

NOBIS Austria

NOBIS MEETING 2024

SYSTEMATICS & COLLECTIONS



November 28th–29th, 2024
Natural History Museum Vienna

NETWORK OF BIOLOGICAL SYSTEMATICS AUSTRIA

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SYSTEMATICS & COLLECTIONS

18th Annual Meeting of NOBIS Austria

Thursday, November 28, 2024 –

Friday, November 29, 2024

Natural History Museum Vienna

Editors: Andreas Kroh & Nicole Grunstra

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Dear fellow NOBISs!

After a break in 2023, when NOBIS Austria co-organized the first Biodiversity Days ("Tage der Biodiversität"), we are back this year and reuniting for our 18th annual meeting. With more than 70 registered participants at the time of writing, the meeting promises to become a fruitful place for discussion, networking and exchange of ideas. This year we were kindly invited by the Natural History Museum Vienna, which hosted the 3rd NOBIS Austria Meeting back in 2009 and the first NOBIS Young Researchers Day in 2013. The Nobis Austria Executive Board thanks Katrin Vohland and Markus Roboch, CEOs of the Natural History Museum Vienna, for their kind support. Likewise, we gratefully acknowledge Martin Kapun, Sonja Steindl & Astra Bertelli, who organized a hands-on bioinformatics workshop on the topic "*AmpliPiper – Applications and pitfalls of multilocus amplicon sequencing with Oxford Nanopore technology*", which is held back-to-back with the NOBIS-Austria-Meeting on Thursday afternoon, before the icebreaker.

As in previous years, junior colleagues will compete for the **NOBIS Awards 2024** for excellent research in the field of biological systematics. Two awards of € 500 and a three-year NOBIS membership each will be conferred, one for a Master and one for a PhD student talk. We are grateful to our scientific jury who will select the winners during the meeting. The evaluation will be based on scientific significance as well as on the quality of the presentation.

This year's annual meeting is dedicated to the topic "Systematics & Collections". Collections provide the raw data from which scientists derive evidence, including knowledge that is directly relevant to key issues faced by our society, such as biodiversity loss, climate change and the origin of life, to name just a few examples. Nesrine Akkari will address the significance and future of collection-based research using Myriapoda as a case study in her keynote and the contribution by Mathias Harzhauser and colleagues will expand on the importance of museum collections for tracing past changes of biodiversity. This year's annual meeting will be concluded with a presentation by the awardee of the NOBIS Grant 2022, Susanne Reier, presenting the initial results of her project, a short project presentation by the NOBIS Grant 2024 awardee, and the announcement of the winners of the NOBIS Awards 2024 will conclude the meeting. We encourage all NOBIS members to attend the general

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assembly following on directly from the meeting, where the new executive board of NOBIS Austria will be elected.

Finally, we would like to promote the upcoming meeting “Tage der Biodiversität 2025”, held at the BOKU Wien, which is again co-organized by NOBIS Austria and will take place from February 25–28, 2025.

We are looking forward to seeing you all at the NOBIS Austria Meeting 2024 and we wish you a great time, filled with interesting talks and fruitful discussions.

The Nobis Austria Executive Board

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Programme

Thursday, November 28th 2024

- 13:00–16:30 Workshop “Multilocus amplicon sequencing / AmpliPiper” held by Martin Kapun, Sonja Steindl & Astra Bertelli (for pre-registered attendees only, Kurssaal, Natural History Museum Vienna, Burgring 7 (staff entrance), 1010 Vienna)
- 16:30–17:30 Guided tours through NHM collections (meeting point: Natural History Museum Vienna, staff entrance)
- 17:30–20:00 Icebreaker in Hall 16 of the Natural History Museum Vienna (use the staff entrance Burgring 7, 1010 Vienna) – **Bring your posters!**

Friday, November 29th 2024

(Hall 16 of the Natural History Museum Vienna – use the main entrance
Maria-Theresien-Platz 1, 1010 Vienna)

- 09:00 Welcome address by **Andreas Kroh**, President of NOBIS Austria

Talks – Session 1

Chair: Andreas Kroh

- 9:10–9:50 **Nesrine Akkari**: Keynote – Towards an integrative future of collection-based systematics, with examples from research on Myriapoda (Arthropoda)
- 9:50–10:05 **Jonas Eberle**: Clarification of the taxonomic status of the North American clerid *Thanasimus nubilus* (Coleoptera: Cleridae)
- 10:05–10:20 **Philipp Hummer**: How museomics may help us detect recent anthropogenic changes in the genomes of insects
- 10:20–10:35 **Elora Marx**: *Basilosaurus* predation and possible sexual dimorphism in a late Priabonian Archaeocete from Fayoum, Egypt
- 10:35–11:00 **Coffee break**

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Talks – Session 2

Chair: Nicole Grunstra

- 11:15–11:30 **Thomas Strohmeier:** Cryptic diversity in snow scorpionflies (*Boreus* spp.) in relation to cuticular chemistry and geography
- 11:30–11:45 **Sarah Saadain:** Unraveling the evolution of the German cockroach *Blattella germanica* using historical specimens
- 11:45–12:00 **Katharina Mason:** Last pieces of the jigsaw – population genetics of the rock-dwelling door snail *Montenegrina* (Gastropoda: Clausiliidae)
- 12:00–12:15 **Daniel Lukic:** Exploring molecular data from pinned beetles: chances and challenges
- 12:15–12:30 **Anna Pyttlik:** Bilateral asymmetry of the mammalian and avian inner ear
- 12:30–13:30 **Lunch Break** (Food & drinks will be provided)

Talks – Session 3

Chair: Dominique Zimmermann

- 13:30–13:45 **Anne Le Maître:** A comparison of the intraspecific variation of middle and inner ear morphology between selected mammals and birds
- 13:45–14:00 **Mathias Harzhauser:** The hotspot in the drawer – the importance of museum collections for tracing past changes in biodiversity
- 14:00–14:15 **Špela Di Batista Borko:** Distribution and diversity of *Gammarus fossarum* in AT
- 14:15–14:45 **Lightning talks** (poster presentations, 3 min. each)
- 14:45–15:30 **Coffee break & Poster session**

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Talks – Session 4

Chair: Andreas Tribsch

- 15:30–15:45 **Tamara Spasojevic:** Deciphering host-related evolutionary patterns in polysphinctine spider parasitoids (Hymenoptera, Ichneumonidae)
- 15:45–16:00 **Harald Letsch:** Phylogenomics elucidates the relationships, biogeography and evolution of host plant associations of minute seed weevils (Coleoptera)
- 16:00–16:15 **Elisabeth Geiser:** Museum collections are the most important basis for studying Donaciinae
- 16:15–16:35 **Susanne Reier:** Overcoming challenges in molecular genetic analyses of *Pomphorhynchus* species (project report NOBIS Grant 2022)

Final Session

Chair: Elisabeth Haring

- 16:35–16:50 **Awards ceremony** (presenter prizes & NOBIS Grant 2024)
- 16:50–17:00 **NOBIS Grant 2024** – Short presentation of the project by the 2024 recipient
- 17:00–18:00 **General assembly** & election of the NOBIS board members

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Abstracts

Towards an integrative future of collection-based systematics, with examples from research on Myriapoda (Arthropoda) [Keynote]

Akkari, N.¹

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Natural history collections are a treasure trove for scientific research and innovation, providing a long-term resource to study the diversity of nature and the evolution of our planet. They are repositories of millions of preserved labelled specimens, including rapidly disappearing or even extinct species. Well curated and preserved scientific collections are unique “archives for biodiversity”. They provide invaluable information on evolutionary processes and changes in species composition across vast temporal and special scales, allowing to answer a number of scientific questions, even those that have not been posed yet. The decline of biodiversity, changing of the climate and destruction of natural habitats continue to impact the humanity and represents a major concern, which renders exploring and understanding the systematic diversity of taxa of a prime importance. A role mainly carried by taxonomists, who themselves have become an “endangered species”. The core task of taxonomists is to discover, describe and name taxa, document their diversity, and understand their phylogenetic relationships. This constitutes the groundwork for any subsequent fundamental or applied research and procures profound insights into the evolution of taxa. Taxonomy continues however to face numerous challenges, such as the lack of prestige and resources, which undeniably humpers the progress of cataloguing the diversity. Natural history museums have however always facilitated the work of taxonomists and continue to be the ideal place for interdisciplinary research and innovation, where novel methods are always applied to bridge the gap between science, art and humanities.

In this talk, I highlight the history and importance of taxonomy as an independent research, yet vital for all other disciplines. Based on examples from own research, I illustrate the immense role of natural history collections as a timeless resource for systematic research, as well as the effort invested by taxonomists in reinventing the taxonomic research as an active discipline, depending on multidisciplinary and integrative approaches.

Distribution and diversity of *Gammarus fossarum* in Austria [Talk]

Di Batista Borko, Š.¹, Grimm, J.¹, Hahn, C.¹, Koblmüller, S.¹, Weutz, E.¹, Schulz, N.¹, Raffler, J.¹, Zettel, C.¹ & Sefc, K. M.¹

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Gammarus fossarum is an amphipod species complex that plays a major role in the food webs of European rivers and streams. It is a morphologically cryptic but genetically highly diverse complex, with an estimated 100+ MOTUs (Molecular Operational Taxonomic Units). Although it is widely used as a sentinel species and as a model system in ecophysiology and ecotoxicology, its taxonomic status has not yet been clarified (Wattier et al. 2019). There are several country-wide sampling gaps with little to no information on the distribution and diversity of potential new species. Systematic sampling in recent years has shown that *Gammarus fossarum* is widespread in Austria. Species delimitation based on the COI (cytochrome c oxidase subunit 1) marker revealed 27 MOTUs from several clades. Nuclear markers (arginine kinase, heat shock protein and elongation factor genes) confirmed the delimitation of most MOTUs, with one case of mitonuclear discordance within three sister COI lineages that needs to be further explored. Most MOTUs are found only in Austria. Few are widely distributed, with a range extending over several hundred kilometres, while 11 have a narrow distribution, with a maximum distance between localities of less than 20 km. Genetic diversity within MOTUs generally increases with the range size, with few exemptions that pinpoint recent range expansion events. Spatial diversity patterns vary through the country. North and west Austria is less diverse, occupied almost exclusively with one widely distributed MOTU, while MOTU richness is highest in the Eastern Alps, where most of narrowly distributed MOTUs occur. Two hotspots are evident: around Graz and in the Soboth. Phylogenetic diversity largely correlates with MOTU richness, but is lower than expected in the two hotspots, indicating local diversification. Diversification, combined with colonisation of different unrelated lineages, and survival of narrowly distributed relicts in glacial refugia along the eastern limits of the glaciated area, seem to be the main factors contributing to the high diversity in the area. Noteworthy, intensive sampling has revealed several cases of possible human-mediated introduction of MOTUs outside their natural range, mainly along the Danube. These introductions are difficult to detect and reliably confirm, but important to consider since they influence diversity patterns and obscure historical processes.

References

Wattier, R., Mamos, T., Copilaş-Ciocianu, D., Jelić, M., Ollivier, A., Chaumot, A., ... & Grabowski, M. 2020. Continental-scale patterns of hyper-cryptic diversity within the freshwater model taxon *Gammarus fossarum* (Crustacea, Amphipoda). *Scientific reports*, 10(1), 1–16. <https://doi.org/10.1038/s41598-020-73739-0>

Clarification of the taxonomic status of the North American clerid

Thanasimus nubilus (Coleoptera: Cleridae) [Talk]

Eberle, J.¹, Schallegger, R.¹, Sikes, D. S.², Lebel, M.³ & Gerstmeier, R.⁴

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The North American checkered beetle (Cleridae) *Thanasimus nubilus* Klug, 1837 is currently listed as a subspecies of *T. undatulus* (Say, 1825) in several publications. Recently, evidence from morphology and genetics has increased, suggesting its species status. We revise the taxonomic status of *T. nubilus* by the investigation of cox1 DNA-barcodes and morphological measurements of multiple specimens of each of the two taxa as well as of multiple specimens of four further species of the genus. We use state of the art species delimitation methods based on gene trees and clustering algorithms. Evidence from mtDNA supported the species status of *T. nubilus*. The results were confirmed by morphometric measurements of the investigated species. Furthermore, genetic data pointed to a potentially highly interesting showcase of North American biogeography.

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A First Look into Lineage-Specific Gene Families in Tintinnid Ciliates (Alveolata, Ciliophora, Spirotricha) [Poster]

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Tintinnids have diversified into more than 1,000 known species predominantly inhabiting the marine plankton since at least the Triassic period. Their systematics are mainly based on the morphology of their remarkable lorica: a robust shell formed from highly resistant, probably proteinaceous material produced during cellular division. Despite their significance in marine ecosystems, the process of lorica formation and the underlying genetic mechanisms remain unknown. Tintinnids are monophyletic and closely related to many species which also share the planktonic lifestyle but do not form a lorica. We assume that genes associated with lorica formation are unique to tintinnids and can be considered lineage specific. We aim to establish the first baseline for lineage-specific gene families (LSGFs) in tintinnids analyzing single-cell transcriptomes obtained from culture material and field samples collected in the Atlantic and the Pacific Oceans. Potential LSGFs are identified utilizing state-of-the-art bioinformatic tools, including TIDeS, Orthofinder, and the phylogenomic pipeline PhyloToL. Our findings not only represent a significant step towards unraveling the genetic basis of lorica formation but also contribute to our understanding of the intricate relationship between gene evolution and emergent biological functions. Tintinnids, with their unique lorica, serve as a model for exploring these correlations and advancing our knowledge of the molecular underpinnings of lineage-specific adaptations.

Taxonomy and diversity of Nemesiidae and Dysderidae (Arachnida, Araneae) in Kosovo [Poster]

Geci, D.^{1,2}, Strohmeier, T.², Ibrahimji, H.¹, Bilalli, A.³ & Koblmüller, S.²

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This study investigates the taxonomy and diversity of the spider families Nemesiidae and Dysderidae in Kosovo, a region characterized by diverse ecosystems and a rich biodiversity. Despite their ecological significance, the arachnid fauna in this area remains one of the most understudied and unexplored in Europe. We conducted field surveys across various habitats, including forests, grasslands, and rocky areas, to collect specimens. Taxonomic identification was performed using morphological characteristics, complemented by DNA barcoding through nanopore sequencing to clarify species boundaries and resolve potential cryptic diversity. Our findings reveal a noteworthy diversity within both families, with several species being reported for the first time in Kosovo, along with new species to be described from both families. This research not only enhances the understanding of arachnid diversity in the region but also provides essential baseline data for future conservation efforts. The results underscore the importance of preserving diverse habitats to protect these often-overlooked yet vital members of the ecosystems.

Museum collections are the most important basis for studying Donaciinae [Talk]

Geiser, E.¹

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Museum collections are essential for systematic studies. Firstly, type specimens are or should be kept in museums; secondly, it is necessary to study specimens from the entire distribution area of a species; thirdly, many areas can no longer be collected today due to the political situation. Therefore, one has to rely on museum specimens.

These reasons apply to practically all species of organisms. In the case of the Donaciinae additional reasons are deteriorating ecological conditions and these beetles are difficult to catch.

Most Chrysomelids are specialized on their foodplants. The Donaciinae develop under water on plants, which grow close to the shore. This habitat has been heavily modified by humans in recent decades. While water pollution in industrialised countries has decreased, ecological conditions have been greatly altered by straightening, drainage and shoreline use by humans. This has led to the decline of some food plants such as *Butomus umbellatus* (flowering rush). However, some species that live on euryoecious plants such as *Phragmites australis* (common reed) have also declined over the last 50 years because the conditions are apparently no longer suitable for these beetles.

It is difficult to specifically collect representatives of the Donaciinae in their habitat. They are only active for a few weeks a year, and this period and their abundance can vary greatly. Therefore, the vast majority of finds are by-catches made by chance during excursions targeting other species. As a result, around 80 to 90 % of all Donaciinae species – at least in the Old World – can almost be studied in museums.

DNA-Barcoding of large branchiopods in Austria, the Czech Republic and Slovakia [Poster]

Greilhuber, M.^{1,2,3,4}, Devánová, A.⁵, Sychra, J.⁵, Kruckenhauser, L.^{2,3} & Schwentner, M.¹

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Large branchiopods (Branchiopoda excluding Cladocera) are prominent representatives of temporary pool fauna. They are an excellent model for studying the ecology of these endangered habitats. In Austria, 16 species have been recorded so far, including *Lynceus brachyurus*, which is presumed locally extinct. Although the faunistics of these species is relatively well-studied in Austria, the populations have rarely been analyzed genetically. Within the frame of the presented study, a part of the COI gene was sequenced in three specimens per species for all species of large branchiopods occurring in the territory of Austria, the Czech Republic and Slovakia, if available. The material included both fresh specimens and historical specimens from the crustacean collection of the Natural History Museum Vienna. The results provide an overview of the variability of the COI gene of large branchiopod species in the area, and the sequences can serve as references for DNA barcoding applications. The study allows a first look at the genetic diversity of large branchiopods in Austria, the Czech Republic and Slovakia.

The hotspot in the drawer – the importance of museum collections for tracing past changes in biodiversity [Talk]

Harzhauser, M.¹, Mandic, O.¹, Landau, B. M.² & Neubauer, T. A.³

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³ SNSB – Bavarian State Collection for Palaeontology and Geology, Munich, Germany

Metanalyses of published taxonomic datasets are amalgamating a multitude of different taxonomic traditions, incongruent species concepts and a generally broadly scattered quality of research. These issues render many taxonomic datasets internally incomparable and can severely bias reconstructions of species richness, biogeographic relationships and evolutionary trajectories – a problem that is frequently underestimated in (paleo)biodiversity research. To overcome this problem and to minimize the impact of taxonomic artefacts we performed critical revisions of many gastropod families from the Miocene of Central Europe during the last 15 years. Our dataset is based on museum collections and comprises 858 species from 95 localities, spanning the entire Early–Middle Miocene. This dataset represents one of the largest consistently and critically evaluated paleontological-malacological species-level datasets. During our presentation, we will demonstrate geodynamics and climate as the main drivers to explain changes in diversity and define a so far underrated hotspot of marine diversity, that developed in an archipelago-like landscape. Data from museum collections even trace changes in past habitat heterogeneity, which boosted species richness. Similarly, the impact of global climate cooling during the Middle Miocene Climate Transition is documented by a drastic decline in biodiversity. Changes in diversity of deep-water faunas can be linked to changing patterns in circulation. Our study underlines the importance of museum collections but also emphasizes the importance of taxonomic revisions (Harzhauser et al. 2024).

References

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How museomics may help us detect recent anthropogenic changes in the genomes of insects [Talk]

Hummer, P.¹, Saadain, S.¹, Cheronet, O.², Pinhasi, R.² & Kofler, R.¹



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During the last few years, the sequencing of specimens from natural history collections, so called museomics, has improved considerably. Such data from 200-year-old *Drosophila melanogaster* specimens has allowed Scarpa et al. (2024) to detect historical transposable element (TE) invasions. In total, eleven TE invasions in 200 years have been discovered in *D. melanogaster*, which have directly led to an increase in genome size of 0.8 - 0.91% (Pianezza et al. 2024). Given what is known about the TE content of the *D. melanogaster* genome, such a high rate of invasions during this time is unexpected and must be inflated relative to the species' broader evolutionary history. Pianezza et al. (2024) hypothesize that this is linked to human activity, specifically global trade, as *D. melanogaster* is a human commensal with a cosmopolitan range that has recently been brought into secondary contact with other drosophilids, e. g., the neotropical *D. willistoni*. If this hypothesis holds, we expect that other insect species – specifically those who have recently become cosmopolitan – may also have an inflated rate of recent TE invasions. We want to test this hypothesis by sequencing and investigating the genomes of historical specimens from a range of different species. For this purpose, I have developed a protocol for non-destructive DNA extraction that causes only minimal physical changes while the captured quantity of DNA is sufficient for whole genome sequencing. At this point we have established collaborations with three institutions – the monastery Stift Seitenstetten, the Natural History Museum of Vienna and the Smithsonian National Museum of Natural History – and extracted DNA from 86 individuals across nine species.

References

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<https://doi.org/10.1101/2024.04.25.591091>

A taxonomic revision of Chimaeridae [Talk]

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² CIBIO – Research Center for Biodiversity and Genetic Resources, Vairão, Portugal

Holocephalans are an exceptionally ancient taxon. Together with the elasmobranchs (sharks and rays), they form the oldest lineage of jawed vertebrates (Benton et al. 2009), providing a crucial reference for our understanding of vertebrate evolution (Inoue et al. 2010). Nonetheless, holocephalans remain severely understudied, with limited knowledge about their ecology, biology or behavior, often derived from a few coastal species accessible to commercial fisheries (Didier et al. 2012). Moreover, ambiguities persist regarding the phylogenetic relationships among extant holocephalan taxa. This is particularly evident in Chimaeridae, the most speciose family, whose two genera, *Hydrolagus* and *Chimaera*, have traditionally been distinguished by the presence or absence of an anal fin (Didier 2004). This distinction, however, is challenged by recent molecular evidence revealing Chimaeridae's paraphyletic nature based on mitochondrial phylogenies (Licht et al. 2012). Consequently, there is need for a comprehensive examination of the family.

We will sequence the whole genomes of all 46 Chimaerid species to construct a phylogenetic tree based on orthologous gene sequences. Depending on whether the phylogenomic analysis indicates paraphyly between the two genera, as suggested by mitochondrial gene trees, we will include morphological data.

References

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A comparison of the intraspecific variation of middle and inner ear morphology between selected mammals and birds [Talk]

Le Maître, A.^{1,2}, Grunstra, N. D. S.^{2,3}, Bravo Morante, G.², Pfaff, C.⁴, Wimmer, W.⁵ & Mitteroecker, P.^{1,2}

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The ear of mammals is particularly complex compared to other vertebrates. During the evolution of mammal ancestors, several bones of the lower jaw and its joint changed morphologically, migrated to the cranium and became part of the middle ear apparatus. Mammals therefore have three auditory or middle ear ossicles – the malleus, the incus and the stapes – compared to only one in other vertebrates: the columella (homologous to the stapes). This complex structure, together with the lengthening and coiling of the cochlea of the inner ear, enabled mammals to increase their hearing range, especially towards high frequencies. The inclusion of extra bones in the mammalian middle ear implies the recruitment of an additional pharyngeal arch during embryonic ear development, as well as additional genetic pathways, relative to other vertebrates. We previously proposed that this higher complexity of the mammalian ear facilitates the independent evolution of the different ear elements, thereby increasing the evolvability of the ear. From this we predict that the mammals exhibit increased morphological variability and modularity of the different ear components *within* species compared to other vertebrates. In other words, the total shape variation of the mammalian ear is expected to decompose into a higher number of independent factors (or dimensions) than in other vertebrates. To test this, we compare inner and middle ear shape variation among a select sample of mammals and birds, two lineages of roughly the same age. Specifically, ear morphology of humans, European red squirrels, common buzzards and house sparrows was obtained from microCT scans. Using 3D geometric morphometrics, we quantify the morphology of the bony labyrinth (osseous moulding of the inner ear) and the middle ear ossicle(s) with a comprehensive set of anatomical and sliding landmarks in a sample of ~30 individuals per species. Using multivariate statistics, we compare the intraspecific patterns of variation and modularity/integration between the inner and middle ear among the four species. Finally, we discuss the implications of our findings for the evolvability of the mammalian compared to the avian ear.

Phylogenomics elucidates the relationships, biogeography and evolution of host plant associations of minute seed weevils (Coleoptera: Curculionidae: Ceutorhynchinae) [Talk]

Letsch, H.^{1,2}, Vukotić, S.¹, Gottsberger, B.¹, Friedman, A.³, Wanat, M.⁴, Beran, F.⁵, Fiedler, K.¹ & Riedel, A.²

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² State Museum of Natural History Karlsruhe, Karlsruhe, Germany

³ The Steinhardt Museum of Natural History, Tel Aviv University, Tel Aviv, Israel

⁴ Museum of Natural History, Wrocław University, Wrocław, Poland

⁵ Friedrich Schiller University Jena, Jena, Germany

Ceutorhynchinae are a diverse weevil subfamily of almost worldwide distribution and considerable economic importance. They also occur in a great variety of habitats: several genera are adapted to an aquatic lifestyle, whereas species adapted to feed on *Ephedra* plants live in desert and semi-desert habitats. Many ceutorhynchine species are monophagous, i.e. tied to a single species or genus of host plants, while others are oligophagous, i.e. using different species of host plants that belong to the same genus or at least the same family of plants. We inferred the relationships among the tribes of this rather neglected taxon, using a phylogenetic workflow that combines both whole genome and Sanger sequence datasets with heterogeneous taxon coverage. We used a dataset comprising about 2600 genes derived from the whole genomes of 85 species and Sanger sequences of seven genes for about 300 species. Our phylogenomic results inferred the mainly African tribe Egrini as sister group to all other ceutorhynchine tribes. All analyses further recovered three well supported clades. All taxa with the ability to jump as adult beetles, are included in one clade, which comprises the tribes Cnemogonini, Hypurini, Mecysmoderini, and Phytobiini. Detected major diversification shifts correlate with both host shifts and major climate events. Ceutorhynchinae experienced an increase in diversification during the Early Eocene Climate Optimum. A second major diversification phase occurred at the end of the Eocene. A third diversification increase is correlated with the rising temperatures of the Late Oligocene Warming Event. The patterns of interactions observed among the radiation of Ceutorhynchinae and environmental factors indicate that the interplay of biotic and abiotic factors might better explain their evolution than each of these factors viewed in isolation.

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Exploring molecular data from pinned beetles: chances and challenges [Talk]



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Molecular data is essential to many biological disciplines, including systematics, taxonomy, population genetics, and conservation, among others. However, obtaining such data often presents significant challenges, such as finding specimens, obtaining collection permits, the political situation in the countries, and the time and financial costs associated with travel. One example is the bee-beetles (Cleridae: *Trichodes*), a well-known genus to most entomologists and well-represented in collections. It has a wide distribution across the Palearctic, North America and Africa, comprising 94 species. While some of them are abundant, others are rarely found and therefore, their evolutionary history is poorly understood. These circumstances make *Trichodes* an ideal model system to explore alternative sources of molecular data. In the dusty drawers of natural history museums and private collections the dry material is a rich source even for rare species from all over the world. These collections represent a valuable yet underutilized resource for obtaining molecular data. To unlock this potential a better understanding of both the quality and quantity of historic DNA, as well as the most effective methods for extracting high-quality DNA isolates from these specimens is required. In this study, we analysed three methods of DNA extraction from dry-preserved material and examined how dry preservation impacts DNA quality. Our findings revealed a large variability in DNA concentration between samples. Fragment length data indicated an initial rapid decline in fragment size, followed by a much slower rate of degradation. On average, the fragment sizes were 78 base pairs (bp), which is shorter than those observed in butterflies. Future research is needed to investigate the reasons behind these differences in fragment lengths across taxa.

Basilosaurus predation and possible sexual dimorphism in a late Priabonian Archaeocete from Fayoum, Egypt [Talk]

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The shallow marine fauna of Al-Fayoum in Egypt, dating from the Middle to Late Eocene, is known for its spectacular early whale fossils, which have significantly contributed to our understanding of cetacean evolution. The Natural History Museum in Vienna houses two previously unpublished archaeocete skulls from this location, acquired in 1907.

In this study, one of these specimens undergoes a detailed examination. Using measurements and morphological analyses of the bones and teeth, supplemented by μ CT scans, the species and ontogenetic stage of the specimen are identified. Additionally, the previously unknown stratigraphic layer of the find is determined with greater precision, combining what is known of the collection history with lithological comparisons. Further characteristics are explored by morphological research. Of particular relevance is the investigation of potential sexual dimorphism in the species based on teeth sizes and the shape of the sagittal crest. Furthermore, the present bone modifications are analysed for evidence of the cause of death.

The specimen represents a dentally mature individual of a medium-sized dorudontine Basilosaurid nearing skeletal maturity. The specimen most likely originates from the Upper Eocene Qasr-El-Sagha formation. It might have died during a *Basilosaurus isis* attack which followed a typical cetacean hunting pattern, giving the first evidence for the occurrence of this predator both in the environment and in time. The hypothesis of sexual dimorphism is supported, potentially offering insights into the sexual development and mating system of these early whales.

Last pieces of the jigsaw – population genetics of the rock-dwelling door snail *Montenegrina* (Gastropoda: Clausiliidae) [Talk]

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Over the last years we comprehensively studied the rock-dwelling door snail *Montenegrina*. It is a hyper-diverse land snail genus, specialised on limestone, with a very patchy and restricted distribution range in the western part of the Balkan Peninsula. Therefore, it is a useful study organism to get deeper insights into speciation processes, morphological differentiation, ecological adaptation as well as genetic differentiation. We performed a comprehensive phylogenetic study based on three markers, partial sequences of the mitochondrial genes coding for cytochrome c oxidase subunit 1, 16S rRNA, 12S rRNA (COI, 16S, 12S). In the resulting tree, only about half of the species and subspecies were monophyletic (Mason et al. 2020). In parallel, anatomical features like specific genital structures were analysed (De Mattia et al. 2020). Combining the genetic and anatomical results, some paraphylies were resolved by taxonomic changes either by reassigning subspecies or raising them to species level. 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. Finally, based on the Biological Species Concept, we addressed the question of species delimitation investigating two co-occurring *Montenegrina* taxon pairs by microsatellite analysis to assess gene flow. Interpreting the results of these two cases illustrates that this approach does not always yield a clear conclusion, even when considering all available information – genetic, morphological and geographic. Sometimes not all pieces of the jigsaw fit together.

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Bilateral asymmetry of the mammalian and avian inner ear [Talk]

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Mammals may owe part of their evolutionary success to an increased evolvability of their ear. The incorporation of jaw elements into the middle ear enhanced the genetic, regulatory, and developmental complexity of the mammalian ear, potentially providing greater evolutionary flexibility for the independent evolution of its functional components. The mammalian ear may thus be more evolvable than the simpler ear structure of other vertebrates, such as birds with one auditory ossicle. Very little research exists regarding the extent to which properties of the developmental system have contributed to the evolvability of the mammalian ear. The higher genetic and developmental complexity in mammals may on the other hand increase the risk of developmental instabilities, which can be assessed through the study of bilateral asymmetry. In contrast, the fewer genetic and developmental factors involved in avian ear development may limit its evolutionary potential, yet this simplicity may simultaneously reduce the risk of developmental disorders. This study focuses on the different patterns of fluctuating asymmetry, which refers to the random deviations from directional mean asymmetry. We compare intra-specific patterns of asymmetry across four species: two bird species (*Passer domesticus* and *Buteo buteo*) and two mammal species (*Homo sapiens* and *Sciurus vulgaris*), with sample sizes of around 30 individuals per species. For both mammals and birds, a large and a small species was chosen in order to test for the effect of size on asymmetry. Landmark-based geometric morphometrics is employed to quantify and analyze morphological shape differences of the inner ear across species as well as discern the different patterns of asymmetry. We test the expectation that mammals show greater fluctuating asymmetry in ear shape compared to birds, owing to the former's increased developmental complexity.

From past to present: Overcoming challenges in molecular genetic analyses of *Pomphorhynchus* species [Talk]

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Thorny-headed worms (Acanthocephala) are obligate parasites of fish, and other vertebrates. In Europe, the genus *Pomphorhynchus* Monticelli, 1905 is common, using gammarids as intermediate hosts and freshwater fish as definitive hosts. In Central Europe, three species are identified: *Pomphorhynchus laevis* (Zoega in Müller, 1776), *P. tereticollis* (Rudolphi, 1809), and *P. bosniacus* Kiskároly & Čanković, 1969. Due to morphological similarities between these species, individuals were mostly recorded as *P. laevis*, probably leading to inaccurate assumptions about species distribution and the displacement of native species by invasive ones.

In 2019, *P. bosniacus*, typically found in the Black Sea region, was discovered in the Danube near Vienna. This raises two key questions regarding these understudied species: (1) Has native *P. laevis* been displaced by invasive *P. bosniacus*, or (2) has *P. bosniacus* been misidentified in former times due to taxonomic confusion?

This project, conducted as part of the NOBIS Grant (awarded to S. Reier in 2022), combines historical and contemporary data to address these questions. The aim is to dissect historical fish specimens (circa 1900) stored in the Natural History Museum in Vienna to obtain preserved parasites. These parasites will then be analyzed and compared with recent *Pomphorhynchus* samples using next-generation sequencing (NGS) data to track changes in parasite fauna over time. However, there are significant methodological challenges in preparing NGS data from these organisms. One major issue is the small size of *Pomphorhynchus* larvae, which results in very limited quantities of DNA. Another issue is the degradation of DNA from historical samples, further limiting the yield of usable genetic material. Additionally, separating parasite DNA from host tissue poses further difficulties. Here, I report on the approaches to overcome these challenges, such as refining DNA extraction and amplification protocols to ensure sufficient high-quality genetic material for NGS.

Unravelling the evolution of the German Cockroach *Blattella germanica* using historical specimens [Talk]

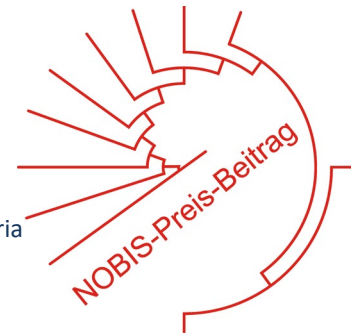
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While the processes behind the rapid adaptation of invasive species are often unclear, these species typically exhibit a relatively high rate of genome evolution. Genomic parasites, such as transposable elements (TEs), have been identified as potential drivers of this process, with recent findings indicating a significant contemporary proliferation of these TEs in commensal species, such as *Drosophilids*. To test if this high rate of evolution can also be observed for other commensal insects, we aim to investigate one of the most widespread invasive pest species, the German cockroach (*Blattella germanica*).

Despite the name, *B. germanica* originated in South Asia, more specifically it originated from the Asian Cockroach *Blattella asahinai* approximately 2,100 ya in the Indo-Burman region. A recent study highlighted a shift of phototaxis and locomotion between the two species. The ancestral species, *B. asahinai*, is attracted to light, while *B. germanica* is repelled by it and has also lost the ability to fly, despite having similar morphological features. Additionally, *B. germanica* exhibits a remarkably high level of insecticide resistance, which in other insects has been shown to be linked to TE insertions. By applying a minimally-invasive protocol, we extracted DNA from 150-year-old *B. germanica* specimens from the NHM Vienna. Comparing this museomic data with recently collected samples, we want to discover whether *B. germanica* has experienced recent TE invasions and if they have contributed to the observed high level of insecticide resistance. Finally, we aim to elucidate genomic changes that may have contributed to the shift in both phototaxis and locomotion.

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Lost but not forgotten: Rediscovery of the Ukrainian *Lepidurus middendorffii* (Braem, 1893) (Branchiopoda: Notostraca) through integrative taxonomy [Poster]

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The taxonomy of the notostracan *Lepidurus* Leach, 1819 is complicated by a large number of synonymised species and extensive intraspecific variability in many relevant characters. We demonstrate, based on an integrative taxonomic approach, that the Ukrainian populations of *Lepidurus* are not conspecific with any currently accepted *Lepidurus* species and assign them to the previously synonymised species *Lepidurus middendorffii* (Braem, 1893). This species exemplarily highlights the problems in the taxonomy of *Lepidurus*. The species was originally described as *Apus extensus* var. *middendorffii* (Braem, 1893), but *L. extensus* is a junior synonym of *Lepidurus lubbocki* (Brauer, 1873), which is currently treated as a subspecies of *Lepidurus apus* (Linnaeus, 1758). Our molecular genetic analyses based on mitochondrial genes COI, 12S, 16S, and the nuclear gene 28S, which included published data, suggest the presence of further, possibly cryptic species that await formal recognition and stress the importance for a more extensive revision of *Lepidurus*. The original type specimens of *L. middendorffii*, previously stored at the Museum of Natural History (Wrocław University, Wrocław, Poland), are lost and a neotype is designated. *Lepidurus middendorffii* is characterised by the dorsal organ position between the ocular tubercle margins, the sharp carapace sulcus spines, the long supra-anal plate with many median spines, a telson length to carapace length ratio 0.18–0.35, and differs by > 9% uncorrected COI p-distances from all other *Lepidurus* species.

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Non-invasive extraction of DNA from tiny arthropods: a step forward for systematics and biodiversity research on soil organisms [Poster]

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Soil arthropods play a vital role in ecosystem processes, yet their diversity remains under-documented due to limitations of current DNA extraction techniques, which typically require destructive methods. Here, we introduce a novel non-invasive method for extracting DNA from small arthropods, preserving the specimens for further morphological and taxonomic studies. By avoiding damage to these often delicate specimens, this approach allows for the repeated morphological analyses and long-term conservation of voucher specimens. We demonstrate the method's applicability across Pauropoda and small soft-bodied mites in yielding DNA of sufficient quality for standard PCR-based genetic analyses while maintaining specimen integrity. We provided the first DNA barcodes plus nuclear genetic data for a number of pauropod species, whose species identity was confirmed by morphological examination of the voucher specimens after DNA extraction. For mites, we mainly focused on members of the Brachychthoniidae, which, with a body length of 120-300 μm , belong to the smallest fraction of oribatid mites. The family includes about 175 described species worldwide, grouped into 12 genera. However, roughly a quarter of these species have been reported for Austria alone. As with pauropods, we sequenced some brachychthoniid species with morphological identification after DNA extraction, but more than half of the specimens could not be assigned to any known species despite perfect morphological preservation. With this new extraction method, it is now possible not only to generate genetic data and then morphologically determine the tiniest fraction of mites, but also to identify and describe the soft-bodied juvenile stages, which have not yet been known for many species. To conclude, this extraction method opens new possibilities for integrative taxonomy, systematic and general biodiversity assessment of minute soft-bodied soil arthropods.

This research is funded by the Biodiversity Fund of the Federal Ministry for Climate Protection, Environment, Energy, Mobility, Innovation and Technology.

The Common Wall Lizard (*Podarcis muralis*) in southeastern Austria – how threatened are autochthonous populations? [Poster]

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The common wall lizard (*Podarcis muralis*), widely distributed across Europe, comprises several recognized subspecies and, based on mitochondrial data, even more genetic lineages. In most areas of Austria, the endangered subspecies *Podarcis muralis muralis* is considered to be autochthonous. As in other regions of their distribution area, allochthonous individuals and populations pose a threat to native populations. Human activities, such as deliberate releases and accidental dispersal via material transport along railways, are major drivers for the spread of individuals to new regions. Furthermore, lower ecological requirements and greater body length grant Italian lineages, which pose the major threat to native populations, a competitive advantage over autochthonous populations. Although there are records of allochthonous individuals based on morphology in southern Austria (in this study limited to southern Burgenland, Carinthia and Styria), genetic data has been lacking. Initial results of cytochrome b sequencing suggest that most populations analysed thus far represent mixtures of the native lineage and a mitochondrial lineage that is attributed to the Veneto region. Additionally, individuals with a minimum genetic distance to a population from Slovakia suggest that at least two allochthonous lineages are present in south-eastern Austria.

This research is funded by the Biodiversity Fund of the Federal Ministry for Climate Protection, Environment, Energy, Mobility, Innovation and Technology.

Redescription of the tadpole shrimps *Triops sudanicus* and *Triops dispar* [Poster]

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In 1877, *Triops dispar* and *Triops sudanicus* were reared from eggs collected in Sudan and described. However, a comprehensive revision of the Notostraca later led to the synonymization of these, along with all African and Asian *Triops* (Crustacea) species, under *Triops granarius*. As a result, *Triops granarius* is recognized as having a remarkably wide geographical distribution and a high degree of morphological variability. Recent phylogenetic studies, however, have suggested the existence of distinct species within *Triops granarius*. Our examination of the morphological traits of the original type material of the previously synonymized species *Triops dispar* and *Triops sudanicus* reveals differences in the structure of the second thoracopod pair and the telson when compared to *Triops granarius* and other African *Triops* species. These findings shed new light on the taxonomic classification and evolutionary diversity within the Triopsidae, emphasizing the need for a revision within this fascinating family.

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Epigean Amphipods in Austria [Poster]

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Amphipods constitute important members of aquatic ecosystems and can locally dominate the communities of macrozoobenthic invertebrates in terms of biomass and numbers of individuals. Nonetheless, nominal species diversity of native amphipod species in the surface water bodies of Austria is low, including *Gammarus fossarum* and *G. roeselii* in streams and rivers and *G. lacustris* in alpine lakes. Not counting substantial cryptic diversity within *G. fossarum* (see contribution by Di Batista Borko et al.), the native species are outnumbered by a growing number of introduced and invasive species, many of them originating from the Ponto-Caspian region. In an ongoing project, funded by the Biodiversity Fund of the Federal Ministry for Climate Protection, Environment, Energy, Mobility, Innovation and Technology, we are currently recording species-level and genetic diversity of epigean amphipods in Austria. The poster will provide an account of amphipod species detected in the course of the sampling campaign, including their geographic distribution, notes on their intraspecific diversity and an assessment of their status as native or introduced taxa.

Deciphering host-related evolutionary patterns in polysphinctine spider parasitoids (Hymenoptera, Ichneumonidae) [Talk]

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A unique parasitoid strategy can be seen in polysphinctine parasitoid wasps—a group of Darwin wasps (Hymenoptera, Ichneumonidae) that exclusively utilises active sub(adult) spiders as hosts. The larvae of many of these wasps not only attach and feed on spiders during their development, but they also manipulate the web-building behaviour of the spiders for their own benefit. Several interesting host-related evolutionary patterns have been observed for the group, but our current understanding of them is seriously hampered by poorly resolved phylogenetic relationships in previous studies. We here reconstruct the first comprehensive phylogeny of the group using museum specimens and targeted capture of ultra-conserved genomic elements (UCEs) coupled with the next-generation sequencing. Based on more than 1,400 UCE loci and 146 species, including the representatives of 23 out of 25 known polysphinctine genera, we recover a group of parasitoids of spider egg-sacks (part of the outgroup) within the parasitoids of active spiders (polysphinctines). This result held up under different outgroup and loci subsampling schemes, as well as when only protein coding UCEs were analysed on nucleotide or amino acid level. Our results challenge a long-standing hypothesis about the single origin of the parasitoidism of active spiders in Darwin wasps and redefine generic limits across polysphinctines, paving a way to further phylogenetic and evolutionary studies on this group.

Cryptic diversity in snow scorpionflies (*Boreus* spp.) in relation to cuticular chemistry and geography [Talk]

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Snow scorpionflies (Family Boreidae) are flightless insects in the order Mecoptera. Two species of Boreidae have been recorded in Austria, *Boreus hyemalis* and *B. westwoodi*, but species delimitation based on DNA barcoding data suggested that species-level diversity is higher than what is captured by current taxonomy (Zangl et al. 2021). Restricted dispersal capacity and (seemingly) small population sizes might facilitate the evolution of genetic structure in these enigmatic insects. In this study, we extended the previous sampling effort in order to investigate the geographic pattern of mtDNA lineage diversity in southern and Eastern Austria. We also generated genomic (ddRAD) data for a subset of samples to test whether the previously proposed cryptic diversity in Austrian *Boreus* is also supported by nuclear data. In addition, GC-MS (gas chromatography – mass spectrometry) was used to examine the composition of cuticular chemical compounds. Body surface chemistry plays a role in the chemical communication of insects and may therefore exhibit lineage-specific divergence (Chung & Carrol 2015). Our data revealed congruent mitochondrial and nuclear genetic lineages. Chemical patterns of cuticular compounds were correlated with the genetic structure, but no lineage-diagnostic compounds were detected. The geographic distributions of some genetic lineages overlapped. Together, these data suggest that Austrian *Boreus* indeed comprise several cryptic species. The local genetic diversity and the phylogeographic signals within genetic lineages were variable – for instance, some mitochondrial haplotypes were shared between distant sampling locations and genetic diversity was high at some locations but not at others. Opposite to expectations based on life history and abundances, the genetic data suggest large effective population sizes and considerable degrees of population connectivity.

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CROBEach: Towards developing an ecological framework for sustainable gravel beach management along the Croatian coastline [Poster]

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Tourism is the predominant economic force in many Mediterranean countries, including Croatia. Consequently, coastal management strategies tend to focus on short-term solutions that are influenced by the seasonality of the tourism industry. This approach often results in unsustainable practices, particularly in highly populated or urban areas. For example, Croatia's unique gravel beaches are currently managed without consideration of the natural resources they support. Additionally, the lack of baseline knowledge about the biota residing on these beaches impedes the development of sustainable management strategies. To address this issue, we will investigate the biotic and abiotic relationships on both urban and non-impacted natural gravel beaches in Croatia. The project will have three main objectives. Firstly, by applying DNA metabarcoding and geological surveys, we aim to illuminate how the habitat and biodiversity change throughout the year due to both anthropogenic and seasonal factors. Secondly, we seek to understand trophodynamics on gravel beaches by analyzing the gut contents of the only vertebrate predators inhabiting these beaches, the blunt-snouted clingfishes. Finally, we aim to understand the recruitment and connectivity patterns of the blunt-snouted clingfishes in the urbanized area of Rijeka by assessing population variation through whole genome sequencing data. The results obtained in this project will be reported to decision-makers (such as municipalities and ministries) and NGOs in the Adriatic region to increase awareness of beaches as natural resources and foster their sustainable management. Ultimately, the goal of this project is to promote ecosystem-based beach management as part of sustainable, long-term solutions for coastal management in Croatia.

A window to the past? Metabarcoding analyses of pollen preserved on historical bee specimens [Poster]

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Plant diversity and species composition in grasslands significantly influence wild bee diversity. However, traditional botanical records often lack detailed historical data on plant abundances, complicating efforts to track changes in floral landscapes over time. DNA metabarcoding provides a powerful method for comparing the foraging plants of wild bees across historical and recent samples. One of the most significant collections of central European bees from the mid-20th century is the Bruno Pittioni Collection, preserved at the NHMUK. The study sites, Oberweiden and Stammersdorf, were selected due to the abundance of specimens from these locations in Pittioni's collection, with recent samples collected for comparison, along with specimens housed in the NHM Vienna. Pollen was extracted from the scopa (pollen-collecting structures) of wild bees, and DNA was amplified from the pollen using *rbcl* and *ITS2* markers through a metabarcoding approach.

Preliminary results showed successful DNA extraction from all recent samples, while most historical samples yielded poor results. Approximately 40% of the Stammersdorf historical samples contained some retrievable DNA, but very little DNA was recovered from the Oberweiden samples. The lack of DNA from Oberweiden is not entirely due to sample age and may be attributed to the use of cyanide during specimen preservation, which likely degraded the DNA. Differences in DNA preservation between the two sites may also be related to differences in specimen handling and storage, with Stammersdorf samples being processed more quickly due to Pittioni's proximity to the site.

Further analysis of the moderately successful historical specimens, along with continued examination of recent samples, will provide valuable insights into the foraging plants, patterns, and networks of wild bees. This research will enhance our understanding of wild bee ecology and the factors shaping their foraging behavior.

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