



Molluscan Forum 2006

Palaeontology Demonstration Room
Natural History Museum, London

2nd November 2006

Organised by:



THE MALACOLOGICAL SOCIETY OF LONDON



NATURAL HISTORY MUSEUM, LONDON

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Foreword

THE MALACOLOGICAL SOCIETY OF LONDON and the NATURAL HISTORY MUSEUM welcomes young researchers to the Forum, and hopes the event will prove both enjoyable and useful to them. Malacologists not presenting work are also invited to attend and take part in the discussions.

This informal, annual 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.

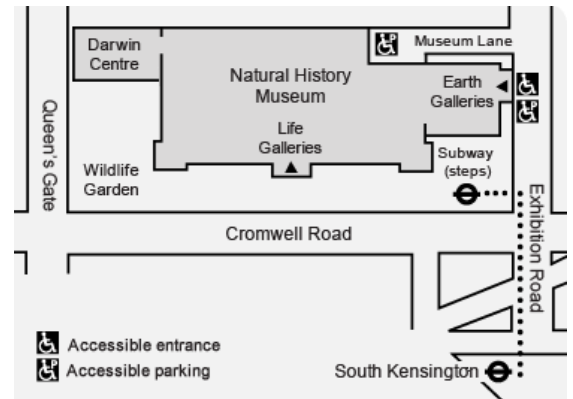
Attendance is open to all, but speakers and poster presenters should be research students, post-doctoral researchers, undergraduates starting molluscan projects or dissertations, and amateurs engaged in substantial projects, which have not yet been published. Any topic related to molluscs is acceptable: palaeontological, physiological, behavioural, ecological, systematic, morphological or molecular.

In addition to talks and posters there will be opportunities to acquire reprints contributed by members of the Society. The forum will end with a wine reception.

Further information available at:

<http://www.malacsoc.org.uk/Molluscanforum06.htm>

How to get to the Natural History Museum



The NATURAL HISTORY MUSEUM is located in South Kensington, and the most convenient way to get there is probably by underground (South Kensington station). There are three underground lines calling at South Kensington (Piccadilly, District, and Circle lines) plus several buses. Visit the NHM website at <http://www.nhm.ac.uk/visit-us/getting-here/index.html>, and find out the best way for you to reach the Museum.

How to find the Molluscan Forum?



To attend the Forum you should enter the Museum by the Main visitors Entrance in Cromwell Road. Once inside please go to the visitor's reception desk (on the left) and tell them that you are coming to attend the Molluscan Forum. They will then give you a Visitor's Pass. Unlike the previous editions, this year the Molluscan Forum will be held in the Palaeontology Demonstration Room (The Dorothea Bates Room). This is two minutes walk from the reception desk in the Green zone at the far end of the Fossil Marine Vertebrates Gallery. The quickest way to get there is to walk right through the shop, continue through the Ecology Gallery on the far side of the shop, and then turn left at the end of the gallery. Continue until you come to the giant ground sloth and the entrance to the Palaeontology Department is the door on the right. Ring the bell and someone will come to meet you.

Molluscan Forum 2006 Programme

<i>Time</i>	<i>Programme</i>
10.20 - 10.30	Welcome
10.30 - 10.50	Land snail distribution patterns within a site: the role of different calcium sources LUCIE JUŘIČKOVÁ, MICHAL HORSÁK, ALENA MÍKOVCOVÁ, JAROSLAV Č. HLAVÁČ and JAN ROHOVEC
10.50 - 11.10	Comparative morphology of the Thraciidae A. F. SARTORI and E. M. HARPER
11.10 - 11.30	Release of reactive oxygen intermediates by <i>Lymnaea stagnalis</i> haemocytes: a pivotal role for Protein Kinase C AUDREY H. LACCHINI, ANGELA J. DAVIES, DAVID MACKINTOSH and ANTHONY J. WALKER
<i>Coffee break / Poster session</i>	
11.50 - 12.10	Towards a phylogeny of <i>Limax</i> (Gastropoda: Stylommatophora) BARBARA KLEE
12.10 - 12.30	The land-snail fauna of fragmented Sri Lankan lowland rainforest and village home gardens DINAZARD RAHEEM
12.30 - 12.50	The influence of species diversity on resource partitioning in intertidal gastropods as revealed by stable isotopes G. M. ANDREW, M. T. BURROWS, S. J. HAWKINS and R. A. R. MCGILL
12.50 - 13.10	<i>Achatina fulica</i>: its molecular phylogeny and genetic variations in global populations IAN K. FONTANILLA
<i>Lunch</i>	
14.00 - 14.20	Is this a sacoglossan? – Computer-based 3D anatomical visualisation of the mesopsammic <i>Platyhedyle denudata</i> SALVINI-PLAWEN, 1973 (Opisthobranchia, Sacoglossa) INA-MARIA RÜCKERT, GERHARD HASZPRUNAR and MICHAEL SCHRÖDL
14.20 - 14.40	Researching <i>Limax maximus</i>: Old literature and new sequences ISABEL HYMAN
14.40 - 15.00	Evolutionary history of molluscs from deep-sea chemosynthetic ecosystems LUCIANA GÊNIO, STEFFEN KIEL, CRISPIN LITTLE, JOHN GRAHAME and MARINA RIBEIRO CUNHA
15.00 - 15.20	Pallet structure of wood borers of the family Teredinidae (Bivalvia) L. M. S. BORGES and S. M. CRAGG
15.20 - 15.40	Taxonomy of the genus <i>Trochulus</i> (Gastropoda: Hygromiidae) in the Czech Republic M. HRABAKOVA, L. JUŘIČKOVÁ and A. PETRUSEK and A. PETRUSEK
<i>Coffee break / Poster session</i>	
16.20 - 16.40	Mobility of <i>Bulgarica cana</i> in a natural habitat MAGDALENA MARZEC
16.40 - 17.00	Species-area relationships in the spring fen mollusc communities NICOLE CERNOHORSKY
17.00 - 17.20	Combining confocal laser scanning microscopy and electron microscopy to investigate the mantle and velar ciliation of larval bivalves SAMUEL STANTON
17.20 - 17.40	<i>Sphaerium comeum</i> / <i>nucleus</i> (Bivalvia: Veneroidea: Sphaeriidae) is a complex of several cryptic species TEREZA KOŘÍNKOVÁ, ADAM PETRUSEK and LUCIE JUŘIČKOVÁ
17.40 - 19.10	<i>Social event</i>

Poster Programme

The phylogeny of mollusks and their relatives within the Lophotrochozoans

ACHIM MEYER and BERNHARD LIEB

**The molluscan collection of the National Museums Scotland
(Royal Museum); significance, value and potential**

CLAIRE PANNELL

Niche creation for cryptofauna by teredinid bivalves in mangroves

IAN HENDY

Seasonal variation of zebra mussel tolerance to toxins

R. COSTA and G. D. MOGGRIDGE

**Co-evolution or easy exploitation?: Trematode prevalence,
diversity and lifecycles in endemic gastropods
of Lake Tanganyika, East Africa**

SARAH M. COLLINS, JULIA HOOPER and ELLINOR MICHEL

**Geometric morphometric analysis of geographic variation
in four endemic gastropod species from Lake Tanganyika**

VIVIANE CALLIER, CATHERINE E. WAGNER, ELLINOR MICHEL
and JONATHAN TODD

Hemocyanin: an appropriate new marker.

Phylogeny of polyplacophorans resolved by hemocyanin genes

KLAUS STREIT, DOUGLAS J. EERNISSE and BERNHARD LIEB

Cryoelectron microscopy and single particle analysis

of *Nautilus pompilius* hemocyanin under different oxygenation states

ARNE MOELLER, CHRISTOS GATSOGIANNIS, FRANK DEPOIX,
ULRICH MEISSNER and JUERGEN MARKL

**Interaction between environmental factors and life history variables
in determining recruitment of the Manila clam**

MATT HARRIS

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Land snail distribution patterns within a site: the role of different calcium sources

LUCIE JUŘIČKOVÁ, MICHAL HORSÁK,
ALENA MÍKOVCOVÁ, JAROSLAV Č. HLAVÁČ
and JAN ROHOVEC

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THE aim of this study was to analyse whether land snail assemblage patterns reflect gradients of calcium content on a very small scale. We chose two sites differing in their calcium richness and source of the calcium ("Tufa site" and "Boulder site"). We tested the predictive power of different sources of calcium (from topsoil, vegetation and leaf litter). At both sites, the main variability in species composition was explained by the calcium gradient. For the "Tufa site", calcium content was a strong controller of species composition and also species richness, total abundances and abundance of almost all species. At the "Boulder site" only species composition was significantly driven by calcium. Content of calcium carbonate was the best predictor of species composition. No significant correlation was observed for leaf litter calcium. Topsoil pH did not explained the observed clear pattern of land snail composition along the calcium gradient.

Comparative morphology of the Thraciidae

A. F. SARTORI and E. M. HARPER

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THRACIIDÆ STOLICZKA, 1870 (Bivalvia: Anomalodesmata) is a cosmopolitan family of marine burrowers, generally regarded to comprise eight extant genera. An analysis of diagnostic characters for the family reveals that most are solely based on the shell, many are rather variable throughout the constituent species, none occur exclusively in thraciids, and several are likely to be plesiomorphies.

Monophyly of the taxon is thus questionable. Although recent molecular investigations provided evidence that the family is indeed non-monophyletic, formal taxonomic treatment is hindered by lack of knowledge of the morphology of most genera. In the present study, the biology, shell structure and anatomy of previously unsurveyed thraciids are investigated by dissections, serial histological sections and scanning electron microscopy. Not only will the results broaden our knowledge of this poorly understood group but hopefully they will form the required morphological basis for a revision of the family.

Financial support: ORSAS; Gates Cambridge Trusts; Emmanuel College.

Release of reactive oxygen intermediates by *Lymnaea stagnalis* haemocytes: a pivotal role for Protein Kinase C

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DAVID MACKINTOSH and ANTHONY J. WALKER

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IN molluscs, Reactive Oxygen Intermediates (ROI), produced by macrophage-like cells called haemocytes, play a major role in innate immune defence and participate in the elimination of pathogens such as parasites. The NADPH oxidase enzyme, responsible for the successive formation of cytotoxic oxidative molecules including hydrogen peroxide (H_2O_2), is in part activated by Protein Kinase C (PKC) in mammalian phagocytes (El Benna *et al*, 2005). We have reported the existence of PKC-like protein(s) in haemocytes from the freshwater snail *L. stagnalis*, host for the avian schistosome *Trichobilharzia ocellata* (WALKER and PLOWS, 2003) and have found that the activity of this signalling enzyme is modulated following challenge with lipopolysaccharide (LPS) and laminarin, a β -1, 3- glucan that occurs in fungal cell walls. The purpose of the present study was to investigate the generation of H_2O_2 by *L. stagnalis* haemo-

cytes, and to determine whether or not the molecular mechanisms underlying "the respiratory burst" involve the PKC pathway. Laminarin promoted extracellular H_2O_2 output by *L. stagnalis* haemocytes in a dose- and time-dependent manner, with 10 mg/ml laminarin stimulating H_2O_2 production approximately 9-fold. The PKC inhibitor, GF109203X (10 μ M), significantly attenuated laminarin-dependent H_2O_2 production by 65% ($P < 0.001$); moreover, the NADPH oxidase inhibitor, apocynin (500 μ M), reduced stimulated H_2O_2 levels by 57% ($P < 0.001$). These results demonstrate that PKC is at least in part responsible for the synthesis of ROI by molluscan haemocytes following immunological challenge and is therefore likely to be important in snail anti-parasite responses.

Towards a phylogeny of *Limax* (Gastropoda: Stylommatophora)

BARBARA KLEE

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THE terrestrial slug genus *Limax* is distributed mainly in Europe (and introduced worldwide) and includes 20 to 30 currently accepted species, which are usually (often poorly) defined by external morphology and genital characters. A phylogeny is entirely lacking. A molecular dataset has been generated for more than 200 specimens of *Limax* and other Limacidæ based on 613 nucleotides of the mitochondrial gene cytochrome oxidase subunit I (COI). Initial tree reconstructions show that the genus *Limax* (*s. str.*) is probably monophyletic within monophyletic Limacidæ. *Limax* itself splits into multiple groups. Each of these groups contains one or several species already defined by morphological characters, but also several still undescribed taxa. These findings indicate that COI-sequences are mostly suitable for the problem, but also indicate the need for wider biogeographic and taxonomic sampling. Future improvement and confirmation are planned by further taxon sampling and AFLP-fingerprinting.

The land-snail fauna of fragmented Sri Lankan lowland rainforest and village home gardens

DINAZARD RAHEEM

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HABITAT fragmentation is one of the major threats to the Earth's biodiversity. Global biodiversity is concentrated in tropical forests, but nowhere in the world is the rate of habitat fragmentation so high as in tropics. In many parts of the tropics, modified habitats increasingly dominate the landscape and it is vital to understand the significance of such habitats to the survival and conservation of tropical forest species. This talk focuses on the structure of the land-snail communities of fragmented rainforest and village home gardens in south-western Sri Lanka. Home gardens are an important type of modified, agricultural habitat in Sri Lanka. Having evaluate the capacity of rainforest snails to persist in home gardens and explore the ecological and conservation implications of this, I show that although a substantial part of the rainforest fauna is restricted to forest, a significant number of both widespread and localized rainforest species can persist in home gardens. Home gardens, therefore, have potential as refugia for Sri Lankan rainforest snails and may have a key part to play in the re-establishment of connectivity in Sri Lanka's fragmented rainforest landscapes.

The influence of species diversity on resource partitioning in intertidal gastropods as revealed by stable isotopes

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IN recent years stable isotope techniques have emerged as powerful tools in trophic ecology. The ratio of ^{13}C to ^{12}C in animal

tissue, measured relative to a standard, provides a $\delta^{13}\text{C}$ value which gives information on the sources of organic carbon in the diet of the animal; the $\delta^{15}\text{N}$ value of the tissue provides information on trophic level. This work uses such isotopic 'signatures' to look at how species diversity influences resource partitioning within the guild of intertidal grazing gastropods found on British rocky shores. Intertidal gastropod species diversity varies with latitude, with more diverse assemblages present on southern shores than those in the north. Such natural variations have been used in this study to examine whether sympatric grazers show increased dietary specialisation and niche differentiation under conditions of different diversity.

***Achatina fulica*: its molecular phylogeny and genetic variations in global populations**

IAN K. FONTANILLA

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THE giant African land snail, *Achatina* (= *Lissachatina*) *fulica* BOWDICH, is a tropical crop pest species with a widespread distribution across East Africa, the Indo-Pacific and the Caribbean. The phylogenetic position of *A. fulica* within the Family Achatinidae and Superfamily Achatinoidea was investigated using segments of the nuclear large subunit (LSU) ribosomal (r) RNA, actin and histone 3 genes as well as the mitochondrial 16S rRNA and cytochrome oxidase I genes. Results support the monophyly of the Family Achatinidae as well as the taxonomic designation of *A. fulica* as *Lissachatina fulica* in order to distinguish it from the Western and Central *Achatina* species. The extent of genetic diversity in *A. fulica* populations was also investigated using a molecular marker developed from the 16S rRNA gene. Preliminary results indicate snails that spread across the globe were derived from a single haplotype.

Is this a sacoglossan? – Computer-based 3D anatomical visualisation of the mesopsammic *Platyhedyle denudata* SALVINI-PLAWEN, 1973 (Opisthobranchia, Sacoglossa)

INA-MARIA RÜCKERT, GERHARD HASZPRUNAR
and MICHAEL SCHRÖDL

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THE tiny marine interstitial species *Platyhedyle denudata* SALVINI-PLAWEN, 1973 has a dorsoventrally flattened, wormlike body which lacks a shell and any tentacles. Initially it was included in the opisthobranch taxon Acochliidae as an own-family Platyhedylidae by SALVINI-PLAWEN (1973). However, the postpharyngeal central nervous system and the monostichoglossan radula pointed towards a sacoglossan relationship. WAWRA (1979, 1988, 1991) corrected the original description regarding several aspects: *P. denudata* is hermaphroditic rather than dioecious, a copulatory organ is present, the cerebral and the pleural ganglia are fused instead of being separate, an ascus for storage of worn radula teeth is present, cuticular jaws appear absent, and the digestive gland is not an acochlidian-like single U-shaped duct but is comprised of two separate glandular ducts which are fused anteriorly and posteriorly. WAWRA (1979) had already transferred *Platyhedyle* to the Sacoglossa. A cladistic analysis of Sacoglossa by JENSEN (1996) placed *Platyhedyle* as the sister group of the evenly aberrant elysioidean *Gascoignella aprica* JENSEN, 1983.

Computer-based three-dimensional visualisation is an ideal tool to analyse and document the anatomy of tiny opisthobranchs, and has thus been applied to critically review the data formerly obtained on *P. denudata*. Several specimens were extracted from subtidal sands of the Mediterranean type locality, Secce della Meloria, and observed in living condition. Fixed specimens were embedded in Spurr's resin and serial histological sections (1,5 μm) were made. One

subadult individual was completely reconstructed using AMIRA software, mature gametes were studied in a second individual. Our results confirm and supplement Wawra's observations and leave no doubts on the sacoglossan nature of *P. denudata*.

JENSEN KR. 1996. Phylogenetic systematics and classification of the Sacoglossa (Mollusca, Gastropoda, Opisthobranchia). *Phil Trans Roy Soc London B* 351: 91-122.

SALVINI-PLAWEN LV. 1973. Zur Kenntnis der Philinoglossacea und der Acochliidae mit Platyhedylidae fam. nov. (Gastropoda, Cephalaspidea). *Zool Syst Evol Forsch* 11: 110-133.

WAWRA E. 1979. Zur systematischen Stellung von Platyhedyle denudata Salvini-Plawen, 1973 (Opisthobranchia Gastropoda). *Zool Syst Evol Forsch* 17: 221-225.

WAWRA E. 1988. Beitrag zur Kenntnis des Zentralnervensystems von Platyhedyle denudata Salvini-Plawen, 1973 (Ascoglossa, Gastropoda). *Ann Naturhist Mus Wien* 90: 401-406.

WAWRA E. 1991. Beitrag zur Kenntnis des Genitaltraktes von Platyhedyle denudata Salvini-Plawen, 1973 (Mollusca: Gastropoda, Ascoglossa). *Ann Naturhist Mus Wien* 92: 269-275.

Researching *Limax maximus*: Old literature and new sequences

ISABEL HYMAN

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LIMAX MAXIMUS is a terrestrial slug belonging to the family Limacidae (Mollusca, Gastropoda, Pulmonata). This species is one of the most widespread and morphologically variable species in the genus *Limax*. In addition, *L. maximus* has been introduced throughout the world. Before any biological control can be considered, *L. maximus* needs to be well understood in its natural environment. An important first step in understanding the true identity of this species involves the sourcing, translation and interpretation of old publications, since *L. maximus* has been described by many early authors. Other important datasets include anatomy, copulation behaviour and molecular data. Preliminary molecular data is based on 613 nucleotides of the mitochondrial gene cytochrome *c* oxidase subunit I (COI) for specimens from Europe, Australia and America. Current work includes the sequencing of additional specimens and a second gene, the nuclear internal transcribed spacer 2 (ITS2) from the ribosomal gene cluster.

Evolutionary history of molluscs from deep-sea chemosynthetic ecosystems

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THE bivalve family Mytilidae has representative genera and species in both recent and fossil deep-sea chemosynthetic communities. The phylogenetic relationships among these taxa and their relation to other mytilids are, however, not yet fully resolved. Molecular phylogenetic data suggest that modern mytilid genera from hydrothermal vents, cold seeps, sunken whales, and wood form one monophyletic group, and should be included in the subfamily Bathymodiolinae. This hypothesis remains untested using morphological data.

Our research aims to identify phylogenetic relationships of the Mytilidae using early ontogenetic shells and shell microstructure characters. Different structures may occur in the outer shell, which can be entirely aragonitic or composed of an outer calcitic sublayer and an inner aragonitic sublayer. Preliminary results indicate that mytilids inhabiting chemosynthetic environments show considerable differences in shell microstructural details, as well as in larval and juvenile shell morphology. Future investigation will evaluate whether those characters can indeed be used for phylogenetic analyses.

Pallet structure of wood borers of the family Teredinidae (Bivalvia)

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SPECIES of wood boring bivalves present in Norwegian waters were investigated with the collaboration of Dr Arne Snøli in the Trondheim Biological Station. Six panels of *Pinus sylvestris* were deployed in Trondheim

Fjord for one year, acting as baits to recruit wood borers. Two bivalve species, family Teredinidae, *Psiloteredo megotara* and *Nototerredo norvagica*, were identified using the key in TURNER (1966). However, discrepancies found in the literature (TURNER, 1966; NAIR, 1971) posed doubts about the initial identification of the species based on the pallets. The external shape, form and colour of the pallets were different when observed under the light microscope. The pallets thought to belong to *Nototerredo norvagica* showed an internal segmented structure, viewed with transmitted light, matching TURNER'S (1966) description of the pallets of this species. On the other hand, pallets which were identified as belonging to *Psiloteredo megotara* did not show signs of segmentation when viewed under the stereomicroscope. Furthermore, TURNER (1966) proposed that *Psiloteredo megotara* belongs to the evolutionary line of species with non-segmented pallet whereas *Nototerredo norvagica* belongs to the evolutionary line of segmented pallet. Thus, it was decided to investigate further the internal structure of the two different types of pallets under the scanning electron microscope. Initially, pellets of *P. megotara* from Norway and *N. norvagica* from Norway, Croatia and Turkey were cut at the blade level and observed under the SEM. The pallets of *N. norvagica* from all sites had a similar structure, but the *P. megotara* pallets had a clearly different structure. Pallets of *P. megotara* and *N. norvagica* were embedded in resin and then ground in the transverse plane at intervals of 250 and 500 µm to show cross sections at different levels. After each grinding they were observed under the SEM. The pallets from Norway identified as *Psiloteredo megotara* showed a different internal structure to the pallets of *Nototerredo norvagica* but, surprisingly, also showed internal segments surrounded by a solid non-segmented calcareous layer. It seems, therefore, that although the pallets belong to different species, the genera are more closely related than has been thought until now. This finding has implications in the model of the relationship between genera proposed by TURNER (1966).

Taxonomy of the genus *Trochulus* (Gastropoda: Hygromiidae) in the Czech Republic

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THE genus *Trochulus* (formerly *Trichia*) was always considered to be taxonomically problematic. Previous research revealed substantial cryptic diversity in this genus in the surroundings of the Alps. Little is known however, about the situation in other Central European regions. Our study focuses on whether the observed morphological differences of populations in the Czech Republic can be explained by the presence of cryptic species, or by intraspecific variation. We analysed 14 populations of two species of the genus – *Trochulus plebeius* and *T. hispidus*. Karyotype analysis revealed that all the studied populations have identical number of chromosomes ($n = 23$) of similar morphology. Sequence analysis of 16S rDNA and COI showed two divergent groups of *T. hispidus* populations, differing in geographic distribution (north-western versus eastern) but with overlapping morphology. To clarify the status of the two clades, we are conducting breeding experiments to test for potential reproductive isolation.

Mobility of *Bulgarica cana* in a natural habitat

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MOVEMENTS of *Bulgarica cana* (HELD, 1836) (Gastropoda: Pulmonata: Clausiliidae) were observed in its natural habitat in a riparian forest in the valley of a small stream

(Romincka Forest; NE Poland). From June to September 2006, 310 individuals of *B. cana* were individually marked and 57 individuals was re-trapped. Most snails (75% - 43 individuals) stayed on the same tree during the whole investigation period. Only 12 individuals moved to another tree and the distance was approx. between 1 to 5 m (measured from tree to tree). The longest distance was 20 m (made during 1 month).

Additionally, for four successive days, movements of *B. cana* were observed every 12 hours. Snails moved from 10 cm to more than 150 cm within the same tree per day. Some specimen stayed inactive for 2-3 days.

Species-area relationships in the spring fen mollusc communities

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WWE studied species-area relationships at nine Western Carpathian spring fens (differing in mineral richness), sampling a set of three nested quadrats in each site. When considering only live molluscs or all shells, principal differences in the numbers of species as well as individuals were found. Differences were also found among the mineral fen types. In mineral-poor fens, the smallest plot (25 cm²), contained a significantly smaller part of the site's species richness than the mineral-rich, and tufa forming fens, due to the sites' lower abundances and higher heterogeneity. The species accumulation curve was therefore steep for mineral-poor sites (especially from the 25 cm² to 50 cm² plots) and became more shallow towards the mineral-richer fens. However at all sites, regardless of mineral type, the largest plot (75 cm²) plot contained 84% of the site's richness (only 2 species short of the total for the whole site). This demonstrates that the 75 cm² plot fairly reflects the site's species richness.

Combining confocal laser scanning microscopy and electron microscopy to investigate the mantle and velar ciliation of larval bivalves

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THE planktotrophic larva *Crassostrea gigas*, has organised ciliation on the mantle and velum that increases in complexity during larval development. Serotonin and catecholamines have been implicated in the control of ciliary activity, as early morphogens, and as triggers in metamorphosis. General catecholamines were imaged with aldehyde induced fluorescence, while serotonin was localised using immunohistochemistry. The current study aims to clarify the localisation of these compounds in specific larval structures through the novel integration of observations from fluorescence microscopy with anatomical information from scanning electron microscopy. SEM has been used to examine the distribution and morphology of the ciliation found on the larvae, and discrete cilia groups were identified and 'mapped' throughout larval ontogeny. SEM and traditional LM sectioning has also indicated the presence of a previously unrecorded row of compound cilia on the velar rim.

Sphaerium corneum / *nucleus* (Bivalvia: Veneroida: Sphaeriidae) is a complex of several cryptic species

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DISTINCTION between cryptic species often depends on the different concepts of species adopted by the respective authors.

Combination of different methods and approaches are therefore needed to reach conclusions about the status of similar forms. A good example is *Sphaerium nucleus*, described by STUDER in 1820, regarded as a subspecies of *S. corneum* for many subsequent decades, and revised and considered a good species by KORNIUSHIN in the 1990s.

We analysed a number of populations putatively identified as either *S. corneum* or *S. nucleus* from the Czech Republic, comparing anatomy, ecology, karyotypes and sequences of mitochondrial gene for 16S rRNA. Whereas the karyotypes differ only slightly and are difficult to compare because of frequent presence of abnormalities (aneuploidy, additional chromosomes), the different habitat preferences and functional adaptations of the latter species to extreme habitats support its distinctness from the former. The analysis of available sequence data suggests that "*S. nucleus*" forms more than one clade of the same rank as *S. corneum*. Thus, the redescription of both species is needed for any potential revision of this complex.

POSTERS

The phylogeny of molluscs and their relatives within the Lophotrochozoans

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THE phylogeny of the Bilaterians and more primitive taxa is partially a still unresolved enigma. To address this question a project called the "Deep Metazoan Phylogeny project" was initiated by thirteen different German scientific groups. As

members of this project, we will try to unravel the mystery of the phylogenetic relationship of all metazoan groups using a large data set of protein sequences of nuclear encoded genes, which derive from both comparative EST (expressed sequence tags) analyses and the amplification of selected, phylogenetically informative genes. The main tasks of our investigations are both to resolve the phylogenetic relationship of the main groups within the molluscs and the positioning of this phylum within the higher order of the Lophotrochozoans, with special respect to the Sipunculida and the Kamptozoa as a potential sistergroup of the Mollusca. However, the preparation and the analyses of the EST data and some specifically selected "house keeping genes", also known from analyses of PETERSON et al. (2004) are still in progress and therefore cannot be used for further analyses. We therefore started to generate and analyse five other genes, the 16S, 18S, 28S, COI and H3 respectively, to reconstruct a molecular tree including most of the Lophotrochozoan taxa.

The molluscan collection of the National Museums Scotland (Royal Museum); significance, value and potential

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THE mollusc collection of the National Museums Scotland is the third largest in the U.K. and is of global significance. Holdings include: type specimens of W.S. Bruce's Scottish National Antarctic Expedition (1902 – 1904); deep-water species from the Rockall Trough and the Portuguese coast from the British Atlantic Benthos Survey (1973); and comprehensive series of land and freshwater molluscs, including the A. E. Salisbury collection (acquired 1961), being

the largest private collection of exotics in the U. K. Our new storage facilities provide ample bench space. NMS seeks to maximise the usage of its collection and offers opportunities for research in, but not only, the areas of taxonomy, morphometrics, isotopic analyses and biogeography. There are further opportunities for public dissemination of research, given the special museum combination of research with a public interface. NMS encourages inquiries from interested visitors and collaborators, both for short visits, loans and longer term projects.

Niche creation for cryptofauna by teredinid bivalves in mangroves

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TEREDINIDS (Family Teredinidæ) are an intriguing collection of morphologically and physiologically diverse assortment of animals. The cosmopolitan diversity observed within this family is facilitated by the myriad of various life histories adopted by these animals. The initial stimulus, which facilitates settlement of planktonic teredinid larvæ, remains ambiguous. These animals are able to process the available carbon provided by the high abundance of dead woody substratum. However, the burrows facilitated by the vivacious feeding activity of the teredinids may magnify potential niche creation for mangrove cryptofauna. This research will focus therefore upon the factors responsible for pediveliger settlement, thereby underlining ecologically important questions such as what factors control the settlement and initial penetration of the wood by the larvae. Furthermore this research will also investigate the potential cryptofaunal diversity facilitated by shipworms in mangrove ecosystems, with the intention of highlighting the ecological role of cryptofaunal populations.

Seasonal variation of zebra mussel tolerance to toxins

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THE zebra mussel, *Dreissena polymorpha*, is an invasive species whose biofouling activity has major impacts on fresh water-dependent industries. A common approach for controlling this pest is to apply suitable biocides at the end of the breeding season in late autumn. The assumption behind this practice is that adult mussels are more sensitive to toxins after spawning when their condition is at its weakest. However, the tolerance of bivalves to biocides is dictated not only by their body condition, but also by other factors, amongst which is their filtration rate. Both body condition and filtration rate undergo seasonal variation related to the species' reproductive cycle and the annual variation of environmental conditions. The seasonal variations of these two factors tend to have opposing effects on the susceptibility of mussels to biocides. In this study, it is hypothesised that the lowest tolerance of the species to toxicants occurs when an optimal combination of body condition and filtration rate is reached, not necessarily when the former is at its lowest or the latter is at its highest. To test this hypothesis, the tolerance of zebra mussels to three reference toxicants, with distinct modes of action is being tracked by monthly measurements for one year. Results of this study may have implications for the appropriate timing of control treatments, as well as for the setting of protocols for conducting toxicological studies with the species.

Co-evolution or easy exploitation?: Trematode prevalence, diversity and lifecycles in endemic gastropods of Lake Tanganyika, East Africa

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LAKE Tanganyika's ancient age (14 MY) and remarkably diverse array of endemic flora and fauna are reasons to expect numerous co-evolutionary developments among its inhabitants. Interactions between host gastropods and trematode parasites remain relatively unstudied in the lake despite potential impacts on evolution of endemic species, and ecosystem function. In this study, we aimed to relate trematode prevalence and diversity in *Lavigeria nassa*, a 'thiarid' gastropod commonly found throughout the littoral zone of the lake, to depth, site characteristics, brood size, and shell morphometric variables. We examined approximately 1200 *L. nassa* at four depths and three sites in the Kigoma, Tanzania area for parasite infection. Smaller samples of *Paramelania damoni* and *Vinundu guillemei* were also surveyed. For each gastropod we measured shell height, width, lip thickness, and scarring due to attempted crab predation. Five morphotypes of trematodes were identified. Parasite prevalence and diversity differed across depths and sites. Shell size was also highly variable, but no apparent connection existed between morphometric data and parasite prevalence. Ongoing work aims to correlate reproductive strategy of brooding females with parasite prevalence in the maternal population, and molecular profiling of the parasites is underway.

Geometric morphometric analysis of geographic variation in four endemic gastropod species from Lake Tanganyika

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LAKE Tanganyika is the largest of the East African rift lakes and home to the endemic gastropod genus *Lavigeria*, a species flock which contains approximately 45 patchily distributed species (MICHEL and TODD, 2003). We used a detailed landmark-based geometric morphometric approach on four species to examine the following questions:

1. Are geographically separated populations morphologically distinct? If so, what shell features differentiate the populations?
2. Do closely related species exhibit similar patterns of morphological differentiation geographically?
3. Do these species exhibit sexual dimorphism? If so, what differences in shell morphology characterize these groups?

Our results indicate that there are different patterns of morphological variation among these species, despite their sympatric distributions (and thus likely similar ecological pressures). In some species, geographically separate populations of the same species may differ greatly (*L. grandis*), or subtly (*L. nassa*). In all species, adult females are on average larger in size than adult males, but dimorphism in shape differs in character between species, with clear differences within *L. sp. J* and *L. sp. W*, and only very subtle differences for *L. grandis* and *L. nassa*.

We conclude that divergence between populations may be the result of drift or of local adaptation to heterogeneous environments. Geometric morphometrics is a powerful tool for detecting fine-scale morphological differences within and among species.

Hemocyanin: an appropriate new marker. Phylogeny of polyplacophorans resolved by hemocyanin genes

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MOLLUSCAN hemocyanins are ancient respiratory proteins estimated to have evolved ~700-800 MYA. The native molecules are formed from 10, 20 or more identical subunits of which each possesses a molecular mass of 350 - 400 kda. The subunits show a repetitive structure of 7 (a-g) to 8 (a-h) functional units. Each domain-coding exon is separated from a paralogous neighboring exon by an intron of variable size. These introns are probably as ancient as the Precambrian duplication events that led to the repeated exons, because all these introns are in phase 1 and are also located at the same positions within the orthologous hemocyanin genes across Mollusca. In contrast to the case of gastropods, bivalves and cephalopods, in which paralogs of the entire hemocyanin gene region can be observed, chitons possess only one type of hemocyanin, and this forms ~4,000 kda homodecamers.

We assessed the phylogenetic utility of hemocyanin for selected chitons. Particular hemocyanin coding regions were compared across diverse chitons and results were consistent with expectations for high-level relationships based on recent morphological and molecular studies. In particular, Chitonida was robustly subdivided into two clades, Acanthochitonina and Chitonina, although these results are preliminary due to still limited taxonomic sampling.

Cryoelectron microscopy and single particle analysis of *Nautilus pompilius* hemocyanin under different oxygenation states

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HEMOCYANINS are the copper-containing respiratory proteins of many molluscs. They are basically composed of ten copies of an elongated 350 to 400 kda polypeptide (subunit). This subunit consists of seven or eight O₂-binding functional units (FUs) termed FU-a to FU-h. The ten subunits form a hollow cylinder (the decamer) of ca. 35 nm in diameter, with an internal collar structure. In gastropods, two decamers assemble face-to-face, comprising a didecamer of 8 Mda (for details, see MEISSNER et al. 2000, J.Mol.Biol. 298, 21-34). In the cephalopod *Nautilus pompilius*, single decamers are present, based on a subunit comprising only seven FUs; its complete primary structure has recently been published (BERGMANN et al. 2006, J. Mol. Evol. 62, 362-374). Although X-ray analysis of single FUs are available that provide near-atomic resolution, the exact path of the elongated subunit within the decamer, respectively didecamer, as well as details of the collar structure are still obscure. Notably, information about possible structural movements within the molecule during cooperative oxygen binding is scarce. According to SAXS analyses (HARTMANN et al. 2004, Micron 6:11-13), such conformational changes should be directly visible at a

resolution between 10 and 20 Å. Computer aided processing of data obtained by cryo-electron microscopy should allow to directly visualize the quaternary structure of different native states. Therefore, we developed a preparation method for respiratory proteins that allows their incubation in different gaseous environments and their subsequent shock-freezing in liquid ethane. To visualize conformational changes during oxygenation, we choose *Nautilus* hemocyanin because of its simpler construction and higher symmetry compared to gastropod hemocyanin. We freshly purified the hemocyanin from *Nautilus* hemolymph and exposed aliquots to two different atmospheres: deoxy (100% N₂) and oxy (25% O₂, 75% N₂). Subsequent high-resolution cryo-electron microscopy, digital image processing, and 3D reconstruction allowed a comparison of both structures at ca. 10 Å resolution which revealed significant structural differences between the putative oxy and the putative deoxy form. The clues of these results, and possible pitfalls such as artifacts will be discussed.

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Interaction between environmental factors and life history variables in determining recruitment of the Manila clam

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RUDITAPES PHILIPPINARIUM is a bivalve mollusc that has become established far outside its traditional range in South East Asia. A breeding population has become established in Poole harbour. There are also reports of populations in the Thames Estuary and Southampton water. In a recent benthos survey of Langstone harbour *Ruditapes* was not found, but conditions are similar to Poole harbour. The mud flats offer a potentially suitable environment for *Ruditapes* to settle. The study's aims are to determine whether *Ruditapes* could settle in Langstone harbour by investigating its life history strategies. The Poole population will be sampled throughout the year to determine the time of spawning. Subject to clearance, a population will be kept adjacent to the institute of marine sciences to compare cycles with the Poole population. Molecular phylogeny will be used to determine whether the south coast populations are separate from one another.

