *N. magellanica* along 2,900km in the Atlantic coast of the Magellanic Province. We compare the present results, based on nuclear markers, with those from a previous phylogeographic study using the mitochondrial COI gene. The values of the Polymorphism Information Content and the Marker Index were relatively low, probably due to a high level of polymorphism homogeneously distributed over the sampling area. All the results presented here suggest little genetic structure within *N. magellanica*, with moderate to high genetic connectivity among its populations. The short time lapse since the expansion of this species plus a possible long lifespan for larva and the oceanographic and environmental conditions of the Magellanic Province, could explain the lack of genetic structuring and the low levels of genetic differentiation in the species over its entire distribution range in the Argentinean coast.



Sculpture characters of the shells of *Cornisepta* (Mollusca: Gastropoda: Fissurellidae) from the northeast Atlantic Ocean

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The family Fissurellidae includes prosobranch gastropods of rocky habitats, from the foreshore to the deep sea. They are characterized by a conical and patelliform shell with a wide aperture and an apical, subapical or marginal foramen. The family classification is only based on morphological characters and is highly discrepant, including from two to five subfamilies, so a broader study of Fissurellidae species is necessary to improve the understanding of this family. The genus *Cornisepta* McLean & Geiger, 1998 comprises fourteen species located all over the world, of which only four are cited in the Atlantic Ocean. In this communication, specimens of the genus *Cornisepta* from the NorthEast Atlantic Ocean are described, from a total of 584 specimens and tree different species: *Cornisepta crossei* (Dautzenberg & Fischer, 1896), *Cornisepta microphyma* (Dautzenberg & Fischer, 1896) and *Cornisepta* sp. The material was collected through French and Spanish excursions and specimens were found in different Banks from NE Atlantic (Galicia, Atlantis, Hyeres, Plato and Irving Banks) and in the drop-off of the Galician coast, between 650 and 1191 m at depth. The type material of *Cornisepta crossei* and *Cornisepta microphyma* was lent by the Oceanographic Museum of Monaco and was included in this study. A detailed X-ray tomography (Micro-CT) and SEM study of the shells of these species is presented, redescribing characters of the sculpture, such as the form of the pustules, their distribution and their density among others. Also, a comparative study with the rest of species of the genus *Cornisepta* is presented. The results of this study provide new data about *Cornisepta* species and their diagnostic characters.



Rissoidea Species Distributed Along the Turkish Levantine Coast

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The aim of this study was to determine the taxonomical, ecological and distributional features of Rissoidea species distributed along the Turkish Levantine coast. The investigated material was collected within the frame of various research projects conducted in the area between the years 2005 and 2011. The faunistic analysis of the benthic samples, taken from various biotopes at depths between 0-200 m in 83 stations, revealed 40 Rissoidea species and 7068 specimens belonging to 7 families (Rissoidea, Barleeidae, Caecidae, Hydrobiidae, Irvadiidae, Tornidae and Truncatellidae). Among the identified species, *Alvania mamillata* Risso, 1826, *Alvania testae* (Aradas Maggiore, 1844), *Pusillina lineolata* (Michaud, 1830), *Setia fusca* (Philippi, 1844), *Obtusella macilenta* (Monterosato, 1880), *Hyala vitrea* (Montagu, 1803) and *Circulus striatus* (Philippi, 1836) are new records for the Turkish Levantine coast. Some ecological and distributional characteristics of the determined species are also provided.



Alcohol dehydrogenases and oxidases in the digestive gland of gastropods

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Alcohol dehydrogenases are enzymes that convert alcohols into aldehydes or ketones, reducing NAD⁺ to NADH. Alcohol oxidases also convert alcohols into aldehydes, but using molecular oxygen as the hydrogen acceptor. These enzymes have been thoroughly investigated in mammals, fungi, plants and bacteria, but much less so in molluscs. In this work, dehydrogenases and oxidases were assayed with spectrophotometric methods in gastropod digestive gland homogenates using mannitol, sorbitol, cinnamyl alcohol, ethanol and methanol as substrates. Mannitol oxidase activity was high in the digestive gland of the herbivorous heterobranchs *Aplysia depilans*, *Cornu aspersum* (= *Helix aspersa*) and *Arion ater*. Moreover, this enzyme was detected for the first time in the digestive gland of herbivorous caenogastropods (*Littorina littorea*, *Marisa cornuarietis*, *Pomacea bridgesii*) and also in the herbivorous heterobranchs *Siphonaria pectinata*, *Bulla striata* and *Planorbarius corneus*. This enzyme was not detected in the digestive gland of carnivorous gastropods nor in the herbivores *Patella vulgata* (Patellogastropoda) and *Phorcus lineatus* (Vetigastropoda). Additionally, mannitol and sorbitol dehydrogenase activities were detected in digestive glands. High oxidase and dehydrogenase activities were recorded with the aromatic cinnamyl alcohol in all species tested so far. Few species showed activities with ethanol, and none with methanol. These enzymes were also detected by gel electrophoresis.



Molecular phylogeny of the land snail genus *Candidula* (Pulmonata: Helicoidea), based on a genomic multi-marker approach

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Candidula Kobelt, 1871, is a land snail genus distributed across Western Europe and Northwest Africa, with two important disjunct centres of diversity in the Iberian and the Italian Peninsulas. The genus contains 24 species, some of them presenting wide distribution ranges, while others have narrow distributions. Anatomically, the genus is characterized by the presence of one relatively large dart-sac, placed close to the vagina, and two or three bifurcated mucous glands. However, the phylogenetic relationships within *Candidula* are not clear due to the simplicity of its reproductive system. Using the transcriptomes obtained from three *Candidula* species (*C. gigaxii*, *C. rugosiuscula* and *C. unifasciata*), we developed new primer pairs for eight nuclear markers valid for all *Candidula* species. In this work, we show a molecular phylogeny based on DNA sequences of these new eight nuclear markers, together with another nuclear gene fragment, *internal transcribed spacer 2*, and one mitochondrial gene fragment, *cytochrome oxidase subunit one*. The study includes 21 species from all distribution range of the genus. Main phylogroups obtained correspond to the geographic distribution of species.



The use of Micro-CT vs classical histological techniques in the study of the internal anatomy of Solenogastres

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Despite the progress made in the last decades the knowledge of the class Solenogastres is still limited. Among other reasons, the organization of the class, based mainly on internal anatomic characters, requires the use of invasive histological techniques which are challenging and time consuming. Additionally, most of the species are described from a single specimen, so a technique that allows the study of the internal anatomy and the preservation of the specimens would be advantageous. X-ray tomography (Micro-CT) is a promising new technique to examine soft-tissue anatomy creating 2D and 3D virtual models. One of its important advantages is the possibility of a non-destructive investigation of internal structures, although it is sometimes difficult to interpret the images correctly. In this contribution, the internal anatomy of two specimens of *Dorymenia* Heath, 1911 (Mollusca, Solenogastres) was studied, using classical histological techniques and Micro-CT in order to compare both techniques, and find the advantages and disadvantages of each other in the study of Solenogastres.



Wider sampling reveals a non-sister relationship for geographically contiguous lineages of a marine mussel

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The accuracy of phylogenetic inference can be significantly improved by the addition of more taxa and by increasing the spatial coverage of sampling. In previous studies, the brown mussel *Perna perna* showed a sister lineage relationship between eastern and western individuals contiguously distributed along the South African coastline. We used mitochondrial (COI) and nuclear (ITS) sequence data to further analyze phylogeographic patterns within *P. perna*. Significant expansion of the geographical coverage revealed an unexpected pattern. The western South African lineage shared the most recent common ancestor (MRCA) with specimens from Angola, Venezuela and Namibia, whereas eastern South African specimens and Mozambique grouped together, indicating a non-sister relationship for the two South African lineages. Two plausible biogeographic scenarios to explain their origin were both supported by the hypotheses-testing analysis. One includes an Indo-Pacific origin for *P. perna*, dispersal into the Mediterranean and Atlantic through the Tethys seaway, followed by recent secondary contact after southward expansion of the western and eastern South African lineages. The other scenario (Out of South Africa) suggests an ancient vicariant divergence of the two lineages followed by their northward expansion. Nevertheless, the “Out of South Africa” hypothesis would require a more ancient divergence between the two lineages. Instead, our estimates indicated that they diverged very recently (310 kyr), providing a better support for an Indo-Pacific origin of the two South African lineages. The arrival of the MRCA of *P. perna* in Brazil was estimated at 10 [0-40] kyr. Thus, the hypothesis of a recent introduction in Brazil through hull fouling in wooden vessels involved in the transatlantic itineraries of the slave trade did not receive strong support, but given the range for this estimate, it could not be discarded. Wider geographic sampling of marine organisms shows that lineages with contiguous distributions need not share a common ancestry.

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Hidden biodiversity of Antarctic *Marseniopsis* (Velutinidae)

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Marseniopsis Bergh, 1886 is a genus of marine gastropods (Velutinidae) which includes nine described species, eight of which endemic to Antarctica. This genus is known to feed on tunicates and is characterized by a peculiar planktotrophic larva, the “limacosphaera”, with a potentially long pelagic life, which is a rare developmental strategy for Antarctic gastropods. In the framework of recent scientific expeditions held in the Ross Sea, at the tip of the Antarctic Peninsula and in the Weddell sector, a special effort was made to document with digital pictures the colour pattern of the different species routinely encountered during sampling activities. Thanks to this live-collected new material, several different colour patterns, within and amongst presumed conspecific samples, were documented, suggesting the existence of at least a partially underestimated diversity. Based on this unprecedented large sampling, our aim was to define the actual diversity of the Antarctic *Marseniopsis*, including the identification of cryptic species through an integrative taxonomy approach. Our dataset included 78 COI barcode sequences, out of which 21 originate from 18 sampling sites in the Ross Sea and other 57 from 13 sampling sites in the Weddell Sea- Antarctic Peninsula. Through genetic distances, we identified 13 MOTUs, 9 of which exclusively from the Weddell Sea-Antarctic Peninsula and four occurring also in the Ross sea. Automatic Barcode Gap Discovery (ABGD) analysis confirmed the same samples partition and identified a barcoding gap around 2% of genetic distance. The isolation-by-distance analysis did not show any significant correlation between genetic and geographic distances among populations of each clade. These results suggest the presence of a hidden biodiversity of Antarctic *Marseniopsis* that, if confirmed by further analysis, will almost double the number of species of this genus. In addition, the absence of isolation-by-distance and the presence of some MOTUs in both seas, are congruent with the long pelagic life of the *Marseniopsis* larva.



The FreshGEN Project: Europe's Neogene and Quaternary lake gastropod diversity - aims, scope and first results

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The FreshGEN project aims to assess the freshwater gastropod biodiversity of European lake faunas over the last 23 million years. This involves the setup of a new database to store all the relevant information including taxonomical data, distributions, stratigraphical age and affiliation to a lake system. The faunas have been studied for over a century from a taxonomic perspective, but were rarely compared statistically. Even for the modern faunas, literature on large-scale freshwater gastropod diversity is scarce and lacks a statistical approach. First results show that a rather homogenous central European Pleistocene and Holocene fauna is contrasted by considerable provincialism during the Miocene. This suggests fundamental differences between modern and pre-Pleistocene freshwater biogeography in central Europe. Aside from the ancient Desarettes lakes of the Balkan Peninsula, Holocene faunas are dominated by planorbids and lymnaeids in species numbers. This composition differs considerably from many Miocene and Pliocene faunas, which comprise pyrgulid-, hydrobiid-, viviparid-, melanopsid- and planorbid-dominated lakes. Future steps include revealing changing evolutionary hotspots, faunal gradients and the evolution of endemic radiations. The results will be discussed in terms of regional and global patterns and will be related to regional and large-scale climatic changes during the Neogene.



Sperm morphology in *Buccinanops monilifer* (Gastropoda: Nassariidae) from the Southwestern Atlantic Ocean

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Buccinanops monilifer (Kiener, 1834), endemic in the Southwestern Atlantic Ocean, is widely distributed in shallow waters up to 50 m deep, from Rio de Janeiro in Brazil (23°8'S) to San Matías Gulf (42°8'S) in Patagonia. In Mar del Plata (Buenos Aires Province), *B. monilifer* lives on subtidal sandy bottoms of temperate waters. It is usually collected with bottom trawling nets between 5 and 20 m in depth. Ultrastructure of the spermatozoa is a useful tool for gastropod phylogeny. We used transmission electron microscopy to study the structure of mature spermatozoa and paraspermatozoa from *B. monilifer* and compared them with those of other caenogastropoda, particularly other neogastropods. The spermatozoa of *B. monilifer* contains an elongated nucleus capped by a conical acrosome with an anterior extension. The nucleus is filiform with a complete and long invagination and contains a centriolar derivative. The mid-piece region consists on an axoneme sheathed by helical mitochondrial elements. The flagellum exhibits the typical 9+2 microtubule structure (9 double outer tubules + 2 single central tubules). The paraspermatozoa of *B. monilifer* are vermiform. They contain 2 axonemes, numerous oblong dense vesicles, numerous less dense vesicles, and mitochondria. Most of the euspermatozoal features of *B. monilifer* are also observed in many neogastropods, with the exception of the number of axonemes in the parasperm.



Timing of diversification and genital system evolution of the western Palearctic Helicoidea

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The Helicoidea, Rafinesque, 1815, is the most diverse group of the terrestrial molluscs of the western Palearctic, with its distribution centre being located in the Mediterranean region where it locally can represent more than half of the molluscan biodiversity. It contains several families and genera of uncertain phylogenetic relationships. The classification of the Helicoidea taxa has been mainly based on the morphology of shell and reproductive system, but there are still some controversies between the main classification systems. After constructing a phylogenetic hypothesis for Helicoidea based on mitochondrial and nuclear rRNA gene sequences for 121 species, this study had two main tasks. Firstly to use phylogenetic reconstruction to evaluate the evolution of different organs of the reproductive system, including the diverticulum of bursa copulatrix, dart sac with dart, accessory sac, type of mucous glands, penis papilla, flagellum, as well as the relationship of the right ocular retractor muscle and genital system. Morphological evolution based on Bayesian trees was reconstructed in Mesquite v2.75. and PAUP 4.0b10. using maximum parsimony; secondly, to estimate divergence times from the Middle Jurassic using different genes and multiple fossil calibration points. This analysis was performed using Beast.



Management actions to recover the populations of *Vertigo angustior* and *V. moulinsiana* in Banyoles lake system (NE Iberian Peninsula)

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Vertigo angustior (Jeffreys, 1830) and *V. moulinsiana* (Dupuy, 1849) are two land snails species listed in the EU Habitats Directive (92/43/EEC 1992). Design of effective monitoring programmes of these two globally threatened species probably remains the greatest challenge to be faced by specialists. Some monitoring and recovery plan actions are included within the LIFE + Nature project “LIFE Potamo Fauna (LIFE12 NAT/ES/001091)” focused on the Banyoles lake system (Girona, Catalonia), a Natura 2000 site. Management actions include: 1) the redaction of a protocol for monitoring both species in this lake system, taking into account the specific environmental characteristics of NE-Iberian Peninsula and testing different collecting methods; 2) to perform population estimates of both species in the lake system; 3) the design and preparation of new ponds for the establishment of new populations; 4) translocation of *V. angustior* and *V. moulinsiana* to the new ponds; and 5) monitoring of translocated populations during four years to evaluate their settlement. We present the new data about the distribution and abundance of both species in this area, as well as the localisation and characteristics of the five new ponds designed. Finally, we report the monitoring protocol that will be used during the period 2014-2017.



Timing of growth line formation in accreted structures of the whelk *Buccinum undatum*

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The common whelk *Buccinum undatum*, a species common to the North Atlantic, supports an economically important fishery in the United Kingdom that has grown substantially since the mid-1990s. The life history strategy of whelks renders them vulnerable to overfishing and can lead to ‘closed’ populations, particularly as they are slow growing, have direct larval maturity and do not show migratory or nomadic behaviour. In order to carry out robust stock assessments, fisheries scientists require accurate and reliable information on the age of individual whelks and to understand the reproductive capabilities of a population. This paper reports on progress into the development of methods for ageing whelks using their shells, opercula and statoliths. Neither of the current methods available are reliable for age determination. Growth lines on the operculum are often unreadable and the outer surface of the whorled shell does not exhibit clear annual growth rings. Statoliths that contain a high resolution archive of the growth history of whelks offer an alternative method for ageing. The timing of formation and the factors controlling deposition of the operculae and statolith growth lines are unclear, but it is thought that they may be related to a peak in summer seawater temperatures causing a slowing of growth, (*B. undatum* is a boreal species), or a cessation of feeding during the reproductive cycle. Opercula, shells and statoliths from whelks, together with their reproductive condition are being assessed in individuals caught monthly in baited traps deployed in the Menai Strait, to determine the timing of formation and the role of environmental factors and reproduction in growth line deposition. To complement the field work, growth line formation in immature juvenile whelks (<1 year old), hatched from egg masses held in laboratory aquaria under ambient (6-15 OC) and constant (10 OC) seawater conditions are being studied to determine whether the seasonal cycle in seawater temperature or the provision of food are responsible for growth line formation. This work is aimed at developing methodologies that will allow fisheries researchers to confidently assess the population age structure and sustainability of a whelk fishery.



Where Bivalves Bite Back: Trophic Shifts in the Deep Sea

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The deep sea has often been described as the last great, unexplored environment on Earth. It poses a number of challenges to invasion by shallow-water lineages, including increased pressure, lack of light, limited food resources and reduced ability to produce calcified shells. One of the most successful groups in the deep sea are the Bivalves and in particular the Anomalodesmata. This highly diverse clade account for around one sixth of the Bivalvia, and more than 50% of molluscs living on the continental slope and abyssal plain making them an ideal model group to study diversification in the deep sea. Anomalodesmatans exhibit a range of lifestyle habits, but shallow water species are typically suspension feeders, whereas some deep-sea taxa have evolved into active carnivores, feeding on small crustaceans. In this study we aimed to investigate

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whether a trophic shift from filter feeding to active carnivory acted as a key innovation leading to massive diversification in organisms living on the continental slope and abyssal plain. We used shotgun sequencing of genomic DNA using an Illumina MiSeq to obtain the first bivalve phylogeny based on Bayesian analyses of complete mitochondrial genomes plus three nuclear genes (18S, 28S and histone 3) to produce a robust phylogeny. We used innovative techniques to determine trophic level using stable isotopes and then mapped trophic habit onto the tree to determine whether carnivory has been acquired along a single evolutionary trajectory or whether trophic habit is more labile, with aberrant morphologies evolving convergently, multiple times in response to ecological pressures? If carnivory has evolved on multiple occasions, are the origins of carnivory convergent in time?



Patterns of diversity within the native and introduced range of the terrestrial slug *Deroceras invadens*

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Deroceras invadens (previously confused with *D. panormitanum*) has spread globally over the last century, sometimes becoming a pest and/or invading natural habitats. We have reviewed and checked museum and literature records and added some of our own. New records reveal that the species is more widespread in the Americas than previously appreciated, but there are no authentic records from Asia. Cold winters probably are limiting its spread into eastern Europe, but it has also scarcely intruded into the eastern Mediterranean. We sequenced 655 bp of the mitochondrial COI gene from much of the range. Diversity was by far highest in southern Italy, including the Aeolian Islands and part of Sicily. Within this region, of the 30 individuals sequenced (one per locality), each was unique, some differing by 7%. The strong relationship between genetic and geographic distance implies that this is the native range. High genetic variation is accompanied by a high diversity in mating behaviour and genital morphology; nevertheless these differences do not prevent sperm exchange. Elsewhere in Europe, three haplotypes predominate with others occurring occasionally; sites mostly contain more than one haplotype. A small number of other haplotypes predominate in Australasia, suggesting that colonisation events there have been rare.



Ecological groups of snails – use and perspectives

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Land snail assemblages have been traditionally used to describe Quaternary environmental changes. There are two advantages of snail fossils over other proxies. Firstly, snail shells can be identified to species level, in contrast to plant pollen, which is the most commonly used palaeoecological proxy, but mostly identifiable only to genus or family level. Secondly, unlike other remains, snail fossils are usually deposited directly in the places where they lived, thus enable fine spatial resolution. Despite these advantages, snails have recently been overlooked in palaeoenvironmental reconstructions, partly because a lack of uniform methodology and interpretation of fossil assemblages. The ecological groups of snails were established by V.Ložek as a tool for such reconstructions. He used detailed knowledge of the ecology of recent populations, and changes in species occurrence during the Quaternary to empirically classify snails in twelve ecogroups. The subdivision hierarchy characterises the species (and thus environment) as terrestrial or aquatic, then terrestrial as woodland, open-country or indifferent, and these three groups are divided into subclasses based on humidity requirements. The final classification contains the following groups of species that mostly inhabit: 1 – woodlands (*sensu stricto*); 2 – woodlands and partly semi-opened habitats; 3 – damp and alluvial woodlands; 4 – xeric open habitats; 5 – open habitats in general; 6 – various predominantly dry habitats; 7 – mesic or various habitats; 8 – predominantly damp habitats; 9 – humid wetland habitats; 10 – periodic waters; 11 – stagnant waters; 12 – running waters. Based on analyses of 828 Holocene mollusc assemblages situated in the Czech and Slovak Republics we slightly modify the species categorization to original ecogroups. Except for a few species, the majority of species displayed stable ecological requirements during the Holocene, in other words the Holocene assemblages of particular habitats are the same as the recent ones. However, the above mentioned subdivision reflects conditions in Central Europe, and may differ in other parts of the continent. We would like to open the discussion to specify ecological requirements of European species and to delimit changes and/or gradients of changes of species requirements throughout Europe. Such specification may result to Europe-wide system of application of ecogroups for reconstructions of palaeoenvironment.



Diversity and phylogeny of *Helix* - insights from mitochondrial data

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The genus *Helix* is well known in most of Europe because of the large size and common occurrence of some of its species, especially *Helix pomatia* and *Helix lucorum*. Nevertheless, *Helix* has an unsettled taxonomy. Here we assess its diversity with emphasis on its centre of diversity in the eastern Mediterranean using fragments of mitochondrial genes (16S LSU and COI). Thanks to use of dried tissue remains from shell collections we were able to sample most species recognised as valid by a parallel morphologic taxonomic revision. The dataset was supplemented by published sequences, reaching an almost complete coverage; only Italian taxa of the complex around *Helix ligata* were not considered. The genus *Helix* was found to be monophyletic, excluding its former subgenus *Maltzanella* from western Turkey, but including the monophyletic genus *Tacheopsis*. *T. nicaeensis*, which resembles more a species of *Cepaea*, was found to be a sister to the polymorphic *H. lucorum*. Instead of the traditional division to some five subgenera (of which only *Pelagosa* received some support), there were four major clades in the genus with a few additional isolated species. Several species, especially among the brown-mouthed taxa related to *Helix cincta*, were not supported in their current limits. Partly this may be attributed to overlooked diversity; conversely, some of the traditionally recognized species seem to represent locally differentiated populations of other taxa. Even the type species of the genus, *Helix pomatia*, is problematic, as it seems to consist of two cryptic species. Parallel evolution and rapid local changes in conchology complicate the taxonomy of *Helix*. The region comprising Greece, the Aegean archipelago, and western Turkey probably represents the major long-term refuge for large-bodied helicid snails, while the highest diversity at the species and intraspecific levels is found along the mountain chains from the western Balkans to southern Turkey. More thorough sampling and multilocus data are needed to unambiguously resolve remaining taxonomic problems within *Helix*.



The importance of the mining subsidence reservoirs in the conservation of biodiversity of freshwater molluscs in industrial areas (Upper Silesia, Poland)

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The study was carried out from 2009 to 2011 in the mining subsidence reservoirs that were created as a result of land subsidence over exploited hard coal seams. The mining subsidence reservoirs are located along the communication routes that have a high volume of vehicular traffic in urbanised and industrialised areas. They have similar types of supply (atmospheric precipitation, surface run-off, groundwater) but differ in the physical and chemical parameters of the water (mainly conductivity, pH, hardness, total dissolved solids, concentration of calcium and chlorides). In total, 15 mollusc species were recorded (from 6 to 11 species in individual mining subsidence reservoirs) including three gastropod species that are alien in the Polish fauna: *Potamopyrgus antipodarum*, *Ferrissia wautieri* and *Physella acuta*. Four bivalve species were also found. Among them *Anodonta cygnea* is protected by the Polish legislation. *A. cygnea* is classified as Endangered (EN) according to the Polish Red Data Book of Animals and also as Near Threatened (NT) according to the European Red List of Non-marine Molluscs. Eleven out of 15 mollusc species are included on the European Red List of Non-marine Molluscs as Least Concern (LC). Mining subsidence reservoirs for this location are characterised by a low mean density of molluscs from 10 to 123 individuals/m². The mean values of the Shannon-Wiener index H' ranged from 0.85 to 1.22. The cluster analysis showed the greatest similarity between reservoirs in which bivalves occurred. Conductivity, pH and the concentration of calcium were the parameters most associated (statistically significant) with the distribution of mollusc species. Canonical correspondence analysis (CCA) showed that *P. antipodarum*, *Radix balthica*, *P. acuta*, *Gyraulus crista* and *Pisidium casertanum* were associated with a higher conductivity and lower pH values. *A. cygnea*, *Anodonta anatina* and *F. wautieri* were negatively influenced by these parameters of the water. The results of this survey showed that the mining subsidence reservoirs that are located in urbanised and industrialised areas provide refuge for rare and legally protected species and that they play an essential role in dispersion of alien species as well.



Differentiation of *Bithynia* snails in Thailand using morphometrics and DNA barcode analyses

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Snails in the family Bithyniidae (Prosobranchia) of the genus *Bithynia* serve as intermediate hosts of a medical important trematode namely *Opisthorchis viverrini*, the major cause of cholangiocarcinoma in humans. The *Bithynia* species/subspecies distribute in different parts of Thailand that is *Bithynia funiculata* in the North, *B. siamensis goniomphalos* in the

Northeast and *B. s. siamensis* in the Central and North. Typically, the morphological characters of the three species/subspecies snails are not easily distinguishable, and often require experienced malacologists for species identification. Moreover, *B. s. siamensis* and *B. s. goniomphalos* are closely related subspecies. The available taxonomic keys are based on morphological characters of size, shape, color, and sculpture on the shell surface and operculum, and shape and arrangement patterns of radular teeth. Thus, the accuracy of species/subspecies identification of those snails serving as host of *O. viverrini* leads to the reliability of prevalence and epidemiologic data. In this study, *B. funiculata*, *B. s. siamensis* and *B. s. goniomphalos* were compared through DNA barcode and morphometric analyses. DNA barcode analysis using 218 cytochrome oxidase subunit I (COI) was applied to differentiate three species/subspecies. Eight primers were used to amplify the 700 bp COI gene and compare the relationship of three species/subspecies by using Neighbor-Joining tree analysis. Most PCR amplification products exhibited a strong single specific band, with success rate of 80-90%. The phylogenetic tree of COI gene showed good discrimination of three snail species/subspecies of family Bithyniidae from Thailand. Morphometrics was also used as a tool for analysing shell shape variation using landmarks on photographs of three snail species/subspecies. Our results showed that these methods could be used as confirmation tools for identification of *B. funiculata*, *B. s. siamensis* and *B. s. goniomphalos* from Thailand.



Rare, threatened and alien species in the mollusc communities of lowland rivers and selected oxbow lakes in agricultural areas with an anthropogenically elevated nutrient concentration (Central Poland)

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The major threat to European freshwater molluscs that lead to population decline is intensification of agriculture, which results in a decreasing water quality in rivers and lakes. An anthropogenically elevated nutrient concentration in surface and ground water causes environmental problems on a worldwide scale. The study was carried out from 2005 to 2009 in the Wkra River (total length 249.1 km), its main tributaries and selected oxbow lakes. The rivers flow through agricultural areas of Central Poland, which comprises part of the Eastern Plains (Ecoregion 16) according to the division of the EU Water Framework Directive. The present results show a relatively high nutrient concentration, especially nitrates of up to 142.20 mg NO₃⁻/dm³ in the Wkra River catchment area (higher than the trigger threshold value set in the EU Nitrates Directive, i.e. 50 mg NO₃⁻/dm³). A long-term survey of mollusc communities revealed the occurrence of 44 species including rare, threatened or legally protected species, e.g. *Borysthena naticina*, *Unio crassus*, *Anodonta cygnea*, *Pseudanodonta complanata* or *Sphaerium rivicola* in the Wkra River catchment area. *A. cygnea* and *P. complanata* are classified as Near Threatened (NT) according to the European Red List of Non-marine Molluscs. *U. crassus* and *S. rivicola*, are included in the IUCN Red List of Threatened Species as Endangered (E) and Vulnerable (V), respectively. The density of *U. crassus* whose conservation requires designation of special conservation areas within the Habitats Directive Natura 2000, ranged from 2 to 20 individuals/m². The density of alien species, *Lithoglyphus naticoides* and *Potamopyrgus antipodarum* ranged up to 50 and 13 individuals/m², respectively. Most of the molluscan species occurred at sites with a median nitrate concentration below 30.0 mg NO₃⁻/dm³ and a nitrite concentration of 0.20 mg NO₂⁻/dm³. Canonical correspondence analysis (CCA) showed that conductivity, hardness, water velocity, river width, temperature, nutrient concentration and the size of sediment particles were the environmental variables most associated (statistically significant) with the distribution of mollusc species. Anthropogenically elevated concentrations of nitrites and nitrates in the water were the most predictive parameters that negatively (i.e. stressors) influenced the structure of mollusc communities.



Extreme habitat disturbances and its influence on *Vertigo moulinsiana* survival

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Vertigo moulinsiana is a poorly known and rare small land snail species, living in wet areas with high pH and calcium content. This poster presents the results of analysis of extreme habitat disturbances such as: winter cold, fire and movement. Over winter survival was found to differ significantly between seasons, but no differences between habitat types was found. A survival was significantly higher in *Carex elata* than in *Glyceria maxima* vegetation type. They did not overwinter in the soil. Survival of 60-70% was not proportional to the number of snails. In relation to fire, fire, fire penetration depth, litter thickness, tussock height and percent of fired area had a significant influence on the number of survivors. Vegetation type and ground water level had no influence on the number of live *Vertigo moulinsiana* specimens. Ground water level had a significant influence on percent of a fired area, fire penetration depth and vegetation type. Tussock height did not relate to fire penetration depth but tussock height and vegetation type had a significant influence on percent of fired area. In relation to vagility (movement), the number of all, alive and dead specimens was significantly different between habitats. Most snails were found in an undisturbed site, less was found in a swath and no specimens were found in stubble. Air temperature over the vegetation at two studied areas was significantly different: it was warmer over the disturbed area compared with the undisturbed area. Also, air temperature in leaf litter was significantly higher in the disturbed area and stubble was even warmer. The described phenomena are disadvantageous to *Vertigo moulinsiana* and, depending on the scale, they negatively affect its abundance. However, the population is able to survive those catastrophes and after some time rebuild in number.



Intrapallial fertilization in *Digitaria digitaria* (Bivalvia Astartidae)

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The eggs of most Astartidae are characterized by a thick adhesive membrane, spawned with a mucous cover. Mucous egg masses are common in molluscs, but rare among bivalves. The fertilization of these species has not been observed but it is expected to take place in the mantle cavity of the female, prior to the formation of the capsules and mucous cover, which constitute a barrier for sperm penetration. *Digitaria digitaria* is a small astartid living in bioclastic bottoms under the influence of strong currents. During the study of its reproductive cycle, we observed morphological changes in the postero-dorsal part of the demibranchs, forming a small chamber in which sperm may be stored. Sperm has been observed inside the female gonad; however the main site for the insemination seems to be outside the gonad, in the dorsal part of the gill, where the oocytes are lined up before they are extruded from the pallial cavity. Fertilization within the shell is believed to be advantageous for small sized species, such as *Digitaria digitaria*, which have a limited egg production.



Western Palearctic Unionidae in the Senckenberg Collection: first results of their revision

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The collection of river mussels (Unionida) of the Senckenberg Research Institute Frankfurt/Main (Germany) is among the largest worldwide and of pre-eminent scientific value. It is estimated at ca. 13 - 15.000 lots and a total of ca. 60.000 specimens. In terms of species diversity it covers ca. 60 % of the global diversity of Unionida. Accessions date back to the early 19th century and they comprise among others the collections of Emil Adolph Rossmässler (1806 - 1867), Wilhelm Kobelt (1840 - 1916) and Fritz Haas (1886 - 1969). Their works, in particular the latest worldwide monograph of Haas (1969), are fundamental for the knowledge of the diversity and distribution of Unionida. At present, unionid mussels are again a focus of systematic and ecological research resulting in a better understanding of their phylogeny and in detection of unrecognized species diversity even in "well-studied" areas like the Western Palearctic (Europe, North Africa, Middle East). Access to historic material, especially type material, is essential for settling relevant nomenclatorial and taxonomic questions. The Senckenberg collection contains about 250 nominal types, 130 of them belong to Western Palearctic taxa. As a part of an ongoing project to inventory and digitize the Unionida collection all Western Palearctic material (estimated at 40.000 specimens/10.000 lots) is being reexamined. The Anodontinae demonstrate the need for a thorough revision of this major part of the collection. Considered a problematic group of difficult species recognition, the specimens already registered as *Anodonta "cygnea"* belong to at least eight different taxa where *A. cygnea* in the present sense has just a 22 % share. Without revision of the identifications, related data would be misleading or useless for any further analysis. The revision of other Palearctic taxa has revealed a 4 - 6 % share of misidentified specimens so far. Another asset of the Senckenberg collection is its detailed documentation of the unionid fauna of all major European rivers that dates back to the period of relatively low human impact, i.e. pollution, habitat destruction and, more recently, global warming. This is invaluable comparison material for scientifically based restoration projects or the study of range shifts.



Cylichna alba: a valid cephalaspid species or a complex of species?

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The Cylichnidae is a family of Cephalaspidea gastropods represented by five species Norwegian waters, namely: *Cylichna alba*, *C. cylindracea*, *C. lemchei*, *C. occulta*, and *C. magna*, the latter a new record for the country. Members of the family have an infaunal lifestyle inhabiting the first few centimeters of soft substrata and occur down to more than 2000m. While most species of *Cylichna* show a fairly conservative morphology, extensive intra-specific variability has been documented in shells of *C. alba* raising the question of whether the latter is a valid species or hides a complex of multiple species. The study presented here is part of a larger project investigating the diversity, taxonomy, and distribution of Norwegian cephalaspidean gastropods and aims to clarify the taxonomy of the *Cylichna alba* species-complex by correlating shell variability with morpho-anatomical (jaws, radula, gizzard plates, male reproductive) and DNA characters within a molecular phylogenetic framework.



Looking like a comb! Preliminary phylogeny of the Genus “*Felimida*”

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The heterobranch genus *Felimida* was originally defined on the basis of the denticulation of the radular teeth. Later it was synonymized with *Chromodoris*, considering the differences in radular denticulation as a normal variation within the genus. In 2012, a new classification of the family Chromodorididae, based on two mitochondrial markers, was proposed. This classification included 14 valid genera, and provisionally re-erected two genera: *Dorisprismatica* and *Felimida*. Since then, *Felimida* has been used for naming the eastern Pacific, Atlantic, and Mediterranean species previously included in the genera *Chromodoris* and *Glossodoris* (except *Glossodoris sedna*). This option was the most conservative choice for this clade, but the authors also encouraged the idea of a broader taxon sampling. We aim to solve the relationships within “*Felimida*” incorporating more species and specimens from the eastern Pacific (including *Felimida sphoni*, the type species of the genus), the Atlantic coast and the Mediterranean, and using two mitochondrial genes -cytochrome *c* oxidase subunit I (COI) and 16S rRNA (16S)- and one nuclear gene -histone-3 (H3). Our preliminary outcomes showed, despite the increased taxon sampling, a high number of unresolved branches that include the specimens attributed to *Felimida* genus, as resulted in the 2012’s phylogenetic study on which the current classification is based. Should we conserve *Felimida* as one unique genus or should it be split into two or even more genera?



The diversity of Philinidae gastropods (Heterobranchia: Cephalaspidea) in light of recent molecular evidence

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Studies on the systematics and taxonomy of the family Philinidae have mostly been based on shell and morpho-anatomical characters and because of similarities, the genus *Philina* has functioned as a repository for most species, with most assignments to other genera considered by many authors of doubtful taxonomic validity. Nevertheless, a recent molecular study with a broader taxon sampling indicates that the Philinidae is polyphyletic, formed by at least four independent lineages (family level) and seven genera. Fine anatomical and SEM work (details of the shell, radula, gizzard plates, foregut morphology and the male reproductive system), showed that this new molecular-based classification is mirrored by morpho-anatomical differences. In this poster the importance of taxon sampling is emphasised and a new systematic arrangement for the Philinidae *sensu lato* is presented, together with the synapomorphies of each new group.



Gene flow between wild banks of the commercially important bivalve *Chamelea gallina* (Veneridae). Present state of genetic variability

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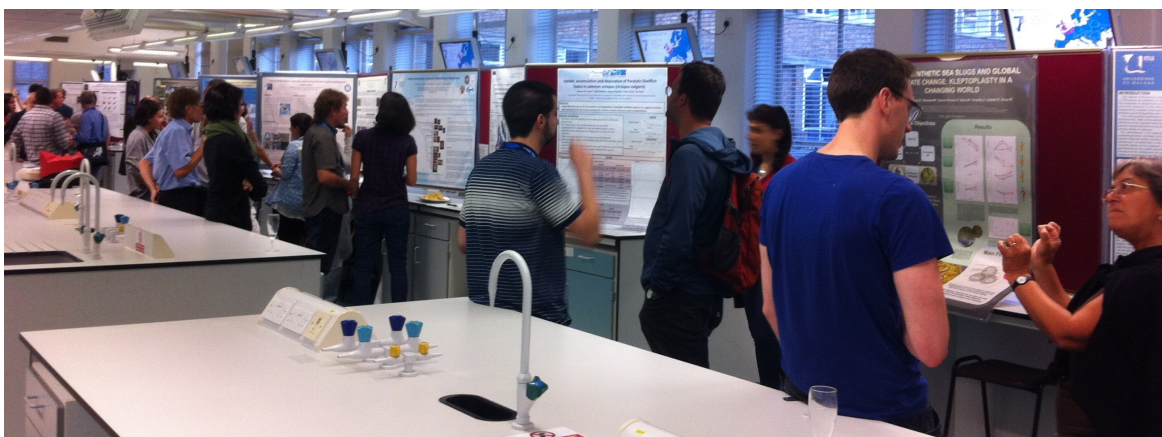
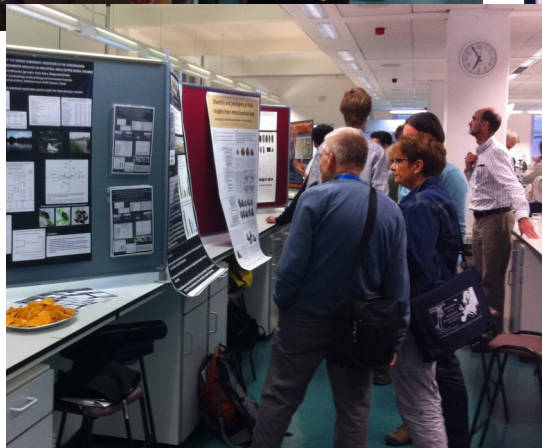
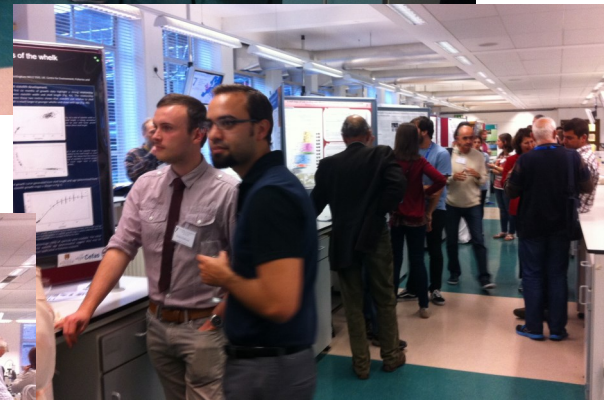
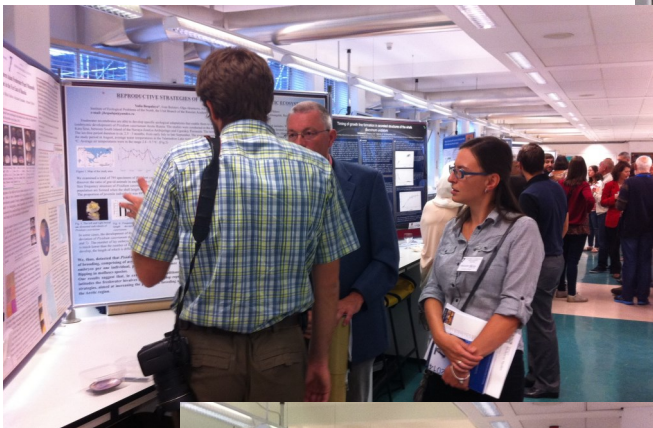
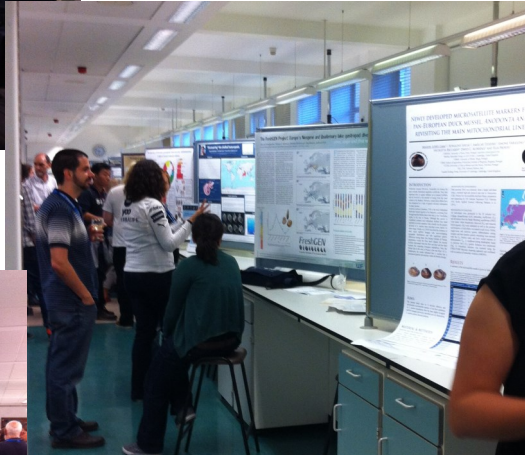
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Bivalve commercial species represent a potentially valuable source to investigate the combined effects of fishery pressure, environmental variability and ecological characteristics on genetic structure. The endobenthic bivalve *Chamelea gallina* is distributed throughout the Mediterranean, the Black Sea, along the Portuguese coast and in a few localities of the Northern Atlantic, living in high-density wild banks on sandy or sandy/muddy seabeds, 1,000-4,000 m off the coastline. There has been strong fishing pressure on *C. gallina* in the northern and central Adriatic Sea for over 30 years. After the first high fishing yields, landings soon declined, together with the observed clear-cut decrease in clam population density. The reduction in clam number was additionally driven by the occurrence of several mortality events. Despite the commercial interest in this species, nothing is known about the genetic sub-structuring at geographic and/or temporal scales and the species potential for genetic variability maintenance. By genotyping 12 microsatellite loci for nine population samples, collected in two years from three sites of the northern Adriatic Sea, we detected weak but significant genetic differentiation at both geographic and temporal scales. These preliminary results suggest the presence of inbreeding and genetic patchiness, typical of marine invertebrates, and do not clearly allow exclusion of a human induced role in the observed pattern. This species might be highly influenced by inter- and intra-annual variability of environmental conditions that typically lead to annual variability of all reproductive traits, such as the timing, frequency, duration, and magnitude of spawning. In addition, human exploitation and disturbance applied during potentially vulnerable life stages of *C. gallina* may enhance the genetic effect of habitat fragmentation, resulting in decreased population sizes and increased inbreeding. The effects of population subdivision and inbreeding on the structure and amount of genetic variability of this species might have important long-term consequences, which are yet not well understood. This kind of research approach should, in the author’s opinion, routinely complement fishery activities.



Photographs of the poster session



A deep-sea *Dorymenia* sp. (Mollusca, Solenogastres) from East Iceland, Norwegian Sea (IceAGE-project)

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The class Solenogastres includes approximately 280 described species, 20 of which can be found off areas near Iceland, but most of them are described from shallow waters off the Norwegian coast. The IceAGE-project (Icelandic marine Animals: Genetics and Ecology) aims to combine classical taxonomic methods with modern aspects of biodiversity research and ecological modeling in the climatically sensitive region around Iceland. In this contribution, five specimens of Solenogastres sampled during the Meteor M85/3 expedition were studied. The specimens came from East Iceland, Norwegian Sea (Area 30 of the expedition) at 662-729 m depth. Based on the study of hard parts and internal anatomy, the five specimens were placed in the Family Proneomeniidae Simroth, 1893 as *Dorymenia* sp. (genus *Dorymenia* Heath, 1911). They are animals of between 3 and 8 cm long and 1 to 3 cm wide with a digitiform projection on their posterior end. The cuticle is thick with numerous hollow acicular sclerites. The digestive system is characterized by an atrio-buccal cavity, a polystichus radula, ventral foregut glandular organs type C and a midgut with regular constrictions. In the posterior part of the body copulatory stylets are present and the existence of dorsoterminal sense organs is unknown.



Molluscs in flood deposits – a tool for the study of river dynamic and species spreading

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River floodplains have been recently under study for several reasons: 1) the heavy damage caused by floods, 2) the impact of anthropic regulatory arrangements on alluvial biota, and 3) as a liner biocorridor in the landscape. Thus, the analysis of flood deposits will be useful for the understanding of dynamics of the flow and dispersion of small organisms along rivers in all the above mentioned cases. Floods can pick up various materials from the riverside – wood and vegetation pieces, debris and molluscs shells – the flood deposit. This material is washed ashore down the stream which is a good opportunity for the caught organisms to spread. Molluscs can survive the transport hidden in their shells or attached on a piece of floating material. The first results of the case study of molluscs in floodplain deposits of three watercourses in the Czech Republic (a river and two tributaries) are presented. Comparing the snail species contained in the flood deposits to the species recorded along corresponding river basin (defines I) the movement of the species along the river II) the area from which the snails are flushed into the river flow or III) the distance which the individuals can cover in the deposit and subsequently colonize new stands. Different representation of particular ecological groups of molluscs shows which biotopes are the most affected by the flood events.



Immune defence proteins expressed in *Bithynia siamensis goniomphalos* upon infection with the human liver fluke

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Among snail species acting as hosts for parasites, *Bithynia siamensis goniomphalos*, a fresh water snail, is responsible for transmission of the carcinogenic liver fluke *Opisthorchis viverrini* to humans. Estimated 10 million people worldwide are infected with *O. viverrini*. Despite its high prevalence in humans and fish intermediate hosts, the prevalence in the snail intermediate host was surprisingly low, which has led to speculations that snail infections by the parasite may cause the activation of defense molecular pathways aimed at eliminating and/or limiting the infection itself. To scrutinize the immune molecular processes, changes in immune protein expression occurring in *B. siamensis goniomphalos* upon experimental infection with *O. viverrini* were conducted using iTRAQ labeling followed by OFFGEL fractionation and LC-MS/MS, respectively. Investigations were carried out 1, 7, 14, 28 and 56 days post infection. The infection with *O. viverrini* induced a strong up-regulation of a number of snail immune proteins. The proteins showed up-regulation during early *O. viverrini* infection (1-28 days post infection) and either returned to their standard expression or, in some cases, showed down-regulation at 56 days post infection and one, complement C1q tumor necrosis factor-related protein 3-like, that remained up-regulated throughout the course of infection. Concerning the success of parasite infection in the snail intermediate host, research has focused on the concept that the parasite either acquires host molecules or produces host-mimicking molecules to escape the defense response. In this study, survival of the parasites during infection suggests either an inadequate immune response or a response actively modulated by the parasites in the early and mid-period of infection. The data contributes to the current research on the molecular biology of *B. siamensis goniomphalos*-*O. viverrini* relationship and ultimately sets the basis for the development of integrated and sustainable strategies for the control of snail-borne infections.



Is shell-shape of rock-dwelling snails affected by environmental factors? The case of *Pyramidula*

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Pyramidula is a genus of terrestrial gastropods whose distribution extends to almost all Europe, Mediterranean area, Central Asia and Japan. Species inhabit limestone rocks from sea level to 3000 m of altitude. Several species have sympatric distributions. They have from flattened to high trochoid shells, not exceeding 3 mm in diameter. Nowadays, six species are proposed for Europe. The identification of the species has been done using morphological studies exclusively based on shell parameters: shell width and height and umbilicus diameter, but these parameters are highly correlated and could be not enough to resolve the taxonomy. After reviewing the phylogeny of the genus analysing 211 specimens from Europe and adjacent areas using molecular methods, we found several incongruences between morphological and phylogenetic species. Therefore, the main objective of the present study is to find whether there are any relationships between shell morphology and environmental factors. The analysis was performed for the two most polymorphic species: *P. rupestris* and *P. jaenensis*. Each of these species was subdivided into two subgroups taking into account shell morphology. The distribution modelling of each subgroup was performed using Maxent and the output response curves were compared.



Revision of the Aclyvolvinae (Cypraeoidea: Ovulidae) based on molecular analyses, morphometrics, mantle patterns and host-specificity

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Worldwide there are around 230 species of Ovulidae in intrinsic association with different species of Octocorallia (Cnidaria: Anthozoa). They occur in temperate and tropical waters of both the Atlantic and in the Indo-Pacific. Molecular research on this family has so far been limited to a single study based on the 16S marker. Those results, in combination with morphological characters, were used to taxonomically revise the family's classification. As a result, the number of subfamilies was doubled from two to four. In the present study these subfamilies are reassessed using additional molecular data with a focus on the Indo-Pacific subfamily Aclyvolvinae. Eight nominal species are currently known in this subfamily. These species are similar, having the same lanceolate shell form. Molecular analyses based on four markers (16S and COI mtDNA, H3 and 28S rDNA), however, show that this subfamily is paraphyletic and that it consists of only five species instead of eight. Morphometric analyses support the new molecular findings. From an evolutionary perspective, these lanceolate shell shapes evolved at least three times within Ovulidae and must therefore be considered homologous. Mantle patterns and host-specificity, in contrast to the shell shape, reflect the molecular findings and are therefore useful characters in clarifying the taxonomic problems within this (sub)family.



Formation of the periostracum in Protobranchia

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The periostracum is the waterproof outermost layer of the molluscan shell and is the first shell layer to be secreted by the mantle edge. Members of the Protobranchia are characterized by a moderate to thick, persistent and smooth periostracum that ranges in thickness from 3 to more than 100 µm. The presence of two basal cells at the bottom of the periostracal groove seems to be the general rule in this clade. Electron microscopy observations in Nuculidae and Nuculanidae point to the presence of a pellicle layer, a dark layer and a translucent layer, although the first is less defined than in other bivalve species. The dark layer thickens by tanning of the translucent layer and, in these clades, frequently forms vesicles which enclose the translucent layer. The shell of *Solemya* exhibits considerable flexibility which is further enhanced by the marked extension of the periostracum beyond the calcareous portions of the valves. We detected the two basal cells in *S. elarraichensis*; later on, the periostracum thickens with secretions from the inner epithelium of the outer mantle fold. Three layers have been observed in *S. elarraichensis*. Beneath the pellicle, there is a dark layer which thickens at the expense of the translucent layer; the latter disappears when the periostracum is projected beyond the periostracal groove, but some vesicles of translucent layer are present at the base of the small projections or folds of the periostracum.



Unexpected patterns of connectivity and phylogeographical breaks in *Unio crassus* across Central and Eastern Europe

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Like many freshwater mussels in Europe, the thick-shelled river mussel *Unio crassus* is threatened with extinction. We combined mitochondrial sequences and nuclear microsatellites to reconstruct the genetic structure and phylogeography of *Unio crassus* from major drainage systems in central and eastern Europe. Such information is crucial for the development of conservation strategies and management programmes. Phylogenetic and multivariate methods were used to describe the genetic and geographical patterns. The mtDNA network showed a clear split into three different haplogroup lineages: Crimean (restricted to Crimean peninsula and Dniester River drainage), Southern (occurring in lower Danube drainage and spreading north to Baltic Sea) and Northern (extending northwards from the Pannonian, middle Danube and Dnieper River drainage). Our results indicate recent population expansion and the mixing of two previously separated lineages (Southern and Northern). Bayesian structure analysis identified three population clusters and also showed strong genetic structure at the nuclear level. Two distinct clusters were detected within the Southern lineage: roughly extending either northwards or southwards from the Carpathian region. Dispersal and evolutionary history of freshwater mussels from family Unionidae is allied to those of host fish. However, the phylogeographical distribution of *U. crassus* populations does not seem consistent with the general scenario proposed for the colonization of Europe by freshwater fishes. The current distribution of genetic diversity was influenced by past climatic events, especially those related to the LGM (Last Glacial Maximum).



Sex ratio, sexual size dimorphism and the fecundity advantage hypothesis in the bivalve *Patinopecten yessoensis*

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Knowledge of the sex structure of Pectinidae populations is limited. This study deals with mobile long-lived scallop *Patinopecten yessoensis* (Jay), a commonly fished and cultured species in the subtidal benthos of the Sea of Japan. In natural scallop populations, the general sex ratios were *circa* 1:1. A pronounced female-based sexual size dimorphism was found between the totality of males and the totality of females within a population. An original method of age determination in *P. yessoensis* allowed us to investigate the sex-age-frequency distribution in population and to compare the parameters of same aged males and females. Young age classes had strongly male-biased sex ratio, and the females became more prevalent as the scallop age increased. The shell growth rates and sizes of both genders were similar, but a female-biased dimorphism in gonad weight was found. The gonad increased until a threshold age was reached, which varied between populations; later the gonad weight was steady in the pre-spawning period. The 'fecundity advantage hypothesis' for *P. yessoensis* with external fertilization is realized by physiological mechanisms if there is a greater number of senior females than males in a population in order to produce a larger clutch. Gregarious settlement aids reproductive success as the energetically costly ovaries may all be fertilized.



Apertural barriers in clausiliids with different reproductive strategies

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Door-snails (Clausiliidae) develop a unique system of apertural barriers in the last shell whorl. It includes several folds and a flexible plate (clausilium) which together almost entirely block the entrance to the shell from outside. The biometrical studies of this structure were previously neglected as its complexity precluded measurements in two-dimensional space. Our comparison of shell morphology between clausiliids *Laciniaria plicata* (oviparous) and *Alinda biplicata* (viviparous) was focused on the diameter of the cross-sectional area between apertural barriers available for the passage of eggs or embryos. Measurements were conducted with novel methods including X-ray microcomputed tomography (XMT) and a specially designed algorithm that mimics the movement of spherical object (egg or embryonic shell) in the lumen of the parental shell. The algorithm worked on a three-dimensional image rather than on a single cross-sectional or longitudinal data and allowed the largest possible sphere that can be entered in the shell channel at a given place to be measured. Thus the diameter of the biggest sphere that can pass between the folds of the clausilial apparatus in the ultimate whorl of *Alinda biplicata* equals 1.25 ± 0.05 mm. The penultimate whorl is more spacious – the fitted sphere reaches 1.71 ± 0.08 mm. In relation to shell width, the patency of ultimate whorl amounts to 32% and for the penultimate whorl it is 44%. In *Laciniaria plicata*, the diameters of the fitted sphere equal 0.61 ± 0.08 mm in the ultimate whorl and 1.46 ± 0.08 mm in the penultimate whorl. In relation to shell width, these are 18% and 42%, respectively. The studied clausiliids exhibit interspecific variation in shell patency. The wider passage through the apertural barriers in *A. biplicata* seems to be an adaptation that enables the release of intrauterine embryos with inflexible, calcareous shells.



Description of a new species of *Piseinotecus* (Gastropoda, Heterobranchia, Piseinotecidae) from the North-Eastern Atlantic

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A new species of aeolid nudibranch of the genus *Piseinotecus* Er. Marcus 1955 is described, based on several specimens from the Atlantic coast of Morocco and the South Western Iberian Peninsula. This new species is characterized by a translucent violet ground colour (very similar to several *Flabellina* species) with minute opaque white spots over the cerata, which emerge from stalks, smooth rhinophores, uniseriate radula and a jaw with a smooth masticatory border.



A new species of *Eubbranchus* (Gastropoda, Heterobranchia) from the North-Eastern Atlantic

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A new species of the genus *Eubbranchus* (Gastropoda, Heterobranchia, Aeolidida) is described based on two specimens collected near the harbour of Agadir, Morocco. The translucent white ground colour with opaque white and red-orange speckles over the dorsum and cerata, smooth rhinophores and morphology of the lateral teeth of the radula characterize this species, which is compared with all the Atlantic and Mediterranean red-spotted species of the genus.



Reproductive seasonality and histochemical profile in *Brachidontes rodriguezii* (D'Orbigny, 1846) from the South-Western Atlantic

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Brachidontes rodriguezii has a wide distribution along 1500 km of the Argentinean coast, from Buenos Aires to Patagonia. It is the most abundant species in the intertidal benthic community associated with rocky shores. In recent years, because of the introduction of hard substrata as docks, sandy beaches became a new habitat for this species. The reproductive cycle was studied, over a period of two consecutive years, through analysis of gonadal samples. Individuals were sampled monthly on hard substrata from Buenos Aires province, the northern limit of its distribution. Stage of gonadal development and oocytes size-frequency in females of *B. rodriguezii* were used to estimate the reproductive events. Preatellogenetic and late vitellogenic and late vitellogenic oocytes were found all the year, with a high frequency of mature oocytes during the late spring and early summer. Spermatogenesis continued throughout the year. The reproductive season at the sampled locality extended from December to February (austral summer). During summer, histochemical characterization showed the neutral lipids in oocytes and the gonadal connective tissue. After spawning, the gonads of *B. rodriguezii* contained oocytes under atresia and a lower concentration of lipids in the connective tissue. The reproductive seasonality was linked to changes in water temperature and photoperiod. These results suggest that *B. rodriguezii* has a simple yearly gamete production cycle.



Discovering' the shelled heteropods

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The shelled heteropods (Pterotracheoidea, Atlantidae) are a family of microscopic (shells <10 mm) holoplanktonic gastropods with highly specialised eyes, a foot adapted for swimming and lenticular, flattened and keeled aragonitic shells. Recent research into their abundances through Quaternary sediments suggests that the Atlantidae are an important constituent of the ocean zooplankton. However, there is currently a lack of research on their morphology, taxonomy, ecology, distribution and importance to the ocean food web. This makes it difficult to understand how the Atlantidae will be affected by current and future global changes, which are predicted to have a significant negative effect on a similar group of holoplanktonic gastropods, the shelled pteropods (thecosomes), generating fears that the Atlantidae may become extinct before they have even been 'discovered'. Our research at Plymouth University aims to address many of these key questions, using a multidisciplinary approach to lay the foundations for future work in this field. Here we present a review of what is currently known

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about the Atlantidae, including an updated and detailed biogeography compiled from museum collections and literature. This information provides a platform from which our future research will be based, including the use of molecular and morphological techniques to improve taxonomy and the collection and analysis of specimens from sites world wide to provide a more complete understanding of the ecology of the Atlantidae.



Distribution, population structure and growth of the fresh water pearl mussel *Margaritifera margaritifera* (Linnaeus, 1758) in the river basin of Narcea (Asturias, North Spain)

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The freshwater pearl mussel *Margaritifera margaritifera* (Unionoida: Margaritiferidae) is a long lived bivalve that inhabits the upper courses of oligotrophic rivers and brooks. Its life cycle includes a parasitic larval stage, the glochidium, which is host specific. In Europe, the glochidia infest the gills of salmonid fishes, the brown trout and the Atlantic salmon, where it remains attached until metamorphosis. The historical distribution of the freshwater pearl mussel is holoartic, with its area spreading from the Peninsula Kola (northwest Russia), along the European Atlantic coast down to the Northwest Iberian Peninsula and along the Western Atlantic coast of North America. Currently, populations are in strong decline across the distribution area. As a result, the species is included in Annex II and V of the European Directive 92/43/CEE and Annex III of the Bern Convention. In the Iberian Peninsula, populations of the naiad are still found in affluents of the Duoro and Tagus River and along the coast of Galicia northwards from the Miño River. In Asturias, the species have been recorded in the rivers Narcea, Nalón, Eo, Navia, Porcía, Esva and Esqueiro. Within the framework of a more comprehensive study whose goal is to determine the temporal trend and conservation status of the species in Asturias, a census of the fresh water pearl mussel was conducted between 1997 and 2000 along the Narcea river basin. Populations of the naiad were found in the lower courses of the Narcea and close to the entrance of its affluents Pigüena and Arganza. Recruitment was low and most individuals fell within the largest size classes. Besides, the growth parameters L_{∞} (the asymptotic length), maximal age and the growth constant K for 9 populations of the Narcea were determined. The maximal age at L_{∞} was calculated from the von Bertalanffy growth curve and the growth constant K and the L_{∞} from growth increment data at five years time interval through a Ford-Walford plot. The age of the individuals were determined by counting the annual concentric growth rings of the shells. L_{∞} ranged from 8.19 to 13.34 cm, the maximum age from 58.38 to 65.76 years and the annual growth rate from 0.03 to 0.06 per year.



Taxonomy and Distribution of the Eastern Asian Freshwater Pearl Mussels (Unionoida: Margaritiferidae) in the Far East of Russia

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The family Margaritiferidae includes 13 species of the genus *Margaritifera*, which are among the most endangered freshwater mussels in the world. Based on a broad spatial sampling of *Margaritifera* spp. in the Far East of Russia (from Kamchatka Peninsula to Kunashir Island), morphological investigation of shells and phylogenetic analyses of mtDNA gene cytochrome oxidase subunit I (COI) sequence data, three valid species were identified: *Margaritifera dahurica* (Middendorff, 1850), *M. middendorffi* (Rosén, 1926) and *M. laevis* (Haas, 1910). *M. middendorffi* was previously considered as an endemic species of the Kamchatka Peninsula. However, *M. middendorffi* is more widespread in the rivers of the Kamchatka Peninsula, Kurile Archipelago (across the Bussol Strait, which is the most significant biogeographical boundary within the Archipelago) and Sakhalin Island. Two NW Pacific margaritiferid species, *M. laevis* and *M. middendorffi*, belong to one mitochondrial clade, together with two North American species. The range of *M. dahurica* includes the Amur basin and some nearby water bodies. From molecular data, this species is identified as the closest to *M. margaritifera* (L. 1758), which occurs in Europe and Eastern North America.



What can be inferred from the shell of *Unio crassus*?

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We have studied relations between morphology, sex (determined on the basis of reproductive features) and habitat in two populations of *Unio crassus*: in a warm environment of the Bieśninka river which is a typical, small Carpathian river, and in the San river, located at a higher altitude, larger, typical for a mountainous river. We sampled 20-30 ind., usually every week (depending on the local water conditions), which were measured and checked for the presence of eggs/glochidia or sperm. We found significant differences in size between males and females (males have narrower shells than females), between the studied rivers (smaller shell size in San and different, curved shape). We analyze the possible ecological factors responsible for the differences: water chemistry, water velocity and energy allocation in shell growth.



Habitat selection of *Unio crassus* in mountainous habitat - a case study in the San river

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Mountainous habitats are expected to be a hostile environment for mussels. Usually, the channel is underlined by solid rock, the channel slope is steep, water dynamics are high with frequent extreme events, and all these factors prevent mussels occurrence. However, when the channel crosses perpendicular layers of rock, the water stream is distorted, creating areas of slow water current and intensive sedimentation. The still water along the bank creates habitat preferred by mussels, with very high densities (up to 1000 ind./100m). Because the habitat is restricted to the very thin strip of sediment at the bank (10-30cm in height), the local density is very high and simply lack of space can limit the mussels occurrence. Fine sediments allow for development of vegetation, which prevents the banks from eroding; however, it also creates a danger of being buried by banks collapsing under the ice load. The middle parts of the channel are deprived of mussels. Behavioural experiments with individuals marked with transponders show that they actively prefer the fine sediment strip over the coarse sediment within the channel. Also recruitment takes place in the fine sediment strip.



A novel symbiotic association of the nudibranch mollusc *Rostanga alisae* with bacteria

Natalia V. Zhukova*^{1,2}, Marina G. Eliseikina¹, Evgeniy S. Balakirev^{1,3} and Francisco J. Ayala³

¹ Institute of Marine Biology, Far East Branch, Russian Academy of Sciences, Vladivostok, 690041, Russia nzhukova35@list.ru

² Far Eastern Federal University, Vladivostok, 690950, Russia

³ Department of Ecology and Evolutionary Biology, University of California, Irvine, CA 92697-2525, USA

Symbioses involving bacteria and invertebrates contribute to the biological diversity of aquatic environments. A new symbiosis between the dorid nudibranch *Rostanga alisae* (Mollusca: Opisthobranchia) and the members of the bacterial groups Rhizobiales and Rhodobacterales, known for their ability to obtain energy autotrophically by the oxidation of carbon monoxide and displaying antimicrobial activity has reported for the first time. Transmission electron microscopy revealed dense clusters of rod-shaped Gram-negative bacteria enclosed with a membrane within bacteriocytes located in the epithelium of the nudibranch foot. The number of bacteria in bacteriocytes varied from one item to a few dozens. There were three main types of bacteria corresponding to the stages of lifecycle of endosymbionts. The presence of three transitional forms, monomorphism of bacteria within each bacteriocyte, and the presence of dividing bacteria suggest that the revealed bacteria are symbionts of the nudibranch. Molecular phylogenetic analyses revealed the bacteriocyte-associated bacteria to be dominated by α -Proteobacteria (*Labrenzia* and *Maritalea* clones). Gram-positive Actinobacteria (*Iamia* and *Iumatobacter*) were found as single clones. Revealed in bacteriocytes were β -Proteobacteria (*Achromobacter*) and γ -Proteobacteria (*Lysobacter* and *Stenotrophomonas*); these were also detected in the intestine and in amicrobic tissues, thereby indicating the nonspecificity of these bacteria. Fatty acid analyses suggest that these endosymbionts probably supply the host with nutrients. Additionally, the abundance of specific bacterial fatty acids in the lipids may serve as an indicator of the presence of symbionts in the mollusc tissues. This study was supported by Bren Professor Funds at the University of California Irvine and by the Government of the Russian Federation grant 11.G34.31.0010.



Previously known only as a fossil, a single specimen of *Wollemia nobilis* was discovered in 1994 in New South Wales. Here, a scion of *W. nobilis* is growing in the Cambridge Botanic Garden.

The Conference Dinner



Previous Euromol meetings

6th Congress

Vitoria-Gasteiz, Spain, 18-22 July 2011

5th Congress

Ponta Delgada, Azores, 2-6 September 2008

4th Congress

Naples, Italy, 10-14 October 2005

3rd Congress

La Rochelle, France, 24-27 June 2003

2nd Congress

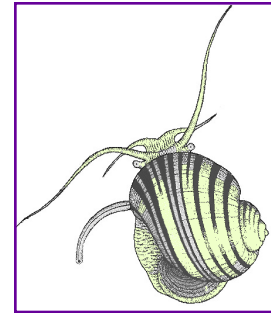
Vigo, Spain, 9-13th September 2002

1st Congress

Genoa, Italy, 12-16 November 2000

The Malacological Society of LondonWWW.MALACSOC.ORG.UK

Molluscan Forum



Thursday 19th November 2015
9:30 am – 6.30 pm
Flett Lecture Theatre
Natural History Museum, London

CALL FOR REGISTRATIONS AND PAPERS

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 Forum will be held the day before the Young Systematists' Forum (www.systass.org/ysf), which will also take place at the Natural History Museum.** This has been arranged so both meetings can be attended, although if attending both you will have to register for both meetings separately.

Attendance at the Molluscan Forum is open to all, but presenters should be **research students, post-doctoral researchers, undergraduate students** starting molluscan projects, 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. They need not be polished accounts of completed work; descriptions of new methods, work in progress, and appeals for assistance with unsolved problems are equally acceptable.

In addition to talks and posters there may be opportunities to acquire books and other items contributed by members of the Society. Lunch will be provided and The Forum will end with a wine reception, both sponsored by The Malacological Society of London.

THERE IS **NO** REGISTRATION FEE AND A LIMITED AMOUNT OF HELP WITH TRAVEL COSTS WILL BE AVAILABLE FOR PRESENTERS WHO CANNOT CLAIM THEM FROM ELSEWHERE.

Enquiries and registrations to:

Andreia Salvador, Curator of Marine Mollusca, Natural History Museum
(a.salvador@nhm.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>

The Malacological Society of London

Molluscan Forum, Thursday 19th November 2015

9:30 am – 6.30 pm

Flett Lecture Theatre, Natural History Museum, London

REGISTRATION FORM

Return before 1st October 2015, by email to:

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

Name.....

Address.....

.....

Tel. No.....

Email.....

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

‘Other’ (please state)

Will you attend the Young Systematists’ Forum on 20st November 2015?

I wish to give a paper / poster (delete as appropriate) entitled:

.....

.....

PLEASE ATTACH, AS A MICROSOFT WORD ATTACHMENT, AN ABSTRACT - SEE BELOW FOR INSTRUCTIONS - OF NOT MORE THAN 350 WORDS. ABSTRACTS OF ACCEPTED CONTRIBUTIONS WILL BE PUBLISHED IN THE SOCIETY’S BULLETIN, *THE MALACOLOGIST*, AND ON ITS WEBSITE.

Posters should be roll-ups or mounted on stiff cards, and should require no more than a 1 metre x 1 metre display area. They will be mounted on boards (velcro supplied).

If you are unable to get financial support from elsewhere (students and amateurs only) and need assistance with travel costs, please enter here the cost of the cheapest possible public transport return fare to London.

£.....

Funding is not guaranteed but we endeavour to support as many presenters as possible. Late registrations may miss the opportunity for financial support. The support will be limited, so funding from elsewhere should be sought first. A provisional programme and confirmation of registration will be sent out late October.

Abstract submission

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

Please use the following format:

Title (12pt, centered)

<blank line>

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

<blank line>

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

Presenting Author email

<blank line>

Abstract (11pt, no indentation, 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 taxa. It is also possible that ecological speciation could result in geographical speciation on a small scale in the presence of wide dispersal. My results suggest that five species of *Stramonita* are present in the Caribbean, at least three of which occur sympatrically. Gene flow is maintained between Caribbean and Mediterranean populations in at least one species, while no genetic differentiation was found along the Eastern Pacific coast. The implications of these results are discussed.

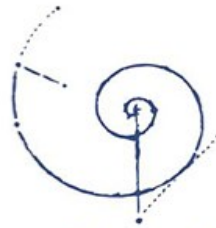
NOTE THAT ABSTRACTS ARE PUBLISHED IN *THE MALACOLOGIST* WHICH IS THE BULLETIN OF THE SOCIETY AND HAS AN ISSN NUMBER. IT IS CIRCULATED TO ALL MEMBERS.

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



mollusks in peril 2016 forum

presented by
The BAILEY-MATTHEWS
NATIONAL SHELL MUSEUM

Bailey-Matthews National Shell Museum
3075 Sanibel-Captiva Road
Sanibel, Florida 33957 USA

- **Forum will be held May 22-24, 2016**
- **Twitter: @mollusksinperil.org**
- **<http://www.shellmuseum.org/learn/mollusks-in-peril-forum>**



Triennial conference of the Malacological Society of Australasia

This year the conference will be held in Coffs Harbour on the mid-north coast of NSW between November 29 and December 2, and we are open for abstract submissions by researchers wishing to present their work.

Delegates can partake in optional post-conference events including a day trip to the World Heritage Listed Gondwana Rainforest of Australia at Dorrigo National Park, a SCUBA diving trip to the Solitary Islands Marine Park, or a two-day nudi-branch taxonomy and ecology workshop.

The society will be offering travel scholarships to students to help with meeting the cost of getting to and participating in the conference. This year we will also be offering community scholarships to applicants who have demonstrated significant commitment to malacology on a voluntary basis. If you know anyone who may be eligible to apply for these please let them know.

For more information including accommodation packages, registration and abstract submission, visit www.malsocaus.org or email conference@malsocaus.org. You can also receive conference updates on facebook by joining our online group at

- www.facebook.com/groups/Malsocaus
- <http://www.malsocaus.org/wp-content/uploads/2015/02/Molluscs-2015-A4-Flyer.pdf>



Grants and Awards

Malacological Society of London Awards and Grants

The Malacological Society of London makes a number of Awards and Grants. These are in addition to financial support for meetings, including travel bursaries to the Molluscan Forum.

Research Grants

The Research Grants Scheme was established to commemorate the Society's Centenary in 1993. Under this scheme, the Society anticipates making at least five awards each year, each with a value of up to £1500 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 professional positions, 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 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. The conditions of the award, notes of guidance and an application form are on the Society's website at www.Malacsoc.org.uk

Travel Grants

Travel Grants are available as bursaries to support attendance at a conference or workshop relevant to malacology. Grants are preferentially conferred on students and researchers without professional positions. The value of each of these awards is up to £500, and the Society anticipates that at least five awards will be made annually. The application should have the support of the project supervisor. In years when a UNITAS Congress (i.e. World Congress of Malacology) is held, a number of these awards are likely to be used to support participation at this meeting. 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. The conditions of the grant, notes of guidance and an application form are on the Society's website at www.Malacsoc.org.uk Preference will be given to members of the Society.

Sir Charles Maurice Yonge Awards

Successful applications for Research Grants or Travel Awards that are concerned with the study of Bivalvia may be awarded as Sir Charles Maurice Yonge Awards.

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, Dr Suzanne Williams, Natural History Museum, London, SW7 5BD, UK. 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 copy of the *Journal* 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 (1976) into the *Journal of Molluscan Studies*. The *Journal* is published in annual volumes consisting of four parts which are received by fully paid-up members and student members. Members also receive the *The Malacologist*, the digital Bulletin of the Society, twice a year.

Meetings

In addition to the traditional researches on taxonomy and systematics, new experimental, chemical and molecular techniques are amongst the topics considered for discussion meetings and papers for publication in future volumes of the *Journal*.

Subscriptions

The Annual Subscription is due on 1st January each year.

- Students £25 (or US\$ equivalent- on-line access only)
- Ordinary members £45 online; (or US\$ equivalent) or £70 with hard copy

Methods of Payment

Sterling cheque to "The Malacological Society of London".

- (2) Banker's standing order to: The Northern Bank (Sort code 95-01-49), 49-51 University Road, Belfast BT7 1ND, for the credit of "The Malacological Society of London" (a/c 70030422).

(Please note-This bank address will change in 2016)

- (3) Credit card: Overseas members ONLY may pay by credit card: the Society can accept VISA and MasterCard payments only. Please provide the Membership Secretary with your card number and expiry date, card type (VISA or MasterCard.), the name on the card, and the cardholder's address (if this differs from your institutional address). Receipts will only be sent if specifically requested. Overseas members wishing to pay electronically should contact the Membership Secretary (Dr R.Whittle at roit@bas.ac.uk for SWIFT/BIC and IBAN numbers of our bank.

Institutional Subscriptions to the Journal

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

Change of Member's Address

Please inform the Membership Secretary of a change of postal or email address. Alternatively, use the address slip on the *Journal* wrapper to inform us, through Oxford University Press, of a change of address.

APPLICATION FOR MEMBERSHIP OF THE MALACOLOGICAL SOCIETY OF LONDON

I wish to apply for Membership of the Society (select one)

- Student Membership £25 (on-line access only)
- Ordinary Membership £45 online Journal only
- Ordinary Membership £70 with Hard Copy (paper) Journal and online Journal

I enclose a cheque payable to "The Malacological Society of London" for my first annual subscription.

TitleName

Department Institution

Street City

Post /Zip Code Country Email

Malacological Interests

Signature Date

Please send the completed form and cheque to the Membership Secretary:

Dr Rowan Whittle, British Antarctic Survey, High Cross, Madingley Rd., Cambridge CB3 0ET roit@bas.ac.uk