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Cover image: Table 14 from the lavishly illustrated catalogue of Ignaz Born from 1780. [Testacea Musei Cæsarei Vindobonensis, quæ jussu Mariæ Theresiæ Augustæ disposuit et descripsit. Kraus, Vindobonæ (Vienna), [I-XXXVI], 1-442, [1-18].] ©NHM Vienna

Abstracts of Talks (in alphabetical order of first author's surname)

Bringing the mollusc collection online: Digitisation efforts at Biodiversity Centre, Upper Austria Landes-Kultur GmbH

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The digitisation of the mollusc collection at the Biodiversity Centre, Upper Austria Landes-Kultur GmbH, has a legacy spanning over 30 years. However, significant progress has been made through two major projects carried out between 2022 and 2024. The first, the 2022 “Pilot Project Mollusca”, involved reviewing and updating over 70,000 metadata records, linking them to 500 specimen images, and making the data publicly accessible via the OSCA platform, ZOBODAT, and the GBIF network. Building on this foundation, the 2024 “Cultural Heritage Digital” project—funded by the Federal Ministry for Arts, Culture, the

Civil Service, and Sport (BMKÖS)—focused on producing high-quality digital reproductions of rare and remarkable specimens from the Fritz Seidl collection, which includes several world-record-sized marine molluscs. Using newly acquired photographic equipment and advanced focus stacking techniques, over 5,400 high-resolution images, representing over 4,000 specimens, were produced and made publicly available. As of today, the collection comprises approximately 165,000 specimen records and 7,728 images accessible online, significantly enriching scientific research and public engagement.

Long-term data analysis of macrozoobenthos over 30 years as part of the Biological Survey Program (BUP) in Upper Austria

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The BUP was established in 1991. The sampling sites were examined at three-year intervals, later adapted where necessary, or expanded to include other rivers. By 2021, 1112 taxa had been identified in 2513 surveys at 375 sampling sites in 132 rivers. 695 taxa were identified at the species level, 69 at the species pair/species aggregate level, 265 at the genus level, and 84 at the family level. The Flysch and Granite-Gneiss Area bioregions exhibit the highest species diversity per site, with medians of 75 and 73 taxa, respectively. The rivers of the Limestone High Alps and Prealps and the Lower Traun River, with medians of 62 and 61 taxa, respectively, are noticeably poorer in species diversity.

Species loss is evident in 57 % of all rivers, or even 70 % of the sites in the granite-gneiss region. In contrast, species gains are observed in only 18 % of rivers. Most of the nine invasive species, such as *Pacifastacus leniusculus* (signal crayfish) and *Potamopyrgus antipodarum* (New Zealand mudsnail), show a significant increase in the long-term period from 1991 to 2021. Other “winners”

include *Cordulegaster boltonii* (golden-ringed damselfly) and the Dryopidae (long-toed water beetles). The “losers” include *Ecclisopteryx guttulata* (caddisfly), *Habrophlebia fusca* (mayfly), *Taeniopteryx kuehntreiberi* (stonefly), *Astacus astacus* (noble crayfish), *Margaritifera margaritifera* (freshwater pearl mussel), and the freshwater mussel genus *Unio*.

Despite the long time series, the analysis of the macrozoobenthos between 1991 and 2021 represents a transitional period. Major negative changes such as water pollution, drainage, and structural engineering, as well as, in a positive sense, the remediation of rivers through the expansion of wastewater treatment plants, mostly occurred before this time series. The impacts of land management that does not protect water bodies and soils are omnipresent. However, the dataset already shows that species loss is occurring in Upper Austria's rivers and that benthic neozoans are expanding both spatially and in terms of population densities.

**Testing genital anatomical characters in clausiliid systematics
on the example of Aloiinae
(Gastropoda: Stylommatophora: Clausiliidae)**

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Among door snails (Clausiliidae), the subfamily Aloiinae is the most species-rich group in the Central and Eastern Mediterranean as well as adjacent regions of Asia and Africa. Its systematics has traditionally relied on shell morphology, which often led to ambiguous or inconsistent taxonomic interpretations. The aim of this study was to assess whether qualitative and quantitative genital traits can improve taxon delineation and provide phylogenetic signal. Two genera were selected for comprehensive investigation: *Montenegrina* Boettger, 1877 and *Siciliaria* Vest, 1867. *Siciliaria* showed high variation in genital anatomy, with 120 specimens from 22 taxa and 44 populations analyzed. Phylogenetic trees from COI and ITS2 sequences placed the species in two well-supported clades. Based on a combined analysis of genital anatomy, shell morphology, and DNA sequence data the genus was revised, including the re-introduction of the genus *Sicania* Tomlin, 1929. In *Montenegrina*, genital morphology was examined in 405 specimens representing 124 taxa from 174 populations, revealing striking variability with taxon-specific anatomical character combinations. In *Montenegrina*, quantitative (morphometric) and qualitative (trait

categorization) data were analyzed using multivariate ordination and clustering to test correspondence with the DNA-based phylogeny. Trees derived from morphological measurements show little concordance with the DNA-based trees. Furthermore, neither morphological nor geographic distances between taxa correlate genetic distances. Thus, while morphological traits prove to be indispensable for alpha-taxonomy, their phylogenetic signal appears weak and largely random in the here treated clausiliid taxa. The results are in accordance with the non-adaptive radiation hypothesis and suggest reproductive character displacement as a plausible mechanism for increasing morphological divergence. These rather unexpected findings motivate to investigate further obligatory rock-dwelling clausiliid genera like, e.g., *Medora*, *Muticaria* or *Charpentieria* or even other families (e.g., Chondriidae) that occupy the same ecological niche.

Invasion genetics of the quagga mussel: Global and regional dispersal dynamics using whole-genome sequencing

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The quagga mussel (*Dreissena rostriformis bugensis*) has become one of the most successful and disruptive aquatic invaders worldwide. Originally native to the Ponto-Caspian region, this species has rapidly expanded across Europe and North America over the past decades, aided by shipping corridors, ballast water, and artificial canals. Unlike its close relative, the zebra mussel, the quagga mussel is able to colonize deep and cold habitats, allowing it to thrive in ecosystems previously considered less vulnerable.

Despite its growing impact, many aspects of the global invasion remain poorly understood. This research aims to clarify when and how the quagga mussel entered Western Europe and Switzerland, and whether previously unde-

tected introduction events occurred. By applying whole-genome sequencing (WGS) to more than 500 individuals from native and invasive populations across Europe and North America, I investigate population structure, genetic diversity, and invasion pathways.

This work addresses the so-called “genetic paradox” of invasion, how quagga mussels succeed despite potential genetic bottlenecks, and explores whether adaptation has played a role in their rapid expansion. The results not only retrace the global journey of a highly adaptive invader but also offer key insights into the genetic and evolutionary forces that drive biological invasions today. These insights form an essential basis for improving future risk assessments and predictive modelling of invasive species.

The species conservation project “Vision Flussperlmuschel” – goals, challenges, successes

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The freshwater pearl mussel (*Margaritifera margaritifera*) faces a dramatic decline throughout its distribution area, including Austria. As a consequence, the Austrian conservation project “Vision Flussperlmuschel” was initiated in 2011. The aim of this project is the establishment of reproductive populations in selected river systems in Upper Austria. In order to reach this goal, two main strategies are being followed. On the one hand, captive breeding of juvenile mussels is performed in order to increase the total number of specimens. For this purpose, adult mussels are kept in two raceways within a custom-built rearing facility. Each raceway runs into a consecutive tank in which juvenile brown trout (*Salmo trutta fario*), the host fish, are kept. This setup enables a natural infestation of the host fish in the course of the serotinal release of glochidia. The infested brown trout are then held within the tanks until the juvenile mussels start dropping off the gills. At

this time, the juvenile mussels are collected in a sieve and then transferred to a laboratory, where they are supplied with fresh water, food and detritus. As soon as all individuals are large enough for surviving in the wild, they are transferred into various rearing systems and placed into selected river sections. The second strategy focuses on restoration measures in the catchment areas. There are hardly any river systems left in Upper Austria that provide suitable conditions for the establishment of pearl mussel populations. Therefore, a detailed mapping of selected rivers was carried out to identify the most promising sites for future resettlement efforts. In these river sections various abiotic and biotic factors with respect to the requirements of *M. margaritifera* are analyzed. Based on these results improvement measures such as the construction of silt traps to reduce fine sediment levels are executed.

DNA Barcoding of native Austrian spring snails – first results on the Stygofauna Austria project

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As part of the Biodiversity Funds project Stygofauna Austria coordinated by the University of Vienna, a basic nationwide survey of biodiversity in groundwater including phreatic, hyporheic, spring and cave waters is carried out and concepts for future ecological monitoring are being developed. In addition to the digitalisation of historical data, new and revised species findings are being systematically documented and archived in cooperation with the Natural History Museum Vienna. Here we present the results from the assessment of the groundwater mollusc fauna compared to data from previous projects (ABOL Mollusca, Hydrobiidae des NP Kalkalpen).

Among the family of Bythinellidae, three species could be found – *Bythinella austriaca*, *Bythinella conica*, and *Bythinella opaca*. Their DNA barcodes reflect the current state of knowledge as separate species and with regard to their geographical distribution. The family of Hydrobiidae is represented by the genera *Alzoniella*, *Belgrandiella*, *Hauffenia* and *Graziana*. For *Alzoniella hartwigschuetzi* DNA barcodes were generated for the first time. In the ge-

nus *Hauffenia* one species could be assessed, i. *Hauffenia wienerwaldensis*. It is genetically clearly separated from its congener *Hauffenia kerschneri*. In *Graziana* two clades show up. One resembles *Graziana pupula*, while it is unclear, if the second one belongs to *Graziana klagenfurtensis* or *Graziana lacheineri*. In *Belgrandiella* species were not clearly differentiated on the basis of DNA barcodes – only *Belgrandiella mimula* and *Belgrandiella parreyssi* seem to be somewhat distinct. While most of the specimens from the genus *Bythiospeum* have identical DNA barcodes, two are differentiated in their DNA sequences. For the hitherto investigated Austrian spring snails, the following facts can be summarized: In *Bythinella*, *Hauffenia* and perhaps *Graziana* DNA barcoding goes conform with the existing taxonomy. For *Alzoniella hartwigschuetzi* no comparable sequences of congeners do exist. In *Belgrandiella* and *Bythiospeum* the unclear results reflect the current controversies concerning different species delimitations and concepts.

Landschnecken-Fauna Süd-Kroatiens, der SO-Herzegowina und W-Montenegros

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Ein Besuch der Stadt Dubrovnik in der Karwoche 2025 bot Gelegenheit Ausflüge in das (süd-kroatische) Umland, sowie nach Montenegro und Bosnien und Herzegowina zu unternehmen. Dabei wurde, neben der Besichtigung kultureller Sehenswürdigkeiten, auch die Gelegenheit genutzt die Landschneckenfauna der Region zu erkunden. In Kroatien wurden die Imperial-Festung außerhalb Dubrov-

niks sowie die Ruine Sokol Grad besammelt, in Montenegro die sogenannte „Spanische Festung“ in Herzeg-Novi. In der Südost-Herzegowina wurde an mehreren Stellen des Gebiets um Gacko gesucht. Marlene Füreder (9 Jahre) wird eine Zusammenfassung der Fundstellen und dort gefunden Arten präsentieren. Die Präsentation erfolgt in deutscher Sprache.

***Parakaliella harimensis* from East Asia: A highly diverse *Euconulus* lineage**

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Euconulus is a widespread Holarctic land snail genus, characterized by small, tightly coiled conical shells ranging from 2.3 to 3.5 mm. Genetic studies often show that species with similar shells belong to separate lineages, reflecting convergent evolution rather than common ancestry. As a result, some species classified as *Euconulus* may belong to other related genera, and vice versa. Additionally, many taxonomic questions about this genus remain unresolved. For example, earlier studies indicated that *Euconulus fulvus* (Müller, 1774) exhibits a polyphyletic structure, with a distinct subclade originating in Japan. However, additional data were required to elevate the Japanese lineage to species level. To further clarify the taxonomic status of this clade, we added samples from Japan and Southeast Asia and used an integrative approach. Phylogenetic relationships in *Euconulus* were reconstructed using two nuclear (ITS1, ITS2) and two mitochondrial (COI, 16S) markers from 53 samples across all five *E. fulvus* species. To have a better resolved tree, two new nuclear markers, ZN507 and TEP1, were also included.

To proceed, we performed morphometric analyses combining shell measurements and geometric morphometry using 19 landmarks. The group containing populations from East and Southeast Asia showed significant genetic divergence and markedly different shell morphology compared to the other species. This group showed a strong morphological resemblance to *Parakaliella harimensis* reported from Japan, confirmed through geometric morphometry using its lectotype and paralectotype. Therefore, we propose reclassifying *Parakaliella harimensis* as *Euconulus*. Examination of type specimens of several *Parakaliella* species revealed that the same species has been described multiple times, primarily due to assumptions about frequent island endemism. This highlights that unrelated snail species can evolve similar shell shapes under similar selective pressures, leading to taxonomic misclassification. Notably, this species shows high genetic variability, likely promoted by climatic stability of the area during Pleistocene, unlike its more widespread sister species.

Mussels of the Vienna Lobau

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The last extensive survey specifically targeting native big freshwater mussels (Unionidae) in the floodplains of the Vienna Lobau in eastern Austria has been conducted in 2007. Since then there have been important changes to ecological factors like local water levels, general habitat conditions and presence of invasive mussel species. Therefore, there is lack of data for the current local diversity of unionid species. More recent superficial surveys however suggest that they may have been in decline.

This master thesis aims to assess the current diversity of native big freshwater mussels (Unionidae) and potentially harmful invasive mussel species in this specific area. Potential threats by the presence of the invasive mussel species and correlations between habitat conditions and species occurrence will also be of relevance. Targeted native unionid mussel species are: Painter's mussel (*Unio pictorum*), swollen river mussel (*Unio tumidus*), swan mussel (*Anodonta cygnea*) and duck mussel (*Anodonta anatina*). The findings

are supposed to provide insights on whether there are still existing vivid populations and/or local extinction trends for these native species. Conducted fieldwork will mainly involve surveys with survey glasses and mussel rakes. This will be complemented by habitat parameter measurements (e.g., water levels, temperature, pH values and conductivity). After identification, all unionid findings will be documented via standardized protocols and photographs. Selected shells will be deposited as vouchers in the mollusc collection of the Natural History Museum of Vienna. If necessary, species identification will be done by DNA analysis. For this task, non-invasive sampling using swabs will be carried out. GIS mapping of local occurrences will visualize spatial distributions for the documented species.

The results will be compiled into a comprehensive master thesis which is also supposed to serve as a basis for a scientific publication. This could potentially contribute to conservation efforts and future monitoring strategies.

“On the Trail of Snails” – A natural trail project in Scharnstein/Almtal

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The nature trail “On the Trail of Snails” in Scharnstein in the Almtal Valley is the first European nature trail to explore the astonishing diversity of snail forms, biology and ways of life. The trail’s history is presented – from the initial idea to its opening. The purpose and benefits of such

projects are briefly reflected upon. Images provide a taste of what awaits visitors upon visiting the trail. Finally, there is a short story about *Bythiospeum elseri*, an endemic species of the Almtal Valley, which is presented on the last panel of the trail.

Digitization of the malacological collection at Haus der Natur Salzburg

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The malacological collection at the museum Haus der Natur Salzburg includes around 55.000 specimen series of terrestrial, limnic and marine molluscs from all over the world. A large part of the specimens originates from the snail collection of Peter Sperling with a focus on the province of Salzburg. With the founding of the malacological working group in 2014, a systematic reorganization, an extensive inventory and a digital acquisition of the whole malacological collection started. The metadata of the specimens were transferred to the Salzburg Biodiversity Database (BioOffice) and the collection sites were georeferenced. This made it possible to use the data for

nature conservation and research and to make the data publicly accessible in global networks such as GBIF. The digital acquisition of the Sperling Collection was intensified with the help of two digitization projects that were financially supported by the BMWKMS (BMKÖS) and the EU. In addition to metadata acquisition, object digitization became an integral part of the daily work-routine. A camera system was purchased to produce high-resolution images of molluscs using focus stacking. At the same time, workflows and strategies were developed in cooperation with the OSCA consortium to improve collection digitization and standardize the data flow to public databases.

Invasive gobiid fishes (Gobiidae) as hosts for native freshwater mussels (Unionidae) in oxbows of the Danube in Austria

Rethinking invasion: Can non-native gobies (Gobiidae) support native mussels (Unionidae) in Danube oxbows?

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Freshwater mussels (Unionidae) are among the most vulnerable inhabitants of freshwater ecosystems, which are experiencing more severe biodiversity losses than those on land or at sea. As long-lived filter feeders, mussels play a vital role in maintaining water quality and ecosystem functions, making their decline both a symptom and a driver of ecological degradation. In Austria's Donau-Auen National Park, a particularly dynamic and free-flowing stretch of the Danube, mussels face multiple pressures including habitat loss from siltation and altered hydrology, pollution, and the spread of invasive species. Yet, invasive species may not solely be detrimental. Because mussel reproduction depends on a parasitic larval stage (glochidia) that must attach to a fish host, new fish arrivals could potentially serve as alternative hosts for native mussels.

Over the past decades, several non-native gobiids from the Ponto-Caspian region have colonized the Danube, with their presence particularly pronounced in the oxbows of the National Park. While these species compete with the native tubenose goby (*Proterorhinus semilunaris*), they may also play an unrecognized beneficial role in supporting mussel reproduction. This study, the first of its kind in Austria, assesses the potential of non-native gobies to act as hosts for native Unionidae.

In spring of 2025, eight electrofishing surveys were conducted across four oxbow sites between Maria Elend and Wildungsmauer. Up to 120 gobies per site will

be examined for evidence of glochidia attachment using visual inspection under magnification. Detailed host data (species, size, sex) and the precise attachment location of glochidia will be recorded. Infection intensity and distribution patterns will be quantified, and glochidia will be genetically identified to confirm mussel species and detect potential multi-species infections. Environmental variables such as water temperature and conductivity will also be considered to explore links between infestation timing and mussel reproductive cycles. Statistical analyses, including regression models, t-tests, and ANOVA, will be applied to test hypotheses on seasonal overlap, sex-related differences, and size dependence in glochidia attachment.

The results will illuminate an overlooked ecological relationship with far-reaching implications for conservation. If non-native gobies are effective hosts, they may inadvertently support the recruitment of threatened mussel populations. Conversely, if they prove unsuitable, the loss of native host fish could further challenge mussel persistence. Clarifying these dynamics addresses a key knowledge gap in Central European freshwater ecology. The findings will also provide actionable insights for biodiversity management, restoration planning, and the integration of fish–mussel interactions into long-term conservation strategies in one of Europe's most valuable aquatic landscapes.

Getting digital – aims, difficulties and results of the digitization of the mollusc collection at the NHMW

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The mollusc collection of the Natural History Museum Vienna comprises a vast number of specimens and it has been the task for many decades now, to account for them and make the meta data digital available. This process is time consuming and with a rather low staff count and many other projects aside, the progress is taking its time. Nevertheless, so far we have around 150.000 series entered into our database, we estimate this is about 1/4 of the whole collection. In recent years 'Digitization' has become a huge word and finally more attention is drawn

to museum collections and their validity. This also results in funded projects, which help to fasten the digitalization process of the mollusc collection. Recently, we were part of the OSCA-initiative and the Kulturerbe-Digital project (BMKÖS), which also focused on producing digital photos of the objects. Currently, the NHMW is implementing a database (DIVINA) for which also a public portal is available and will therefore open our collections to the public.

Musculature of the invertible foot of gadilid Scaphopoda in 3D view

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Scaphopoda live burrowing in marine sediments. The foot can be extended through the anterior shell opening for locomotion and to produce a feeding cavity. The Dentaliida, as one of the two major taxa of Scaphopoda, have a contractible burrowing foot comparable to that of Bivalvia. The foot of the other taxon, the Gadilida, however, is invertible and functionally similar to the introvert of Sipuncula or the proboscis of Nemertini. This derived function is achieved by the detachment of a considerable part of the longitudinal musculature from the pedal wall to form central retractor muscles. The number of central retractors and their point of detachment varies among the gadilid subgroups. Whereas the Entalimorpha have several small pairs of retractor muscles detaching from the pedal wall in the area of the pedal ganglia, the Gadilimorpha sport a single large pair separating from the body wall further posterior at the level of the visceral ganglia. A fine-scaled 3D-reconstruction of histological serial

sections of two gadilimorph and one entalimorph species, complemented by checking histological sections of other species, revealed new details on the branching sequence of the dorsoventral musculature in the formation of the pedal muscles. In the Entalinidae, three pairs of central retractors separate from the lateral foot wall posterior of the pedal ganglia, and a fourth pair anterior of them. Several accessory retractor muscles branch from and re-fuse again with the central retractors in the distal part of the foot. This is also the case in the examined species of Gadilidae and Pulsellidae in the Gadilimorpha. The latter further have two pairs of delicate connecting muscles originating from different parts of the central retractors in the middle part of the foot and attach to the longitudinal musculature of the pedal wall. These hitherto unexplored details of the gadilid muscle system raise questions about functional and systematic implications that require a broader taxon sample to be answered.

Abstract of Poster

Methods for visualizing and analyzing the structure of the shell *Caucasotachea vindobonensis*

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The shells of the south-eastern European land snail *Caucasotachea vindobonensis* were examined in terms of morphometric, structural, chemical, phase and mechanical properties. The shells (n= 90) were collected at xerothermic sites in Janowiec, Chęciny and Olsztyn, Poland, located along the northern boundary of the species' distribution. Morphometric and structural studies of the shells were carried out using digital, epifluorescent and polarizing microscopes, as well as SEM and micro-CT. The crystalline phase of the shells was identified using the XRD method. The chemical composition was determined using the EDS technique, while microhardness was measured by the Vickers method. The studies showed that the shells of *C. vindobonensis* have a crossed-lamellar structure. Beneath the periostracum, four mineral layers are present, composed of first-, second- and third-order lamellae, each with varied geometric orientation. The average thickness of the shell walls is 215.8 µm. Pigments in the shell walls

are distributed throughout almost the entire thickness or are concentrated in the upper parts. Some shells have deformations that cover a large part of the surface or only the last whorl. In the chemical and phase composition of the shells, an average 99.13 % by weight consisted of the major elements forming calcium carbonate in the aragonite phase. In addition to the major elements, there are trace elements such as strontium, magnesium, iron, and manganese, whose total content is 0.8 % by weight. Their presence in the shells is associated with the calcium carbonate, which may contain impurity-forming elements in its crystal lattice. The average microhardness of the shells is 327.93 HV at a load of F=0.025 HV. The presented results are part of an interdisciplinary project aimed at investigating the compositional, structural and mechanical properties of the shells of *C. vindobonensis* from different biotopes.