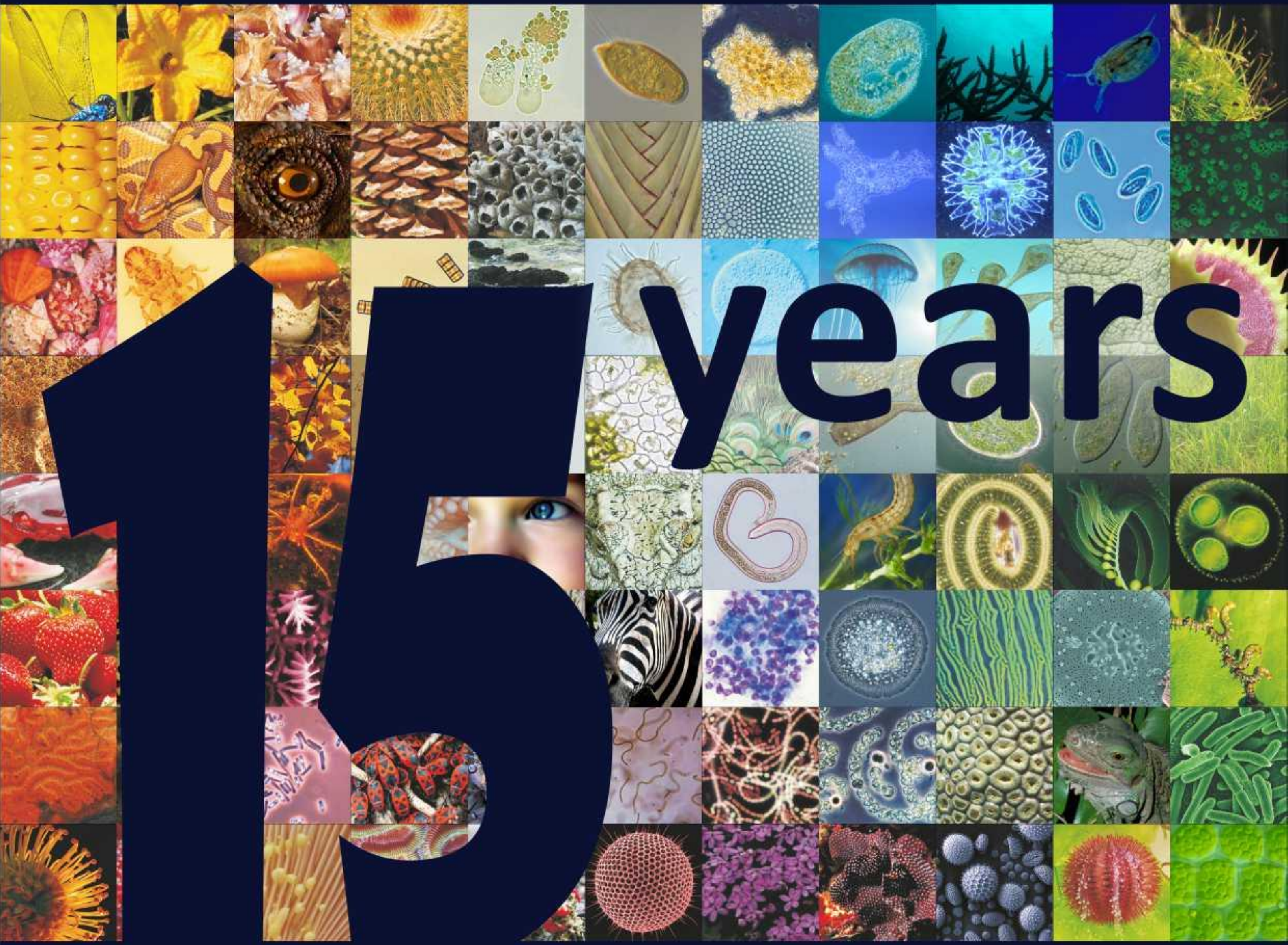
NOBIS Austria

NOBIS MEETING 2021

15 Years NOBIS Austria!



November 26th 2021

Online Meeting

NETWORK OF BIOLOGICAL SYSTEMATICS AUSTRIA

Online 2021 NOBIS AUSTRIA 15

15 Years NOBIS Austria!

15th Annual Meeting of NOBIS Austria

Friday, November 26, 2021

Online

Editors: Dominique Zimmermann, Nicole Grunstra & Andreas Kroh

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Dear fellow NOBISts,

as in 2020, the precautions related to the coronavirus pandemic prevent the 15th meeting of NOBIS Austria from physically taking place in Graz this year. In order to keep up the tradition of the popular annual meetings of NOBIS Austria, we have once again arranged an online meeting on the afternoon of Friday, November 26th, 2021. Based on the success of last year's meeting, which was attended by more than 60 participants, we have largely kept the same format. After an opening keynote on *Novel developments in the systematics of the colonial Bryozoa* delivered by Björn Berning (Biologiezentrum Linz, Geoscience Collections), there will a combination of oral presentations by junior colleagues who compete for the NOBIS awards for the best students' talks, and presentations by established researchers. A ceremony during which the winners of the NOBIS Awards will be announced will conclude the meeting.

To accommodate all presentations in the programme, individual contributions are restricted to 12-minute presentations plus 3 minutes for discussions. Breakout rooms will be provided during the lunch break and the coffee breaks, which can be used for further discussions with the presenters and general chat among the participants. The workshops planned to take place back-to-back with the NOBIS Meeting 2021 had to be cancelled due to the COVID-19 precautions and the current general lockdown. We hope to offer workshops again next year. Attendance of and participation in the NOBIS Meeting 2021 is free of charge. With almost 70 registered participants, we are confident that this years' meeting will be a successful event with an active audience, and we look forward to a positive and appreciative atmosphere for all presenters.

As in previous years, junior colleagues will compete for the **NOBIS Awards 2021** for excellent research in the field of biological systematics. Two awards of 500 € each and a three-year NOBIS membership will be conferred, one for a Master and one for a PhD student talk. We are grateful to our scientific jury which will select the winners during the meeting. The evaluation will be based on scientific significance as well as on the quality of the presentation.

We gratefully acknowledge financial support of the **NOBIS Awards 2021** by the Open Access journal *diversity* by the publisher MDPI. A special issue on “DNA Barcodes for Evolution and Biodiversity” edited by Stephan Koblmüller will appear in *diversity* in 2022. Submissions for the special issue is still open and participants of this year’s NOBIS Meeting are eligible for a 20% discount on the Article Processing Charges.

diversity
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We are looking forward to seeing you all again during the NOBIS Meeting 2021 and wish you interesting talks, fruitful discussions, and a great time. It has never been more important than now during the current global pandemic to stand united and support each other during these difficult times.

The Nobis Austria Executive Board

Programme

Friday, November 26th 2021

12:00–12:05 Welcome address by **Andreas Kroh**, President of NOBIS Austria

12:05–12:25 **Ulrike Aspöck & Andreas Kroh**: Looking back on 15 years of NOBIS Austria

Talks

Chair: Andreas Kroh

12:25–13:00 **Björn Berning**: Novel developments in the systematics of the colonial Bryozoa [Keynote]

13:00–13:15 **Philipp Resl** & Christoph Hahn: Fast and reproducible phylogenomic analyses with phylociraptor

13:15–13:45 Lunch break

Session 1

Chair: Sabine Agatha

13:45–14:00 **Constantin Kopper** et al.: Testing pollination syndromes in Melastomataceae [NOBIS Awards MSc]

14:00–14:15 **Zita Roithmair** & Nesrine Akkari: Morphology and diversity of sexually dimorphic characters of the ultimate legs in selected lithobiomorph centipedes (Myriapoda, Chilopoda, Lithobiomorpha) [NOBIS Awards MSc]

14:15–14:30 **Samuel Leeming** et al.: A new record of *Sphyranura euryceae* (Monogenea, Sphyranuridae) from the Oklahoma salamander and its position in a mitochondrial phylogeny of the monogeneans

14:30–14:45 **Christoph Hahn** et al.: Disentangling the evolution of obligate parasitism in flatworms

14:45–15:00 **Alexey Reshchikov**: The Tea Fauna: an initiative citizen science biodiversity project

15:00–15:15 Coffee break

Session 2

Chair: Dominique Zimmermann

15:15–15:30 **Susanne Reier** et al.: Underground connections and paleohydrology rather than human translocations are causing the genetic complexity of *Phoxinus lumaireul* (Leucisidae) in the Slovenian Dinaric Karst [NOBIS Awards PhD]

15:30–15:45 **Mildred Johnson** & Thomas Schwaha: The morphology of an endolithic ctenostome: *Immergentia* [NOBIS Awards PhD]

15:45–16:00 **Gernot Englmaier** et al.: A phylogenetic perspective on the sexual dimorphism of graylings (*Thymallus*, Salmonidae) [NOBIS Awards PhD]

16:00–16:15 **Julian Bibermair** & Thomas Schwaha: The ‘unplumatellid’ freshwater bryozoan *Plumatella fruticosa*? The morphological approach [NOBIS Awards PhD]

16:15–16:30 **Eva Strasser** et al.: Evolutionary significance of mitochondrial genomes in saxicolous *Pyrenodesmia* (Teloschistaceae) [NOBIS Awards PhD]

16:30–16:50 Coffee break

Session 3

Chair: Nicole Grunstra

16:50–17:05 **Ahmed Saadi** et al.: Phylogenomics reveals deep relationships and diversification within phylactolaemate bryozoans

17:05–17:20 **Maximilian Wagner** et al.: Parallel evolution and genomics of adaptations in interstitial clingfishes

17:20–17:35 **Silas Bossert**: The phylogeny of andrenid bees and their diversification in the Neogene

17:35–17:50 **Frank Zachos** & the Global Species List Working Group: Towards a global list of accepted species: A new initiative to deal with taxonomic conflict

17:50–18:00 **Announcement of Nobis Prize Winners & Final Words**

Abstracts

Novel developments in the systematics of the colonial Bryozoa [Keynote]

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Bryozoa is a phylum of exclusively aquatic and colonial animals with over 6500 known recent species (and many, many more undescribed ones) that occur at all latitudes and from intertidal to abyssal depths. In some environments, bryozoans are present in such abundance, and their calcified colonies reach such a great size, that they are habitat-forming and provide an important contribution to the carbonate factory. Bryozoans are also well-represented in the fossil record since the early Paleozoic, resulting in numerous landmark studies on large-scale patterns of evolution.

What has stayed largely obscure to date, however, is the higher-level systematics of Bryozoa, and not just of the extinct Paleozoic taxa but also of the recent ones. The reasons for this lie, on the one hand, in the repeated evolution of calcified taxa from stem lineages that remained uncalcified throughout the Phanerozoic, and which are therefore largely unnoticeable in the fossil record. On the other hand, the repeated origin of characters, and their subsequent convergent and parallel evolution, in the newly evolved calcified taxa render it extremely difficult to distinguish homology from homoplasy. The definition and coherence of, as well as the systematic relationships between, taxa above family level are therefore difficult to assess when solely based on morphology.

Until very recently, the few existing genetic analyses of bryozoans were limited to studies addressing interrelationships with other phyla or aimed at identifying single species, while phylogenetic analyses at intermediate taxonomic levels were almost entirely lacking. This has fortunately changed in the last few years, while currently two large international projects are underway that will drastically increase the number of sequenced taxa, significantly alter our view of bryozoan systematics, and raise our knowledge of bryozoan genetics and genomics to an entirely different level.

In this talk, I will summarise the latest developments in bryozoan phylogeny and evolution, starting in the early Cambrian and combining information from the fossil record with the morphology and genetics of recent taxa, especially referring to the contributions made by scientists and research groups in Austria.

The ‘unplumatellid’ freshwater bryozoan *Plumatella fruticosa*?
The morphological approach

NOBIS-Preis-Beitrag

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Bryozoans are colonial, suspension feeding lophotrochozoans. Within the phylum, two major groups are recognised: the vast majority of predominantly marine Myolaemata and the rather minute group of limnetic Phylactolaemata that includes only 70 species and is regarded as earliest branching clade and thus sister taxon to myolaemates. Single zooids consist of a retractive polypide surrounded by a protective cystid/body wall. In phylactolaemates, the latter forms either a gelatinous or chitinous cuticle. Gelatinous representatives mainly belong to the Lophopodidae, Cristatellidae and Pectinatellidae, which are nowadays considered earlier branching than the encrusting Fredericellidae and Plumatellideae. Plumatellids are by far the most speciose family of phylactolaemates, but detailed morphological analyses of its species are rare. *Plumatella fruticosa* is of particular interest as it shows a mosaic of plumatellid and fredericellid features and a closer relationship of to fredericellids rather than plumatellids has been confirmed by molecular data. Consequently, new morphological data of *P. fruticosa* and possibly closely related species is required to identity apomorphic characters that can be used for supporting new clades. Hence, this study uses a series of modern analysis methods of *P. fruticosa* such as confocal microscopy and section based serial reconstruction in order to contribute to this topic.

The phylogeny of andrenid bees and their diversification in the Neogene

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The mining bees (Andrenidae) are a major bee family of over 3,000 described species with a nearly global distribution. They are a significant component of northern temperate ecosystems and are critical pollinators in natural and agricultural settings. Despite their ecological and evolutionary significance, our knowledge on the evolutionary history of Andrenidae is sparse and insufficient to characterize their spatiotemporal origin and phylogenetic relationships. This limits our ability to understand the diversification dynamics that lead to the second most speciose genus of all bees, *Andrena*. Here I present a comprehensive genomic dataset of 195 species of Andrenidae, including all major lineages, to illuminate the evolutionary history of the family. Using fossil-informed divergence time estimates, I characterize macroevolutionary dynamics, incorporate paleoclimatic information, and embed my findings in the context of diversification rate estimates for all other bee tribes. I find that diversification rates of Andrenidae steeply increased over the past 15 million years, particularly in the genera *Andrena* and *Perdita*. My results suggest that these two groups and the brood parasites of the genus *Nomada* (Apidae), which are the primary parasitic counterparts of *Andrena*, are all similar in age and represent the fastest-diversifying lineages of all bees. Using my newly developed timeframe of andrenid evolution, I estimate a late Cretaceous origin in South America for the family and reconstruct the past dispersal patterns that led to their present-day distribution.

A phylogenetic perspective on the sexual dimorphism of graylings (*Thymallus*, Salmonidae)

NOBIS-Preis-Beitrag

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Graylings (*Thymallus*) are freshwater resident fish species inhabiting northern temperate to arctic regions throughout much of Eurasia and parts of western North America. Their taxonomic diversity and phylogenetic relationships have been under revision for some time and progressive use of genetic information (primarily the mtDNA control region) has contributed much to an improved understanding of species diversity and range distributions. Recent application of genomic approaches (complete mtDNA genomes and nuclear ddRAD-seq) has significantly advanced our understanding of grayling diversity and currently 15 species across the global distribution range of the genus have been recognized and supported. Diversity hot spots were found associated with allopatric differentiation around the Asian Altai-Sayan region (*T. baicalensis, T. nigrescens, T. brevirostris, T. brevicephalus, T. nikolskyi, T. svetovidovi*) and the European Alps (*T. aeliani, T. ligericus, T. thymallus*). Additionally, the presence of four sympatric species within the Amur drainage in Far Eastern Russia (*T. baicalolenensis*, *T. burejensis, T. grubii and T. tugarinae*) and ancestral trait reconstruction based on mitochondrial genomes supported the Amur catchment as the origin for the extant grayling diversity. The recovered phylogenetic relationships not only provide opportunities for in depth analyses on contact zones and biogeographic patterns, but have also opened up tremendous potential to analyse macroevolutionary trends such as patterns in sexual dimorphism. To this end, a comprehensive morphometric data set of >1,500 individuals across 11 of the 15 currently recognised species revealed general patterns of intersexual morphological variability particularly relating to size dimensions of the dorsal, anal, pelvic and pectoral fins. These patterns were compared via a literature review to sexual dimorphism across the family Salmonidae which allowed some inferences or hypotheses concerning the drivers of sexual dimorphism in salmonid fishes.

Disentangling the evolution of obligate parasitism in flatworms

Hahn, C.[1], Resl, P.[1], Kasny, M.[2], Kmentova, N.[2, 3], Hansen, H.[4], Zangl, L.[1, 5], Leeming, S.[1], Koblmüller, S.[1] & Vanhove, M.[2, 3]

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Neodermata (Platyhelminthes) is a highly diverse assemblage of obligate parasitic flatworms, many of biomedical, veterinary and economic importance, and constitutes one of the three largest groups of metazoan parasites of vertebrates. In other major parasitic groups, such as nematodes, vertebrate parasitism has evolved multiple times, while in Neodermata the transition has likely been a single evolutionary event. Neodermata currently comprises three groups: Monogenea (Monopisthocotylea and Polyopisthocotylea), Cestoda (tapeworms; Eucestoda and Cestodaria), and Trematoda (flukes; Aspidogastrea and Digenea). Cestoda and Trematoda are characterized by an endoparasitic lifestyle and complex life cycles, infecting a vast diversity of intermediate invertebrate- and final vertebrate hosts, including our own species. Monogenea on the other hand is characterized by a direct, primarily ectoparasitic lifestyle, mainly infecting (semi-)aquatic vertebrates, predominantly fishes. Despite decades of research, however, the interrelationships of Neodermata remain controversial. Given the distinct lifestyle characteristics (ecto- vs. endoparasitism; direct vs. complex life cycles), only through resolving the phylogenetic relationships, can we hope to understand the early stages of evolution of parasitism in the group. We present new insights into neodermatan interrelationships based on phylogenomic analyses utilizing whole genome and transcriptome data of over 80 flatworm species (52 Neodermata, 35 free-living 'Turbellaria'). The underlying project "Deep Evolutionary Genomics of Monogenea", funded by the FWF, represents a large international collaborative effort currently supported by a consortium of Monogenea experts from 15 countries and 17 research institutions.

The morphology of an endolithic ctenostome: *Immergentia*

NOBIS-Preis-Beitrag

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An endolithic lifestyle has evolved multiple times in the phylum Bryozoa and at least twice in recent ctenostomes. Recent species are assigned to four families namely, Immergentidae, Penetrantiidae, Spathiporidae and Terebriporidae. *Immergentia*, the only genus in the family Immergentidae, possesses two striking characteristics that set them apart from other boring ctenostomes. Firstly, autozooids of immergentiids do not have a gizzard. Secondly, immergentiids possess analogous stolonate structures called cystid appendages which differ from true stolons, i.e. kenozooidal polymorphs, in other stolonate forms. To date, 17 species are assigned to *Immergentia*, comprising 11 recent species. The majority of species descriptions were based on external characteristics such as zooid shape, aperture shape and colony growth patterns. The soft body morphology of representative species however is largely lacking, with a detailed histological examination of *I. californica* in 1947 being the only the exception. Therefore, the objective of this study is to gain further insights into various zooidal aspects of this family. To achieve this, we use a combined approach which includes traditional histological sectioning methods and resin casts, examination of zooids after decalcification of shells, as well as visualization with confocal laser scanning microscopy and imaging software. Preliminary results reveal the presence of a cardiac constrictor in the gut, a characteristic found in other non-boring ctenostome species with cystid appendages and anastomoses. We suggest that combined descriptions of colony structure, external characters of autozooids and soft-body morphology could be essential to adequately identify species.

References

Schwaha, T. 2021. Phylum Bryozoa. In T. Schwaha (Ed.), Handbook of Zoology. De Gruyter, Berlin/Boston. https://doi.org/10.1515/9783110586312

Silén, L. 1947. On the anatomy and biology of Penetrantiidae and Immergentiidae (Bryozoa). Arkiv För Zoologi, 40A(4), 1–48.

Testing pollination syndromes in Melastomataceae

NOBIS-Preis-Beitrag

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Pollination syndromes are defined as suites of floral traits, which have evolved repeatedly across angiosperms in adaptation to distinct functional pollinator groups. In Melastomataceae (ca. 5750 sp.), pollination syndromes have only been described in one tribe of ca. 300 species, the Merianieae. For Merianieae, three well differentiated pollination syndromes ("buzz-bee", "birds", "mixed-vertebrate"; e.g. hummingbirds, bats, rodents) were reported. Importantly, these syndromes were best characterized by highly system-specific traits.

In my thesis, I tested whether the three pollination syndromes put forward for Merianieae can also be found in three other Neotropical Melastomataceae tribes where pollinator shifts occurred (Melastomeae, Blakeeae, Miconieae), and whether the same traits are important in differentiating syndromes across these tribes. Further, I investigated whether the different pollination syndromes differ in morphological diversity (i.e. disparity). To answer these questions, I collected flowers and observed pollinators during a fieldtrip to Costa Rica and Colombia in February and March 2020 and compiled a trait matrix of 74 functional traits across 59 species of the four Neotropical tribes. I used statistical classification methods (Random Forest Analyses) to sort flowers into pollination syndromes, and multivariate statistics based on a dissimilarity matrix to test for differences among the pollination syndromes.

I detected two of the three pollination syndromes ("buzz-bee" and "mixed-vertebrate") found in Merianieae in the three other tribes, while the "passerine" pollination syndrome only occurs in the tribe Merianieae. I found that the highly system-specific floral traits identified as most important in delineating pollination syndromes in Merianieae appear useful also across Melastomataceae. Furthermore, I calculated the highest disparity for the "buzz-bee" syndrome, followed by the "mixed-vertebrate" syndrome. Finally, I found strong evidence for an extreme case of self-pollination in *Miconia reducens*, and possibly, a "selfing" syndrome needs to be included in future studies in Melastomataceae pollination syndromes. Additional fieldwork in the Old World Tropics, a wider taxon sampling as well as the potential consideration of additional (i.e. selfing, generalist) syndromes are planned for my PhD project.

A new record of *Sphyranura euryceae* (Monogenea, Sphyranuridae) from the Oklahoma salamander and its position in a mitochondrial phylogeny of the monogeneans

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Monogenea is a class of parasitic flatworms which typically parasitise fish. Polystomatidae is an exception, representing a large radiation infecting (semi)-aquatic tetrapods. Sphyranuridae with its single genus (*Sphyranura*) was traditionally considered a sister-group to Polystomatidae based on morphological features, namely the presence of a single pair of haptoral suckers, as opposed to the three pairs present in polystomatids. However, more recent molecular work supported its inclusion within the Polystomatidae at an early diverging, yet currently unresolved, position in the clade of polystomes that infect batrachian hosts. Records of this genus are relatively scarce with phylogenetic studies of this group only ever having included data from *Sphyranura oligorchis*. Based on detailed morphological examination and comparison with type material, *Sphyranua* worms infecting Oklahoma salamander (*Eurycea tynerensis*) at Greathouse Spring, Arkansas (USA), were identified as *S. euryceae*, a new record for the species. Diagnostic features, as compared to congeners, include the position, size and arrangement of testes, oral suckers, and posterior attachment hooks. Along with a detailed redescription we provide the first molecular data for *S. euryaceae* and discuss its placement in Polystomatidae based on an updated phylogeny of Monogenea using 18S, and 28S genes, as well as whole mitochondrial genomes. The latter were obtained with a newly developed computational pipeline (MitoComp; https://github.com/SamLMG/MitoComp), which automatically assembles mitochondrial genomes from short-read WGS data using five well established third-party, command-line based assembly tools then annotates the genomes and generates graphical maps to allow easy comparison of the performance of the five assemblers.

Underground connections and paleohydrology rather than human translocations are causing the genetic complexity of *Phoxinus lumaireul* (Leucisidae) in the Slovenian Dinaric Karst

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NOBIS-Preis-Beitrag

The Dinaric karst on the Balkan Peninsula is known as a hot spot of European biodiversity. Karst landscapes exhibit specific underground drainage systems and complex connections to the surface water. The most common method to study underground hydrological connections in karst are tracing tests, whereby tracers are substances carried by water. In this study a biologically orientated approach of water tracing was applied, namely the analysis of the genetic structure of fish populations inhabiting a hydrological network with underground connections. Thus, populations of the species *Phoxinus lumaireul* (Schinz, 1840) in the Slovenian Dinaric karst were densely sampled and analyzed for different genetic markers (*COI*, *cytb*, *RPS7*). Subsequently, the genetic structure was compared to the database of tracing tests and paleohydrology of the area in order to evaluate three different scenarios: the genetic structure (1) is a consequence of the ongoing geneflow through underground connections, (2) reflects a past hydrological network, or (3) is an outcome of human translocations. Although none of the three possible scenarios can be unambiguously confirmed as the main driver for shaping the current genetic composition, the population structure indicates a natural distribution influenced by a mixture of current and past gene flow rather, than human-mediated translocations.

The Tea Fauna: an initiative citizen science biodiversity project

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The Tea Fauna is an initiative project https://www.teafauna.com. It has brought together researchers, tea businesses and farmers. The tea plants *Camellia sinensis*, *C. sinensis* var. *assamica*, and *C. taliensis* are native in the Eastern Himalaya Region, from the Assam State in India to the Vietnamese and Chinese mountain ridges around the Southern Chinese Sea, and their use has a long history. Some local communities still practice wild tea picking when the tea production is based on forest use. But at the same time, the tea plantations broadly caused deforestation of vast areas in native tea ranges as well as globally in places with subtropical climate where the tea plant was introduced. I aimed to run long term monitoring of Darwin wasps (Hymenoptera, Ichneumonidae) diversity in both natural tea habitats and mass plantations. This survey will allow to reveal trends in Darwin wasps diversity in native forest and agrocoenosis. I want to test if tea plantations serve as a refuge for the insect fauna in disturbed habitats. I started from Northern Thailand with a Thai tea company, the Monsoon Tea, which introduced a Forest Friendly Tea concept. The tea grown and harvested with sustainable methods can protect the forest if its production is sourced either from completely wild tea plants, or are agroforestry-planted. Tea consumption then is a way of environmental activism. We set a sampling plot with Malaise traps serviced by local tea farmers on private land with an old grown Dipterocarp forest. These communities help us to sample and keep research plots. Later, sampling plots were established also in China at the Institute of Eastern Himalaya Biodiversity Research, Dali University. Here we do long term research at an experimental organic tea garden right at the university campus by the Cang Mountain foothills. Here, the Himalaya rise formed the Three Parallel Rivers region featured by a strongly vertical relief. We sample here with two Malaise traps in a tea garden and two traps outside, in a pine forest. Samples are collected weekly. Another sampling plot was established in collaboration with Wu Yi Star Company and Fuzhou University on Wuyi Mountain in Northern Fujian, the largest and most representative example of Southern Chinese subtropical forests.

Fast and reproducible phylogenomic analyses with phylociraptor

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In the genomic era phylogenetic hypotheses are being tested based on the combined information of hundreds to thousands of genes. Analyzing such large datasets present exciting opportunities but also a great number of challenges. In addition to their sheer size, handling genome-scale datasets reliably, reproducibly and fast can be difficult, and often imply access to complex software- and computational environments. Consequently, large-scale phylogenomic analyses are typically tailored to individual datasets and computational environments, and thus hard to reproduce.

Here we present phylociraptor, a pipeline facilitating streamlined phylogenomic analyses based on hundreds to thousands of genomes. Starting from genome assemblies (local files or downloaded automatically from NCBI), phylociraptor identifies genes, infers orthologs, performs and filters multiple sequence alignments and calculates phylogenomic trees.

Based on the workflow-management system Snakemake and version-controlled container images of state-of-the-art phylogenetic software, phylociraptor runs on Linux/Unix desktop machines, servers and high-performance computing (HPC) cluster environments. Phylociraptor is currently controlled through a simple yet customizable command line interface. Results from each processing stage (gene/ortholog identification, alignment and trimming, phylogenetic inference) are presented in html reports for quick evaluation. As a proof of concept, we apply phylociraptor to test data from fungi, arthropods and vertebrates, utilizing 2298, 633, and 1100 publicly available genomes, respectively. Phylociraptor is open-source software and freely available on GitHub: http://github.com/reslp/phylociraptor.

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Morphology and diversity of sexually dimorphic characters of the ultimate legs in selected lithobiomorph centipedes (Myriapoda, Chilopoda, Lithobiomorpha)

NOBIS-Preis-Beitrag

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Lithobiomorph centipedes present a pronounced sexual dimorphism reflected in remarkable modifications and structures on the ultimate legs of male specimens in some species. Most records of these male secondary sexual characters were of taxonomic importance, helping to identify and characterize species, however information on their diversity, detailed morphology and possible function(s) is scarce. In this study, nine species of the two lithobiid genera *Lithobius* Leach, 1814 and *Eupolybothrus* Verhoeff, 1907 were investigated, using light microscopy and scanning electron microscopy (SEM) to examine and document the detailed morphology of secondary sexual characters on male ultimate legs. Secondary sexual cuticular modifications were described in detail and found to be often associated with sensilla, interpreted here as chemo- and mechanoreceptors, and with clusters of pores, a hitherto undescribed pore-distribution. The sexually dimorphic cuticular structures of the species *L. nodulipes* Latzel, 1880 were additionally examined with micro-computed tomography (μ-CT) and histological semi-thin sections, which revealed that the clustered pores are probably related to the glandular system found inside the cuticular modifications. The presence of an extensive number of sensory and glandular structures associated with secondary sexual characters indicate their possible role during courtship and mating. The closely related species examined in this research show similarities in their secondary sexual structures, which are on the other hand species-specific.

Phylogenomics reveals deep relationships and diversification within phylactolaemate bryozoans

Saadi, A.J.[1], Bibermair, J.[1], Kocot, K.M.[2], Hirose, M.[3], Calcino, A.[1],
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Bryozoans are aquatic, mostly sessile colonial invertebrates that inhabit all kinds of aquatic ecosystems. Extant bryozoan species fall into one of three classes with Phylactolaemata being the only exclusively freshwater clade. The phylogenetic relationships within the class Phylactolaemata have long been controversial owing to the absence of obvious characteristics that reflect evolutionary relationships. Previous molecular evolutionary studies based on a single gene or a combination of few loci have failed to fully resolve the interfamilial relationships of phylactolaemates. Here, we present the first phylogenomic analysis of the Phylactolaemata using transcriptomic data combined with dense taxon sampling to better resolve the interrelationships and to estimate divergence time within this class. Our results fully resolve interrelationships among phylactolaemate families with strong support. Our results show a principal division between Stephanellidae and a clade comprising all other phylactolaemate groups followed by a subsequent division within this latter clade between Lophopodidae and the remaining phylactolaemate families. The Plumatellidae is a polyphyletic family with *Plumatella fruticosa* clearly falling outside Plumatellidae as previous investigations had suggested. Our preliminary results indicate that the most common ancestor of the Phylactolaemata appeared in the early Cambrian (534 Ma) and the oldest lineage of the phylactolaemate tree (Stephanellidae) appeared in the late Ordovician (443 Ma). The diversification of the largest phylactolaemate family (Plumatellidae) began at the early Permian (276 Ma) with most of the plumatellid lineages diverging in the late Cretaceous and in the Paleogene, highlighting post-extinction diversification.

Evolutionary significance of mitochondrial genomes in saxicolous *Pyrenodesmia* (Teloschistaceae)

NOBIS-Preis-Beitrag

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The lichen genus *Pyrenodesmia* stands out within the large and widespread family Teloschistaceae by its morphological diversity and the difficulty of its taxonomic treatment. We have identified signatures of extant hybridization in the genus, and hypothesize that the species behaves as an interbreeding species complex. In this survey we examined 23 mitochondrial genomes of *Pyrenodesmia* sensu stricto, with the aim to (1) evaluate if differences in gene content and structure allow mitochondrial compatibility in a hybridization scenario, (2) test for possible recombination and finally (3) discuss the usability of mitochondrial genes in low level phylogenetic surveys.

The mitochondrial genomes examined are widely conserved in terms of gene content and shared synteny, but contain certain variability in their tRNA content (25-28), integrated segments of DNA polymerase (dpo), homing endonuclease genes, as well as in genome size. On the whole, comparative genomics suggests that mitonuclear incompatibility does not play a major role in reproductive isolation within the genus. A widespread discordance in phylogenetic signal is shown in comparisons based on 16 mitochondrial genes and 6 nuclear loci, using both Maximum Likelihood and Bayesian Methods. We identified discordance in phylogenetic signal between nuclear and mitochondrial loci, and additionally, between mitochondrial loci. After discarding heteroplasmy, we interpret the results as signs of recombination within the mitochondrial genomes.

Parallel evolution and genomics of adaptations in interstitial clingfishes

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Hidden in deep layers of Mediterranean intertidal gravel beaches, clingfishes of the genus *Gouania* show remarkable adaptations to an interstitial lifestyle. An elongated wormlike body combined with morphological truncations and small eyes allow members of this genus to survive and thrive in otherwise hostile conditions. Our recent phylogenetic and taxonomic revision of the genus resulted in the description and redescription of five species. Remarkably, coexisting, “slender” and “stout” ecotypes independently evolved in the Adriatic Sea and the eastern Mediterranean basin. Building upon these initial findings, we aim to analyse this parallel evolution from different ecological, morphological (microCT scans) and genetic angles. The latter includes whole genome resequencing and comparative phylogenomics, and profits from a high-quality reference genome of one of the five species that we have recently produced with collaborators. Through whole-genome re-sequencing of several individuals of each of the five species we aim to illuminate the genomic basis for adaptations and infer loci under divergent selection (e.g., by running selection scans). These results may serve as a baseline for the understanding of the evolutionary success and the parallel evolution in *Gouania*.

Towards a global list of accepted species:
A new initiative to deal with taxonomic conflict

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Taxonomic decisions at and around the species level are often inherently fuzzy, and there is no such thing as one correct taxonomic list, and accordingly, taxonomists differ in their evaluations of the same raw data. As a consequence, some well-studied taxa have several global species lists that are used by different stakeholders such as CITES, the IUCN and others, which creates problems of inconsistency and incommensurability. I will present a new initiative by the recently founded *Global Species List Working Group* whose aim, in close collaboration with the Catalogue of Life, is a set of explicit governance rules by means of which the taxonomic community transparently decides on a single species list for all taxa on Earth (see Garnett et al. 2020). Importantly, there may not be any infringement on the freedom of scientific research and opinion. The species lists must come from within the different taxonomic communities, but to be approved as part of the single global list they must also meet certain criteria, e.g., as wide a representation as possible, transparency of collation principles and reports on how conflicts were solved. The initiative is still in its infancy, and ultimately its principles will have to be accepted and approved by the wider taxonomic community, but the first steps like workshops and foundational publications have been taken. I will give a brief overview on what has happened so far and how the *Global Species List Working Group* envisions the road to a single and truly global list of species for taxonomists and users of taxonomy.

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