Euromal 2024

ABSTRACT BOOK

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The Hellenic Malacological Society (HMS), founded in 2018, is a scientific, non-profit organization dedicated to the study and protection of molluscs, both extant and fossil, and their habitats in Greece, Cyprus, and the wider Eastern Mediterranean region. Welcoming professionals and amateurs, the HMS aims to educate and raise public awareness about the importance of molluscs. The Society's activities include studying all molluscan taxa, advising the government on mollusc-related matters, promoting collaborations among various stakeholders, and organizing educational events such as meetings, conferences, and symposia.

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Why are there so many kinds of snail?

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Keywords: Land snails, distribution, morphology, co-existence

There are almost certainly more than 40,000 species of land snails and slugs. More are discovered each year. In accounting for this diversity, we can find many case-histories that involve vicariance and dispersal following environmental change or tectonic shifts; cases of dispersal into habitats that are scattered; the effects of poor powers of active dispersal, and cases where diet, substrate and resistance to environmental extremes dictate range limits. While such case-histories, often backed by molecular analyses, build a bottom-up basis for accounting for diversity, it is the substance of my talk to query some of the assumptions on which they are based. What do we mean by niche in the context of geological time? What is the impact of phylogenetic constraint and physical limitation on evolutionary change? How do form and function align? By examples, I will show the shakiness of some assumptions, and examine the role of competition or interference in structuring diversity. At the core of my argument is doubt about the equation between species and kinds. Further, I will argue that we wallow in a sea of ignorance when it comes to questions of traits that might determine the history of given kinds, and pay insufficient attention to the power of natural selection to overcome abiotic constraints.

Using integrative phylogenetic approaches for inferring species richness, macroevolution and extinction risk in continental aquatic gastropods

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Keywords: Conservation, diversification, Hydrobiidae, species delimitation, systematics

The continental aquatic ecosystems of the western Palaearctic and Nearctic regions are dominated by a remarkable family of microgastropods: the Hydrobiidae. With over 1,000 nominal species, these intriguing snails have adapted to diverse habitats, ranging from top mountain springs to brackish environments, lakes and subterranean waters. They have also successfully colonised most Mediterranean islands, including numerous Greek islands. Their impressive adaptability and limited dispersal ability within hydrological basins make them ideal candidates for testing various evolutionary and ecological hypotheses in aquatic organisms. However, for decades, malacologists have encountered significant challenges in delimiting and identifying species due to their minute size (0.5-8 mm in height), inconspicuous shells, simple anatomy and narrow geographic distribution. Most species live in ecosystems with limited fossilisation potential (e.g. spring, subterranean and karstic waters), resulting in a sparse fossil record. While molecular data can overcome some limitations of morphology-based identification and systematics, the most effective approach combines multiple data types. Integrating morphological and geographical data with molecular phylogenies has proved promising in establishing a robust taxonomic framework, crucial for advancing our understanding of gastropod systematics, biodiversity patterns and evolutionary processes. Recent multilocus phylogenies of hundreds of species, combined with multiple internal calibrations, have revealed that the Hydrobiidae family is younger than previously thought, beginning to diversify around 60 million years ago, shortly after the fifth mass extinction event. Phylogenetic diversity inferred from these phylogenies will be used to assess the contemporary extinction risk of numerous species that are underrepresented on official Red Lists. In this session, we will explore integrative phylogenetic approaches for disentangling the taxonomy of cryptic groups and inferring biogeographic history, morphological evolution, and diversification dynamics over time and across clades. Additionally, new deep-learning techniques to predict extinction risk for a large number of species will be introduced.

Malacological data from the past, some leftovers for Greece

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Keywords: Taxonomy, species, evolution, predation, Greece

As usual near the end of a career, there are leftovers from several projects that are worth being published. Here, I use the opportunity to add data on some hydrobioid spring snails from Greece, with critical comments on their treatment in the recent literature. Two genera of Clausiliidae are common in Greece, but very different in many aspects. For the genus Tsoukatosia, overlooked a long time, 8 (sub)species are 'known' now, that may be called living fossils, such as two more clausiliid genera, i.e. Graecophaedusa and Sciocochlea. These animals live subterraneously, in a habitat that is virtually inaccessible to humans, as I once more discovered last year. The contrasting genus Albinaria, that has been repeatedly and confusingly defined in the literature, is abundantly and conspicuously present in Greece. It is an ideal subject for ongoing theoretical discussions about the species concept, following in Albert Mousson's and Adolf Schmidt's footsteps, without any relevant proceeding. The snails suffer from predatory Drilus beetles, so that the Albinaria-Drilus relationship became a model for predation research. Some characters of the Albinaria shells may be considered an adaptive response to the actions of the hole-boring beetles. We add some data that ask for further research. Finally, the forgotten (?) fossil Albinaria's that lived in the geological past in Crete, are dealt with. Those days, the island was inhabited by fancy species of deer. The shells are compared with those from recent populations that live in the same area now.

The Miocene roots of the Circum-Mediterranean gastropod diversity – the combined terrestrial and marine record

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Keywords: Neogene, Mediterranean, Paratethys, biogeography

Hundreds of papers were devoted to Neogene gastropods from the Mediterranean Sea and the Paratethys Sea, and a huge bibliography exits describing terrestrial and freshwater gastropods of Europe. In the marine records, we recognized that literature data (referring to the latest available revision) were incorrect at genus level by 58% and by 33% at species level per family. Similarly, the terrestrial record suffered from numerous misidentifications and broad or incongruent species concepts. For more than a decade our working group has been re-examining numerous gastropod groups and was critically revising their taxonomic systematic and geographical distributions. The Neogene record of terrestrial gastropods has never been compared to its marine counterpart. Based on our revised dataset we elucidate the response of marine and terrestrial biota to global changes of the climate such as the Miocene Climate Optimum and the subsequent cooling during the Miocene Climatic Transition and detect differences and similarities in the marine and the terrestrial spheres. In addition, we date and quantify the appearance of extant species in the fossil record. This holistic approach provides new insights into the evolution and diversification history of gastropods in this important biogeographic region.

Socially transferred materials in molluscs

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Keywords: Conflict, Copulation, *Cornu aspersum*, Egg laying, Hermaphrodite, *Lymnaea stagnalis*

Individuals can influence conspecifics through a diversity of interactions. Such positive and negative social effects caused by relatives, competitors or mating partners affect fitness. Well-studied interactions include visual, pheromonal and auditory communication, but senders can also transfer biological materials that intentionally bypass sensory organs and directly affect the physiology of the receiver. Examples of such socially transferred materials (a.k.a. allohormones) can be found in mucus, yolk, milk, saliva and ejaculates. After briefly covering some of this biological diversity, I will present examples from love darts 'shot' by land snails and ejaculates transferred by freshwater snails as well as touch upon how these are affected by anthropogenic effects. In both cases accessory gland proteins are transferred by the donor that affect the reproductive physiology of the recipient (i.e. mating partner). Because these snail species are simultaneous hermaphrodites, this also allows me to assess whether predictions from sexual selection theory, which is generally still framed from a separate sexes perspective, apply to species that are male and female at the same time. I will illustrate that with the right hermaphroditic model species and using an integrative approach, one can still experimentally and genomically disentangle female from male processes, and understand both why and how accessory gland proteins (and other socially transferred materials) have evolved.

Mainstreaming Mollusc Conservation into Biodiversity Planning

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Keywords: Mollusc, conservation, biodiversity targets

Between 1996 and 2024, the IUCN SSC Mollusc Specialist Group has assisted with the assessment of nearly 10,000 species of Mollusc on the IUCN Global or Regional Red Lists (latest version 2024.1). This spans marine (18.6%), Freshwater (41.5%) and Terrestrial (38.5%) ecosystems. The most severe threats to Molluscs remain 1) habitat loss through urban expansion, 2) pollution from sewage, 3) pollution as result of agricultural activities, 4) mining and quarrying and 5) exploitation of water sources. However upcoming threats that have become more dominant in the last 5 years include "increased frequency and intensity of fires" and include "increased frequency and intensity of drought events", and "impact from named invasive non-native species" such that these three threats are becoming common threats at a global level, rather than more localised threats. The Red List documentation allows for the identification of actions required to mitigate and reduce the threats to Molluscs on a world-wide basis and this data could be used to streamline conservation actions into country-level plans. At Conference of the Parties in 2022, nations agreed to a new action plan for the decade 2020-2030: the Kunming-Montreal Global Biodiversity Framework. This plan is designed to halt and reverse biodiversity loss by 2030, to stop extinctions and recover species populations, and restore ecosystems by the end of the decade. This provides an opportunity for malacologists to champion the integration of more molluscs. To improve conservation action, we need to:

1) Create multispecies conservation plans eg. European freshwater bivalves with policy actions at regional levels, conservation and monitoring actions at catchment levels.
2) Identify species and sites for CBD Target 1: reduce biodiversity loss - freshwater littorinids in India and the Partula programmes.
3) Undertake Action plans for threatened species CBD Target 4: Bermuda Land Snail project.
4) Where threatened species occur in an existing Key Biodiversity Area get them added to the local management plan.
5) Suggest methods for monitoring threatened species
6) CBD Target 2: 30% restoration of degraded areas by 2030: ensure any actions are not damaging to existing fauna and will benefit threatened molluscs where present.

What do whole genomes tell us about molluscan evolution?

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Keywords: phylogeny, genomics, evolution, molluscan weirdness

The molluscan genomic landscape has long been a largely uncharted wilderness, but we are rapidly making progress in sequencing, assembling, and understanding mollusc genomes. Until recently, the risk and expense of undertaking whole genome sequencing for molluscs tilted scientific attention toward species with striking adaptations, anomalies, or commercial importance. This generated a set of genomes that are each interesting, but not an effective sampling strategy to establish a dataset to test deep phylogenetic questions. Nonetheless the rapid advance of genome sequencing on many fronts has filled in many gaps, and targeted efforts have concentrated on gathering new data for some of the most rare and elusive clades. New chromosome level genomes for Polyplacophora reveal new and interesting features of molluscan genomes with extreme syntentic rearrangement even between closely related species. Comparison with other genomes from conchiferan clades allowed us to confidently identify a set of common Molluscan Linkage Groups that represent the 20 ancestral molluscan chromosomes, and track their rearrangement including in genome duplication events. The flexibility of the molluscan genome may explain both the success of molluscs, and our challenges in sequencing them.

Natural Distribution of Terrestrial Gastropods in Delta Region and its impact on food security in Egypt

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Keywords: Distribution, terrestrial, gastropods, Egypt

As a significant contribution to the malacofauna of Egypt, an extensive inventory of terrestrial gastropods, including both snails and slugs, was recorded in the Delta region. This study highlighted the spread of many invasive terrestrial snail and slug species in the Delta region, primarily due to climatic changes and breaches of agricultural quarantine rules. These invasive species have been recorded in agricultural areas associated with economically important field crops and vegetables. Sample collection and data recording took place during the activity season. However, numerous observations suggest that terrestrial gastropods remain present in agricultural fields throughout the year, even during the high temperatures of the summer months and low level of humidity. Live snails and slugs were gathered from various sites, and their species were illustrated and described in detail, accompanied by a comprehensive report on their distribution in the Delta region of Egypt. The collected data linked terrestrial gastropods to economic damage and crop losses, highlighting their negative impact on crop yield productivity. This inventory serves as a crucial resource for understanding the distribution and impact of terrestrial gastropods on agriculture in the Delta region, emphasizing the need for effective management strategies to mitigate their adverse effects on crop production.

Phylogeny and species delimitation in *Albinaria* from western Crete (Gastropoda: Clausiliidae)

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Keywords: admixture, double-digest restriction site-associated DNA, Greece, isolation by distance, systematics

We studied the phylogenetic relationships and species delimitation of the *Albinaria* species from western Crete classified in the *Albinaria candida* group based on sequences of 2050 loci generated by double-digest restriction site-associated DNA sequencing. It turned out that neither the *A. candida* group nor the *Albinaria cretensis* group is monophyletic and that the anterior palatal folds that allegedly characterize the species of the *A. candida* group were convergently reduced several times. That these folds are not suitable for diagnosing species groups became especially clear in the populations from Gramvousa Peninsula and adjacent areas, in which the development of the anterior palatal folds is variable. Previously, populations with anterior palatal folds were classified as *Albinaria loosjesi*, a species of the *A. candida* group, whereas populations without anterior palatal folds were classified as *Albinaria tenuicostata*, a species of the *A. cretensis* group. Our analyses showed that they belong to a single species, *Albinaria grabusana* (= *A. loosjesi*), which is not related to *A. tenuicostata*, but to *Albinaria xanthostoma* from the neighbouring Rodopos Peninsula. Admixture analyses and isolation-by-distance tests confirmed the specific distinctness of *A. grabusana*, *A. xanthostoma*, *Albinaria amalthea*, and *A. candida*.

Evolution of sexuality in Sepiolinae (Cephalopoda: Sepiolidae)

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Keywords: Cephalopoda, hectocotylus, bursa copulatrix, mating, coevolution

The subfamily Sepiolinae is characterized by the hectocotylized left dorsal arm in males and the occurrence of a bursa copulatrix (copulatory pouch) in the left ventral side of the mantle cavity in females. Mating occurs in the parallel position: the male holds the female – its dorsal side adhering to the mate's ventral side – and introduces its dorsal arms into the female's mantle cavity to transfer its spermatophores to the bursa copulatrix. As a matter of fact, consistently with the topography of the copulatory organs, mating in the parallel position allows the alignment of the spermatophore-carrying hectocotylus with the bursa copulatrix, which indicates coevolutionary correspondence among the morpho-topography of the hectocotylus, that of the bursa and the mating position.

The sepioline hectocotylus is very complex and mostly species-specific. Its morphology follows either of two distinct main bauplan: bipartite structure, with the suckers in the distal portion forming a palisade (*Eumandya* and *Euprymna*); tripartite structure, where the suckers in the middle part – the copulatory apparatus – are deeply modified (all other genera).

The bursae copulatrices too are morphologically diverse across genera and species, and may be allocated into two main types: closed (the plesiomorphic state) and open (the apomorphic state); anyway, the genera grouping according to the bursa type does not match exactly the hectocotylus-based grouping.

Seemingly, the male and the female copulatory organs coevolved. This supposition is well supported at the tribe level (Sepiolini vs. Euprymini), less so at the genus level, but is very well backed in a few species. The best hypothesis for such coevolution implicates a combination of lock-and-key mechanism and cryptic female choice of hectocotylus morphology.

Lastly, the high diversity of both the hectocotyli and the bursae copulatrices throughout Sepiolinae constitutes a powerful tool in systematic and biogeographic investigations. Moreover, the subfamily common mating ethogram corroborates its monophyly.

Towards the new Croatian Natural History Museum – Fossil molluscs collections under pressure

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Keywords: curation, conservation, collection management, relocation

Events in recent years have put the museums worldwide in a challenging position. Along with the pandemic, earthquakes and managing new ways of communication with the public, the Croatian Natural History Museum has faced one of the biggest challenges since its establishment: complete museum building renovation, preparations for the new natural history permanent exhibition, and relocation of the museum collections in a new depot facility. These activities encompassed different techniques of fossil molluscs preparation and protection for their relocation, conservation in the new depot, as well as the collection management in the focus of the new permanent exhibition and promotion activities of the Museum renovation.

Since March 2020, the Croatian Natural History Museum has been closed for public. To continue presenting collections to the audience, in 2023 the Museum also launched the virtual exhibition on the topic of fossil oysters. The exhibition includes 3D views of chosen fossil oysters made on these specimens for the first time. Everything was designed from the beginning, not on already available classic exhibition, enabling us the opportunity to learn more about the exhibition possibilities in a virtual environment.

Based on the recent experience of the Croatian Natural History Museum, this paper shows the examples of fossil molluscs' conservation and collection management in a demanding time.

Lymnaeid gastropods of the late Miocene Lake Pannon (Pannonian Basin, Central Europe): taxonomic revision and their biostratigraphic and palaeoenvironmental importance

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Keywords: biostratigraphy, brackish-water, Lymnaeidae, pulmonate, taxonomy

At the beginning of the late Miocene period, ca. 11.6 Ma ago, Lake Pannon was formed due to isolation from the Paratethys Sea. This vast brackish-water and long-lived lake existed through 7 Ma and generated a large extent of sedimentary infill. Wide distribution of the lake sediments can be studied in the present-day countries in Central Europe. These sediments hide important geo-energy resources that induced the born of an inevitable chronostratigraphic system. This system mostly relies on the evolution of endemic molluscs and dinoflagellates. Mollusc species are originated from marine relict and freshwater immigrant taxa.

In the present study, a special lineage of lymnaeid gastropods was revised. The studied material came from museum collections of Hungary, Croatia, Austria, and Romania, and new fossil material was also collected from different parts of the Pannonian Basin System. At least 30 lymnaeid species were described from the Lake Pannon deposits but based on the recent study of more than 500 specimens, they belong to 13 species of 7 genera. We concentrated on the evolution of Radix-Velutinopsis-Undulotheca-Provalenciennesia-Valenciennius lineage, but some shallow-water lymnaeids were also included in this study. A new Corymbina species is reported here that is the first mentioned Corymbina species in the late Miocene of Lake Pannon. This brackish-water endemic genus is mostly characteristic for the Pliocene of the Aegean Basin.

Lake Pannon lymnaeids are one of the most unique groups of Lake Pannon molluscs. Their interest lies in their specific morphological features (large size – sometimes more than 10 cm, wide, flat, cap-like shell with reduced coiling and undulated ribs) and deep-water lifestyle confirmed by drill core occurrences and seismic sections. Due to the present taxonomic revision, the studied lineage can be used in the deep-water biostratigraphy of Lake Pannon sediments.

This research was funded by the National Research, Development and Innovation Office of Hungary (NKFIH K 143787 grant).

Insights into the systematics of the Iberian land snail genus *Iberus* s. l. (Stylommatophora: Helicidae) inferred from molecular multilocus data: new taxonomical proposal

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Keywords: *Iberus*, molecular phylogeny, multilocus, diversity

The genus *Iberus* includes some of the largest and most spectacular land snails of the European malacofauna. With all the species endemic to the Iberian Peninsula, it is a well-known genus locally as many of their species are highly appreciated gastronomically, which poses an important pressure on their populations. Moreover, the genus is widely known and has been comprehensively studied by malacologists, yet its systematics has been and still is very controversial. Without evident diagnostic anatomical differences, Iberus systematics has been based mainly on shell characters, but several of the problems known to affect this character in gastropods have been identified for this genus: local adaptations, homoplasies and also the presence of cryptic species. To overcome this problematic, in this study we have reconstructed the phylogeny of Iberus using a multilocus approach with 2 mitochondrial genes (COI & 16S) and 2 nuclear regions (ITS1-5.8S-ITS2-28S & adenine nucleotide translocase gene) along with the most comprehensive sampling to date covering the complete genus distribution and diversity with 170 specimens. We recovered 24 well supported clades grouped in 5 main clades. 23 of these clades could be assigned to already described species and we were able to establish the synonymies for all but one of the available names. One of the clades could not be related to any nominal species and is therefore assigned to a new species status. We also discuss the taxonomic status of *Pseudotachea* and *Tartessiberus* with respect to *Iberus*. Thus, this work provides a solid systematic framework for *Iberus*, necessary for effective conservation of its species and for understanding the evolutionary processes shaping its diversity.

Distribution and ecology of three habitat-specialized terrestrial snail species of the genus *Vertigo* (Gastropoda: Eupulmonata: Vertiginidae) in Europe

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Keywords: EU Habitats Directive, IUCN Red List species, *Vertigo lilljeborgi*, *Vertigo genesii*, *Vertigo geyeri*

Species of the genus *Vertigo* O. F. Müller, 1773 are tiny land snails with shell height around 2 mm. Many of them are restricted to colder climate areas and their centre of distribution lies in higher latitudes, such as *Vertigo lilljeborgi*, *V. genesii* and *V. geyeri*. These species are habitat specialists that are restricted to minerotrophic fens with stable water regime and their main area of distribution lies in boreal and arctic zones. To the south, their occurrence is a relict of more continuous distribution during the late glacial and early Holocene. Their occurrence indicates sites of ancient origin and conservation importance. By the end of the last century, only a few sites were known from temperate Europe. With the onset of new millennium, the number of known sites had started to grow rapidly, partly due to enlisting the latter two species in the Annex II of the EU Habitats Directive (94/43/EEC). Despite the increased number of records, there is no comprehensive study documenting their European distribution. Therefore, we compiled all published distribution data including original unpublished data and created distribution maps. Moreover, their ecological preferences were analysed using data spanning their whole range of distribution.

Oral Presentation

Interplay of UV-filter pollution and temperature rise scenarios on *Mytilus galloprovincialis* health: unveiling sperm quality and adult physiology, biochemistry, and histology insights

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Keywords: Climate change related factors, sunscreens and cosmetics, adult responses, sperm quality impairments, mussels

Marine-coastal organisms face increasing stressors, leading to ecotoxicological risks at various life stages. Among these, changes in abiotic factors related to climate change (i.e., rising sea temperatures) and pollutants (i.e., ingredients from personal care and cosmetic products) pose significant threats. One emerging pollutant of concern is 4-methylbenzylidenecamphor (4-MBC), a chemical UV-filter commonly found in sunscreens and cosmetics. Continuously released into aquatic environments, 4-MBC's lipophilicity and persistence present risks to marine biota. However, its toxicity under predicted climate change scenarios remains largely unexplored. This study investigated the effects of environmentally relevant concentrations of 4-MBC, combined with current and predicted warming scenarios, on the performance and male reproductive health of the marine mussels *Mytilus galloprovincialis*. Using biomarkers across sub-cellular, cellular, tissue and individual levels, the study revealed significant physiological and biochemical impairments in both sperm cells and adults exposed to 4-MBC. Temperature emerged as a primary driver of mussel responses, modulating the impacts of 4-MBC. Mussels showed heightened sensitivity to temperatures outside their optimal range, with interactive effects between stressors. Specifically, sperm motility declined with increasing UV-filter concentrations, while temperature alone influenced reactive oxygen species production, leading to compromised mitochondrial activity and DNA damage under combined stressor conditions, indicative of potential reproductive impairments. Adults exhibited high bioconcentration potential of 4-MBC in tissues, compromised physiological status, morphophysiological changes in digestive glands, oxidative stress, and alterations in metabolic capacity, as well as antioxidant and biotransformation defense mechanisms, correlating with UV-filter exposure and increased temperature. The observed histopathological and biochemical alterations underscore the substantial ecological risk posed by environmental contaminations of UV-filters, especially in the context of anticipated climate warming, along with the vulnerability of *M. galloprovincialis* to cumulative stressors. Effective conservation strategies and proactive measures are essential to mitigate the adverse effects of climate change and pollution on these keystone species, preserving their habitats.

How species concept can affect the conservation of freshwater snails? Exploring ecological niche modeling and coalescent species delimitation approaches in Physidae and Lymnaeidae (Hygrophila)

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Keywords: mPTP, PTP, putative species, coalescence, ecological niche divergence

A common issue for the freshwater snail families Physidae and Lymnaeidae is the fact that the criteria for species delimitation are scarce, subjected to intraspecific and ontogenetic variation, or insufficiently discrete to allow a clear distinction between species. For some genera, the use of molecular approaches is decisive in recognizing and validating species. The use of the molecular approach to investigate cryptic diversity in freshwater snails has consistently demonstrated that several widely ranging nominal species correspond, in fact, to geographically restricted lineages. There is a perception that freshwater snails have relatively high niche flexibility. Nonetheless, niche shifts within a species should be considered cautiously, due to the well-known problems in establishing species limits in Physidae and Lymnaeidae. Occurrence records attributed to one species may in fact correspond to a complex of cryptic species. Niche differentiation has been used in the investigation of species limits and cryptic diversity. Herein we explored these two approaches, ecological niche modelling and molecular delimitation methods, to investigate cryptic diversity in Physidae and Lymnaeidae, respectively. We provide the first comprehensive study to specifically address the issue of species limits and cryptic diversity within Lymnaeidae, using coalescent delimitation methods. Our results evidenced the presence of cryptic diversity, revealed candidate species, validated recently created genera, and confirmed the synonym between some nominal species. To address the issue of cryptic diversity in neotropical physids, we constructed ecological niche models for two nominal species and seven candidate species and measure the niche overlap using a novel approach based on ellipsoid envelopes. Our findings revealed that the knowledge on physid species identity and geographic distribution are probably weakened by taxonomic impediment. Consequently, the diversity of physid species may have been underestimated in South America. We further discuss the consequences of cryptic diversity for species conservation and epidemiology of snail-born parasitic diseases.

Mitochondrial data reveals a high genetic diversity in the alien oyster *Dendostrea* sp. (Mollusca: Ostreidae) spreading in the Eastern Mediterranean Sea.

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Keywords: non-native, Ostreinae, barcoding, Lessepsian, Mediterranean Sea

The ongoing global change and intensified human-exchanges have facilitated the spread and establishment of marine alien species worldwide. The Mediterraenan sea has seen a significant increase in alien species, especially molluscs, through natural dispersal or intensified maritime traffic since the opening of the Suez Canal in 1869. Among these, the oyster *Dendostrea* sp. spread notably since its discovery in 1998 in Turkey. This study aims to provide a taxonomic assessment and update the distribution of *Dendostrea* sp. in the Mediterranean Sea through molecular analyses. Seventy-seven specimens collected from 25 sites across the eastern Mediterraenan Sea were sequenced for the mitochondrial marker COI. These sequences were compared with 572 sequences, previously generated in our lab from alive (17) and museum specimens (133) or retrieved from GenBank (422), using a Neighbor-Joining (NJ) phylogenetic tree and a species delimitation analysis (ASAP). All Mediterranean *Dendostrea* sp. clustered with a single molecular operational taxonomic unit (MOTU) together with sequences of *Dendostrea* oysters from the Rodrigues island demonstrating an Indo-Pacific origin for the Mediterranean population. Phylogenetic and haplotype network analyses revealed a remarkably high genetic diversity and a lack of geographical population structure. These findings, combined with the observation of the abundant and widespread presence of this species across the eastern Mediterranean, suggest an old introduction, a high propagule pressure and perhaps high level of migration from the Red Sea. This study highlights the importance of molecular surveys to clarify the identity and the origin of *Dendostrea* sp. Further study will be necessary to assign a name to this Indo-Pacific taxon and characterize gene flow between native and introduced range, as well as to evaluate the ecological impact of this alien oyster and to develop suitable mitigation strategies.

Effects of foliar pathogens and insects on mollusc abundance in grassland

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Keywords: Mollusc, Fungi, community ecology

Plant consumers such as, insects, fungal pathogens, and molluscs can have large impacts on plant diversity, community structure and ecosystem functioning. However, molluscs are frequently underestimated as drivers of plant community composition and functions, despite their abundance in many environments. Different plant enemy groups are also known to interact with each other and could potentially affect each other's abundance through a variety of mechanisms, e.g., via changing plant species composition. However, these interactions are poorly studied and it is not clear whether changes in the abundance of insects or pathogens could impact molluscs. We use a global network of experiments excluding molluscs, insects and pathogens from grasslands, BugNet, to test how reductions in insect and pathogen abundance affect molluscs. We trapped molluscs on plots of the experiment at 10 sites across Europe. Initial data from the network indicates that foliar fungal pathogens and molluscs interact to affect plant biomass. In addition, results from Switzerland and Greece show that the removal of pathogens with fungicide mainly leads to a decrease in mollusc abundance. We will also present data exploring the mechanisms behind this interaction: whether pathogens affect mollusc abundance because molluscs avoid feeding on infected leaves or whether pathogens change plant composition, microclimate or litter, with cascading effects on molluscs. Our results show that very different enemy groups such as fungal pathogens and molluscs can interact with each other, and demonstrate for the first time that foliar pathogens might be important drivers of terrestrial mollusc abundance.

The effect of acclimation at four developmental stages, under four temperature regimes, on the development of deformities during the embryonic stages of *Charonia seguenzae* (Aradas & Benoit, 1870)

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Keywords: *Charonia seguenzae*, temperature, embryonic development, deformities

The Mediterranean Triton, *Charonia seguenzae*, is an endangered marine gastropod affected by embryonic deformities, significantly impacting offspring survival and quality. Optimal development occurs at 23°C, a temperature at which tritons naturally reproduce. At 29°C, projected for 2100, the embryos are lethal. At the environmental minimum of 17°C, nearly all specimens (96.66%) are deformed at eclosion.

This study examines the effect of acclimation at four developmental stages (morula, trochophore, shell formation, and veliger) on deformities under four temperature regimes (17°C, 23°C, 26°C, and 29°C). Seventy-two egg capsules, laid on the same day by one individual at 23°C, were collected. At each stage, 18 capsules were divided into groups and acclimated at 17°C, 26°C, and 29°C, with 23°C as the control. At eclosion, three capsules per group were opened, and 50 larvae per capsule were sampled.

Acclimation at the morula and trochophore stages led to the highest deformity rates at eclosion, reaching 71.33% and 51.33%, respectively. The morula stage acclimation also resulted in smaller veliger larvae. Except for larvae acclimated at the trochophore stage at 26°C, all other conditions led to significantly smaller veliger larvae compared to the control group at 23°C. Acclimation at later stages resulted in developmental times closer to the control group. Early developmental stages, especially morula and trochophore, were more sensitive to temperature changes, with higher deformity rates at all tested temperatures.

Oral Presentation

The mollusc fauna of the Vienna woods, Viennese municipal part: a synopsis

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Keywords: Vienna woods, molluscs, Gastropoda, Bivalvia

The Vienna Woods are a forested hillside area on the Northeastern margins of the Alps. Part of its range covers the western municipal area of Vienna, an area of interest for nature conservation. A synopsis of several past and present surveys within this region shows 136 mollusc species in total, including 105 land snails, 19 freshwater snails and 12 mussels. Only a few of them could not be recorded in the last ten years. With a few exceptions, the impact of invasive species is comparatively low. The most frequent habitat type are deciduous and mixed forests. As many of them are close to nature-near management, the mollusc fauna of the forests is relatively unaffected. Typical east-Alpine species like *Aegopis verticillus*, but also some endangered species like the local endemic *Orcula dolium* infima have been detected in the forests. Dry meadows and vineyards underwent strong decline during the last century due to intrusion of shrubs, intensification of agriculture and building development. These trends have now been stopped and landscape management activities have been taking place since around the year 2000. In some areas, endangered xerothermophilic species like *Zebrina detrita* are therefore still common. The same applies to wet meadows, which inhabit also more endangered or protected species, e.g. *Vertigo angustior*, Ponds and pools are in most cases artificial. Nevertheless, they provide a habitat for some species, which became rare in other areas of Vienna, e. g. *Viviparus contectus*. Within springs and creeks more specialized species like spring snails (*Bythinella austriaca*) and even groundwater snails have been recorded. Both wetlands and small water bodies might be affected by climate change, as longer drought periods could affect the groundwater level. Therefore, the Vienna Woods can be regarded as an area with the highest diversity of molluscs in Vienna.

Trail Watch: Investigating Gastropod Mucus Trails using Optical Profilometry

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Keywords: optical profilometry, gastropod, mucus, trail topography, locomotion

Gastropods use adhesive locomotion to successfully traverse a range of substrates by adapting the properties of a thin mucus layer. Sample collection methods can disrupt the native mucus structure, so to investigate this system effectively a method for visualising the native deposition of gastropod mucus trails in situ was developed. Optical profilometry and video analysis were utilised to uncover how animal behaviour impacts mucus structure and analysis of the dried trail topography provided insight into mucus alignment and deposition rate.

Our results revealed that dried gastropod trails have a non-uniform deposition profile with ridges visible along both edges of the trail. This phenomenon was independent of specimen size for the slug species *Arion vulgaris*, *Arion flagellus* and *Limax maximus*, but direction and velocity did impact the prominence of the trail ridges. The dried trail topography was the inverse of the convex deposition profile observed in the rehydrated mucus trails of a marine gastropod, indicating a potential difference in mucin deposition or alignment that is independent of the mucus hydration state. When compared to the model slug species, *Ariolimax columbianus*, the species from this study had thinner dried mucus trails, highlighting potential variations in the cost of adhesive locomotion between species. Our results suggest that mucus deposition rate and animal behaviour have a greater impact on mucus trail topography than species or specimen mass. Moreover, analysis of the dried mucus trails can provide invaluable insight into the relationship between the hydration and mucin costs associated with mucus excretion and adhesive locomotion.

Survivors of the Ice Ages: Phylogeographic patterns and population dynamics of trans-Arctic nudibranch species

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Keywords: Evolution, speciation, trans-Arctic species, Bering Strait, Isthmus of Panama, Gastropoda

It is widely known that marine boreal and Arctic areas are inhabited by many widely distributed species, characterized by amphiboreal, arcto-boreal, or circumpolar distribution patterns. However, in the past years, the extensive use of molecular phylogenetic methods revealed a significant genetic heterogeneity within these species, many of which are now understood to be species complexes. Despite this, species with a circumpolar or amphiboreal distribution do indeed exist, but less abudant than previously believed. The species criteria for trans-Arctic species and their complexes, however, are still not well-defined, and the relationship between geographically distant populations warrants further verification.

Our research perform a study on the genetic structure of several trans-Arctic nudibranch species, which are common in the boreal and subpolar regions of the Northern Hemisphere, including Coryphella verrucosa, Onchidoris muricata, Dendronotus frondosus and Aeolidia papillosa. For these species, we have estimated the divergence times of individual mitochondrial haplogroups, reconstructed ancestral ranges, performed neutrality tests, and examined changes in the dynamics of effective population size over time. The divergence time reconstructions for these trans-Arctic species, based on the COI gene, were overlaid with paleotemperature data and sea-level dynamics reconstructions from the Pleistocene epoch.

All studied genera are suggested to have Pacific origins, as indicated by phylogenetic data, divergence time estimates using molecular clocks, and ancestral range reconstructions. A distinct separation into Atlantic-Arctic and Pacific haplogroups was observed for all the trans-Arctic species studied, and these splits align with the interglacial periods. Except for D. frondosus, the Pacific is presumed to be the donor region, with the Arctic and Atlantic are recipient regions. The divergence of all studied nudibranch species is consistent with paleoclimatological dynamics, with populations enduring through glaciations in multiple refugia.

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Molecular characterisation of some Cernuellini Schileyko, 1991 (Geomitridae, Helicellinae), from Tunisia with description of *Sabessebia* nov. gen.

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Keywords: Cernuellini, new genus, *Sabessebia zitanica,* Tunisia

Despite recent research efforts, the malacofauna of Tunisia and North Africa remains inadequately studied and necessitates further investigation. Some taxa have been identified as endemic to North Africa, including the Tunisian genus *Xeroplana*, which has been anatomically confirmed as separate from Cernuella for over a century. However, no molecular characterization of this genus has been conducted, so far. Among a *Cernuella*-like group, common in Tunisia, *Helix zitanica* (Bourguignat & Letourneux, 1887) appears to exhibit some conchological differences compared to *Cernuella* and *Xeroplana*, although it was initially misidentified as *Cernuella caruanae*.

In the present study, we conduct the first molecular investigation of some Cernuellini, analysing two mitochondrial and two nuclear markers to estimate their phylogenetic relationships and confirm the relative status of *H. zitanica* and *C. caruanae*. The results of the molecular analysis corroborate the separation of *Xeroplana* from *Cernuella* at the genus level, as previously demonstrated by the anatomical differences in the genitalia. Furthermore, the results support the status of *C. caruanae* and *H. zitanica* as separate species. Additionally, the taxon H. zitanica exhibits significant anatomical and molecular differences compared to the genera *Cernuella*, *Xerosecta*, and *Xeroplana*. Consequently, it is here described as a new genus, namely *Sabessebia*, which is endemic to North Africa. The new combination for *Helix zitanica* is therefore *Sabessebia zitanica*.

From marine sands to terrestriality: phylogenomics shed light on the evolutionary pathway of the minute Acochlidia slugs (Gastropoda: Heterobranchia)

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Keywords: Mollusca, Panpulmonata, ultra-conserved elements, systematics, habitat shifts

Phylogenomics has significantly contributed to understanding the molluscs' terrestriality, providing deeper insights into their evolutionary history and systematics. Recent genetic analyses have prompted a redefinition of the traditional pulmonate clade within the diverse gastropod subclass Heterobranchia, leading to the establishment of Panpulmonata, which encompasses traditional pulmonate (air-breathing slugs and snails) and various marine and limnic groups. Among these, the enigmatic superorder Acochlidia is notable for its unique anatomical and reproductive traits, with most representatives inhabiting the sandy interstices of marine environments. Despite a modest richness of ca. 50 recognised species, acochlids have adapted to various environments beyond the sea, including marginal coastal habitats, freshwater ecosystems, and even fully terrestrial environments. This ecological versatility has expanded the evolutionary scenario of this group of minute slugs and increased scientific interest in their study. Using a target enrichment approach of ultra-conserved elements and benefiting from a dense taxon sampling of 40 newly sequenced species, which encompass all families and almost all genera, this study represents the most comprehensive phylogeny of Acochlidia to date. Our analyses address outstanding systematic issues within the clade and elucidate their evolutionary history, particularly the complex biological process of conquest of non-marine habitats. The results reveal new lineages, including a putative undescribed genus within the family Parhedylidae and another within the previously monotypic Tantulidae. Additionally, we re-erect the family Strubellidae and delimit Acochlidiidae to the genera *Wallacellia*, *Palliohedyle*, and *Acochlidium*. Furthermore, we provide the first molecular systematic assessment of the freshwater genus *Helicohedyle*, proposing its inclusion in a new family alongside a putative new genus. Regarding the conquest of out-of-sea habitats, our genomic analysis identifies three independent habitat shifts: one to a (semi) terrestrial environment in Aitengidae, and two to limnic habitats in Strubellidae and Acochlidiidae.

Planktotrophy vs. lecithotrophy: a study of three Cone snail species reproduction

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Keywords: planktotrophy, lecithotrophy, cone snails

With around 1,000 species, cone snails (family Conidae) form a highly successful and diverse group of Gastropoda. They are found in the tropical and subtropical waters of all oceans and seas, from intertidal areas to deep sea. These venomous snails, depending on the prey, can be vermivorous, piscivorous or molluscivorous. Besides, some of them show widespread distributions, even across oceans, whereas others are restricted to small geographic areas. The question about why such a difference in distributions exists may have multiple answers. However, one that might contribute significantly is whether their reproduction cycle includes a veliger larval stage or not. In contrast to lecithotrophic larvae that directly develop into a juvenile without almost no displacement, planktotrophic larvae may swim and reach wider areas before their final metamorphosis into a fully developed cone snail.

We have been able to maintain in salt-water aquaria several species of cone snails from the Mediterranean and West African Atlantic coast and islands. The adult specimens fully adapted to live in captivity and were able to complete their reproduction cycle up to the stage of hatching. Here, we present the results of a study about the development within the egg sac of three cone snail species from three different genera: *Lautoconus ventricosus* (Gmelin, 1791), *Kalloconus byssinus* (Röding, 1798) and *Varioconus guanche* (Lauer, 1993). All of them had lecithotrophic larvae. The number of eggs per sac, the size of the egg and the time before hatching correlated well with previous studies and with the model proposed by Perron in 1991. The question whether they produce conotoxins since the very moment they get out of the sac is now under current study by our group.

Monitoring molluscan diversity of Cretan fresh waters

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Keywords: gastropods, wetlands, conservation, environmental parameters, species richness

Freshwater molluscs are an important component of freshwater ecosystems and excellent water-quality indicators. Aquatic molluscs can be found in a variety of habitats, natural or artificial. Regarding the island of Crete (Greece), little is known about the molluscan diversity of its freshwater ecosystems and even less about the species habitat preferences. In the current study, selected Cretan wetlands, protected under a national regime (Presidential Decree, Government Gazette AAP 229/19.06.2012) and other nearby water bodies (e.g. rivulets, water pools), were searched for freshwater molluscs. In each sampling station, physicochemical parameters including water temperature, pH, electrical conductivity and total dissolved solids were measured in order to explore the potential effect of environmental conditions on the molluscs. In addition, historical records of freshwater molluscs from 1801 up to the present were assembled and georeferenced in order to aquire a complete overview of the species distribution in Crete. The research revealed at least 14 species of freshwater molluscs including 1 bivalve, although few species were represented only by empty shells, while in 11 stations (out of 29) we did not find molluscs. Most common species were *Galba truncatula* (Müller, 1774) and *Theodoxus* sp., while most abundant were *Theodoxus* sp. and *Melanopsis* sp., locally reaching abundances of about 200 individuals/m^2. Most tolerant species to environmental conditions were *G. truncatula* and *Theodoxus* sp. although this requires further investigation. The investigated water bodies are a refuge for at least half of the species (including endemics) known from the island of Crete so far. The current protection scheme should be maintained and potentially expanded to other water bodies. Conservation of Cretan freshwater molluscs could be supported by regular monitoring of the environmental conditions and the species presence in selected freshwater bodies of Crete.

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Distinguishing occupancy from sampling biases to infer the extinction dynamics of marine bivalves over 450 million years

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Keywords: diversification, neutral theory, palaeoenvironment, population size, traits

Neutral evolutionary theory predicts that a taxon's occupancy, manifesting in its population size, abundance or geographic range, follows a hump-shaped trajectory: it is low at the taxon's origination, peaks somewhere during its lifetime, and then declines prior to its extinction. Alternatively, stasis – a prolonged constant occupancy – necessitates a change in biotic interaction strength over the taxon's lifespan while a linear rise followed by an abrupt population collapse suggests a rapid change in climate or a catastrophic event. Occupancy dynamics can help us validate alternative hypotheses about the causes and drivers leading to the extinction of taxa and are therefore pivotal to our understanding of macroevolutionary diversification processes. Previously, occupancy history has been approximated from fossil occurrences, with selected marine gastropods constituting one of the prime test cases. However, the inevitable incompleteness of the fossil archive, affected by spatial, temporal and taxonomic biases, means thvat fossil occurrences cannot be reliably taken at face value. Here we present a novel Bayesian model to analyse the fossil record using an unsupervised neural network and explainable artificial intelligence techniques to infer the dynamics of occupancies throughout the lifespan of lineages while accounting for sampling biases. The model also incorporates the effects of life history traits, biogeography, systematics, major biotic events and spatiotemporal environmental conditions on sampling rates, allowing us to test hypotheses about the link between these factors and occupancy. After benchmarking the model with simulations, we apply it to a fossil dataset of 2500 marine bivalve genera spanning 450 million years. Our approach advances our ability to infer occupancy in deep time and our understanding of the population dynamics preceding extinction.

Non-marine gastropods of Iceland: biogeographical affinity and glacial analogy

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Keywords: Iceland, snails, biogeography, diversity, Pleistocene analogy

Although the existence of the LGM refugia in the arctic is anticipated, most of the Icelandic non-marine flora and fauna is of Holocene origin. The geographical position of the island makes it most likely to be colonised from the European mainland or British Isles. About 51 gastropod species have been reported from Iceland, from which at least 20 are of recent anthropogenic introduction. During the sampling of 88 natural sites in 2016-2023, we documented 26 terrestrial and 5 freshwater gastropod species; with *Pupilla alpicola*, *Vertigo substriata* and *Euconulus alderi* being recorded for the first time. All these 51 species are of East Atlantic origin, with the populations of Holarctic species (e.g. *Euconulus fulvus*, *Vitrina pellucida*) being of European affinity based on molecular data. Phylogenetic analyses also revealed that earlier findings of *Pupilla muscorum* represent in most cases *P. alpicola*. This discovery helped to encrypt one of the mysteries of Pleistocene loess snail faunas, a unique co-occurrence of nowadays strictly wetland species such as *Pupilla alpicola*, and strictly steppe species such as *P. sterrii*. Perhaps, the fossil record represents a mixture of multiple microhabitats or time periods and these species have never met. However, Icelandic populations revealed that P. alpicola can prosper on moderately dry sites with sandy substrates. These sites may represent a possible analogue to its occurrence in the glacial period. In Central Europe, there was a clear shift in the realized niche at the beginning of the Holocene, most likely driven by climate. The shift to calcareous wetlands was probably related to their thermal stability, as groundwater buffers the effect of high summer temperatures. In permanently humid and oceanic Iceland, however, *P. alpicola* is protected from temperature extremes. Moreover, dry steppe-like habitats are the only ones in Iceland that meet the high calcium requirements of this species.

On the way to the Carpathians: Postglacial colonization dynamics of two rock-dwelling snails based on genes and fossils

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Keywords: Disjunctions, land snails, phylogeography, postglacial colonization, *Pyramidula*

Various species distributed in the Alps have their disjunct occurrences in the Carpathians. Fossil evidence for some woodland snails suggests that they colonized the Carpathians during the Holocene forest optimum or later. Here, we focus on disjunct Carpathian populations of the alpine land snail *Pyramidula saxatilis*, a minute rock-dwelling species which was only recently genetically distinguished from a more widespread *P. pusilla*. As it occupies very stable habitats of high-elevation limestone rocks, one can assume its potential survival in the Carpathian refugia over the glacial period(s). To test this hypothesis, we analysed the genetic diversity of mtDNA and nDNA markers of both *P. saxatilis* and *P. pusilla* across their entire ranges. We also analysed seven fossil radiocarbon-dated mollusc successions from the Carpathians where *P. saxatilis* occurs nowadays, and calculated habitat suitability models for selected time periods since the LGM. All Carpathian *P. saxatilis* populations were genetically homogeneous and similar to those from the Eastern Alps. In *P. pusilla*, which prefers warmer climate, we found a genetically distinct lineage in the southern Western Carpathians. Both species were found in three fossil profiles since the Middle Holocene, and in one already in the Late Glacial. Habitat suitability models suggested the fluctuations of suitable conditions in the Carpathians driven by summer precipitation, especially for *P. saxatilis*. Our results suggest that the Carpathian populations of *P. saxatilis* represent a post-LGM colonization from the Eastern Alps, triggered by climatic changes, mainly by the increase in summer precipitation. The evidence for *P. pusilla* is similar, but also suggests rare long-term survival in the Carpathian microrefugia. The palaeoecological evidence indicates a possible threat to high-elevation species from future fluctuations in precipitation regimes.

Aquatic Guardians: The Role of *Corbicula fluminea* in Reducing Pathogen Spread

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Keywords: *Angiostrongylus cantonensis*, ecosystem function, invasive pathogen, filtration

Invasive bivalves significantly alter the dynamics of aquatic ecosystems. One of their most notable impacts is their high filtration activity, removing particles from the water column. This includes also planktonic animals, whose populations can be strongly influenced and reduced due to such filtration activity. While this effect can have negative consequences for native populations of zooplankton, our study presents a potentially positive perspective: invasive bivalves may act as protectors against the spread of planktonic pathogens. In our study, we investigated the impact of *Corbicula fluminea*, an important freshwater invasive species, on the transmission dynamics of the globally invasive zoonotic nematode *Angiostrongylus cantonensis* (AC) to gastropods (Biomphalaria glabrata), serving as intermediate hosts. The transmission experiments were conducted in controlled microcosms designed to identify factors influencing the success of AC infection, measured by the number of developed 3rd stage larvae of AC found within the host body. Both abiotic factors (water turbulence and physical complexity) and biotic factors (filtration activity of *Corbicula fluminea*) significantly influenced the success of nematode´s transmission. These findings underscore the role of invasive bivalves as potential ecological regulators of globally invasive pathogenic nematodes.

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Mating behaviour of six species of terrestrial slugs in the genus *Lehmannia*

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Keywords: mating behaviour, slug, *Lehmannia*, sperm exchange, genitalia

For similar reasons as for genital morphology, mating behaviour often provides diagnostic characters distinguishing closely related species; it also reveals how the genitalia function. Video records unravel the mating of six species of slugs in the genus *Lehmannia* sensu stricto and were also used some rapidly frozen copulating pairs. The usual pattern is that one slug follows another, the leader turns back, and they briefly nibble each other's flanks. Then, part of the penis everts, forming a rounded knob in most species, which is more elongated in *L. brunneri*, while having a long stalk in *L. carpatica*. Usually, contact of this part of the penis with that of the partner's is the trigger for further rapid penis eversion, but there is a delay of some seconds in *L. macroflagellata*. The eversion leads to reciprocal sperm exchange. In most species sperm is deposited onto the base of the partner's penis, but in *L. carpatica* the long penes coil around one another forming a double helix, and sperm is exchanged at the tips. In this species, penis length varies geographically. In *L. rupicola*, *L. macroflagellata* and *L. brunneri*, eversion of the flagellum deposits a secretion over the partner's body. The shorter flagellum of *L. marginata* appears not to contact the partner, so might be vestigial. The process, from the rapid eversion to retraction of the penis within the body, lasts from 5–6 s in *L. rupicola* to 42 s in *L. brunneri*, while *L. szigethyae* is aberrant in taking over 50 min. After retraction of the penes, *L. macroflagellata* pairs may continue circling around each other for hours. In conclusion, *Lehmannia* species show consistent and marked qualitative differences in mating behaviour. These differences appear idiosyncratic, meaning that mating behaviours would be an unsuitable basis on which to reconstruct a phylogeny.

Effects of antidepressant water pollution on freshwater mussels: a climate change scenario

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Keywords: freshwater mussels, antidepressants, water pollution, climate change

The global use of pharmaceuticals is systematically rising and over the past few decades, they have become a new type of environmental pollutant. Antidepressants are a class of medications used to treat major depressive disorder, anxiety, chronic pain, and addiction. One of the most commonly prescribed antidepressants is venlafaxine which belongs to the norepinephrine-serotonin reuptake inhibitors, and fluoxetine (selective serotonin reuptake inhibitor). These pharmaceuticals are widely found in freshwaters at varied concentrations. Considering the progressive development of medicine and the demand for drugs, their further release to aquatic ecosystems seems inevitable. It is expected that their concentrations in water will increase and therefore influence aquatic biota, posing a threat to ecosystem structure and functioning. Simultaneously, climate changes and water warming have the potential to magnify these substances' adverse effects on freshwater organisms. Those effects have not yet been recognized.

Due to their unique filter-feeding and sedentary life cycles, mussels are particularly sensitive to environmental disturbances. They typically keep their shells open to breathe and filter suspended matter from the water, but in stress conditions, they close the shells, and decrease activity.

In this study we aimed to analyze the effects of venlafaxine and fluoxetine on the filtering behavior of freshwater mussel *Unio tumidus* Philipsson, 1788 (Bivalvia: Unionidae). In a series of experiments, a self-designed shell-opening mussel biomonitoring system based on measuring changes in magnetic field with Hall sensors was used to analyse mussels' activity. Experiments were conducted in two thermal regimes: optimal and elevated water temperature: 17℃, 22℃ respectively. The following concentrations of venlafaxine, and fluoxetine were used: l00 ng/L, 1 µg/L, 10 µg/L and 100 µg/L.

The obtained results give a better understanding of mussels' responses to emerging antidepressant water pollution, combined with thermal stress, which is crucial to identifying effective conservation and environmental management practices during climate change.

East Asian *Parakaliella harimensis* is in fact *Euconulus* of a remarkable genetic diversity

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Keywords: Holarctic, integrative taxonomy, intraspecific variability, geometric morphometrics, Phylogeny

Euconulus is one of the most widely distributed genera of land snails in the Holarctic. It is characterized by a simple shell morphology and minute size ranging from 2.3 to 3.5 mm in diameter. About ten nominal *Euconulus* species have been described from the Holarctic, however, there are several unresolved taxonomical issues, among which is the existence of potentially species-level phylogenetic clades in the *Euconulus fulvus* group. Our previous molecular data identified such a distinct clade in Japan, which seemed to be a new species candidate. By including more samples from Japan and southeast Asia, we aim to further explore the taxonomic status of this clade, using an integrative approach. Two nuclear (ITS1, ITS2) and two mitochondrial (COII, 16S) markers were used to reconstruct the phylogenetic relationships of the genus *Euconulus*, using 51 samples of all five nominal species from the *E. fulvus* group. We also tackle the aim by morphometric analysis, using classical shell measurements and geometric morphometry with 19 landmarks. Based on the phylogenetic tree reconstruction we documented six distinct groups. The group including the populations from east and southeast Asia was genetically highly divergent and significantly different in shell morphology from all the remaining species. This group resembled *Parakaliella harimensis*, and this similarity was confirmed by including a lectotype and paralectotype in geometric morphometric analysis. We, therefore, propose this species to bear the name *Euconulus harimensis*, by changing the taxonomical status of *P. harimensis*. Its exceptional degree of genetic intraspecific variability can be explained by climatic stability in its range through the Pleistocene climatic cycles, contrary to the remaining *Euconulus* species, whose distributions were more dynamic in response to sharp climatic shifts during the Pleistocene.

A precious gem of the freshwater biodiversity of Greece

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Keywords: freshwater gastropods, Lake Trichonis, conservation

Greece is considered a hotspot of biodiversity and endemism regarding hydrobiid fauna, especially for hydrobiids with valvatiform shells. Up to date, nine genera and sixteen valvatoid species have been recorded in Greece, with 55% of the genera and >90% of the species being local endemics in lakes and springs and most of them assessed as Critically Endangered (CR) or Endangered (EN) in the IUCN Red List of Threatened Species. One of the most important yet mainly unknown species is *Pseudoislamia balcanica*, a Critically Endangered local endemic valvatiform species of Lake Trichonis (Aitoloakarnania, Greece) and the surrounding lotic freshwater. In this study, all the known localities where *P. balcanica* has been recorded, as well as, additional sites with suitable habitats for this taxon were surveyed several times during one-year period, in order to unravel populations' distribution, elucidate its dubious systematics and reveal the previously unknown phylogenetic relationships. Other threatened freshwater gastropods inhabiting the same localities as *P. balcanica* were also collected during samplings, enabling a better understanding of Lake Trichonis's malacofauna composition. According to the results, new sites were successfully discovered, although both known and new populations of *P. balcanica* were extremely small-sized. The fact that these populations are also severely threatened by habitat loss and anthropogenic modification, raises even more the necessity for appropriate conservation of this minute hydrobiid, preventing it from extinction.

The project was founded by the Hellenic Foundation for Research & Innovation (H.F.R.I.) in collaboration with Natural Environment and Climate Change Agency (N.E.C.C.A.) under the action "Studies for the preservation of endemic, endangered and species of national importance for Greece" (Project Number 14859).

Mitonuclear incompatibility contributes to the persistence of Helix thessalica in the *Helix pomatia* range

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Keywords: genomic cline, hybrid zone, land snail, mitonuclear incompatibility, speciation

Interbreeding and introgression between recently diverged species is common. However, the processes that prevent these species from merging where they co-occur are not well understood. We studied the mechanisms that allowed an isolated population group of the snail *Helix thessalica* to persist within the range of the related *Helix pomatia* despite high gene flow. Using genomic cline analysis, we found that the nuclear gene flow between the two taxa across the mosaic hybrid zone was not different from that expected under neutral admixture, but that the exchange of mtDNA was asymmetric. Tests showed that there is relaxed selection in the mitochondrial genome of *H. thessalica* and that the substitution rate is elevated compared to that of *H. pomatia*. A lack of hybrids that combine the mtDNA of *H. thessalica* with a mainly (>46%) *H. pomatia* genomic background indicates that the nuclear-encoded mitochondrial proteins of *H. pomatia* are not well adapted to the more rapidly evolving proteins and RNAs encoded by the mitochondrion of *H. thessalica*. The presumed reduction of fitness of hybrids with the fast evolving mtDNA of *H. thessalica* and a high *H. pomatia* ancestry resulted in a relative loss of *H. pomatia* nuclear ancestry compared to H. thessalica ancestry in the hybrid zone. This probably prevents the *H. thessalica* populations from merging quickly with the surrounding *H. pomatia* populations and supports the hypothesis that incompatibilities between rapidly evolving mitochondrial genes and nuclear genes contribute to speciation.

Reconstructing the evolutionary history of continental *Zonites*: phylogeography, morphometrics, and environmental influences

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Keywords: diversification, extinction, climate, variation, land snail

Zonites Montfort, 1810, is a genus of land snails distributed throughout the circum-Aegean region, which includes western Turkey, several Aegean islands, and southern mainland Greece (Peloponnese and Euboea). The genus exhibits a patchy and disjunct distribution, with some species known only from fossil records or considered rare and nearing extinction. Previous phylogenetic analyses suggest that the diversification of *Zonites* dates back to the Neogene period, influenced by palaeogeographic events in the Aegean archipelago.

In this study, we focus on the continental distribution of *Zonites*, examining the impact of processes such as vicariance, dispersal, and particularly extinction, which appears to have played a significant role in its evolution and current distribution. We integrate molecular phylogenetics, geometric morphometrics, and niche modeling (Maxent) to uncover phylogeographical patterns, estimate divergence times, reconstruct the evolutionary history of morphometric traits, and account for the effects of phylogeny in trait variation. Ultimately, we aim to predict the actual and potential distribution of *Zonites* and illustrate the environmental differences among its various clades.

Mitochondrial markers (16S and CO1) reveal three distinct lineages within mainland Greece: one in central Euboea, a second comprising species from western and northern Peloponnese, and a third that includes the remaining Peloponnesian and southern Euboea populations. The absence of *Zonites* from central Greece, which connects the Peloponnese and Euboea, combined with the observed phylogeographical pattern, estimated divergence times, and predicted distribution from Maxent models, underscores the influence of past and present climatic conditions on the diversification of *Zonites*. The found absence of a phylogenetic signal in shape coordinates and size suggests that morphometric variation of *Zonites* may be attributed to differing environmental conditions and local adaptations.

Enhancing collection data management at the Museum of Paleontology and Geology of Athens in the European DiSSCo Research Infrastructure era

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Keywords: Collection Management, Database, Museum of Paleontology and Geology NKUA, Greece, DiSSCo European Research Infrastructure

The Museum of Geology and Paleontology at the National and Kapodistrian University of Athens houses exceptional fossil collections from Greece and abroad, representing over 500 million years of geological heritage. It features world-renowned collections such as the Late Miocene Pikermian vertebrate fauna. The collection of fossil molluscs alone comprises several thousands of specimens ranging from Cambrian to Holocene, with many Neogene gastropod and bivalve type specimens. However, the availability of primary collection data is currently scattered and incomplete due to variable and frequently outdated indexing systems.

The Distributed System for Scientific Collections (DiSSCo) is a new European Research Infrastructure for natural science collections, which aims to create a new structural model that will digitally unify all European natural science assets by building on shared access and common curatorial policies and practices across countries, while ensuring that all the data complies with the four FAIR principles (Findable, Accessible, Interoperable and Reusable data). Implementing unified and standardised policies for developing natural science databases ensures consistent data quality and compatibility across various institutions and digital platforms, making data sharing and interoperability more efficient. These policies simplify data entry and management, by reducing errors and increasing maintenance efficiency.

Standardising digital records facilitates interdisciplinary research and improves significantly the accuracy of research outcomes by minimising variations and discrepancies during data evaluation and analysis. For instance, integrating accurate datasets with Geographic Information Systems allows for sophisticated spatial analysis of fossil distributions and the reconstruction of ancient ecosystems and climate changing models through time. Such analyses are crucial for understanding the geographical and temporal evolutionary patterns of molluscs, including significant migration, adaptation and extinction events, e.g. during the Messinian salinity crisis. These insights can be also highly informative for current mollusc biodiversity and conservation strategies by providing a long-term perspective on the impact of ecological changes.

Snails in the Zoo – visitors or residents?

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Keywords: outdoor expositions, *Hygromia cinctella*, *Cepaea nemoralis*, Prague Zoo, non-native pulmonates

The study of mollusc biodiversity is crucial for understanding ecosystem health and species interactions, in “free” nature as well as in urban and human-influenced environment. The presented research focuses on inventory of free-living molluscs inhabiting areas outside of formal expositions of Prague Zoological Garden.

Field surveys were conducted in various habitats surrounding exhibition areas such as around the walkways, rocky bases of pavilions, picnic areas, small water bodies and their banks, as well as in two small-scale nature reserves present in the area of the Zoo. Specimens were collected using standard malacological techniques (individual collecting and bulk sampling), and species identification was performed through conchological analysis.

In total, 52 mollusc species from 23 families were found. 15 of them were freshwater snails (4 prosobranchs and 11 pulmonates), 35 are landsnails, and 2 are bivalves. Stagnicola palustris is the only species included in Red List of Threatened Species of the Czech Republic. 10 species are non-native to the Czech Republic, including some of the most common in Prague Zoo area: *Cepaea nemoralis, Arion vulgaris, Hygromia cinctella, Monacha cartusiana, Arion distinctus and Boettgerilla pallens.*

The inventory revealed that areas outside of formal expositions host a significant diversity of mollusc fauna, with notable differences in species composition in various parts of the Zoo. The findings underscore the importance of preserving natural habitats surrounding exhibition areas to maintain mollusc biodiversity, although almost a fifth of the species found are non-native species. This research provides a comprehensive baseline for future biodiversity monitoring and conservation efforts.

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Using ultra-conserved elements (UCEs) to clarify problems in respect to gastropod phylogeny

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Keywords: Mollusca, freshwater, phylogenomic, target enrichment, ultra-conserved elements

Caenogastropoda, which includes 60% of all extant gastropods, is one of the most diverse groups in Mollusca. This diversity is the consequence of extensive adaptive radiation. We used a newly developed probe set to collect ultra conserved elements (UCEs) from 24 species representing 21 mostly freshwater gastropod families in an attempt to generate a stable evolutionary framework for the Caenogastropoda. A total of 12092 probes in the probe set are intended to target 1224 UCE loci. These UCEs' phylogenetic analysis resulted in a highly resolved gastropod tree that is generally in line with transcriptome-based phylogenies and other recent UCEs. In contrast to earlier research, our findings pointed to a sister relationship between the first two groups of the three major groupings of Caenogastropoda, Neritimorpha, and Heterobranchia, strongly supporting their monophyly. Unlike earlier research, our data indicated a sister relationship between the first two groups and firmly supported the monophyly of the three main groups: Neritimorpha, Heterobranchia, and Caenogastropoda. Most relationships within the Caenogastropoda were strongly supported. Our analysis resolved topologies within Heterobranchia that are generally consistent with other, recent molecular phylogenies, despite the small sample size for this group. Overall, our results show strong promise for use in gastropod research and support the idea that UCEs are an important source of phylogenetic information.

Rare Earth Elements and Warming: Implications for Adult Mussel Health and Sperm Quality

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Keywords: Europium, temperature rise, adult mussels, mussels' sperm, Integrated Biological Index

The present study aimed to investigate the effects of europium exposure (10 µg/L), warming (a 4 °C rise), and their combined impacts on *Mytilus galloprovincialis*. Biochemical and histopathological changes in adult mussels were evaluated after a 28-day exposure. Additionally, biochemical and physiological alterations in sperm were measured following a 30-minute exposure. The overall responses to each treatment were assessed using the Integrated Biological Index. In adult mussels, warming elevated metabolism and activated glutathione S-transferases, leading to redox imbalance and cellular damage. Europium exposure alone slightly enhanced metabolism and glutathione S-transferases activity, resulting in cellular damage and histopathological injuries in digestive tubules. The combined exposure to europium and warming was the most detrimental treatment for adults, as indicated by the higher Integrated Biological Index value. This treatment slightly increased metabolism and uniquely elevated the activity of antioxidant and biotransformation enzymes. Despite these responses, they were inadequate to prevent redox imbalance, cellular damage, and histopathological injuries in digestive tubules and gills. Regarding sperm, warming reduced reactive oxygen species production but raised lipid peroxidation levels and decreased sperm velocity. The Integrated Biological Index indicated that europium alone was the most harmful treatment for sperm, significantly increasing reactive oxygen species production and notably decreasing sperm velocity. When combined with warming, europium elevated superoxide anion production, lowered sperm velocity, and increased oxygen consumption. This study underscores the importance of investigating the effects of rare earth elements and their interaction with climate change-related stressors.

Lifting the dust – digitizing an entire Mollusc collection

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Keywords: digitization, malacology, natural history collections, workflows, data integration

Most Natural History collections struggle to inventory the objects they are holding within a decent amount of time. Therefore, several larger museums developed action plans addressing a digital transformation which focusses mainly on digital cataloguing of metadata related to the collection objects and stored in central databases. In addition, new ways of fast, precise and effective inventory and semi-automated imaging need to be brought into the community. The Museum für Naturkunde Berlin started an action plan in 2020 regarding the full inventory of the approx. 30 million collection objects creating a complete digital catalogue of its holdings within 10 years. Biggest challenges here are the object rich collections like molluscs, fossil invertebrates or insect collections. Therefore, the managers of digitization and collection staff have teamed up with partners from other institutions as well as industry to develop and create ways of digitization using new techniques.

One of those new workflows uses next generation digitization stations ("DORA") jointly developed by the Museum für Naturkunde Berlin and the Fraunhofer Institute for Factory Operation and Automation IFF. DORA combines four high-resolution cameras (three of them optimized for focus stacking) to image labels and molluscs with extended depth of field and accurate colour rendition. We introduce QR-codes with persistent identifiers into the collection enabling automated connection between digital assets and real-world objects. Additionally, we sub-contracted ArchivInForm, a company specialised in the digitisation of cultural heritage, which allowed us to focus on project management, restructuring the workflows, setting up user-friendly online tools and bringing in scan operators to scaling up the collection disclosure (dust). This way the complete inventory as well as digital imaging of the most relevant objects (type material and groups that are currently in high demand for research) until 2026 became a reachable goal.

Imported ornamental molluscs as a source of *Digenea* larvae – preliminary research results

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Keywords: ornamental molluscs, Digenea larvae, parasitology, aquaristics, exotic snails

Exotic snails are among the most valued ornamental species in aquaristics. These animals are often collected from their natural habitats in areas where they are endemic and are attacked by numerous pathogens and parasites. Among the parasites found in snails, digenetic trematodes (Digenea) are particularly noteworthy as they complete their life cycle in various groups of vertebrates, including humans. In preliminary research, diagnostic studies were conducted to detect the presence of Digenea larvae in molluscs imported from Thailand that had positive evaluations on EU veterinary certificates. A total of 742 snails belonging to nine species were subjected to parasitological examination: *Anentome helena* (100 specimens), *Clithon corona* (78 specimens), *Faunus ater* (80 specimens), *Filopaludina martensi* (77 specimens), *Neritina natalensis* (87 specimens), *Neritina pulligera* (120 specimens), *Plotia scabra* (80 specimens), *Tylomelania* sp. "Golden Rabbit" (60 specimens), and *Tylomelania* sp. "Yellow Spot" (60 specimens). Parasites were detected in 4.1% (29 specimens) of all examined molluscs, of which 86.2% (25 specimens) were infected with digenean trematodes. Parasites were found in individuals of three species. *Tylomelania* sp. "Yellow Spot" served as the first intermediate host (1.7%), C. corona as the second intermediate host (1.3%), and *F. martensi* were the source of cercariae (2.6%) and metacercariae (27.3%). The obtained results show that imported snails, even under harsh transport conditions, can retain live parasite stages, which may lead to the uncontrolled spread of parasites, posing a potential threat to species kept in aquariums to and to human health. Our future work will focus on the molecular species identification of the detected Digenea to verify their veterinary and medical significance on developing practical solutions and methods for controlling unwanted parasites.

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Plio-Pleistocene continental molluscs from the Bresse (Eastern France): early steps in the reappraisal of J.J. Puisségur's collection

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Keywords: Pliocene, Early Pleistocene, gastropods, extinct species

France is a country with numerous Cenozoic continental deposits that are rich in terrestrial and aquatic mollusc shells. However, there is a paucity of palaeontological syntheses on a regional scale for these malacofauna. In the 1970s the French Geological Survey planned a major program of drilling in the Bresse region to renew the geological map. A multi-disciplinary scientific team was formed, with malacological studies carried out by J.J. Puisségur. The Bresse is a tectonic trough that opened in the Oligocene and was then filled during the Miocene by sedimentary deposits of various origins (marine, fluvial). The research programme focuses on the final part of this filling, which took place during the Plio-Pleistocene by the formation known as the "Marnes de la Bresse" (Bresse marls).

More than 200 boreholes have been surveyed, yielding hundreds of thousands of specimens. J.J. Puisségur was already at the end of his career when this work was carried out and was only able to produce a short publication on this very rich data set. He lists 77 gastropods, 47 of which are extinct taxa whose stratigraphic occurrence allows him to define 12 malacozones, however not described in detail.

Recent work has focused on producing a revised taxonomic list of the species recorded, accompanied by high quality iconography. The systematic recording of species occurrences in a database will then allow the production and refinement of a detailed description of the malacological zonation and the interpretation of their palaeoenvironmental and climatic significance. The considerable value of this corpus represents a significant challenge for French palaeontology and palaeomalacology in terms of heritage. The first stages of the review are outlined here.

Niche-based modelling and geographical analysis to assess the influence of climate change on the terrestrial gastropod *Elona quimperiana* in Spain

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Keywords: *Elona quimperiana*, distribution area, habitat conservation, climate change, niche-based modelling

Elona quimperiana (Blainville, 1821) is a land gastropod of Community Interest listed in Annexes II and IV of the Habitats Directive 92/43/EEC. It has a disjunct geographical distribution and inhabits deciduous forests and humid areas of the Cantabrian region and Brittany in France. Within the Iberian Peninsula, the distribution of *E. quimperiana* extends along the north-west region, from the French Basque Country to the river Miño in Galicia, living also in the mountain ranges of southern La Rioja. During the period 2023-2024, a literature review, citizen science contributions compilation and fieldwork have been carried out throughout the distribution area, with the aim of updating the distribution data of the species in Spain. Based on these data and environmental variables that condition its presence, ecological niche models have been developed for the present day climate and under different climate change scenarios. These frameworks classify the territory according to its capacity to host populations of *E. quimperiana*. The results have been used to assess the effect that climate change could have on this terrestrial gastropod species and to identify the most vulnerable areas of its range. This work has been developed in the context of the EU-funded project: PRTR-ESMOLINCO 'Technical assistance for the improvement of knowledge of the conservation status of terrestrial and continental fauna in Spain (native and invasive alien species: molluscs and coastal invertebrates), six-yearly reports on Article 17 (Habitats Directive) and Article 24 (invasive species), and updating of Atlases and Red Books'.

This project is the result of a contract established between the Euskoiker Foundation and the company TRAGSATEC, in collaboration with the Spanish Society of Malacology (SEM).

Review of the coleoid fauna from the Late Triassic Polzberg Konservat-Lagerstätte (Lower Austria, Northern Calcareous Alps).

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Keywords: Belemnoids, Konservat-Lagerstätte, *Mojsisovicsteuthis*, palaeobiology, *Phragmoteuthis*, Triassic

The well-known, almost complete specimens of the basal coleoid cephalopod *Phragmoteuthis bisinuata* from the Carnian Polzberg Konservat-Lagerstätte near Lunz am See (Lower Austria, Northern Calcareous Alps) come from historical collections. Of course these specimens do not reflect the entire coleoid assemblage of this Mesozoic environment. In order to obtain a more complete picture of this coleoid fauna, 490 specimens from Polzberg and from the contemporaneous fossil locality Cave del Predil (Northern Italy) were studied in detail. The available elements such as phragmocones, proostraca, cartilage, hooks, beaks and ink sacs, were recorded, measured and evaluated taphonomically and taxonomically. Reviews of historical collection material permitted comparisons with specimens from recent excavation campaigns. Particularly the recently collected material refutes the previous assumption of a monospecific composition of the coleoid Polzberg fauna. Instead, we report the occurrence of the newly described *Phragmoteuthis polzbergensis* nov. sp. with differentiated arms and a third, to date undetermined, member of the Phragmoteuthida. A newly excavated specimen confirms the presence of ten arms within the group of the Phragmoteuthida for the first time. The character combination of phragmocones with small opening angles combined with roundly closed (tubular) final chambers, a dorsal crest and curved arm hook types, suggests the presence of the rostrum-less coleoid genus *Mojsisovicsteuthis* in Polzberg. Three types of cephalic cartilage with a preserved channel system support the assumption of the different coleoid groups in Polzberg.

Long lost type material resurfaces in the discovered Heinrich Hauffen Collection in Vienna, Austria (University of Natural Resources and Life Sciences, BOKU)

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Keywords: Dominik Bilimek, Heinrich Hauffen, history of sciences, museum collections, *Zospeum*

Type material of *Carychium bidentatum* Hauffen, 1856 and *Carychium reticulatum* Hauffen, 1856 was long considered lost to science. Now, it has been rediscovered in a recent inventory of the Dominik Bilimek (1813-1884) Collection at the University of Natural Resources and Life Sciences in Vienna, Austria (BOKU). In our work we discuss the historical context of the Heinrich (also: Henrik) Hauffen (1836-1866) and the Dominik Bilimek Collections and provide a contemporary image dataset of Hauffen's type material, while considering today's taxonomic understanding of the genus *Zospeum*. We clarify the taxonomic status of the syntypes by the use of light microscopy, 3D X-ray Micro-CT data and Scanning Electron Microcopy (SEM) in conjunction with Hauffen's original illustrations and compare them with their closest congeners. The recognition of *Zospeum reticulatum* Hauffen, 1856 is supported by historical documentation from Hauffen's annotations, from original collection labels, as well as from Bilimek's diary entries. Hauffen's descriptions were based on micro-sculpture and aperture morphology. Our re-investigation of *Z. reticulatum* provides corroborating evidence supporting its assignment to *Zospeum spelaeum* (Rossmaessler, 1839), while that of *C. bidentatum* corroborates its status as junior synonym of *Zospeum costatum* (Freyer, 1855).

Discovering Hauffen's material underscores the importance of preserving and processing historical natural science collections. The present work also forms a first step for the future scientific treatment of the remaining malacological collection of Heinrich Hauffen at the BOKU, including original material of *Valvata spelaea* Hauffen, 1856 and *Paludina pellucida* Hauffen, 1856.

Diversity, composition and distribution pattern of marine gastropods in the Cape Verde islands (West Africa)

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Keywords: taxonomy, richness analysis, endemism rate, biogeography, Macaronesian region

Darwin visited Cape Verde during his famous voyage around the world. He considered the volcanic islands to be "utterly sterile" in terms of the terrestrial environment but most interesting in terms of marine diversity. Since then, the Atlantic islands have continued to exert an attraction for travellers and scientific expeditions. Despite the high number of scientific publications on marine molluscs in the archipelago, all of them focus on taxonomic aspects, with no studies carried out on other aspects, such as abundance, diversity, geographic, bathymetric, or habitat distribution, among others. This study aims to be the first estimate of the diversity of marine gastropods in these islands through the study of bioclastic sediment samples spread out from coastal beaches. To review the list of marine gastropod species and their occurrences on each island, a total of 10010 specimens were taxonomically identified, representing 134 species belonging to 93 genera and 53 families. Statistical analyses corroborate the Cape Verde Islands as a hotspot of marine gastropod diversity, with high species richness and a significant rate of endemism (59 species, 44%). The similarity in species composition between islands shows two groups matching the two geological chains. Mollusc biodiversity surveys require a long period of time and a large amount of funding to sample most of the species. The results obtained demonstrate that studying molluscan death assemblages in the marine intertidal zone provides a first representative projection of regional biodiversity, with low cost and effort. In addition, this study highlights the importance of complementing the knowledge of Cape Verde marine molluscs, which until now has focused mainly on taxonomic studies, with genetic analyses, ecological, and biogeographical research.

The type room of the fossil invertebrate collection at the Muséum national d'Histoire naturelle in Paris

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Keywords: fossils, type material, managment

The fossil invertebrate collection at the Muséum national d'Histoire naturelle in Paris contains around 7 million specimens and is one of the richest in the world. The d'Orbigny's collection is the founding collection. During the second half of the 19th century, it was enriched by the addition of other collections by illustrious naturalists such as Faujas de Saint-Fond, Lamarck, Brongniart, Tournouër, Toucas, Vasseur, de Morgan, Milne Edwards and Cossmann. Molluscs are abundantly represented mainly by cephalopods and bivalves from the Palaeozoic and Mesozoic, as well as Cenozoic bivalves and gastropods. They come from various parts of the world, but mainly from the major sedimentary basins of Western Europe. Given the importance of the historical material, the idea was born to place the type material of species in a dedicated type room: the typothèque. Jean-Claude Fischer set up it in the 1980s. From a small number of specimens in the early 2000s, the typothèque has grown considerably. After more than twenty years' work, it now contains around 40,000 types and figured specimens, including many molluscs. This means that the type specimens have been brought together and clearly identified, and are no longer scattered throughout the general collection. In addition, the precise status of each type specimen (e.g., holotype, syntype, paratype…) is distinctly identified, and all the material is cataloged in a computerized database. The digitization of the type material marks a new development phase, allowing data to be accessed online through the Museum's website. Researchers worldwide can now virtually access this data, potentially obviating the need for a challenging in-person visit.

The Slug Lab – Complementary molecular tools for exploring the systematics and radiation of Heterobranchia

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Keywords: Mollusca, Gastropoda, phylogenomics, mitogenomes, Sanger-sequencing

Although snails and slugs significantly impact our economy and ecosystems globally, studies using genomic data to investigate their evolutionary history and diversity remain scarce. In this presentation, I will discuss the research focus of our group, The Slug Lab, which combines morphological and molecular tools to elucidate the diversity and evolutionary history of heterobranchs worldwide. We employed a target enrichment approach to explore the phylogenetic relationships within this major clade of gastropods (comprising approximately 44000 species, including opisthobranchs, pulmonates, and other ecologically diverse groups) through a comprehensive genomic, museomics, and all-family approach encompassing 1000 targeted species.

I will introduce a probe set for the target enrichment of ultra-conserved elements (UCEs) as a benchmark genomic technique capable of assembling up to 2259 genes. This high-throughput data, derived from museum specimens, surpasses any currently available method. I developed and rigorously tested this innovative genomic approach on a selection of heterobranchs and further assessed the universality of this set across all six subclasses of Gastropoda and the remaining seven classes of Mollusca. This study reveals the enigmatic position of Acteonimorpha, with significant implications for our understanding of body detorsion and the euthyneurous nervous system.

Students from our lab will present at this congress on various topics, including the rise of Heterobranchia and the morphological innovations associated with the transition from marine to limnic and terrestrial habitats in the minute Acochlidia. In this talk, I will emphasize the importance of complementary tools such as mitogenomes and multilocus analyses based on Sanger sequencing data to investigate intriguing topics such as the radiation of side-gilled slugs, pteropods, cephalaspideans, specific nudibranch families, and even the Cuban *Polymita* jewels.

Octopus Optics and Mussel Memories: communicating and contextualising mollusc conservation research through artistic projects outside the museum

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Keywords: audience engagement, freshwater mussels, *Octopus vulgaris*, art

How can transdisciplinary, artistic projects contribute to wider public awareness of and engagement with mollusc conservation? How might they help with using and improving collections? This presentation discusses two recent mollusc-based artistic projects the author collaborated on: (1), a speculative project to design an AI that might communicate through visual artworks with an octopus (*Octopus vulgaris*) in its environment; and (2), a project to reimagine the freshwater mussel collection of a natural history museum from the perspective of the mussel species' in the collection from one river. The first culminated in an archive of designs, talks, videos and articles about the imaginary project that continues to engage arts, cultural and scientific audiences around the world. The second resulted in an epic poem of species love, loss and extinction, as well as a series of paintings and a prototype for a new role-playing game designed for non-specialist audiences. These collaborative projects were developed by transdisciplinary teams from artistic, zoological, psychological, computational and museums backgrounds. They combined methods from visual art, computational art, 3D coding, data visualisation, literature, creative writing and gaming in order to create works that aimed to draw attention to other animals' lifeworlds and the different ways they perceive and inhabit our shared environments.

This presentation discusses lessons learned from the two projects, arguing that artists working in collaboration with zoologists can help to communicate and contextualise zoological research for diverse communities of interest. It aims to highlight some methods and approaches for art-zoology collaborations that can engage audiences beyond the museum and academia, while using and improving collections, from an artist's perspective. It also suggests that arts-based projects outside the museum could help to connect with new biodiversity and conservation stakeholders by facilitating collective emotional engagement with climate and social change scenarios through the eyes of other species.

Ethnomalacology: bridging biological diversity and traditional knowledge on Mollusca

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Keywords: Ethnozoology, ethnobiology, malacology, snail, Gastropoda

Biological diversity always has a strong bond with cultural diversity. Antropogenic and local culture influence the changes in biodiversity and its ecosystem, and vice versa. Based on ethnozoological studies, fauna is culturally used for various commodity such as consumption, feed, decoration, belief symbols, currency exchange tools, environmental bioindicators, cosmetic ingredients, including traditional medicinal. Here, we review the traditional knowledge on the use of Molluscs especially in Indonesia. Molluscs were used in daily life since the ancient Greek, and the use is not limited to its shells. Other than famously known for human consumption, snail has become part of traditional medicinal culture in China, Africa, the Mediterranean, and Europe. It was used as medicine for wounds and skin diseases in India, for asthma, irritated wounds, burns, and hemorrhoids in Brazil, snail shells for foot pain medicine, and snail mucus for wound medicine in East Africa, as well as hereditary medicinal ingredients in West Africa. In Indonesia, land snails can be used culturally for various functions such as consumption, feed, decoration, and environmental bioindicators, including as ingredients for traditional. Molluscs were even engraved on the walls of Borobudur temple, an ancient temple built in the 8th century, known as the Shanka. The use of Molluscs (not only their shells) as part of human life i.e. socio culture, economy, health, etc is very common. Thus, the terms of Ethnomalacology, ethnological study on Molluscs, should be acknowledged and should have its own place in Ethnobiology.

Land snails of Izmir (Türkiye) and its environs from 1839 to 2024

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Keywords: Gastropoda, Stylommatophora, biodiversity

The city of Izmir in western Türkiye is the type locality of at least 5 land snail species and thus occupies a significant place in malacological history. Izmir has grown tremendously since the 1960s and continues to do so. Development and limestone mining are especially threatening the limestone hills around the city where the snail diversity is the highest. To assess the state of the snail fauna, I have been doing surveys in and around the city and also on the Karaburun Peninsula to the west. The present species total is more than 40. Among the relatively common species are *Thiessea matrella* (Westerlund, 1898) and *Zonites smyrnensis* (Roth, 1839) whose type localities are Izmir. *Zonites chloroticus chloroticus* (Pfeiffer, 1852) is also present and the ranges of the two *Zonites* species almost overlap. Additionally, several other species that Roth reported from Izmir in 1839 may still be found on the limestone hills. One of the rarest species is *Vitrea storchi* described by Pintér in 1978 from the island of Chios across from the Karaburun Peninsula. The species has not been collected on the island since then. Shells referrable to that species have been found at a location on the Karaburun Peninsula. The distribution patterns of other species, including an undescribed *Vitrea*, collected during the surveys will also be discussed.

Diversity of marine snails at Phaselis in southern Türkiye

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Keywords: Gastropoda, Caenogastropoda, Mediterranean, biodiversity

The ruins of the antique city of Phaselis, located at the western shore of the Gulf of Antalya, are situated along two small bays. Thanks to its archeological significance, the inland area surrounding the ruins of Phaselis and the shores are mostly protected from development. We have been surveying the marine gastropods in the bays of Phaselis since 2021. Our methodology includes visual surveys for live species along the rocky shores and the collection of shell grit by snorkeling. Among noteworthy findings were the minute species *Cima cylindrica* (Jeffreys, 1856) and *Cima minima* (Jeffreys, 1858) that were recorded for the first time from the Turkish coasts. Other small species collected include *Oscilla galilae* Bogi et al., 2012, *Williamia gussoni* (O. G. Costa, 1829) and *Eatonina pumila* (Monterosato, 1884). Another significant find was the second ever Mediterranean record of the Lessepsian species *Coriophora lessepsiana* Albano, Bakker & Sabelli, 2021. The preliminary species total exceeds 110 species. Considering the limited survey area where the shoreline is only about 3 km and the collection depths are less than 5 m, the marine snail diversity at Phaselis is unusually rich compared to the results of previous surveys along Turkish coasts that covered larger areas. We believe that the lack of development around Phaselis is one factor that is contributing to the high species diversity.

Recurrent evolution of breathing microtunnel system in terrestrial operculate snails (Gastropoda: Caenogastropoda: Cyclophoroidea)

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Keywords: gas exchange, respiration, land snails, Alycaeidae

The Cyclophoroidea is a group of land snails with an operculum closing the aperture tightly when the animal retracts into the shell. Gas exchange remains a challenge when the aperture is closed. Several cyclophoroid taxa have solved this problem by developing snorkel-like tubes in the shell that open at their outer ends. These structures facilitate breathing in retracted condition. However, the tube of the family Alycaeidae ends blindly to the outside, so its function remained a mystery for a century. In 2016, we showed that there are openings: the alycaeid tube is connected to several long, perpendicular microtunnels that open near the umbilicus. The question arises whether other members of the Cyclophoroidea also have microtunnel systems. We examined taxa similar to Alycaeidae and discovered three more types of gas exchange systems in the genera *Platyrhaphe*, *Laotia* and *Boucardicus* that differ from each other and also from that of the Alycaeidae. Both the different organization and our molecular phylogeny based on 28S, H3 and COI genes suggest that the microtunnel systems of these four groups have evolved independently.

The “slow(est) smart”: predator-induced freezing in Pachyoliva

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Keywords: *Agaronia propatula*, freeze response, *Pachyoliva semistriata*, predator-prey interaction, sandy beach intertidal

Intertidal invertebrate communities on many sandy beaches of the Central American west coast are dominated by gastropods of the family Olividae. The suspension-feeding *Pachyoliva* (formerly *Olivella*) *semistriata* and the predatory *Agaronia propatula* provide a convenient model for studying the behavioural basis of complex predator-prey interactions in the natural habitat. Here we focus on so-called freezing behaviour. By definition, freezing is the cessation of all motion that is induced in a potential prey animal when it becomes aware of a predator. Freezing reduces the probability of the prey being detected by the predator; this defensive function distinguishes freezing from other types of voluntary immobility. According to behavioural theory based on studies in vertebrates and arthropods, freezing occurs before physical contact is made between predator and prey. This may seem obvious in animals with long-distance sensory capabilities, in which physical contact implies awareness of each other. However, the theory does not necessarily apply to gastropods with comparatively limited sensory capabilities. We will demonstrate freezing of *Pachyoliva* in response to direct contact with *Agaronia*, and discuss the sensory basis of its defensive effectiveness.

Integrative taxonomy helps uncover hidden diversity of dart-bearing land snails of *Hygromia* Risso, 1826 (Gastropoda: Hygromiidae: Hygromiini)

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Keywords: love dart, microsculpture, morphology, phylogeny, systematics

A love dart is a sharp calcareous stylet-like structure formed in a dart sac in several taxa of simultaneously hermaphroditic terrestrial gastropods. Its shape is often used to identify and classify species. In this study, we applied a comprehensive approach to assess species limits through the use of molecular and morphological information in dart-bearing *Hygromia* populations collected across Europe. We found two groups of snails that corresponded to two subgenera among which seven monophyletic clades could be distinguished. To the subgenus *Hygromia* s. str. one species *Hygromia cinctella* belonged. The second subgenus *Riedelia* included *Hygromia limbata, Hygromia sublimbata, Hygromia tassyi, Hygromia hylonomia* and *Hygromia veprium*. Additionally, one more clade represented an independently evolving lineage and therefore potentially a new species, whose taxonomic status cannot be assigned yet. Genetic uncorrected p-distances among clades based on COI sequences ranged from 8.31% to 19.27%, while in the case of 16S rRNA they were larger (7.67-25.55%). Conchological delineation of *Hygromia* species appeared to be challenging due to their notable variation and microsculpture instability. Likewise, no morphometric genital characters could ensure species determination. The most reliable diagnostic feature appeared to be the morphology of a love dart, indicating reproductive isolation between *Hygromia* species. Most of the recognized species are endemics restricted to narrow geographic ranges mainly in the south of France, implying a complex evolutionary history of the genus in this relatively small area. Our study also highlighted the need to verify reports of the occurrence of *Hygromia* (*Riedelia*) in both native and introduced areas.

Lower Pleistocene Freshwater Mollusk from the sedimentary basin of Sousaki Ag. Theodoroi, Greece

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Keywords: Lower Pleistocene, non-marine gastropods, non-marine bivalves, Sousaki Ag. Theodoroi, Greece

A Lower Pleistocene freshwater malacofauna from the Sousaki sedimentary Basin has been investigated. The studied area lies next to the Sousaki volcano, which is the westernmost end of the South Aegean volcanic arc, about 15 km west of Corinth, southern Greece. Eight samples were collected from a section, consisting of alternations of marly and conglomeratic layers and were located in the area of the youngest group of volcanic rocks, which comprises the substrate of the respective deposits. As a result, the malacofauna consists of 2 bivalve and 24 gastropod taxa. Concerning the bivalves, a species of Sphaeriidae family and remains of a species from Unionida were found. The gastropods belong to 9 families and 21 genera, namely Neritidae, Planorbidae, Lymnaeidae, Acroloxidae, Hydrobiidae, Bithyniidae, Viviparidae, Melanopsidae, Thiaridae. Five new species have been determined and are listed herein, *Islamia* n. sp., *Bania* n. sp., *Falsipyrgula* n. sp., *Graecamnicola* n. sp., as well as a possible a new species which belongs to a new genus of the subfamily Pseudamnicolinae as they were not detected in the literature. Caenogastropoda are dominating the assemblages, whereas the most diverse family is Hydrobiidae and second one is the Planorbidae. Representatives of the Superfamily Lymnaeoidea (i.e., Lymnaeidae, Planorbidae, Acroloxidae) appear in the study area as well, including some extant species, such as Armiger crista, or widespread extinct species in various Pliocene and Pleistocene basins such as *Lymnaea megarensis*. According to the ecological preferences of the studied taxa, a lacustrine palaeoenvironment could be inferred. This palaeofauna eventually disappeared from the study area, due to the collapse of the ecosystem after the loss of this freshwater environment.

Revisiting Conidae evolution: Present insights and future challenges in taxonomy and palaeobiogeography

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Keywords: Fossil, gastropod, colour patterns, Rhodes, UV light

Conidae (cone snails) are carnivorous gastropods predominantly found in tropical regions, with a rich evolutionary history spanning from the early Eocene (55 Ma) to the Holocene. Today, cone snails comprise about 900 species, inhabiting various depths and feeding on specific prey, with Conus species also present in the Mediterranean Sea. Conidae are venomous, and their toxins, used for hunting, have significant medical applications. Despite their diversity, cone snails exhibit limited interspecific morphological variability, and intraspecific variation can sometimes lead to misidentifications. However, colour patterns are invaluable for identifying extant species, alongside radula characteristics and mitogenome sequences for phylogenetic reconstruction. For fossils, UV light reveals colour pattern variations, aiding in species identification.

Recent taxonomic revisions have focused on Miocene (23.03 – 5.3 Ma) Conidae in Europe and North America, using colour patterns to redefine species diversity. For instance, we studied the Conidae diversity of Tortonian (11 – 7 Ma) outcrops in Crete, Greece, initially thought to consist of only eight species, revealing a rich fauna of 33 species, eight of them new to science. Yet, Pliocene (5.3 – 2.58 Ma) and Pleistocene (2.58 – 0.01 Ma) assemblages remain largely unexamined. Drawing on Miocene studies, it is evident that many Pliocene and Pleistocene species are likely misidentified in collections and literature. To clarify the taxonomy and palaeobiogeographic evolution of Conidae, revisiting these younger species is essential.

To that end, we studied a Pleistocene assemblage (241.8 – 212.9 ka) from the island of Rhodes, Greece, identifying three species of Conidae under UV light, with at least one being new to science. Their palaeobiogeographic inferences are important for understanding climate change and the colonisation of the Mediterranean by different species during specific interglacial periods. Therefore, a comprehensive revision of fossil Conidae globally would significantly elucidate the evolutionary history of this diverse and important gastropod group.

Conservation status and prospects of freshwater molluscs in the Iberian Peninsula

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Keywords: Bivalves, endemism, gastropods, red lists, threatened

Freshwater molluscs in the Iberian Peninsula are experiencing severe conservation challenges, following the global trend of biodiversity loss in freshwater ecosystems. This region, encompassing Spain and Portugal, harbours a rich diversity of mollusc species, many of which are endemic. However, much of this diversity is poorly known, with many species described in the last two decades. This is a main constraint for conservation efforts, emphasising the urgent need for updated species Red Lists. In Portugal, the first national invertebrate Red List was published in 2024, evaluating the risk of extinction of 28 freshwater molluscs: nine were classified as Critically Endangered (25%), six as Endangered (21%) and one as Vulnerable. In Spain, the national Red List last updated in 2007, listed 47 freshwater molluscs: five Critically Endangered (10%), six Endangered (13%), and 20 Vulnerable (43%). The IUCN Red List includes 128 freshwater mollusc

species out of ~200 species found in the Iberian Peninsula, categorizing eight as Critically Endangered (6%), 12 Endangered (12%), and 21 Vulnerable (16%). Approximately a fifth are Data Deficient. However, most of these assessments date back to 2010, and urgently need revision. Most Iberian freshwater mussel species are now endangered according to the updated IUCN list, with half being Critically Endangered. In Spain, a government-promoted national project is expected to produce a revised Red List by 2025. These efforts are essential to implement effective conservation measures for this highly endangered group. This is especially important in the Iberian Peninsula, which faces increased threats to freshwater habitats due to climate change, including altered temperatures and flow regimes, prolonged droughts and heatwaves, and irregular precipitation patterns. Coordinated efforts at local, national, and international levels are essential to mitigate threats and ensure the long-term survival of these ecologically important organisms.

The enigmatic *Deroceras klemmi*, a puzzle resolved

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Keywords: museum collection, terrestrial slug, Eupulmonata, Agriolimacidae, taxonomy

The Balkans is a biodiversity hotspot, also for terrestrial eupulmonate slugs, including the most speciose genus *Deroceras* Rafinesque, 1820, a notoriously difficult group taxonomically. One example is *D. klemmi* Grossu 1972. Described from specimens collected 60 or 80 years earlier in Trieste (now at the Italian/Slovenian border) and at another locality 400 km further north, it has remained a somewhat enigmatic species with unclear identification characters and an uncertain distribution. An increasing number of records lead to the picture of a species widely distributed not only in the Balkans but also Central Europe.

We reinvestigated the type specimens as well as new material with an integrated approach including morphology, genetics and mating behaviour, and searched for further information in the literature. We also tried to examine specimens behind various published and unpublished records in central Europe.

Our results show that *D. klemmi* is a very different species to *D. lothari*, with which it had been synonymised, but more difficult to distinguish from the widely distributed and co-occurring pest species *D. reticulatum*. We redescribe *D. klemmi* and differentiate it from the most similar species. Four out of six type specimens of *D. klemmi* belong to other species. The two remaining types are now in the natural history museums in Vienna and Bucharest. An ambiguous species description, combined with a mix-up of type specimens and some further curating mistakes, led to too broad an interpretation of the species' morphological variability, which in turn led to the idea of a widely distributed species with a high ecological tolerance. In fact, *D. klemmi* seems common in Slovenia and Croatia, but all records from Germany, France, Italy (except for the type locality), Switzerland, and also Austria need verification, even though parts of Austria may well belong to its natural range.

Gastropods as climatic indicators: Insights from Southern Caucasian loess sequences

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Keywords: palaeoecology, stratigraphy, climate change, Quaternary gastropods, geochemistry

Subfossil gastropod assemblages in terrestrial sediments offer valuable insights into the effects of climatic changes on ecosystems and species distributions. They also allow us to reconstruct past environmental and climatic shifts. This study presents findings from loess-palaeosol sequences in the Armenian highlands, highlighting multiple glacial-interglacial transitions over the past 400 thousand years. Our primary aim is to generate reference data essential for the improvement and calibration of earth system models. Therefore, we combine ecological analyses with quantitative approaches, including the mutual climatic range method and stable isotope analyses of the snail shells. The gastropod assemblages revealed distinct variations within the sequences, enabling us to reconstruct vegetation types and humidity conditions across time. Specific ecological groups of gastropods showed distinct patterns related to the oxygen isotopy ($\delta^{18}O$) of the analysed shells. Predominantly xerophilous assemblages from glacial phases were associated with more negative $\delta^{18}O$ shell signals, while mesophilous assemblages corresponded to warmer phases with more positive $\delta^{18}O$ shell signals. $\delta^{18}O$ shell signals in our deposits provide information on the isotopic composition of ingested precipitation, allowing us to reconstruct average temperatures. The mutual climatic range method is used to compare these results with climate data derived from modern species distributions. Both quantitative analyses could be significantly improved and made more precise by expanding the database of modern species distributions and deepening our understanding of ecological dependencies.

Revision of the Holarctic genus *Perpolita* (Gastropoda: Gastrodontidae) and its diversification through time

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Keywords: Beringia, climatic cycle, cryptic species, land snails, misidentification

Robust taxonomy that integrates evolutionary history is the foundation for biological conservation and understanding biodiversity patterns. However, an integrative taxonomic revision for most land snails is still lacking, partly because of the outstanding species diversity of this group. We focused on the Holarctic land snail genus *Perpolita*. We integrated mtDNA and nDNA data including genomic information, geographic and ecological range and identified five empirically-supported temperate-boreal species (*P. binneyana, P. electrina, P. hammonis, P. petronella*, and *P. radiatella*). On the other hand, there was no genetic distinction between *P. dalliana* and *P. suzannae* being limited to North American subtropical areas and these species were highly distinct from the other high latitude Perpolita species. Only *P. petronella* remained unchanged in both nomenclature and diagnostic characteristics with the remainder requiring alterations. In particular, *P. radiatella* had been previously lumped either under the European *P. hammonis* or the North American *P. electrina*. Although the differences in shell shapes among these five species were limited based on morphometric analyses, the combination of microstructure and color provided diagnostic features. The divergence times of 18.7-10.0 Ma were suggested by genomic data in combination with the fossil record, indicating a pre-Pleistocene origin for all temperate-boreal *Perpolita* species. Using genetically-confirmed diagnostic features, we accumulated >2000 valid occurrences and used these to estimate appropriate modern and the Last Glacial Maximum climate extents for all species. These models suggested that modern intra-specific gene pool diversity reflects climate changes during the Pleistocene. Our results show the close relationship between evolutionary history and species taxonomy and the importance of establishing validated taxa for practical identification.

South American terrestrial gastropods: past, present and future

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Keywords: biogeography, Gondwana, fossils, phylogenetics, taxonomy

There is an astounding diversity of terrestrial gastropods in South America across its many biomes: from the Andes through the Amazon Forest to the coastal Atlantic Forest and the Pampas. For many species, all our knowledge is restricted solely to alpha taxonomy; even so, it is estimated that we are still far from knowing the real biodiversity of snails and slugs on the continent. Likewise, the phylogenetic relationships of South American taxa remain understudied. In the past two decades, there has been an increase in the number of studies involving terrestrial gastropods, and many discoveries and interesting new interpretations have emerged. Naturally, new species (both living and fossil) have been constantly described and taxonomic revisions have improved our understanding of genera and families (e.g., Scolodontidae). Moreover, the oldest fossils in the continent have been found in Uruguay, and Urocoptidae, a typically Central/North American family, was found in southern Brazil. New phylogenetic studies have improved systematic classification and shed light on the relationship of taxa within South America and in relation to our neighbours from Gondwana time (e.g., Orthalicoidea, Punctoidea). Those studies have also produced a wealth of genetic data. Finally, there has been increased awareness regarding exotic species and species of economic interest. Despite the usual problems of conducting research in the Global South, these past advances hopefully signal the beginning of a new age of terrestrial malacology in South America. The increase in the number of promising graduate students is an encouraging indicator. Furthermore, researchers in South America are in the initial stages of establishing wider networks of national and international collaborations in the continent; the new technologies not only facilitate this process but also help sustain it, keeping partnerships viable and active.

Multilocus phylogenetic assessment of species and lineages of rock oysters (*Saccostrea* Dollfus & Dautzenberg, 1920) across the Indo-Pacific Ocean

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Keywords: Rock oyster, DNA barcoding, species delimitation, molecular systematics, multilocus phylogeny

Indo-Pacific rock oysters, genus *Saccostrea* Dollfus & Dautzenberg 1920, play a key role in subtropical and tropical ecosystems as well as in aquaculture industry of Australia and Asia. The taxonomy of this genus remains challenging due to the high phenotypic variability and plasticity of shells, which lead to morphological misidentifications. Molecular data demonstrate to be useful for oyster identifications and several lineages have been discovered using a phylogenetic approach. However, a few of them were formally described as new species and significant knowledge gaps for *Saccostrea* species taxonomy, distribution, and evolutionary patterns exist. In this study, we assessed molecular operational taxonomic units (MOTUs) based on thousands of DNA sequence from specimens sampled across the Indo-Pacific Ocean and gathered from GenBank. We used single-locus and multilocus species delimitation methods and combined these results with morphology and geographic distribution data to provide an integrative assessment of the taxonomy of the group. This study allowed to resolve the taxonomy of several lineages and to describe new species of *Saccostrea*. It also provides an updated (molecular-based) picture of the distribution of *Saccostrea* species and lineages across the Indo-Pacific and Atlantic Ocean.

Subcellular effects of imidazolium-based ionic liquids with varying anions on the marine bivalve *Mytilus galloprovincialis*

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Keywords: *Mytilus galloprovincialis*, ionic liquids, biomarkers, ecotoxicology, S9 fractions

Green Chemistry involves applying a set of principles aimed at minimizing or eliminating the use or generation of hazardous substances in the design, production, and application of chemical products. In recent decades, Ionic Liquids (ILs) have emerged as more environmentally friendly substitutes for traditional organic solvents. This preference is primarily due to their low vapor pressure, which results in minimal atmospheric pollution and enhanced industrial safety. However, existing literature highlights the toxicity of ILs towards aquatic invertebrates. Consequently, this study aims to assess the biochemical effects of a selection of ILs through an in vitro approach. Specifically, cellular fractions (S9) from the digestive gland and gills of the marine bivalve *Mytilus galloprovincialis* were exposed to varying concentrations (0.05-2 μM) of three ILs featuring identical cations but different anions. The ILs tested were 1-ethyl-3-methylimidazolium octanoate ([EMIM][Oct]), 1-ethyl-3-methylimidazolium acetate ([EMIM][OAc]), and 1-ethyl-3-methylimidazolium ethyl sulfate ([EMIM][EtSO4]). The results indicate that [EMIM][Oct] induces higher toxicity in both S9 tissues, highlighting a strong effect of the anion. Overall, antioxidant and biotransformation defenses were significantly altered for all three ILs assessed. While acetylcholinesterase activity was significantly inhibited, of about half of control activity, indicating neurotoxicity as part of the toxicity mode of action of these ILs, neither lipid peroxidation nor alterations to DNA integrity were observed (≥ 100 %). This study supports the use of in vitro methodologies as important screening tools capable of generating reliable ecotoxicological data, which can be further considered before in vivo testing and used for in silico modeling.

"Balbúrdias Malacológicas" strikes again: the importance of Education for Health and Conservation

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Keywords: Malacology, popularization of science, teaching of science

Molluscs are the second group in terms of biodiversity. Teaching about Malacology is relevant considering both the species richness and the variety of ecosystems in Brasil, the interfaces that Malacology presents with public health and economy, and the relative rejection of people of snails. The Project "Malacology at School", aimed at disseminating the molluscs to students of all levels, in formal and non-formal spaces, besides training futures teachers of Biology. Among the various activities developed, we highlight those aimed at clarifying and recognizing the differences between the African giant snail *Achatina fulica* Bowdich, 1822, an invasive species and the native species of *Megalobulimus* spp, our Atlantic Forest giant snail, the "aruá-do-mato". *Megalobulimus* can occur in areas of secondary forests bordering the urban areas of small towns and villages, where it can be confused with *A. fulica*. Therefore, pointing out the differences between the two species is relevant for the conservation of *Megalobulimus*, avoiding its undue elimination. We also address the diseases transmitted by *A. fulica* and the necessary precautions to avoid contamination. We use exhibitions of shells and live animals, as well as posters, demonstration boxes and playful activities such as games, modelling clay and drawings. Visits to schools take place especially in the annual events of the "Universidade do Estado do Rio de Janeiro Environment Week", the "National Week of Science and Technology", the "University Without Walls" and other exhibitions at the invitation of other institutions. We will show the results of the work carried out in the last five years, which reached more than 1200 children and teenagers. We believe that young people cannot keep what they do not know. Outreach activities are key to developing love and empathy for molluscs as well preventing diseases.

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Initiatives of the Brazilian Society of Malacology in addressing the theme of One Health

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Keywords: Scientific Societies, malacology congresses

The Brazilian Society of Malacology (SBMa) was founded in 1962 to bring together Brazilian scholars in the field. Every two years, it promotes a national event (Encontro Brasileiro de Malagologia - EBRAM) where relevant topics for Brazilian society are discussed and studies in various areas of Malacology and related areas are presented. The concept of One Health emerged in the early 2000s strengthening the perception that there is a close relationship between human, animal and environmental health. Since then, SBMa has been highlighting the theme, through plenary lectures, symposiums, workshops, discussion tables and presentation of papers addressing health in all its aspects: questions about epidemiology, cultivation, use of molluscs to produce pharmaceuticals and biomarkers, parasitosis of human and veterinary interest, invasive species, species extinction, health surveillance, among others were debated. The abstracts of the papers are published in the EBRAM Summary Books, available on the Society's homepage (http://sbmalacologia.com.br/). In addition to the national congresses, in 2012 it was organized the XI International Congress of Medical and Applied Malacology (XI ICMAM, Rio de Janeiro), on the theme "Crossing Boundaries: Integrative Approaches to Malacology", which resulted in a book of the same title. Another SBMa participation occurs in the Brazilian Zoology Congresses, where we have been debating the theme in discussion tables focused on Malacology. In this regard, we will present a historical synthesis of the themes that have been addressed, which mostly privilege medical malacology and, more recently, the environmental issue.

Support: SBMa, CNPq, Capes.

Notes on the size and maturity of the species *Rondeletiola minor* and *Sepietta oweniana* (Cephalopoda: Sepiolidae) in the Eastern Mediterranean

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Keywords: Sepiolidae, E. Mediterranean, body weight, mantle length, size-at-maturity

The lentil bobtail *Rondeletiola minor* and the common bodtail *Sepietta oweniana* are the most common species of the family Sepiolidae in the Mediterranean Sea and the northeast Atlantic Ocean, exploited mainly as bottom trawl by-catches. Their biological parameters have been sporadically studied, however due to the general plasticity of cephalopod growth, affected primarily by sea temperature and food availability, a systematic study is required to understand their populations response through the years. The specimens of this study were caught during bottom trawl surveys conducted by the Hellenic Centre for Marine Research, in the framework of the Research Projects "Selectivity of the diamond and square mesh of the trawl cod end, biological and economic consequences, and fish behaviour comparative study (EPILEXIS)" (May-June 2015) and "National Fisheries Data Collection Project (DCF) - Research Bottom trawl Survey-MEDITS"(6-28/8/2019, 5-24/8/2020), carried out respectively in the southwestern Aegean and the Ionian Seas. During the dissection of individuals at the laboratory, data concerning dorsal mantle length (mm), total body weight (grams), sex and maturity were reported. A total of 156 individuals of *R. minor* and of 173 individuals of *S. oweniana* were examined. In both Sepiolid species females attained larger sizes of mantle length (ML) than males, indicating morphometric sexual dimorphism due probably to the need of mature females for larger space during ovary development. Maximun size of dorsal ML observed was 20.5 and 29.2 mm for *R. minor* and *S. oweniana* respectively, whereas minimum ML of fully mature females was 9.9 and 13.3 mm, sizes considerably smaller than those reported for these species in the Aegean Sea during the two previous decades, a fact that might be attributed to global warming.

The importance of coarse woody debris and beech trees for land snail diversity in managed spruce forests

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Keywords: forest, gastropods, conservation, management, CWD

Terrestrial gastropods are important components of various ecosystems, contributing to litter decomposition, nutrient cycling, and food webs. As most Central European malacofauna consists of forest species, snails are particularly important in forest environments. Forest malacofauna diversity responds positively to soil calcium and pH, humidity, and the amount of coarse woody debris (CWD), positively affecting key environmental variables. Current forest management in the Czech Republic threatens many forest species, including snails, mainly due to the conversion of forests to spruce monocultures with zero or minimum amount of CWD. Gastropods are good indicators of long-term ecosystem stability because of limited dispersal ability, and they can potentially serve as an umbrella taxon.

Our research investigates the influence of CWD and beech trees on mollusc diversity in managed spruce forests, aiming to propose optimal management strategies that maintain biotic diversity. Field research was conducted in four locations of managed forests (5 plots sampled in each) and four nature reserves (3 plots sampled in each) nearby to each location. We collected four individual leaf litter samples from each plot, representing four mesohabitats: Spruce trees, Beech trees, CWD, and Matrix. This design allowed comparisons on two scales: between forests and between mesohabitats. The data revealed a positive correlation between CWD and both the number of snail species and their abundance. Additionally, the degree of debris decomposition and the presence of beech trees were significant factors. After accounting for soil pH, we found that a minimum of 6.5 m^3/ha of fallen wood can already support higher snail diversity, provided the logs are large and in an advanced stage of decomposition. Furthermore, the presence of beech trees, especially in groups, helped mitigate the negative effects of uniform spruce stands.

Molluscs in environmental analyses: from biomonitoring to ecotoxicological assays

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Keywords: Ecotoxicology, bioindicator, monitoring, environmental assessment.

The search for products to meet human needs of the most varied orders generates several problems for the environment, many of which are irreversible. Environmental changes affect the health, safety and well-being of exposed populations, as well as aesthetic and sanitary conditions and the quality of environmental resources. Consequently, the risk of living beings not being able to survive on our planet increases. In this scenario, concern for the environment and all measures to mitigate, preserve, and conserve ecosystems have become eminent. Among the animal groups, molluscs play an important role in food chains and are vital organisms to sustain many habitats. This group is a focal point and of great value due to its function generating diverse ecosystem services. Molluscs serve as excellent models for environmental health assessments since they inhabit almost all environments, with highly varied representatives. These organisms can reveal important responses to stressors in both natural environments and laboratory settings, providing relevant information for decision-making by environmental regulatory and governmental agencies. Globally most of the studies focus on bivalves and gastropods, followed by cephalopods. Such organisms are called bioindicators of environmental changes, whether *in situ* or in laboratory. Environmental assessments, with several approaches of molluscan studies concern as example, analysis of fossil records, morphometric analysis of shells, physiological and biochemical changes. Research on climate change, plastics, pesticides, industrial products, pharmaceuticals, and personal hygiene products constitute high relevance in terms of impacts on the environment. In this context, the *status quo* of different approaches using molluscs will be discussed, as well as the challenges and perspectives in the use of this group in the Ecotoxicology.

Comparative venomic study of *Lautoconus ventricosus* populations from the Eastern and Western Mediterranean

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Keywords: *Lautoconus ventricosus*, transcriptomics, proteomics, conotoxin

The Mediterranean cone snail, *Lautoconus ventricosus* (Gmelin, 1791), has been considered for a long time a unique species that inhabits the entire Mediterranean basin and neighbouring Atlantic coasts. A recent phylogenetic study based on complete mitochondrial genomes and nuclear markers derived from low coverage genome sequence data disclosed a mito-nuclear discordance. Species delimitation tests proposed the existence of at least three species, one with western distribution and partially sympatric with another having an eastern distribution, separated one from the other by the Sicilian-Tunecine biogeographical barrier.

Taking advantage of the availability of the chromosome-level genome of *L. ventricosus*, and transcriptomic data from the venom gland for several individuals, we have now carried out a comparative proteomic study of the venom gland extracts of individuals from Western (Algarve, Portugal) and Eastern (Crete, Greece) locations, each of the populations corresponding to putative separate species.

The venom extracts were analysed by liquid chromatography coupled to mass spectrometry (LC/MS), and tandem LC-MS/MS. The analysis by LC/MS for 5 specimens of *L. ventricosus* from the Algarve yielded 94 monoisotopic masses, of which only 39 were present in single individuals. In contrast with this, the analysis by LC/MS of 4 specimens from Crete yielded 109 monoisotopic masses, with 86 of them present in single individuals, indicative of a greater intraspecific variability. Only 2 masses were found in common among the Algarve and Crete populations. Tandem LC-MS/MS of the pooled extracts of the Algarve and Crete individuals allowed the identification of a total of 698 sequences, of which 253 (36 %) were common to both populations. The reference database used for conopeptide identification contained 3083 sequences of species in the West African genera *Lautoconus*, *Varioconus* and *Africonus*. These results are consistent with the close phylogenetic relationship among species of cone snails from West Africa and the Mediterranean.

Re-organising a type collection

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Keywords: fossils, museum collections, nomenclature, taxonomy, systematics

The "invertebrate" fossil type collection of the Natural History Museum Basel (NMB) includes about 10000 type-series material of molluscs. Its establishment started in the mid-20th century, growing steadily until today. Historically, the type and published material has been separated from the rest of the collections, and kept in proximity to the relevant literature for easier access. In light of the scientific developments of the last decades and the growing interest of scientific research based on natural history collections, there is a real need to modernise the structure of the type collection.

Starting from locating the different molluscan specimens, we proceed to locate physically the specimens in the collections before establishing a new organisation plan. One of the biggest challenges is to characterise the taxonomic status of specimens, knowing that previous curators and managers have used a special vocabulary to the NMB to designate figured and cited specimens.

Oral Presentation

Exploring the Genome's Dark Matter: The Impact of Satellite DNAs and Transposable Elements on the Architecture and Evolution of Oysters' Genomes

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Keywords: oysters, satellite DNA, transposable elements, heterochromatin

Segments of the genome enriched in repetitive DNA sequences like satellite DNAs (satDNAs) and transposable elements (TEs), are often referred to as the "dark matter" of the genome. These sequences are also acknowledged as important factors in genome architecture, and drivers of its evolution. Consequently, research focused on all apect of the genomes' satDNAs and TEs is expanding. By employing different experimental and bioinformatic methods, we have determined that oysters have unique traits that make them useful organisms for studying repetitive DNAs. We found that the centromeric chromatin of the Pacific oyster *Crassostrea gigas* lacks uniformity in the composition of DNA sequences, and that the heterochromatin of this species is extremely scarce and predominantly constituted of DNA transposons. We have characterized the satellitomes (the entirety of satDNA sequences) of six oysters from the Ostreidae family, revealing not only a substantial number of satDNAs per genome (33 - 61), but also peculiarities in their composition. We have observed novel, highly interspersed patterns of satDNA organization throughout the genome, differing from conventional concepts. An extensive number of detected satDNAs was found to be either associated with TEs or derived from TEs. Through comparative satellitomics, we were able to confirm the applicability of the "satDNA library hypothesis" to this set of related species. Within this organism group satDNAs and TEs were also found to be strongly interconnected in numerous aspects and to form intricate networks. Studies of these important components of the genome are anticipated to continue playing a significant role in advancing our understanding of oysters' genome structure and evolution.

Slugs of Hungary – an identification guide

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Keywords: species identification, introduced species, invasive molluscs, terrestrial gastropods, distribution

We have been investigating terrestrial slugs in Hungary for six years. Our aim was to cover the entire slug fauna and write a monographic identification guide. We collected specimens from as many habitats and regions of Hungary as possible and photographed them alive in the laboratory to document the intraspecific variation in colouration. Special attention was given to garden centres, botanical gardens and cemeteries in Budapest as they are likely hotspots of introductions. For some introduced species new to the fauna we launched "citizen-science" campaigns (e.g. Facebook posts) to reveal their distributions. In the case of Limacus maculatus, we collected every specimen reported by citizen scientists and confirmed the identities by dissection. We also examined slugs in the Hungarian Natural History Museum to confirm previous identifications and locality data. Specimens of all Hungarian slug species were dissected in order to examine the variability of their genitalia, to look for novel species-specific characters and to assess which species are identifiable without dissection. Morphology-based species identifications were confirmed by DNA barcoding.

Our research has revealed nine species that were new to the Hungarian fauna or whose earlier records had been considered doubtful: *Arion intermedius, Arion transsylvanus, Ambigolimax parvipenis, Ambigolimax valentianus, Deroceras invadens, Krynickillus melanocephalus, Limacus maculatus, Milax nigricans, Tandonia kusceri*. Specimens previously recorded as *Arion rufus* are *A. ater ruber*, and those of *A. subfuscus* s.l. are *A. fuscus*. Records of *Deroceras lothari* refer to *D. klemmi*. We could not confirm earlier records of Arion owenii: at least one was based on misidentified A. distinctus; A. hortensis also occurs. A recent report of *Deroceras panormitanum* is also a misidentification. The Hungarian slug fauna now consists of 33 species.

Here we present the process of preparing the book and provide a brief presentation about the slug species new to the Hungarian fauna.

Disentangling the species boundaries of Indo-Pacific cone snail complexes (Neogastropoda: Conoidea) using a genomic approach

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Keywords: Gastropoda, phylogenomics, cryptic species, venomous snails

With circa 1,000 species, cone snails form a highly diversified gastropod clade that lives in tropical and subtropical marine waters worldwide. They are a key predatory group that uses a venom cocktail loaded into harpoon-like radula for hunting and defense. The higher diversity of cone snail species is concentrated in the Pacific Ocean. Based on the shape and coloration pattern of the shells, some of these species have been postulated to have a wide distribution from the Western Pacific to the eastern coast of the Indian Ocean. However, recent phylogenetic studies have demonstrated that shell phenotypic traits are often prone to convergence and cases of cryptic species hide the real diversity of the group. In this study, we performed low-coverage (10x) sequencing of the genomes of 65 specimens assigned to cone snail species that have a distribution throughout the Pacific (collected in Okinawa) and Indian (collected in Mauritius) oceans. We evaluated species boundaries and phylogenetic relationships based on nuclear and mitochondrial sequence data using probabilistic methods. Preliminary analyses uncover cases of sister species inhabiting at both sides of the distribution. Future transcriptomic analyses of the venom glands could reinforce new species hypotheses.

How adverse are Mediterranean waters to the deep-sea fauna? A study of the Gibraltar exchange based on Mollusca from the "BALGIM" expedition

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Keywords: species distributions, deep-sea fauna, Alboran Sea, Gulf of Cadiz

The BALGIM expedition in May-June 1984 was designed to assess the distribution of marine organisms in the transition from the Gulf of Cadiz to the Mediterranean Sea across the Strait of Gibraltar. There were 115 successful hauls, ranging from 115 to 2110 m. Two matrixes with abundance data were constructed using the data of gastropods and scaphopods from this study and those of bivalves studied earlier. Species were scored according to their bathymetric and geographic distribution as (1) deep-sea species occurring exclusively in the Atlantic, (2) deep-sea species reported as living both in the Atlantic and inside the Mediterranean and (3) shallow water species, occurring normally on the continental shelf.

A total of 6035 live-taken individuals corresponding to 212 species of molluscs collected alive were identified, and almost twice as many (408 species) if adding those collected as shells only.

The samples do not form clearly defined clusters based on their faunal content. A majority of species (139) occur both in the Mediterranean Sea and the Atlantic Ocean. Most of the species with an Atlantic-only distribution (60 species) are associated to the cool or cold waters below 600 m depth along the Moroccan margin, and below the Mediterranean Outflow Water in the northern part of the Gulf of Cadiz. There are no deep-sea species restricted to the Mediterranean. The areas within the high-saline (> 38 psu) in the Alboran Sea and along the Mediterranean outflow in the Gulf of Cadiz largely share a set of species, most of them also occurring in less saline (≈ 36.2 psu) Atlantic waters. Therefore variation in salinity in a range of 1-2% is not critical compared to temperature which explains most of the restricted distributions.

Changes in terrestrial malacofauna of the Aegean islands during Holocene

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Keywords: Gastropods, biodiversity, extinction, alien species, Greece

The Aegean Islands are renowned for their high diversity and endemism of terrestrial gastropods. We conducted a comparative study of the terrestrial malacofauna across many Aegean islands, spanning over 40 years. The faunal changes – such as the decrease or increase of distributions, new arrivals and extinctions – were analysed in the context of human presence over thousands of years, characterised by intense cultural and commercial activity, as well as geological events during the Holocene. Key geological events include a) sea-level transgression that resulted in either a decrease in island area or fragmentation of land and formation of new islands, and b) the major eruption of the Santorini volcano. Gastropod changes, particularly the presence of alien species, are significant on islands with intense touristic and residential activities, such as Santorini and Mykonos. Conversely, on islands where traditional activities like agriculture and livestock farming have been abandoned, species seem to be withdrawing. Most alien species originate from the western Mediterranean, while declining species are often eastern Mediterranean or endemics.

On the rise of Heterobranchia (Mollusca: Gastropoda): a thorough insight using genomic tools

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Keywords: "Lower Hetrobranchia", phylogenomics, systematics, early evolutionary history, ultra-conserved elements

Heterobranchs represent a diverse subclass of gastropods with approximately 44000 valid species. This taxonomic group exhibits a broad spectrum of ecological and morphological adaptations across all environments and includes the grade 'lower heterobranchs' and the clades Mesoneura and Euthyneura. The 'lower heterobranchs' comprise six superfamilies, namely Architectonicoidea, Cimoidea, Mathildoidea, Omalogyroidea, Orbitestelloidea, and Valvatoidea. While the relationships among the members of these superfamilies are uncertain, there is evidence suggesting that they represent early offshoots of Heterobranchia. Combined morphological and phylogenomic analyses have refined the understanding of heterobranch evolution, encompassing even the most ancient evolutionary events within the group. The inclusion of minute and difficult-to-collect taxa, such as many representatives of these early splitting groups, has further improved the resolution of this early evolution but this no published assessments using genomic tools. The main objective of this study is to shed light on known controversies and to understand the emergence of heterobranchs by analysing for the first time all early lineages or "basal" heterobranchs. To address this objective, we sequenced hundreds of loci using a target enrichment approach, benefiting from an extensive taxon sampling of over 98 species, which covers all superfamilies of 'lower heterobranchs'. The phylogenetic relationships among the 'lower heterobranch' superfamilies here reveal the re-establishment of their taxonomic classification. Architectonicoidea, Mathildoidea, and Omalogyroidea are revealed to form the most basal clade within Heterobranchia. On the other hand, Cimoidea, Orbitestelloidea, and Valvatoidea form a clade sister group to Mesoneura + Euthyneura. This study re-establishes a new phylogenetic framework for the more basal groups of Heterobranchia, thus providing a new evolutionary framework to this diverse group. In addition, morphoanatomical data are collected to situate and understand the ecological and morphological adaptations within this new evolutionary scenario.

Ecology and distribution of the terrestrial molluscs living in the 'Catacombs of Paris' (France)

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Keywords: biospeleology, Paris, land snails, subterranean

Since the birth of the discipline in the XIXth century, biospeleologists have studied all groups of invertebrates living in subterranean ecosystems. French karsts show a strong malacological potential with more than dozens of endemic stygobite and one troglobite species. Like natural caves, artificial cavities are suitable habitats with peculiar underground fauna which is, however, poorly known. Underground quarries seem indeed little investigated because of their poorer malacological biodiversity.

At 10 to 40 metersdeep beneath Paris and in the surrounding area, kilometers of galleries resulted from the former exploitation of the Lutetian limestone. For centuries, the whole underground network has been used and frequented by underground workers and explorers.

This work presents an overview of the malacological diversity, ecology and distribution in the Parisian underground quarries commonly called 'The Catacombs'. 7 troglophiles and 1 endogean taxa were identified. *Oxychilus species*, *Discus rotundatus*, slugs, and *Cecilioides acicula* are commonly observed. The discovery of several living populations of *Zonitoides arboreus* appear unusual and suggest human introduction.

Most of the species identified are tolerant taxa for which the trophic condition is a characteristic that could explain their success in this particular environment. This supports the assumption that human activities (quarrying, consolidation, exploration) have an impact on mollusc biodiversity.

COST Action SaltAges: a new international collaboration network of interest to malacologists

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Keywords: salt giants, molluscs, macroecology, global biodiversity

Giant salt deposits have formed in restricted evaporitic basins controlled by dynamic marine gateways throughout the history of the Earth, altering the physical and chemical properties of the ocean, and affecting regional and global climate, and biota. Salt giants mark relatively abrupt and short-lived major water-body disconnection events that affect both the marine and terrestrial realms, with major implications for biodiversity, ecosystem structure and functioning and facilitating or hindering the flow of larvae and genes, thus driving evolution. Many major biotic and abiotic changes originated in restricted evaporitic basins, but the global processes and mechanisms associated with them remain unclear.

The new COST Action CA23124 *Social, biological and climatic impacts of salt ages* (SaltAges) aims to bring together scientists working on different regions and time periods to clarify and quantify the biotic impacts of basin restriction across scales and identify overarching patterns.

The fossil record of molluscs can offer unique insights into the global biodiversity and macroecological impacts of salt giant formation throughout their appearance, and especially during the Cenozoic. The SaltAges COST Action will run until 2028 and is open for participation to all interested researchers and stakeholders. The topics related to molluscs will be dealt mostly within Working Group 1 (WG1) "Climatic and biological impacts of marine gateway reconfigurations", whose objectives include evaluating the effects on biodiversity hotspots, biogeography, extinctions, endemism, and repopulation. Additionally, WG4 "Salt Deposition through Earth's History" will explore the importance of salt cycles for tectonics and climate that lead to the closure of drainage basins through the ages, and WG5 "Education and Public Engagement" will coordinate the training of young researchers as well as the production of an online educational resource and a moving museum exhibition on salt and salt giants.

Malacological studies on marine cores in the outer shelf west of Mar del Plata, Buenos Aires province, Argentina

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Keywords: Mollusks, marine cores, Pleistocene-Holocene, Argentina

The aim of this research is to carry out malacological and sedimentological studies of 4 marine cores (C4, C22, C19 and T1) located in the 38° S - 38° 40'S, 55° 48' to 57°W quadrant on the Argentinean outer marine shelf. All cores are characterized by bioclastic levels (N) represented by bivalves and marine gastropods. In core C4 (depth 52 m), level 2 (N2) stands out, represented by *Brachidontes* sp., *Spisula* sp. and *Aitepecten* sp., shallow polyhaline-euhaline environments typical of Lower Pleistocene fauna. Core C22 (depth 63 m) is characterised by level 3 (N3) with abundance of *Spisula isabelleana*, and the presence of *Glycymeris* sp., *Ostrea* sp., *Mytilus* sp., *Tawera gayi, Panopea abreviatta, Corbula patagonica* and *Notocholis isabelleana*, distributed in two sublevels, characterizing a sublittoral environment (<100 m depth) of sandy sediment with gravel belonging to the Pleistocene-Holocene boundary. Core C19 (depth 68 m), level 2 (N2) is represented by: *Ennucula nucleus, Ostrea* sp., *Brachidontes* sp., *Aitepecten* sp., *Spisula* sp., *Pitar rostratus, Corbula lyoni, Macoma* sp., *Amiantis purpurata, Bostrycapulus odites, Notocholis isabelleana, Zidona dufresnei, Olivancillaria carcellesi, Trophon lacianatus, Parvanachis isabellei*, and *Turbonilla paralamilata*, is interpreted as a storm deposit of Holocene age. In core T1 (depth 95 m) near the shelf break, N3 stands out with two sublevels (N3a and N3b); N3a with the presence of *Uncancylus concentricus*, and *Biomphalaria* sp. characteristic of a shallow freshwater body with abundant vegetation, and N3b with an abundance of *Macoma uruguayensis, Corbula patagonica*, and the presence of *Ennucula nucleus, Mytilus edulis, Spisula* sp., *Pitar rostratus, Heleobia* sp., *Corbula lyoni*, characteristic of a low-energy Pleistocene sublittoral environment. The latter level shows a decrease in sea level associated with marine regression. These investigations confirm previous studies and ^{14}C dating from the early 1960's.

Malacological associations in a marine core from the Neogene period of the Argentinean outer shelf

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Keywords: Bivalves, gastropods, marine cores , Quaternary, Argentina

The analysed marine core C22 (depth: 63 m; length: 94 cm) (38°10’40 “S/56°30’18 “W) is 49 km from the current coastline of the Argentinean outer shelf. It is composed of three levels (N3, N2, N1). At N3 (base of the core) N3 is composed of fine to medium sands with a pelitic matrix. At this level, 4 bioclastic sublevels are differentiated according to malacological criteria. In sublevels N3a and N3c there is an abundance of *Tawera gayi* characteristic of temperate to cold waters with the presence of *Tegula* sp., *Spisula* sp. and *Aitepecten* sp., organisms mostly from polyhaline-euhaline water environments with depths < 80 m, with sandy and gravelly sediments. While in sublevels N3b and N3d, *Spisula isabelleana* from temperate to warm waters is abundant, making up 90% of the faunal content, with the presence of *Mytilus* sp., *Glycymeris* sp., *Panopea abreviatta, Corbula patagonica*, and *N. isabelleana* from polyhaline-euhaline environments, characteristic of sandy sediments with depths < 100 m, corresponding to the Pleistocene–Holocene boundary. In the N2 composed of gravel-sized shell fragments in a sandy matrix. The molluscs found are: *Aitepecten* sp., *Ostrea* sp., *Corbula patagonica, Pitar rostratus, Corbula lyoni*, and presence of *Spisula* sp. and *Olivancillaria urceus* from euryhaline environments of sandy sediments, they are infaunal organisms as epifaunal, with depths < 120 m, presenting fragmented shells with signs of abrasion possibly corresponding to an Early Pleistocene. The N1 (top of the core) is composed of fine to medium dark brown sands and fragments of *Aitepecten* sp, *Spisula* sp. and cirripedium plates characteristic of sublittoral environments, corresponding to the Holocene period. The faunal changes between levels, and the different sublevels would be evidence of environmental and climatic variations within the Early Pleistocene to Holocene period.

Hidden in the Deep: Unveiling the Subterranean Biodiversity of the Caucasus Hydrobiids

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Keywords: molecular phylogeny, biodiversity, groundwater, Hydrobiidae, Caucasus

The Caucasus is one of the most unique, interesting and, at the same time, understudied regions of the Palaearctic in terms of zoogeography and freshwater hydrobiology. Both the southern and northern slopes of the Greater Caucasus Range boast a wealth of underground aquifers, leading to an abundance of watered caves and springs. The Hydrobiidae family, which includes minute snails and is among the least examined groups of freshwater invertebrates in the Caucasus, occupies local and often hidden biotopes across the region. This study aims to reconstruct the phylogenetic relationships of stygobiotic hydrobiids in the Caucasus region based on multigene analysis and morphological data.

The basis for this study was an extensive collection including long-term (2014-2023) collections of hydrobiid molluscs. To date, the material includes over 3000 individuals collected in the Caucasus (western Georgia, Abkhazia, Krasnodar Krai, Adygea, North Ossetia) and Crimea. The study is based on an integrative approach combining morphological data and molecular phylogenetic analysis based on COI, 16S, H3, 18S and 28S gene fragments.

Our analysis has shown that Caucasian hydrobiids belong to at least three separate subfamilies: Belgrandiellinae, Horatiinae and Islamiinae. Representatives of the subfamily Horatiinae are the most diverse in deep groundwater and include at least 20 species and 5 genera. The subfamily Belgrandiellinae mostly includes crenobiotic snails inhabiting springs and headwaters of streams; this subfamily also includes the stygobiont genus *Sitnikovia* Chertoprud, Palatov & Vinarskii, which includes 4 separate species. The subfamily Islamiinae is represented in the Caucasus by a single genus and species new to science.

On a small collection of land snails from Europe (Geomitridae, Helicidae, Helicodontidae, Hygromiidae, and Sphincterochilidae) in the Malacological Museum Prof. Maury Pinto de Oliveira, Brazil

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Keywords: Small collection, terrestrial gastropods, Helicoidea, Eupulmonata

The malacological collection Maury Pinto de Oliveira (CMMPO) incorporates specimens from Europe donated by renowned malacologists, as J-J van Mol, Richard van Belle, Alexandru Grossu, William Erwood Old Jr, Morris Karl Jacobson, among many others. We revisited the species of the families Geomitridae, Helicidae, Helicodontidae, Hygromiidae, and Sphincterochilidae housed in the CMMPO, providing the associated data. The study involved data compilation, reconditioning of the specimens, image acquisition, and taxonomic revision. The most representative families were Helicidae and Geomitridae. Helicidae is represented by 138 lots, including 437 specimens from 17 European countries. Most of the specimens lots came from Belgium, Italy, Spain, and Portugal. A total of 42 species was recovered, i.e.: *Arianta arbustorum; Campylaea planospira; Cantareus apertus; Cattania polinskii; C. sztolcmani; C. trizona; Caucasotachea vindobonensis; Causa holosericea; Cepaea hortensis; C. nemoralis; Cernuella virgata; Chilostoma cingulatum; C. gonatum foetens; Cornu aspersum; Eobania vermiculata; Faustina faustina; Helicigona lapicida; H. lapicida andorrica; Helix lucorum; H. lutescens; H. melanostoma; H. pomatia; Iberellus minoricensis; Iberus angustatus; I. alonensis; I. alvaradoi; I. gualtieranus; Isognomostoma isognomostomos; Loxana beaumieri; Macularia sylvatica; M. melitensis; M. muralis; M. serpentina; M. signata; Monacha cantiana; Otala lactea; O. punctata; O. xanthodon; Pseudotachea splendida*; and *Theba pisana*. Geomitridae is represented by 38 lots, including 289 specimens from 12 countries. Most of the specimens came from Spain, Belgium, Italy, and Romania. A total of 26 species was recovered. i.e.: *Backeljaia gigaxii; Candidula unifasciata; Cernuella cisalpina; C. neglecta; C. virgata; Cochlicella acuta; C. barbara; C. conoidea; Helicella itala; H. stiparum; Helicopsis striata; Trochoidea elegans; T. pyramidata; T. spratti; Xerocrassa montserratensis; X. seetzeni; Xerolenta obvia; X. spiruloides; Xeropicta candaharica; Xeroplexa intersecta; Xerosecta adolfi; X. cespitum; X. explanata; Xerotricha apicina; X. huidobroi*; and *X. madritensis*. Hygromiidae included 23 species from 11 countries, Helicodontidae included three species from five countries, and Sphincterochilidae included two species from three countries.

Slugs or Snails - Which is more to blame for feline lungworm infections?

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Keywords: Gastropods, *Aelurostrongylus abstrusus*, *Troglostrongylus brevior*, *Angiostrongylus chabaudi*, felids

Terrestrial slugs and snails serve as intermediate hosts for metastrongyloid nematode parasites infecting the cardiopulmonary system of domestic cats and wildcats. These nematodes include *Aelurostrongylus abstrusus*, *Troglostrongylus brevior*, and *Angiostrongylus chabaudi*, parasitizing the lung parenchyma, the bronchi, and the pulmonary arteries of felines, respectively. Under experimental conditions, various snail species have been shown to allow the development of the infective third stage larvae (L3) of these nematodes. A few studies on wild-caught gastropods, both slugs and snails, have provided information about the species involved in the life cycle of these parasites under natural conditions. While slugs and snails share many morphological and biological characteristics, they also show some conspicuous differences. On this basis, the aim of this study was to compare the frequency and intensity of infection with feline metastrongyloid larvae between slugs and snails. Slugs and snails were collected from the field in each of 6 different locations in Greece, (3 in islands and 3 in continental Greece). In total 276 slugs and 536 snails (165/184, 9/41, 18/38, 27/94, 21/16, and 36/163 slugs/snails from each location) were collected and examined by artificial digestion for the presence and number of metastrongyloid larvae. The gastropods and the parasites found were morphologically and molecularly identified to the species level. Overall, 81 out of the 276 (29.34%) slugs and 37 out of the 536 (6.90%) snails were positive for at least one metastrongyloid species. In all locations but one, slugs were more frequently infected than snails. The average number of larvae found in infected slugs was 21 (range 1-204) and in infected snails 6.3 (range 1-58). These results suggest that slugs are more susceptible to metastrongyloid infections. Possible causes for the observed infection rate difference between slugs and snails are discussed.

Microbiome of the land snails *Cornu aspersum* and the enhancement of their immune system

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Keywords: probiotics, *Listeria monocytogenes*, symbiosis, dysbiosis, rebiosis

The interactions of the gastrointestinal microflora with host immune system constitute a mechanism assisting the maintenance and enhancement of homeostasis. Genetic and environmental factors disrupt the gut microflora and impair homeostasis, leading to dysbiosis. Rebiosis can be achieved by manipulation of gut microflora by probiotic administration. The aim of this work was to investigate the symbiotic and dysbiotic interactions between gut microflora and innate immune responses in *Cornu aspersum* snails. Totally, 48 presumptive probiotic *Lactobacillus plantarum* strains and 15 potential pathogenic *Listeria monocytogenes* strains were isolated and investigated phenotypically, functionally and/or genetically. Probiotic activity was associated with cell surface properties (hydrophobicity, autoaggregation, biofilm-formation ability), the capacity to survive gastrointestinal tract barriers (pedal mucus, gastric mucus, gastric juices, acidic pH), to adhere and interact with intestinal epithelium and enhance cellular and humoral immune responses. Snail-derived *Listeria monocytogenes* strains were characterized as hypervirulent, virulent or non-virulent, according to mortality caused after injection to snails' haemocoel. Hypervirulence was associated with cell surface properties and the capacity to tolerate the haemolymph's bactericidal activity, to invade amebocytes and modulate immune responses. Hypervirulent strains suppress phagocytosis by amoebocytes and induce immune responses which enhance their virulence (apoptosis, phenoloxidase, ROS-NO^- production). Cooperative genomic analysis revealed that virulent strains harbor a complete functional mogR gene, coding a transcriptional repressor of flagellin, whereas the non-virulent SOUR strain, harbors a premature stop codon in mogR gene resulting in a frameshift mutation, coding for a shorter non-functional peptide. Last, a snail-dysbiosis/rebiosis model was developed. *Listeria monocytogenes* SN3-dysbiosis was characterized by high mortality and pathological phenotype (immobilization of snails' headfoot outside the shell, alterations in intestinal morphology, increased mucus-secreting cells in intestine and feces, inflammation in haemolymph). Rebiosis was achieved by administration of the snail gut-commensal probiotic *Lactobacillus plantarum* Sgs14 which abolished the SN3-dysbiosis and increased survival, exhibiting antibacterial and immunomodulatory activity.

Periostracum fraction and pedal mucus as sources for non-invasive DNA isolation in the terrestrial gastropods *Cornu aspersum*, *Helix lucorum*, and *Eobania vermiculata*

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Keywords: DNA sequencing, non-invasive sampling, terrestrial gastropods, conservation genetics

In this study, a non-invasive sampling technique for genetic analyses was developed and evaluated in three terrestrial snail species, namely, *Cornu aspersum*, *Eobania vermiculata*, and *Helix lucorum*. Traditional tissue collection methods often present serious drawbacks related to ethical concerns and the conservation status of many species. Our approach involves the sampling of minimal amounts of periostracum and pedal mucus, providing a viable alternative that does not harm the organisms. Mitochondrial CO1 and 18S rRNA genes were successfully amplified from both pedal mucus and periostracum samples, with sequences matching those obtained from tissue samples as well as with those – depending on their availability – in GenBank records. This non-destructive method provides a promising advancement for conservation genetics, allowing for the study of protected species while maintaining their well-being. The results demonstrate that this technique is an efficient and ethically sound tool for genetic studies, with potential applications in biodiversity monitoring and conservation research. By facilitating minimally invasive sampling, this approach supports ethical research practices and promotes the conservation of biodiversity without the legal and ethical complications associated applying more invasive techniques.

Nudibranch molluscs of Sakhalin Island, Northwestern Pacific: potentially species-rich but understudied fauna

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Keywords: Nudibranchia, Gastropoda, populations, connectivity, diversity, North-West Pacific

Sakhalin Is. occupies a unique position in the North-West Pacific; it is elongated in the meridional direction and extends 948 km from 45°54′ N to 54°25′ latitude, separating the Sea of Japan and the Sea of Okhotsk water basins. The different coasts of Sakhalin Is. are influenced by the warm Tsushima Current (southwestern side of Sakhalin), the Soya Current (southern side, including Cape Crillon), and the cold Eastern Sakhalin Current (northern and eastern side). These currents impose temperature limits for species distribution. Many researchers designate Sakhalin Is. as an important biogeographical boundary dividing temperate and boreal marine fauna: this boundary is located either between its southwestern/southeastern coasts or between Sakhalin Is. and Hokkaido Is.

Studies of the nudibranch fauna of Sakhalin Island (North-West Pacific) are scarce in comparison to adjacent waters of the Sea of Japan and the Sea of Okhotsk. To date, no dedicated studies have been ever published listing the biodiversity of nudibranchs of this area.

We investigated a collection of nudibranch molluscs from Sakhalin Is. by means of integrative taxonomy, including morphological analyses, and molecular data from four partial gene sequences. Material was collected during two independent research programs: the expedition of the R/V “Akademic Oparin” (Russia) to the Sea of Okhotsk, July 2019 at depths of 38–282 m, and the survey of Cape Crillon biodiversity in August 2023, at depths of 0.5–20 m. This work reports 21 nudibranch species found in Sakhalin Is., including two species new to science, and four species recorded for Sakhalin Is. for the first time.

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Ignaz von Born's Heritage

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Keywords: Ignaz von Born, history, mollusca, types, catalogue

Almost two hundred and fifty years ago, in 1776, the mineralogist, metallurgist and malacologist Ignaz von Born, was appointed by empress Maria Theresia to systematically arrange the enormous collection of her deceased husband. Randomly, Born started with the molluscs and published two unique books, describing and figuring also many types. With his scientific approach and the use of the recently established taxonomic system of Linnaeus, Born lay the foundation for the oldest and most valuable part of the mollusc collection of today's Natural History Museum Vienna. Over the centuries, not all curators and collaborators appreciated the importance of these objects: some were used for exhibitions, others exchanged or just replaced by "better looking" specimens. Friedrich Brauer was the first curator to realise the importance and worthiness of tracing every single species described in Born's books. He found the key to interpret the strange labels and codes and compiled the first comprehensive list, which he published in 1878, exactly hundred years after the publication of Born's "Index Rerum Naturalium Musei Cæsarei Vindobonensis". In the following centuries the "Born Collection" – still incomplete – was kept separately from other objects, in the original drawers to honour and retain its uniqueness. To date, efforts have been made to locate missing specimens; not least thanks to the digitisation of the collection, these efforts have been crowned with some success. In spite of the importance and value of the specimens, no type catalogue has been published so far. Following the digitisation of the whole Born collection, the publication of a comprehensive type catalogue will be our next step. Once this is completed, the aim is to make all pictures and data available online, to facilitate easy access of this highly requested research resource to the scientific community.

Comparative proteo-transcriptomics analysis of the closely related cone snails Rhombiconus fuscatus (Born, 1778) and Rhombiconus imperialis (Linnaeus, 1758)

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Keywords: transcriptomics, proteomics, bioinformatics, venomics, cone snails

Rhombiconus fuscatus (Born, 1778) and *Rhombiconus imperialis* (Linnaeus,1758) are two closely related cone snails present in the Western and Eastern Indo-Pacific region, respectively, that feed on polychaetes, known as fireworms, belonging to the family Amphinomidae Lamarck, 1818. Their venom duct, where conotoxins are produced, is noticeably divided into two sections distinguished by their colour (red in the distal part from the bulb and pale yellow in the proximal region).

A transcriptomics analysis was carried out using a custom-made bioinformatics pipeline that allowed us to greatly reduce the time employed in the filtration of the sequences. This novel tool called Transcripto-filter consists of a sliding window algorithm and a series of bioinformatics filters based on the similarity of the query sequence with a reference database. We have applied this tool to the study of the two sections of the venom duct of one individual of each species, which allowed us to identify 185 sequences.

The identification of these sequences permitted us to carry out a comparative proteomics analysis using two spectrometric techniques: ultra-high performance liquid chromatography coupled to mass spectrometry and liquid chromatography coupled to tandem mass spectrometry. Combining both techniques, we have identified 79.9% of the sequences detected at the transcriptomic level, which validates the pipeline employed in this work. We have also gathered these sequences with other transcriptome sequences already published of *R. imperialis* and conducted the same proteomics study which allowed us to identify 82,2% of them. The heatmap of the conotoxins normalised intensity groups the samples by species, but not by region of the venom duct. This analysis shows the differences in the venom composition of these two species and supports their differentiation.

The alien land snails and slugs of Greece

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Keywords: non-indigenous, terrestrial gastropods, geographic distribution, literature review, iNaturalist

Alien species may become a serious threat after their introduction to new environments. These species are characterized as invasive when their establishment out of their native range leads to biodiversity loss, has an effect on public health and causes financial hardship on local or regional level. In Greece, our understanding of alien terrestrial molluscs is at least to say limited. Very little is known of the pathways of alien land snails and slugs introduction, distribution and current population trends. In this study, a thorough literature review was conducted in order to track and compile a list of all occurrences of alien land snails and slugs in Greece since the beginning of the 20th century. Data on collection dates, habitats, and other relevant ecological information were gathered. Records of species from the iNaturalist platform were also taken into consideration. In total, 11 species were found: *Ambigolimax valentianus* (Férussac, 1821), *Ambigolimax parvipenis* Hutchinson, Reise & Schlitt, 2022, *Boettgerilla pallens* Simroth, 1912, *Deroceras invadens* Reise, Hutchinson, Schunack & Schlitt, 2011, *Gonyodiscus rotundatus* (Müller, 1774), *Hawaiia minuscula* (Binney, 1841), *Lucilla singleyana* (Pilsbry, 1889), *Lucilla scintilla* (Lowe 1852), *Paralaoma servilis* (Shuttleworth, 1852), *Zonitoides arboreus* (Say, 1817) and *Polygyra cereolus* (Megerle von Mühlfeld, 1818). The species are known from a variety of habitats. Most widespread species are *P. servilis* (46 occurrences) and species of the genus *Ambigolimax* (21 occurrences). The remaining species are represented by less than five occurrences each, spread all over continental and insular Greece. A systematic effort to validate the presence and potential establishment of the alien land snails and slugs in Greece is pressing.

Endless forms most beautiful and most wonderful have been, and – hopefully! – are being evolved: History and future of New Caledonian microgastropods

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Keywords: biogeography, diversity, endemism, groundwater, Tateidae

So far, a total of 62 species of freshwater gastropods of the family Tateidae have been described in the South Pacific biodiversity hotspot of New Caledonia, most of them dwelling on non-ultramafic bedrock. During expeditions between 2016 and 2023 focusing mainly on ultramafic areas including the Grand Massif du Sud as well as smaller outcrops further North, an estimated 100 additional species have been discovered. Most of the known species belong to the Hemistomia-clade. In contrast, most of the new species, many of them around 1 mm small, belong to four different groups of which some may predate the Hemistomia-clade, whose most recent common ancestor was estimated to 28.5 (34.9-22.7) Ma. Therefore, Tateidae may be of special interest for our understanding of the geological evolution of New Caledonia and its unique biota. According to a recent review of the geological history, there is no geological evidence for subaerial land throughout most of the Oligocene (34-25 Ma). A dated phylogeny of Tateidae may provide biological evidence for continued persistence in situ, hence informing geology. Our evidence so far is based on a fragment of COI. Obviously, the resolution of this tree is poor and the topology probably suffers from artefacts like long-branch-attraction. Therefore, we aim at establishing a phylogenomic analysis of the family. While New Caledonian Tateidae probably had a spectacular history, their future may not be that bright. Ultramafic rock harbours several minerals of industrial importance including nickel. Open-cast mining is threatening large parts of the areas where the new and highly endemic species have been discovered. It is not difficult to predict the winner of the conflict between the intrinsic value of tiny snails and the billion-dollar business for mineral resources. Therefore, developing conservation strategies is of utmost importance to minimise the impact of mining.

Unravelling the origin and evolution of conotoxin diversity in cone snails through a comparative genomic approach

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Keywords: Cone snails, comparative genomics, conotoxin precursor genes, venom gland transcriptomes

Cones (Caenogastropoda: Conidae) are predatory venomous marine snails with more than 900 described species living in tropical and subtropical marine areas worldwide. They elaborate complex venoms composed of hundreds of short peptides named conotoxins, which are used both for preying and defense. They feed on worms, snails and fish. These venoms are highly variable, not only among different species, but also among individuals within the same species. This great variability makes cone snails a group of great interest for research. On one hand, conotoxins allow the study of neuromuscular receptor functioning, and moreover, they have significant potential for drug discovery. On the other hand, these venoms are a highly interesting model system for attempting to understand the underlying evolutionary mechanisms generating molecular variability, their adaptive importance, and their role in the extensive diversification of cones. Here, we compare for the first time, the organization (synteny) of conotoxin genes in the only two available high-quality genomes of cone snails i.e., *Kalloconus canariensis* and *Lautoconus ventricosus* finding interesting evolutionary patterns for conotoxin gene superfamilies. We detected cases of gene duplication/loss in some superfamilies between both species. These comparative genomics analyses shed light on the origin and evolution of conotoxin gene families and how the extraordinary diversity of the venom cocktails is generated.

Updated distribution of *Geomalacus maculosus* in Spain

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Keywords: distribution, *Geomalacus maculosus*, Spain, threats

The arionid slug *Geomalacus maculosus* Allman, 1843 is a typical Lusitanian species. This species occurs only in Northern Iberia and Ireland, where it is protected by EU as well as national laws. Within the Iberian Peninsula the specie's distribution extends throughout the North-Western coast as far south as the Serra da Estrela in Portugal, and as far east as the Basque Country in Spain. It is predominantly found in montane forests and chestnut- and oak-tree groves as well as on different types of rock outcrops and walls.

Throughout the years 2023 and 2024, we carried out field sampling and compiled bibliographic information and information generated by Citizen Science with the aim of updating the available data on the distribution of the species in Spain and evaluating the conservation status of its populations and of the habitats it occupies.

We will present the data obtained on its distribution, as well as the conclusions drawn on its conservation status and the main threats to which it is exposed.

This work was carried out within the framework of the PRTR-ESMOLINCO Project "Technical assistance for improving knowledge of the conservation status of the terrestrial and continental fauna of Spain (native and invasive exotic species: molluscs and coastal invertebrates), six-year reports of article 17 (habitats directive) and article 24 (invasive species), and updating of Atlas and red books - Recovery, Transformation and Resilience Plan - financed by the European Union - Next Generation EU". The project is the result of a contract signed between the Euskoiker Foundation, in collaboration with the Spanish Society of Malacology (SEM), and the company TRAGSATEC.

Preliminary data on genetic diversity of *Vertigo geyeri* in Lithuania: a step to adequate protection of an EU importance species

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Keywords: *Vertigo geyeri*, habitat preferences, genetic diversity, land snails

Researchers find that maintaining genetic variation is critical to allowing wild populations to survive, reproduce, and adapt to future environmental changes. This would be particularly important for species as *Vertigo geyeri* Lindholm, 1925 with very low dispersal abilities and a considerable ecological specialization. *V. geyeri* is a tiny land snail and a rare relict from the Late Glacial period, inhabiting treeless spring fens. This species is listed in Annex II of the EU Habitats Directive and in the IUCN Red List of Threatened Species. The EU conservation regulations oblige the member countries to ensure their protection. This species has been protected in Lithuania since 2003 and is categorized as a rare species in the Lithuanian Red Data Book. To ensure the long-term maintenance of viable populations, genetic diversity of *V. geyeri* should be evaluated. The aim of this study was to assess the genetic diversity of *V. geyeri* using both mitochondrial and nuclear markers. Data from 83 ecologically suitable sites, covering the entire Lithuanian distributional range of the species, were analyzed to select collection sites of *V. geyeri*. Sampling for the assessment of genetic diversity was performed in 2019-2020 at 12 different wetland sites in Lithuania. The DNA barcoding region of cytochrome c oxidase subunit I (COI) and the internal transcribed spacers of the nuclear ribosomal RNA complex (ITS1 and ITS2) were used to evaluate genetic diversity within and between populations of *V. geyeri*. This presentation will review the main criteria for the protection of *V. geyeri* populations in Lithuania and analyze preliminary data on the genetic diversity of the studied snails, which should be taken into account in future conservation actions.

Mytilus galloprovincialis as a model organism to assess the adverse effects of Disposable Face Mask (DFM) presence in coastal areas

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Keywords: mussels, disposable face masks, transcriptomics, stress indices, leaching substances

The present study investigated the impact of Disposable Face Masks (DFMs) on coastal areas as a result of their wide use, irresponsible disposal and inefficient waste management, using the marine bivalve mollusk *Mytilus galloprovincialis*. Specifically, slightly fragmented DFMs were left in tanks containing Artificial Sea Water (ASW; 1 mask L^{-1}) for 20 days under standard conditions (continuous aeration and stirring, light/dark 12h:12h). ASW_{DFM} were analyzed for the presence of polymeric fibers (Raman spectroscopy), as well as both inorganic and organic substances (ICP-MS and GC-MS analysis, respectively). In parallel, mussel individuals were exposed to ASW_{DFM} tanks for 4 days and a battery of cytotoxic (in terms of Neutral Red Retention Time/NRRT), oxidative (i.e. superoxides, nitric oxides and lipid peroxides), and genotoxic (in terms of Micronuclei/MN formation) stress indices were determined in their hemolymph. According to the results, a plethora of organic and inorganic substances, as well as polypropylene (PP) fibers were detected on ASW_{DFM} samples, while the challenged mussels showed significantly enhanced cytotoxic and oxidative damage, followed by high frequencies of MN formation. Additionally, gills of control and challenged mussels were dissected and prepared for RNA extraction to determine differential gene expression via comparative transcriptomics. Following a de novo assembly and annotation of each conditions' transcriptomic data, the preliminary results reveal that the challenged mussels show enrichment in several COG categories (eg. Defense mechanisms, protein turnover and chaperones, intracellular trafficking, inorganic ion transport and metabolism). More specifically, we document differential expression of many putative genes related to ion channels and transporters, apoptosis (eg. caspases), oxidative stress (thioredoxin, G6PD) and stress related genes such as Heat shock proteins, ubiquitin, etc. Overall, the findings of the present study highlight the potential hazards from DFM's presence in coastal areas along with their negative impact on aquatic organisms like *Mytilus galloprovincialis*.

Needle in a haystack: on the finding of live *Pinna nobilis* (Linnaeus, 1758), a Critically Endangered mollusc, via Citizen-Science and Social Media platforms

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Keywords: *Pinna nobilis*, endangered species, citizen science, Eastern Mediterranean

Several groups of people such as birdwatchers, scuba divers and hikers are environmentally aware and, in these times, are acknowledged, as an important conservation initiative for several species, groups of different taxa or even habitats. Their valuable contribution, and their direct involvement in the field is recognized by the E.U. as "a good practice" tool and by the U.N. as a procedure that eventually increases environmental protection. The 'Red Fish Project' Facebook group which has been utilized during this study aims to study the distribution, density, and habitat use of certain threatened marine biota like the European spiny lobster, the dusky grouper, and, more recently, the Mediterranean endemic noble fan shell Pinna nobilis. Populations of the later present a substantial decline due to mass mortality events (MMEs) that emerged across the Mediterranean (mostly linked to the presence of the parasite *Haplosporidium pinnae*). Nowadays the specie's conservation status has been evaluated as "critically endangered" on the IUCN Red List. The 'Red Fish Project' group consists, up to May 2024, of 668 active members, from different Mediterranean countries and of a wide range of ages (13 - 65+). Different pinnid individuals were recorded by 2023 onwards. Most of the records were coming from the Northern Aegean Sea, with the majority regarding dead individuals of *Pinna nobilis*. The most striking and well documented record was from Southern Peloponnese where five live juveniles were reported by Scuba divers. It is worth mentioning that, apart to the *P. nobilis* records, the 'Red Fish Project' has contributed on the first verified occurrence of the congeneric P. rudis from the coastal waters of Greece and Cyprus, and it seems that in these regions the species expands its distribution to the Eastern Mediterranean covering rapidly the available niches in the absence of *P. nobilis*.

Fossil record of molluscs from the Museum of Paleontology and Geology NKUA

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Keywords: fossils, molluscs, open science, museum collection, database

The Museum of Geology and Paleontology of the University of Athens was founded in 1835 as Physiographic Museum, and since 1981, it has been housed in the building of the Faculty of Science of the University. Its collections consist of several thousand fossils from all various places in Greece, covering over 300 million years of the country's geological history. The Museum hosts many fossil invertebrates, vertebrates, plants. Particularly important is the collection of Gastropods, Bivalves and Ammonites.

In recent times, there has been a push for scientists to publish datasets used in original research. However, this was not the practice in earlier years, and the publication system was different from the current one. As a result, data from that era are often only available in Greek or have outdated names (e.g., *Trigonostoma* (*Trigonostoma*) *scrobiculatum* (Hörnes, 1854), now recognized as *Scalptia scrobiculata* (Hörnes, 1854)). Furthermore, the species concepts employed by previous authors differ from contemporary paleontological standards. Consequently, specimens from Greece collected between the 1960s and 1980s urgently require taxonomic revision. The so-called dark data must be utilized, so it can be made available to the global community as open data. Such an effort should be founded on the principle that scientific results should be accessible to everyone (Findable, Accessible, Interoperable, and Reusable – FAIR). This shift towards open research results is expected to drive significant advancements and foster better collaboration among geoscientists. The aim of the museum researchers is to make this data available in an online repository, or to be entered into a Paleobiology Database, making it accessible to the global community. This approach ensures that collection management aligns with the new era of open science.

Phylogeny of Littorinimorpha aiming at prioritizing conservation efforts

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Keywords: European gastropods, freshwater snails, phylogenetics, molecular systematics, extinction risk

Gastropods constitute the majority of freshwater molluscs and include a number of phylogenetically diverse lineages (Littorinimorpha is the largest Order; about 700 species). They play key roles in ecosystems by contributing to water quality, nutrient cycling, primary and secondary productivity and as a food source for other species. They are also highly endemic (more than 93% of freshwater gastropod species) and the most threatened group (about 43% of freshwater gastropod species) among all groups assessed by the IUCN at the European level. However, the taxon is seriously under-represented in conservation efforts since our basic knowledge is highly incomplete, hampering the implementation of effective conservation strategies. To determine conservation priorities, a robust taxonomy is needed. However, for freshwater species, the degree of taxonomic uncertainty is comparatively high. Our incomplete knowledge of taxonomic diversity in combination with their high risk of extinction may lead to a number of "silent extinctions" (i.e. species may go extinct before they are formally described). The use of molecular systematic methods for species delineation represents an important tool that contribute to mitigate taxonomic uncertainties and reveal possible cryptic diversity. Here, we use five genetic loci from published sequences comprising a dataset of more than 3800bp in total, and we attempt to reconstruct the phylogenetic relationships among all European species of Littorinimorpha (about 80% of all European freshwater gastropods) assessed by the IUCN. Our phylogenetic tree confirms the monophyly of some lineages and shed light on the phylogenetic relationships among species and/or genera, also supporting several recent suggestions for taxonomic revisions. We also take into account the species threat category as well as the phylogenetic endemism, a concept that can be used to indicate the uniqueness of specific freshwater habitats and contribute to conservation actions.

The research project was supported by the Hellenic Foundation for Research and Innovation (H.F.R.I.) under the "3rd Call for H.F.R.I. Research Projects to support Post-Doctoral Researchers" (Project Number: 7339).

One-legged traveller conquers the Czech Republic: *Hygromia cinctella* 13 years after first finding

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Keywords: Gastropoda, non-indigenous species, passive dispersal

The Girdled snail (*Hygromia cinctella*), a medium-sized stylommatophoran with a whitish and slightly transparent shell with a prominent white keel, belongs to the family Hygromiidae. The native area (probably) lies between south-east France and north-west Croatia. Since 1930, when it started its spread throughout Europe, this species "conquered" a number of countries and now lives from the United Kingdom to Ukraine. In 2015 it first appeared in New Zealand where it is also rapidly spreading. The first record in the Czech Republic dates back to 2011 when it was found in Prague-Holešovice. Other localities present in cities, suburbs or intravillans quickly followed. The first occurrence outside man-made sites was documented in 2023.

In the Czech Republic, as in other European countries, the projects of citizen science (iNaturalist or City Nature Challenge) are used to track the current current distribution of species in different territories. Since several native species (Urticicola umbrosus or Perforatella incarnata) look quite similar, the results of this "citizen mapping" must be treated with care.

This study was supported by the Institutional Support for Long-term Development of Research Organizations – Cooperatio HUM – Charles University, Faculty of Education (2023); financial support of Prague Capital City Environmental Improvement Project No. 258/2021, 213/2022; and the Ministry of Culture of the Czech Republic (DKRVO 2024–2028/6.II.a, National Museum, 00023272).

Pyrite in the Palaeontological collections of the Natural History Museum in Basel (CH). Detection to treatment.

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Keywords: Pyrite, palaeontology, Mollusca, ammonia, paraffin bath

The conservation of palaeontological heritage is one of the fundamental missions of Natural History Museums and other institutions housing patrimonial collections. Among the most prevalent risks menacing fossil specimens, the problem of pyritisation is of particular importance. The presence of pyrite or marcasite (a polymorph of pyrite, FeS_2) in rocks and/or fossils and exposure to poor conditions of oxygen and humidity causes pyrite to disintegrate, sometimes very fast. This transformation process can alter specimens, increasing their volume and even destroying them completely if nothing is done to stop the reaction. Some affected specimens can be easily identified by a characteristic sulphur smell. To remedy this problem, the preparators of the Natural History Museum of Basel (NMB) have developed a treatment that consists of four steps: (1) removing pyrite residues from the specimen, (2) neutralising the pyrite reaction, (3) stabilising the specimen and (4) ensuring its long-term preservation. These steps include several ammonia gas baths to stop the reaction, followed by a paraffin bath to prevent any restart of the reaction, and finally a long-term preservation under controlled temperature and humidity conditions and in neutral, non-acidic containers.

From seas to shelves; a glimpse at the Moazzo's bivalve collection of the Goulandris Natural History Museum

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Keywords: bivalves, collection, comparative tool

Marine invertebrate collections constitute a large part of the Goulandris Natural History Museum as it contains more than 120.000 lots. In order to shed light on some of the hidden treasures of the Museum, this study investigates the bivalve Moazzo Collection. Polychronis G. Moazzo (1893-1975) was a passionate conchologist and collector. He studied zoology at the Natural History Museum of Paris, and worked alongside molluscan experts of his time, having the opportunity to participate in expeditions around the world. He is best known for his research on molluscs of Suez Canal that was published in 1939. Moazzo's collection was donated to the Goulandris Natural History Museum after his death. It counts approximately 80.000 specimens of molluscs, echinoderms, arthropods and corrals. Out of 14.640 lots registered in the database of the Museum up to now, 2.610 belong to the Phylum Bivalvia, classified under 66 Families, 316 Genera and 536 species. The material was collected from 510 different localities globally between the First and the Second World War. The majority of bivalves derive from the Mediterranean Sea, the Pacific Ocean and the north eastern Atlantic Ocean. Families with the most marine representatives are Tellinidae (373 lots), Pectinidae (296 lots) and Mytilidae (205 lots). From the 2.610 lots, 206 are fresh water representatives (Unionidae, Sphaeriidae, Iridinidae, and Dreissenidae). The wide geographical range of the Moazzo collection, along with the good preservation state of the specimens and the digitization process ongoing, constitute the collection a valuable comparative tool for molluscan studies, which adds to the Museum's impact. As such, the need of curation, scientific revision and digitization is highlighted, especially in times of losing habitats and biodiversity.

The Quaternary legacy in non-marine molluscs European biogeography

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Keywords: Phylogeography, climatic cycles, gastropods

Quaternary climate cycles have strongly influenced the diversity and distribution of continental molluscan fauna. This is especially true for European areas located at the edge of Pleistocene ice sheets. Studies of the Quaternary malacofauna developed in Western and Central Europe provide a great deal of information on the past distribution of species that is relevant to the current geographical expansion of European species. In recent years, many papers have focused on the location of glacial refugia and possible recolonisation pathways during interglacial periods, using either or both Quaternary and phylogeographic approaches. The Quaternary malacological record can provide insight into the evolution of group diversity and the associated causes of variation over long periods of time, as well as the timing of both species retreat/expansion and extinction rates during climatic cycles. Mapping the expansion of snails over time is an important key to understanding the current status and distribution of species, and to help accurately predict potential changes in distribution. The European Quaternary Mollusc Database project aims to provide maps of species distribution at different time periods and tables of reliable, well-dated malacological counts from Quaternary deposits across Europe. Particular attention has been paid to the time table in order to minimise regional discrepancies in the interpretation of chronological attributions. Originally developed at the LGP (Meudon, France), the project has received strong support from the Czech Quaternary Malacology Group. Today, the database includes 528 sites with Pleistocene and Holocene records distributed across the Palaearctic province. Further contributions from other countries are now highly desirable to improve the database and make it a useful tool for the European malacological scientific community.

Land snail co-occurrences in islets of the East Aegean archipelago

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Keywords: community assembly, competition, islands, gastropoda

Species co-occurrence is crucial for understanding many ecological processes. It measures how often two or more species appear together in various locations and determines whether this frequency is random, positive, or negative. The association between species pairs can suggest or support evidence for the ecological processes or factors leading to these patterns. Although a specific co-occurrence pattern does not definitively indicate a particular process, co-occurrence patterns are crucial for understanding the mechanisms that enable or prevent species coexistence. In this study, we analyse land snail occurrence data from 33 islets of the East Aegean Archipelago to pinpoint whether any of the 47 species (1081 species pairs) exhibit negative or positive co-occurrences and, more importantly, whether this pattern can be translated into information regarding processes such as competition, predation, or facilitation. We identified 34 positive and 32 negative correlated species pairs and discuss those where biological significance can be inferred from their deviation from random frequency.

Small snails, big rocks and huge trees – a phylogenetic revision of the door snail *Montenegrina* (Mollusca: Gastropoda: Clausiliidae)

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Keywords: Ignaz von Born, history, mollusca, types, catalogue

Montenegrina is a hyper-diverse land snail genus that is specialised on limestone and has a very restricted distribution range in the western part of the Balkan Peninsula. As common in molluscs, the existing systematics of *Montenegrina* was established mainly based on conchological traits. To extensively revise the taxonomy, a comprehensive phylogenetic study based on three mitochondrial markers, cytochrome c oxidase subunit 1, 16S rRNA, 12S rRNA (COI, 16S, 12S), was conducted. In the resulting tree, about half of the species and subspecies are monophyletic, but several remained paraphyletic. To gain better insight into the incongruencies, anatomical features like specific genital structures were analysed as well. Combining the results, some of the paraphylies could be reasonably resolved by taxonomic changes by reassigning subspecies or raising them to species level. However, in other cases, also introgression even between distant clades could be the reason for the paraphylies. This integrative taxonomic approach led to a revised taxonomy of *Montenegrina* with 110 valid taxa, raising the number of species from 29 (conchologically based) to 69 species. As a next step, population genetic analysis based on newly established microsatellite markers will be performed, helping to get insights into population structure and testing for possible gene flow between selected populations.

When a University collection moves to a Museum

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Keywords: palaeontology, scientific specimens, storage, limitations, museum mission

The Natural History Museum Basel (NMB) houses 12 million objects in its collections. A new building is being constructed for the NMB, which will better accommodate these collections (expected to open in 2029). At the same time, the University of Basel's Geological and Paleontological Institute (GPI) houses many of its collections, deposited there since many decades. The GPI is also moving to a new building, and, in contrast to the Museum, it is no longer planning to house such large collections. It is currently examining which collections the Museum should, may and would like to take over from the University. This includes objects that are registered with NMB inventory numbers, but also other specimens that have scientific significance. Various factors play a role here, such as the Museum's legal mandate, the ownership structure of the University/canton (state)/Museum, the quality of the University collections, the importance of the University collections, and ultimately the quantity and space available in the new facilities of the NMB. In this poster, we will examine the following questions: How does the Museum proceed? What are the biggest challenges? What are the considerations for possible solutions?

A trans-Pacific split: species identity of nudibranch Hermissenda from the Sea of Japan (Heterobranchia: Nudibranchia)

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Keywords: Phylogeny, phylogeography, species delimitation, marine gastropods, diet preferences

Facelinidae s.l. is a highly diverse group of nudibranch gastropods. It includes several family-level lineages and show a high level of heterogeneity, making the taxonomical revision a necessity. In Russian waters, there are representatives of the genus *Hermissenda*, which now belongs to the family Myrrhinidae, one of the lineages of Facelinidae s.l. This genus has a Pacific origin and includes three closely related species: *H. opalescens, H. emurai*, and *H. crassicornis*. However, the species identity of *Hermissenda* in the Russian Far East (the Sea of Japan) has not been determined.

In the present work, we used an integrative taxonomic approach to study relationships within the genus *Hermissenda*, focusing on specimens from the Russian Far East. For this purpose, we used a set of four standard mitochondrial and nuclear markers: COI, 16S, H3, and 18S, and a large variety of species delimitation, phylogenetic, and phylogeographic methods. We also investigated morpho-anatomical characters and the food spectrum with light and scanning microscopy. The cnidosac morphology was studied by confocal laser scanning and transmission electron microscopy.

Based on our integrative results, we show that the specimens of *Hermissenda* from the Russian Far East are closely related to the species *H. emurai* found near Japan and Korea. The studied specimens show significant variability in external and internal features which overlaps with states in North Pacific species *H. crassicornis*. *Hermissenda emurai* also has a wide range of feeding objects. The nuclear genetic markers of specimens from the Russian Far East do not demonstrate phylogenetically significant differences from *H. crassicornis*. This suggests a possible gene flow between two species, questioning their distinct species status.

This study was supported by the Russian Science Foundation, Project No. 20-74-10012.

A species for every bay? Towards the species identity of *Asperspina* (Heterobranchia: Acochlidiimorpha) from the White Sea

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Keywords: acochlidian, species delimitation, Arctic

To date, *Asperspina murmanica* (Kudinskaya & Minichev, 1978) has been a rare case of the mesopsammic acochlidian species inhabiting the subpolar region, specifically the Barents Sea. However, there have been reports of *Asperspina* in Kandalaksha Bay and Onega Bay in another subarctic sea, the White Sea. These specimens were previously misidentified as *Hedylopsis spiculifera* (Kowalevsky, 1901), which led to uncertainty in their true species identity.

To solve this question, we conducted an integrative study on *Asperspina* from the White Sea. In our work, we used a set of standard mitochondrial and nuclear markers, as well as a range of species delimitation methods. To perform the morphological analysis, we used light and scanning electron microscopy as well as computer-based 3D reconstruction.

Our finding revealed the presence of two species of Asperspina in the White Sea, both falling into the *Asperspina murmanica-brambelii* species complex. Furthermore, one of the species is found in both Kandalaksha Bay and Onega Bay, while the other is exclusive to Onega Bay.

This study was conducted in the frame of scientific projects of the State Order of the Russian Federation Government to Lomonosov Moscow State University No. 121032500077-8 and No. 121032300121-0.

Publish your research in the journal Folia Malacologica

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Keywords: Folia Malacologica, international journal, research papers, short communications

Folia Malacologica is the first Polish malacological journal founded in 1987. It is published by The Association of Polish Malacologists (Stowarzyszenie Malakologów Polskich, www.malakologia.org) in co-operation with The Faculty of Biology, Adam Mickiewicz University in Poznań and Bogucki Wydawnictwo Naukowe. Here are some reasons to submit your manuscripts to our journal:

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Late Pleistocene Mollusc Communities of Karpathos Island and their palaeobiogeographic significance

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Keywords: Fossil, climate, migration, MIS 5, Greece

Marine terraces represent the former shoreline of a sea, hosting shallow-water faunas. They constitute excellent environments for the development of rich, shallow-water invertebrate faunas, especially molluscs (gastropods, bivalves) or other organisms such as corals and crustaceans. In the eastern Mediterranean, tectonics has been the main controlling factor of the landscapes of the southern Aegean Sea, shaping the morphology of modern-day islands. This holds particularly true for the island of Karpathos located in the south-eastern part of the Aegean Sea, where a multitude of marine terraces of different ages can be found. Here, we focus on the analysis of a superimposed terrace, which crops out onshore along the southern coast of the island and which has deposited during the interglacial period MIS (Marine Isotope Stage) 5 (130.000 – 80.000 years before present), also known as Tyrrhenian.

Bulk and hand-picked samples were collected in the field. The results reveal a rich fauna of 66 species (45 gastropods and 21 bivalves), where the gastropod *Babelomurex cariniferus* (G. B. Sowerby II, 1834) is found for the first time in the Tyrrhenian fossil record. Additionally, the warm temperatures of this interglacial period are highlighted by the presence of tropical species [e.g., *Thetystrombus latus* (Gmelin, 1791)], which indicate the migration of the so-called Senegalese fauna to the eastern Mediterranean. The communities are characteristic of shallow marine sandy to rocky bottoms, with patches of vegetation. The comparison of the fauna to other Tyrrhenian localities sheds light into the paleobiogeographic evolution of molluscs through time. Finally, the composition of the interglacial interval of MIS 5 is a good analogue for present day's faunas that are affected from climate change, due to the ongoing warming.

In high mountains: Molluscs of Králický Sněžník Mountains (Czech Republic)

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Keywords: Hercynian high mountain forest, Lehmannia macroflagellata, singletracks

Králický Sněžník Mountains with an area of 276 km^2 and the highest peak reaching 1423.7 m above sea level represents the smallest high mountains in Central Europe. Slopes are covered with spruce forests including Acer pseudoplatanus, Fagus sylvatica and Sorbus aucuparia. Majority of this area is situated in Poland, while smaller part is located in the Czech Republic. Crystalline limestone outcrops are present on southern slopes.

Malacozoological survey was carried out in years 2023 and 2024. Standard malacozoological methods (individual collecting, bulk sampling and wet sieving) were used on 76 surveyed sites. In total, 52 species of molluscs were found: one bivalve (Pisidium casertanum), and 51 gastropods. Only one of the species (Platyla polita) belongs to the terrestrial "prosobranchiate" gastropods, the other 50 species are pulmonates. Six species (Bielzia coerulans, Lehmannia macroflagellata, Eucobresia nivalis, Perpolita petronella, Clausilia cruciata and Vertigo alpestris) are included in the Red List of Invertebrates of the Czech Republic.

The malacofauna of Králický Sněžník Mountains represents typical and yet unique fauna of Hercynian high mountain forests on acidic soils. The most abundant species is Arion fuscus which also occurs at the highest altitudes. The local biodiversity hot-spots, lime outcrops, host up to 31 species of land snails. Non-indigenous species like Arion vulgaris or Arion distinctus are present in human influenced localities.

However, the local mountain ecosystems are threatened by human activities, especially by the "loosening" of forest stands through construction of singletracks, hiking trails, and intensive logging. Increased attention in terms of proper forest management and responsible reforestation is needed.

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Sclerites morphogenesis and phylogenetic relationships in aculiferan molluscs

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Keywords: Solenogastres, Caudofoveata, Polyplacophora, sclerites, crystallization chamber

The phylogenetic position of the Aplacophora (Solenogastres + Caudofoveata) and Aculifera (Aplacophora + Polyplacophora) has been subject of debate for decades. Recent molecular studies strongly supported the monophyly of Aplacophora and a sister group relationship of Aplacophora and Polyplacophora, but the relationships within Aculifera have hardly been analysed further. An analysis of the polarity of some aplacophoran-polyplacophoran morphological characters seems necessary in order to understand the relationships within Aculifera. The plesiomorphic state of the molluscan scleritome (shells and other calcified elements) remains ambiguous. The formation of the conchiferan shells is extracellular and involves organic molecules and calcareous secretions of the mantle towards the extrapallial space. Several authors also indicated an extracellular formation of the scales and spicules in Polyplacophora, and in Aplacophora based only on samples of Solenogastres.

We have analysed the formation of the sclerites in five species of Solenogastres, two species of Caudofoveata and five species of Polyplacophora at ultrastructural level by transmission electron microscopy. The pattern of secretion of the sclerites in the studied Polyplacophora is similar to that observed in most of the studied Solenogastres. In both groups, an invagination of the microvillous epithelial cellular membrane forms a crystallization chamber, which presents microvilli in its secreting wall. This pattern reminds that of the shell secreting mantle epithelium of bivalves, therefore it should be considered plesiomorphic within Aculifera. The analysed species of the Caudofoveata form the sclerites in a different manner, below the basal lamina and the crystallization chambers do not have microvilli, therefore this pattern would be considered as derived.

“Snail lab” - a tool to study the evolution of biological clocks under the Arctic daylight

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Keywords: colonization of the Arctic, global changes, land snails, range shifts, Wild Clocks

Due to worldwide changes in climate and increasing temperatures, many species are shifting their geographical ranges towards higher latitudes. In doing so, these species come into contact with an often-ignored challenge in ecological research: highly different photoperiodic regimes. The photoperiod is largely responsible for synchronizing daily and seasonal rhythms of uni- and multicellular organisms and such synchronisation is a crucial aspect of an organism’s life and survival. Can populations migrating to higher latitudes (polewards) adapt to such novel light conditions? To test this, we must integrate principles and practices from the fields of Evolutionary Ecology and Chronobiology into an approach that has become known as “Wild Clocks” in the past decade or so. In our study, we aim to establish the copse snail (*Arianta arbustorum*) as a novel model species in Evolutionary Chronobiology. We seek to understand if and how biological clocks adapt to extreme variations in daylight by using a combination of field and laboratory studies. We are based in Tromsø, Norway, within the Arctic Circle, in a strategic position for studying adaptation to extreme daylight. Our project started earlier this year and we have just finished building the “Snail Lab”, part of the Arctic Chronobiology and Physiology group. Currently, we are in the initial steps of breeding the snails and using a camera setup to record their activity patterns, with which we can then characterise their biological clocks.

Hydrobiidae in Cyprus's freshwater systems: Diversity, Endemism, Conservation Status

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Keywords: Mediterranean Basin, freshwater gastropods, hydrobiids, extinction risk

Cyprus is an oceanic island that originated from the seabed and one of the most biogeographically isolated islands of the Mediterranean Sea. It is included in the Mediterranean Basin biodiversity hotspot, one of the richest hotspots in terms of the number of endemic species. Cyprus could be considered an under-studied region when it comes to the gastropods of its freshwater ecosystems. Up to date, five hydrobiid species assigned to three genera have been found and described from this island, i.e. *Pseudamnicola malickyi* Schütt, 1980, *Pseudamnicola aphroditae* Glöer & Kolokotronis, 2023, *Pseudamnicola despinae* Glöer & Kolokotronis, 2023, *Islamia mylonas* Radea, Parmakelis, Demetropoulos & Vardinoyannis, 2017 and *Kitrinomatousa nikolinae* Glöer & Kolokotronis, 2023. The description of most of the above species was based on characters of shell and male genital system and their phylogenetic affinities remain completely unknown. The purpose of this study is to further investigate the species richness of hydrobiids in Cyprus, to elucidate their taxonomic status and phylogenetic relationships using both morphological and molecular data, and to evaluate the conservation status of their populations. A small number of hydrobiid specimens was collected from rivers, streams and springs during two sampling periods, in August and September 2023 and in December 2023 and January 2024. Among the areas sampled were Troodos Mt., Machairas Mt. and Paphos forest. The results of our study provide new data on the number and endemism of hydrobiid species in Cyprus and contribute to the evaluation of the extinction risk these gastropods face and to the identification of conservation priorities.

The contribution of palaeodata to conservation: insights from Spanish and Moroccan Holocene land snails

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Keywords: Holocene, conservation palaeobiology, past vs modern distribution

In Quaternary studies, fossil land shells are usually studied to investigate past environments and climates across various spatial and temporal scales. Over the last ten years, new molluscan successions from northeastern Morocco and southern Spain have revealed a high diversity of land snail assemblages during the Holocene. Nowadays, the highly anthropized Mediterranean Basin is considered one of the most sensitive areas to landscape and biodiversity modification due to climate changes driven by human activities. As one of the most threatened invertebrate groups, many Mediterranean land snail species require major conservation measures to ensure their survival. On the basis of new Moroccan and Spanish sequences (Aït Said ou Idder, Blirh, Oued Charef, Galera) and a review of the existing palaeomalacology literature, we discuss the significance of Holocene molluscan records from a perspective of palaeobiology conservation. Most of the sequences provide records from the Middle Holocene (8200 – 4200 Before Present) consisting of a rich hygrophile fauna as common components. *Vallonia moulinsiana* and *V. angustior,* both protected species under the European Directive, occur regularly. *Vallonia enniensis* is common in several Holocene sites, but has a current distribution limited in Spain and it is unknown if the species survives in Morocco. Likewise, the occurrence of the endemic *Orculella aragonica* at Galera and Baides shows that this species had much larger populations and a wider distribution during the Holocene which support its endangered species status. Middle Holocene molluscan successions provide a historical perspective of the occurrence of hygrophilous species before aridification and increased human impact that led to the disturbance and fragmentation of wetland habitats. Molluscan fossil records are an ideal temporal tool to better understand the parameters that have shaped today's biodiversity and to identify the most vulnerable taxa.

Islands of History: exploring land snail diversity across Greek archaeological sites using an Island Biogeography approach

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Keywords: land snails, species-area, island biogeography, human impact, community similarity

Archaeological sites can be viewed as “islands” of distinct human history amidst a “sea” of peripheral human activities. This study investigated patterns of land snail diversity across 18 island-like archaeological sites, located across mainland Greece and Aegean and Ionian islands. Specifically, we sought to (i) assess the species richness and identities of each site, (ii) test the species-area relationship, (iii) quantify among-site compositional similarity, and (iv) investigate potential human influence on species richness and community similarity. A total of 87 species belonging to 52 genera were morphologically identified (mean=11.94 species/site), the most frequently occurring ones being Monacha (13 sites) and Lindholmiola (12 sites). Some species exhibited unique distribution patterns, including species of the genus Lindholmiola –present throughout mainland Greece but not found on most insular archaeological sites. Area did not exert a significant influence on species richness, which may partially reflect a small “island” effect, as all sites were small-sized (<1.004 km^2). We tested potential human effects on community features – richness and similarity – after assigning each archaeological site to a specific historical period (i.e. ancient, <50 BC, Roman-Byzantine, 50 BC-1500 AD, recent, >1500 AD) or to current levels of human presence (i.e. within or outside urban landscape). Species richness differed significantly between ancient and recent archaeological sites (mean=13.1 and 5.5 species/site, respectively). While the pairwise community similarity across all 18 sites was low (Jaccard range=0-0.41, mean≈10%), we observed a tendency for increased homogeneity among sites located outside urban areas (n=11, mean $\text{Jaccard}_{\text{outside}}$=0.13) compared to those within (n=7; mean $\text{Jaccard}_{\text{within}}$=0.06). These results indicate that the diversity patterns of land snails observed today may depend on both historical and modern human presence. This underscores the significant influence of human activities, both past and ongoing, in shaping biotic communities at some of Greece’s most culturally and touristically significant archaeological sites.

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