NOBIS Austria NOBIS-MEETING 2022 SYSTEMATICS & CLIMATE CHANGE

November 25th–26th, 2022

University of Graz

Field of Excellence University of Graz

NETWORK OF BIOLOGICAL SYSTEMATICS AUSTRIA

SYSTEMATICS & CLIMATE CHANGE

16th Annual Meeting of NOBIS Austria

Friday, November 25, 2022 – Saturday, November 26, 2022

University of Graz

Editors: Nicole Grunstra & Andreas Kroh

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Dear fellow NOBISts!

We are very happy that we can meet in person again at the 16th annual meeting of NOBIS Austria! While the virtual meetings in 2020 and 2021 were regarded as successful by the participants, discussion between talks and during poster sessions suffers a lot from the virtual format that was chosen due to the precautions related to the coronavirus pandemic. This year we were finally able to accept the kind invitation of the University of Graz, which also hosted the 4th NOBIS-Austria-Meeting, back in 2010. The Nobis Austria Executive Board thanks Stephan Koblmüller and Kristina Sefc, as well as their team, for the local organization of the meeting. Likewise, we are indebted to Matthias Affenzeller and Flavia Nardi from the University of Salzburg, who organized a hands-on bioinformatics workshop on the topic "Phylogeny & diversification rates", which is held back-to-back with the NOBIS-Austria-Meeting on Friday afternoon, before the icebreaker.

As in previous years, junior colleagues will compete for the **NOBIS Awards 2022** for excellent research in the field of biological systematics. Two awards of \in 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 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 years' annual meeting is dedicated to the topic "Climate Change", which is one of the five "Fields of Excellence" of the University of Graz. The keynotes by Jan Christian Habel and Wolfgang Schöner will explore the effects of climate change on arthropod diversity and whether the Alps are particularly sensitive to climate change. A brief presentation by the awardee of the NOBIS grant 2022, Susanne Reier, of her proposed project and the announcement of the winners of the NOBIS Awards 2022 will conclude the meeting.

We are looking forward to seeing you all again in person in Graz during the NOBIS-Austria-Meeting 2022 and we wish you interesting talks, fruitful discussions, and a great time.

The Nobis Austria Executive Board

Programme

Friday, November 25th 2022

- 13:00–17:00 Workshop "Phylogeny & diversification rates" held by Matthias Affenzeller & Flavia
 Nardi (for pre-registered attendees only, Institute of Biology, Seminar room 0002-01 0006, Universitätsplatz 2, 8010 Graz)
- 17:30–21:00 Icebreaker in the glasshouse of the Botanical Garden (Botanical Garden, "Gewächshaus", Schubertstraße 59, 8010 Graz)

Saturday, November 26th 2022

(Institute of Biology, Hörsaal, Universitätsplatz 2, 8010 Graz)

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

Talks – Session 1

Chair: Stephan Koblmüller & Kristina Sefc

- 9:10–9:50 Jan Christian Habel: Climate change effects on arthropod diversity (Keynote 1)
- 9:50–10:15 **Wolfgang Schöner**: Are the Alps more sensitive to climate change? (Keynote 2)
- 10:15–10:30 **Dominique Zimmermann**: Changes in the wild bee communities over 100 years in relation to land-use: A case study in a protected steppe habitat in Eastern Austria

10:30–11:00 Coffee break

Talks – Session 2

Chair: Andreas Kroh

- 11:00–11:15 Kristina Sefc: A diversity hotspot of stream amphipods in the Eastern Alps
- 11:15–11:30 Anna Götz: Taxonomy and diversity of crustose lichens in Sary Chelek, Kyrgyzstan
- 11:30–11:45 **Raphael Schmid**: Mitochondrial diversity and a bar-HRM assay for rapid species identification of *Romanogobio* (Actinopterygii, Cypriniformes, Gobionidae) species from the Danube drainage
- 11:45–12:00 **Martina Topić**: Gudgeons of the genus *Gobio* in Austria and Croatia, and their monogenean parasites: mystery of their diversity
- 12:00–12:15 **Johannes Schlagbauer**: Phylogenomic insights into adaptive radiations of *Gyrodactylus* (Monogenea, Platyhelminthes) ectoparasites on European freshwater fishes
- 12:15–13:30 Lunch Break (Food & drinks will be provided)

Talks – Session 3

Chair: Dominique Zimmermann

- 13:30–13:45 Maximilian Wagner: Parallel genomic signals in an interstitial clingfish radiation
- 13:45–14:00 **Susanne Reier**: Near vs. wide: Comparative phylogeography of four fish species in the Dinaric Karst
- 14:00–14:15 **Anne Le Maître**: The bony labyrinth: a good tool for systematics? A case study in cercopithecine monkeys
- 14:15–14:30 **Nicole Grunstra**: Climate, not biogeography, explains divergence in skull morphology of the long-tailed macaque on the Sunda Shelf
- 14:30–14:45 Klaus Schliep: Phangorn 3.0: New trees in the forest
- 14:45–15:30 Coffee break & Poster session

Talks – Session 4

Chair: Nicole Grunstra

- 15:30–15:45 **Harald Letsch**: Diversification in flea beetles (Coleoptera: Chrysomelidae: Alticini) in the context of their host use, with a special focus on crucifers (Brassicaceae)
- 15:45–16:00 **Tetiana Pachschwöll**: Mismatching ecology should be pursued: cryptic diversity in *Saussurea discolor* s.l. (Asteraceae)
- 16:00–16:15 **Thomas Strohmeier**: Cryptic diversity in snow scorpionflies (*Boreus* spp.) in relation to cuticular chemistry and geography
- 16:15–16:30 **Cyprian Katongo**: Towards establishing a DNA barcoding database for Zambia
- 16:30–16:45 **Frank Zachos**: A single list of the world's species background information and results of a recent large-scale survey

Final Session

Chair: Elisabeth Haring

- 16:45–16:50 NOBIS Stipendium presentation of the proposed project
- 16:50–17:00 Announcement of Nobis Prize Winners & Final Words

Abstracts

Climate change effects on arthropod diversity [Keynote 1]

Habel, J.C.¹

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Climatic changes influence the distribution and interactions of species, ecosystems and functions. Biodiversity of the Western Palaearctic have been strongly shaped by climatic shifts. Climatic fluctuations of the Pleistocene have led to significant shifts in distribution areas of species. The geographical isolation of populations during the glacial periods into Mediterranean refugia (southern Europe, North Africa) led to a strong differentiation of numerous species, and in some cases resulted in micro-allopatry within refugia (such as around the Atlas Mountains of North Africa). The subsequent postglacial warming favoured the expansion of warm-loving species, and simultaneously cold-loving species largely vanished or occurred in small and isolated relict population remnants across Central Europe. Current anthropogenically induced climate change is causing rapid shifts in distributions (altitudinal and latitudinal shifts) and is putting especially mountain species such as the numerous alpine endemics under severe environmental stress. In my talk I will highlight the effects of climate changes, starting with the Pleistocene cycles, the postglacial warming, to the current anthropogenic climate warming, based on examples of various arthropod groups.

References

Husemann, M., Schmitt, T., Zachos, F.E., Ulrich, W. & Habel, J.C. 2014. Palaearctic biogeography revisited: evidence for the existence of a North African refugium for Western Palaearctic biota. *J. Biogeogr.*, 41, 81–94.

Habel, J.C., Rödder, D., Schmitt, T., Nève, G. 2011. Global warming will affect the genetic diversity and uniqueness of *Lycaena helle* populations. *Glob. Chang. Biol.*, 17, 194–205.

Habel, J.C., Teucher, M., Gros, P., Schmitt, T. & Ulrich, W. 2021. Land use and climate change affects butterfly diversity across northern Austria. *Landsc. Ecol.*, 36, 1741–1754.

Are the Alps more sensitive to climate change? [Keynote 2]

Schöner, W.¹

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The study of climate change and its consequences is a core task in research and must also include an understanding of regional differences. Some regions of the earth are characterised by particularly pronounced climate change, which is significantly greater than the global average. The Arctic is such a hot topic in this respect with highly relevant consequences for nature and humans. Mountain regions are also repeatedly described as such a particularly sensitive region (e. g., Pepin et al. 2015). In general, temperature is referred to in order to characterise climate change. The presentation tries to contrast the results from the analysis of climate data with the process understanding of climate change in mountain regions. It is shown that the greater sensitivity of mountain regions to global changes can be clearly demonstrated, but that a comparison of e. g., the Alps with the corresponding forelands does not show this effect or shows it only seasonally. Possible atmospheric processes are described to understand the observations. Finally, a comparison on a global scale (Pepin et al. 2022) is shown in order to generalise the statements for mountain regions.

References

Pepin, N.C., Arnone, E., Gobiet, A., Haslinger, K., Kotlarski, S., Notarnicola, C., Palazzi, E., Seibert, P., Serafin, S., Schöner, W., Terzago, S., Thornton, J.M., Vuille, M. & Adler, C. 2022. Climate changes and their elevational patterns in the mountains of the world. *Reviews of Geophysics*, 60(1), e2020RG000730. <u>https://doi.org/10.1029/2020RG000730</u>
Pepin N., Bradley R.S., Diaz H.F., Baraer M., Caceres E.B., Forsythe N., Fowler H., Greenwood G., Hashmi M.Z., Liu X.D., Miller, J., Ning, L., Ohmura, A., Palazzi, E., Rangwala, I., Schöner, W., Severskiy, I., Shahgedanova, M., Wang, M.B., Williamson, S.N. & Yang, D.Q. 2015. Elevation-Dependent Warming in Mountain Regions of the World. *Nature Climate Change*, 5, 424–430. <u>https://doi.org/10.1038/nclimate2563</u>

Taxonomy and diversity of crustose lichens in Sary Chelek, Kyrgyzstan [Talk]

Götz, A.¹, Paukov, A.², Knudsen, K.³, Søchting, U.⁴, Türk, R.¹ & Ruprecht, U.¹

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Kyrgyzstan is characterized by a diverse landscape structure which results in a rich biodiversity. Lichenologically, most of the areas are vastly under-researched and especially knowledge about crustose lichens is rare. For this study the diversity of saxicolous crustose lichens was analyzed in the Sary Chelek Nature Reserve, Kyrgyzstan. This area is mainly influenced by two high mountain ranges in the north and east and due to this sheltered topography is known for its high biodiversity. Tectonic activity with accompanying landslides has shaped the prevailing landscape and ecosystems and therefore, the investigated habitats differ in their formation history, which results in a high number of lichen species. To investigate the influence of geomorphological processes on species composition, lichen samples were taken from different depositional zones. Taxonomic classification was carried out with morphological, chemical and molecular methods. Additionally, newly generated sequences of species that previously had only been described morphologically were included. Altogether 143 species were investigated and most of them could be assigned to the genera Aspicilia, Lobothallia, Caloplaca and Xanthocarpia. Several species were re-evaluated based on existing literature and/or newly described. Species composition varies a lot among different depositional zones (no deposits, toma-hills, debris cones). Especially toma-hills formed by landslides include a high diversity of saxicolous lichens. Those geomorphological processes which intensively shape the landscape and environment in Sary Chelek, are also reflected in the diversity and composition of the local lichen community.

Climate, not biogeography, explains divergence in skull morphology of the long-tailed macaque on the Sunda Shelf [Talk]

Grunstra, N.D.S.^{1, 2}, Louys, J.³ & Elton, S.⁴

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- ³ Griffith University, Australian Research Centre for Human Evolution, Environmental Futures Research Institute, Brisbane, Australia

⁴ University of Durham, Anthropology Department, Durham, UK

Sundaland, comprising the low-lying Sunda Shelf, the major islands of Borneo, Sumatra, and Java, as well as many smaller surrounding islands, formed a contiguous landmass through much of the Pliocene and Pleistocene. Subsequent late-Pleistocene rising sea levels have often been invoked as major zoogeographic barriers to gene flow and associated phenotypic and taxonomic divergence of Sundaic mammals. However, previous examinations of mammalian biogeography have painted a complex picture, suggesting that mammalian diversification in the region cannot easily be explained by a single overarching biogeographical phenomenon. Instead, it may be that the significant climatic changes and their concomitant impacts on local environments were the more significant control. In this context, we studied adult skull morphology of a widely distributed primate in insular and continental Southeast Asia, the long-tailed macaque (Macaca fascicularis), using 3D geometric morphometrics. We analyzed the associations between morphological divergence and island biogeography, subspecific taxonomy, and phylogeny. We also investigated associations with climate of the present and last interglacials and the last glacial maximum (LGM). There was very poor morphological divergence and discrimination among specimens from different biogeographical zones. There was also large overlap between M. fascicularis subspecies in skull size and shape, although sundaic M. f. fascicularis and M. f. philippinensis, restricted to the Philippines, were successfully discriminated on size and shape. There was moderate morphological differentiation associated with the deepest split in mitochondrial DNA lineages in skull size and shape. Contrary to biogeography, we detected strong associations between skull morphology and climate. Skull form (size and shape combined) was better explained by climate closer to present conditions and correlated most strongly with the current interglacial. In conclusion, we found no compelling evidence that cranial and mandibular variation in *M. fascicularis* consistently tracks insularity caused by Quaternary sea level change. Instead, the morphological overlap evident in our sample indicates connections between subspecies and is consistent with the history of Sundaland as a single landmass for large portions of the Quaternary.

Towards establishing a DNA barcoding database for Zambia [Talk]

Katongo, C.¹, Seemani, B.², Nkunika, P.¹, Likulunga, E.¹, Phiri, M.¹, Mbindo, K.³, Muyaba, N.⁴, Szucsich, N.⁵, Sonnleitner, M.⁵, Hahn, C.⁶, Zangl, L.^{6, 7} & Koblmüller, S.⁶

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The world is currently facing an unprecedented loss of biodiversity. Many animal and plant species are threatened with extinction, and the average abundance of many species has been declining rapidly over the last few decades. While these data and projections are highly alarming, one needs to keep in mind that there are many regions, especially in the "lower and medium income countries" that are notoriously understudied, especially with regards to less charismatic taxa. This is particularly true for Zambia, for which data on general distribution and genetic characterization of many animal, plant and fungal species are scarce. Yet, many of these species have the potential to support and secure human livelihoods in the country, directly as food source, source of medical agents and raw material for clothing and building material, or indirectly via ecosystem services like clean water and air or climate regulation. For documenting, maintaining and monitoring changes in biodiversity and its numerous functions it is necessary to be able to identify the contributing entities. For many taxa, reliable species identification is only possible by taxonomic experts, whose numbers have been drastically declining over the last few years. Thus, there is a clear need for i) data on species identity and occurrence, ii) generating taxonomic expertise, and iii) efficient means to identify and characterize biodiversity even in the absence of taxonomic expertise. DNA barcoding has great potential to fulfil these needs and move biodiversity research and data generation forward in Zambia. Here, we provide a brief overview about ongoing activities that should act as starting point for establishing a national DNA barcoding initiative/database for Zambia, and briefly also discuss the potential challenges associated with such an ambitious endeavour.

DNA barcoding of the intertidal clingfish genus Gouania [poster]

Klar, N.¹, Koblmüller, S.¹ & Wagner, M.^{1, 2}

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The clingfish (Gobiesocidae) genus *Gouania* Nardo, 1833 is endemic to the Mediterranean Sea and inhabits, unlike any other vertebrate species in Europe, the interstitial of intertidal gravel beaches. Various adaptations in morphology and potentially also physiology allowed *Gouania* to colonize this harsh environment. Recent studies demonstrated that *Gouania*, long considered to be monotypic, comprises a radiation of at least five distinct species (Wagner *et al.* 2019, 2021). Based on sequences of the DNA barcoding region (5'-part of the mitochondrial COI gene) from ~650 samples, covering large parts of the Mediterranean Sea, we inferred levels of inter- and intra-specific diversity in these fishes. Depending on the specific method used, molecular species delimitation suggested a different number of molecular operational taxonomic units (MOTUs), but the consensus confirms the previously described five species. Inconsistencies in species delimitation were mainly observed in nominal taxa from the eastern Mediterranean basin. Contrary to *Gouania* from the western Mediterranean basin and the Adriatic Sea, the species from the eastern Mediterranean basin exhibit fairly high levels of mitochondrial marker gene diversity, with some of the distinct clades within the species identified as distinct MOTUs by the tree-based molecular species delimitation methods. Some of the tree-based methods are known to have a tendency for over-splitting and our study once more shows that it is prudent to not only rely on a single method of molecular species delimitation for assessing species diversity in taxonomically difficult taxa.

References

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Wagner, M., Kovačić, M. & Koblmüller, S. 2021. Unravelling the taxonomy of an interstitial fish radiation: Three new species of *Gouania* (Teleostei: Gobiesocidae) from the Mediterranean Sea and redescriptions of *G. willdenowi* and *G. pigra. J. Fish Biol.*, 98, 64–88. <u>https://doi.org/10.1111/jfb.14558</u>

New insights into the diversity of Austrian ground beetles from high throughput DNA barcoding [Poster]

Koblmüller, S.¹, Paill, W.², Gunczy, J.², Klar, N.¹, Grimm, J.¹, Zangl, L.^{1, 2}, Sturmbauer, C.¹, Hahn, C.¹ & Resl, P.¹

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With 660 reported species, ground beetles (Coleoptera, Carabidae) are a fairly species rich insect family in Austria. Many species are habitat specialists and threatened by habitat loss, and thus listed in the national red list. To inventory/characterize the Austrian ground beetle diversity, we collected about 75 % of the Austrian ground beetle species diversity and employed Nanopore sequencing (ONT's MinION and Flongle systems) to barcode close to 3000 samples in a high throughput manner. For the majority of samples high quality barcodes could be generated. We found that currently available bioinformatic pipelines allow for the generation of high-quality barcodes (as verified by comparing barcoding data from a subset of sample generated by both Nanopore sequencing and traditional Sanger sequencing), despite the high inherent error rate of Nanopore sequencing. Thus, Nanopore sequencing is clearly an efficient means for generating high quality DNA barcodes from a large number of samples. The newly generated barcoding data revealed some interesting and in part unexpected insights into the Austrian ground beetle diversity. We found glacial relicts (Paill *et al.* 2021), some species with high intraspecific diversity (i.e. distinct clusters related to geography and/or ecology), potential cryptic species, new records for Austria, and some species that cannot be distinguished based on their DNA barcodes despite clear morphological differences. These DNA barcodes provide a robust reference system for reliable species identification of the majority of the Austrian ground beetle species.

References

Paill, W., Koblmüller, S., Frieß, T., Gereben-Krenn, B.-A., Mairhuber, C., Raupach, M.J. & Zangl, L. 2021. Relicts from glacial times: the ground beetle *Pterostichus adstrictus* Eschscholtz, 1823 (Coleoptera: Carabidae) in the Austrian Alps. *Insects*, 12, 84.

Molecular phylogeny and taxonomic revision of the cichlid genus *Hemichromis* (Teleostei, Cichliformes, Cichlidae) [Poster]

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The tribe Hemichromini is an early diverging, mainly Central and West African lineage within the species rich African cichlid fishes (Cichliformes, Cichlidae). It includes two genera, Hemichromis Peters, 1858 and the monotpypic Anomalochromis Greenwood, 1985. Though many of the species are popular aquarium fish, the number of hemichromine species is still unclear and their phylogenetic relationships are largely unknown. Based on DNA sequence data of two mitochondrial and two nuclear genes we present the first comprehensive phylogeny of the Hemichromini. Using an integrative approach based on these DNA sequences data, morphometrics, meristics and a qualitative assessment of body coloration, we revise the genus Hemichromis and discuss intrageneric relationships. Two major groups within the genus Hemichromis that diverged roughly 6–12 MYA are recognized, of which the first one represents *Hemichromis* sensu stricto, for the second one a new genus is proposed. Diversification within these two main groups started about 3-6 MYA, with different trajectories of colonization in the two groups. In some lineages, diversification happened only fairly recently, possibly related to colonization of new habitat in the wake of climatically and/or geologically induced episodic connections between distinct hydrological systems. Hemichromis populations from the most southern (Cuanza, Zambezi and Okavango) part of the genus' distribution range constitute a well-supported clade distinct from all other members of Hemichromis, for which the taxon H. angolensis Steindachner, 1865 is confirmed (Lamboj & Koblmüller 2022).

References

Lamboj, A. & Koblmüller, S. 2022. Molecular phylogeny and taxonomic revision of the cichlid genus *Hemichromis* (Teleostei, Cichliformes, Cichlidae), with description of a new genus and revalidation of *H. angolensis*. *Hydrobiologia* <u>https://doi.org/10.1007/s10750-022-05060-y</u>

The bony labyrinth: a good tool for systematics? A case study in cercopithecine monkeys [Talk]

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Reconstructing the systematics of past species is challenging, because of a fragmented fossil record and unavailable molecular data. Palaeontologists use anatomical characters to reconstruct the taxonomy of fossil taxa; however, these traits tend to reflect adaptations rather than phylogenetic relationships. On top of that, body mass diversity imposes different functional constraints, leading to huge morphological variation even for closely related species. In this study, we investigate whether the morphology of the bony labyrinth (the bony moulding of the inner ear) can be used to reconstruct phylogenetic relationships among cercopithecine monkeys. Based on microCT-scans of the skull, we virtually reconstruct the bony labyrinth of a taxonomically diverse sample of extant cercopithecines (n = 80). Using a geometric morphometric approach, we explore allometry, morphological variation and phylogenetic signal in the bony labyrinth. We demonstrate that, despite a statistically significant association between labyrinth morphology and body mass, the proportion of labyrinth shape variation due to allometry is only minor. Cercopithecine clades at higher taxonomical levels (tribe, subtribe) can be separated based on labyrinth morphology; however, the fine phylogenetic pattern cannot be reconstructed, probably because of an adaptive signal. We applied these results to the cranium LGPUT DFN3-150 from the lower Pleistocene (2.3 Ma) site Dafnero-3 in North-western Greece, attributed to the fossil monkey taxon Paradolichopithecus aff. arvernensis. Contrary to the traditional hypothesis of a grouping with Macacina (macaques), the morphology of the bony labyrinth supports closer affinities with Papionina (baboons and relatives). This finding sheds a new perspective on the evolution of a key member of mammalian faunas in Eurasia, during a period of cooler climatic conditions at the Plio-Pleistocene transition.

Diversification in flea beetles (Coleoptera: Chrysomelidae: Alticini) in the context of their host use, with a special focus on crucifers (Brassicaceae) [Talk]

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Within leaf beetles (Chrysomelidae), the flea beetle tribe (Alticini) forms by far the largest group. It comprises about 8500 species in about 500 genera and is nowadays distributed on every continent except Antarctica, being most diverse in Central and South America. Given these enormous species number, flea beetles are associated with probably up to 100 different plant families. Conspicuously, a quarter of flea beetle diversity is displayed by only ten species-rich genera, whereas about 380 genera comprise less than ten species. This indicates differential modes of host plant adaptations and subsequent diversification in this tribe. Two species-rich alticine genera are associated with plants of the order Brassicales as host plants. *Phyllotreta* comprises about 300 species, which almost exclusively feed on Brassicales. In contrast, only about 50 of the about 240 species of *Psylliodes* are specialized on Brassicales, whereas the remaining species are associated with at least 20 different host plant families including species specialized on Solanaceae, Poaceae or Fagaceae, as well as polyphagous species. We investigated the history of crucifer feeding among flea beetles and its potential impact on the diversification of *Phyllotreta* and *Psylliodes*. 1) Do the diversification rates of the crucifer-feeding genera differ from those feeding on other host plant families? Here, increased diversification rates would indicate that crucifer-feeding would have provided new ecological opportunities for both groups. 2) Do diversification rates in other groups or genera differ from the mean diversification rates in Alticini?

To test for differential diversification patterns among alticine groups in the context of their host plant associations, we constructed the phylogenetic relationships of 628 alticine species and applied several frameworks of clade-specific diversification rate analyses. We found that diversification significantly differs between alticine groups. However, this pattern is only partly associated with crucifer host use.

Association of moss mites with the lichen Cladonia norvegica

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It is known that several species of moss mites are living associated with lichens. The association ranges from a simple use of the lichen as a food source to the use of the lichen as a habitat and protection of juvenile stages against external influences, such as predators. *Cladonia norvegica* is characterized by unique red spots induced by rhodocladonic acid, which are even used as a diagnostic character. However, the lichen seems to produce these red spots only in places where mites feed on the lichen or in places where the juveniles are supposed to feed and develop within buried cavities (Edmund *et al.* 1984; Schindler 1991).

We discovered three different species of moss mites, i.e. *Carabodes areolatus, Carabodes labyrinthicus* and *Hermannia gibba*, feeding on *Cladonia norvegica*. We could observe juvenile stages of a *Carabodes* species being endophagous within the lichen. The nymphs were enclosed in red-colored podecia or primary squamules, where they buried holes by feeding on the lichen.

We reared one of the nymphs until the adult stage, and then we could determine it as a *Carabodes areolatus* specimen.

Until now, we only found female mites foraging on the lichen. If males are absent from the lichen will be clarified in further investigations.

The reason for the red stains produced by the lichen seems to be associated with the presence of the mites, but details of this correlation are yet unclear. In this masters' thesis, the following points should be clarified:

1) Which mite species are specifically associated with Cladonia norvegica?

2) What is the nature of the mite-lichen association? What do the mites exactly feed on? Do they harm the lichen?

3) Are there only female mites associated with the lichen and if yes why?

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Edmund, L. & Mark, R. 1984. The association of oribatid mites with lichens. *Zoological Journal of the Linnean Society*, 80, 369–420.

Rampant hybridization of Saussurea alpina and

S. discolor (Asteraceae) in the Eastern Alps

Pachschwöll, C.¹, Pachschwöll, T.¹, Larsson, D.J.¹, Temsch, E.M.¹, Weiss-Schneeweiss, H.¹ & Schneeweiss, G.M.¹

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Tetraploid Saussurea alpina (2n = 4x = 52) and diploid S. discolor (2n = 2x = 26) are two ecologically vicariant plant species in the European Alps found on siliceous bedrock versus mostly on limestone, respectively. There are only few and rather cursory reports about hybridization (based solely on morphology) of these two alpine species exclusively in older literature, but no such hybrids are mentioned in current floras covering this area. In the course of recent molecular-taxonomic work on S. alpina and S. discolor (Pachschwöll et al. 2021), herbarium vouchers of putative hybrids from the Eastern Alps were discovered in several herbaria. To test their potential hybrid status, material from 5 putative hybrid populations from the eastern Central Alps (Niedere Tauern, Gurktaler, Seetaler Alpen and Eisenerzer Alpen) in Austria was collected in the field. For genetic comparison, 8 populations of S. alpina (Scandinavia, Alps) and 11 populations of S. discolor (Eastern Alps, Western Carpathians, Northern Dinarides) were included as well. The molecular data (RADseq data, nuclear ITS sequences) were complemented with absolute genome sizes calibrated by chromosome counts. We could show that hybrid swarms exist in the entire eastern Alps not only in areas where both species occur, but such hybrid forms also occur as orphans or half-orphans. Hybrid populations prefer intermediate bedrock like basic schists and are characterized by grey tomentose lower leaf surfaces (vs. grey-arachnoid-villous in S. alpina and densely whitishtomentose in S. discolor), although the morphological variation between hybrids and parents is continuous. All analysed hybrids were tetraploid and the S. alpina genepool was prevailing. This suggests gene flow from the diploid S. discolor into the tetraploid S. alpina likely via unreduced gametes of S. discolor. We could show rampant hybridization and introgression between these two high mountain species in the Eastern Alps.

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Mismatching ecology should be pursued: cryptic diversity in *Saussurea discolor* s.l. (Asteraceae) [Talk]

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In the European Alpine System, one of the largest angiosperm genera, the genus *Saussurea* (Asteraceae), is represented by only four species, i.e. *S. alpina, S. discolor, S. porcii* and *S. pygmaea. Saussurea discolor* is a taxonomically undisputed European endemic growing in alpine grasslands and crevices on calcareous bedrock. Whereas in the Alps it is a high mountain species growing above the timber line, we could find it growing in montane spruce forests in the Eastern and Southern Carpathians. This triggered us looking in more detail at the morphology, ecology, distribution, taxonomy and phylogeny of *S. discolor* s.l. (i.e. *S. discolor* in Europe and *S. controversa* in Siberia and adjacent regions). To accomplish this we did morphometric analyses, counted chromosome numbers, measured absolute genome sizes, inferred a RADseq based DNA phylogeny, and did taxonomic hypothesis testing using BFD* (Bayes Factor Delimitation). In this group, cryptic allopatric diversity has been detected. Consequently, *Saussurea discolor* s.l. in Europe anust be revised taxonomically.

Near vs. wide: Comparative phylogeography of four fish species in the Dinaric Karst [Talk]

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The Dinaric Karst is a biodiversity hotspot, especially known for its speleofauna. However, there is also a high species richness of epigean organisms and the region is especially known for a diverse freshwater fish fauna, which is characterized by numerous endemics. The distribution patterns of fishes in the Dinaric karst can roughly be divided in two categories: (1) Genera, which include both widespread species, distributed in several river drainages in- and outside of the region, as well as species with ranges restricted to the Dinaric karst e. g., *Phoxinus, Telestes.* (2) Genera endemic to Dinaric karst (e. g., *Phoxinellus, Delminichthys*). The present study compares the distribution ranges and the biology of the two categories, including genera *Phoxinus, Delminichthys, Phoxinellus* and *Telestes*, based upon their mitochondrial genetic lineages. While *Delminichthys, Phoxinellus* and Dinaric *Telestes* have a similar lifestyle, specialized for dwelling in sinking streams in karst poljes, the genus *Phoxinus* is ubiquitous with numerous species common all over Europe. Yet, *Phoxinus* have an unusual distribution pattern, which, in contrast to other members of Leuciscidae, do not seem to be affected by current hydrological barriers, often traversing drainage and basin boundaries. One possible reason for that is the biology of *Phoxinus* that includes high migratory potential. In other three genera some limited ability to migrate underground is exhibited, but they cannot disperse along main river courses due to their specific adaptation for dwelling in the sinking streams of karst poljes.

Phylogenomic insights into adaptive radiations of *Gyrodactylus* (Monogenea, Platyhelminthes) ectoparasites on European freshwater fishes [Talk]

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The hyperdiverse genus Gyrodactylus has a circumpolar distribution and includes more than 400 described and a total estimate of 20,000 species worldwide. Apart from a few exceptions on amphibians, these tiny parasitic flatworms (<1 mm) infect predominantly bony fishes (Bakke et al. 2007). In the course of the Austrian Barcode of Life (ABOL) initiative we aspire to unveil Austria's Gyrodactylus diversity in unprecedented detail. More than 20 species have been identified as of now based on nuclear ribosomal ITS sequences. This allowed us to confirm the presence of members of at least two sub-genera, G. (Limnonephrotus) and G. (Gyrodactylus), the relationships within groups, however, are poorly resolved. Using newly designed primers and ONT's MinION sequencing platform we inferred mitochondrial COI diversity across more than 40 species, which yielded the first reliable divergence estimate between the subgenera, but did not significantly increase the resolution within groups. We aim to revise Gyrodactylus taxonomy and resolve controversial relationships, particularly those in the wageneri-group of G. (Limnonephrotus), an adaptive radiation of parasites infecting salmonids, cyprinids, percids, esocids, and gasterosteids, based on hundreds of Single-Copy genes. To this end we generated Illumina data for 17 distinct Gyrodactylus spp. infecting 13 host species. The subset of species was chosen strategically to maximise taxonomic breath and also include Gyrodactylus spp., which, according to the marker genes (ITS and COI), appear to have colonised the same host species independently. Data are being assembled using multiple correction- and genome assembly approaches, yielding results comparable to or in some cases better than previously published genomes both with respect to continuity and completeness. Against the backdrop of a resolved phylogeny these data will provide a paramount foundation for the identification of genes associated with host specificity and -preference in *Gyrodactylus* and potentially beyond.

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Phangorn 3.0: New trees in the forest [Talk]

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Since its first release in March 2008, the R (R Core Team, 2017) package phangorn (Schliep 2011) has developed steadily to provide a set of tools for researchers in evolutionary biology who want to infer phylogenetic trees and networks and seek to phylogenies. Phangorn is a popular R package which is cited around 2500 times according to google scholar and is used by around 50 packages on CRAN (<u>https://cran.r-project.org</u>) and Bioconductor (<u>www.bioconductor.org</u>). A recent addition to the package the feature to estimate ultrametric and tiplabeled phylogenies with a strict molecular clock. For the release of version 3.0 we took the opportunity to simplify the workflow of some common analyses and improve and rewrite some of the documentation. For example, we added a dataset and examples for handling morphological data. Phangorn is freely available at <u>https://CRAN.R-project.org/package=phangorn</u> and <u>https://github.com/KlausVigo/phangorn</u> (development version).

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Mitochondrial diversity and a bar-HRM assay for rapid species identification of *Romanogobio* (Actinopterygii, Cypriniformes, Gobionidae) species from the Danube drainage [Talk]

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Gudgeons of the genus Romanogobio are small benthic fishes that live both in lentic and lotic systems. Six species are known to occur in the Danube system, some of which are listed on national Red Lists. However, as these species are in part difficult to distinguish, especially as juveniles, little is known about their phylogeographic and population genetic structure across the Danube system. Based on sequences of the DNA barcoding region (5'end of the mitochondrial COI gene) of 237 Romanogobio specimens collected from across the whole Danube system, we aimed at i) investigating the genus' actual species diversity in this river drainage, ii) inferring the phylogeographic structure within species, and iii) developing a bar-HRM (barcode high resolution melting) assay for the time- and cost-efficient identification of the Romanogobio species present in the Danube system. Our DNA barcoding results fit well with the current taxonomy of Danubian Romanogobio, but also indicate a potential cryptic species in the Olt River, requiring further scrutiny. Intraspecific divergence in Romanogobio species is very shallow with little to no phylogeographic structure across the Danube system, which is in stark contrast to the patterns previously found in the sister genus Gobio. The observed low intraspecific variation in the COI region allowed for identifying minibarcode primer pairs that should reliably distinguish among species based on bar-HRM. The findings from our study thus increase our knowledge on the diversity of Romanogobio species, both at the inter- and intraspecific level in the Danube system and provides a reliable and cheap method for identifying these species that can be easily used by taxonomic laymen, thereby facilitating monitoring activities to inform conservation management of these fishes.

A diversity hotspot of stream amphipods in the Eastern Alps [Talk]

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The amphipod Gammarus fossarum is an abundant member of the macrozoobenthic communities of European streams and rivers. Genetic analyses have recently revealed that the species is in fact a complex of numerous, genetically divergent but morphologically undistinguishable MOTUs (Molecular Operational Taxonomic Units), whose common ancestor dates back to the mid-Oligocene (Wattier et al. 2019). On several occasions, divergent mtDNA-based MOTUs have been shown to be reproductively isolated from each other (Bystřický et al. 2022). The distribution of the cryptic diversity of G. fossarum across Europe is highly uneven: While large areas of central and western Europe are occupied by representatives of few MOTUs belonging to a single major clade, other areas, such as the Carpathian Mountains, are hotspots of lineage diversity. Except for very few locations, previous studies did not include Austria in their sampling efforts, but the diversity in the neighbouring regions as well as geographic features of the eastern Alpine region predict high levels of cryptic G. fossarum diversity in Austria. Our recent COI (mitochondrial cytochrome c oxidase subunit 1 gene) sequencing effort, using Nanopore technology and covering > 100 sampling locations in eastern and southern Austria, confirmed this prediction, as most of the major European clades are represented in the area. Within these clades, several of the Austrian G. fossarum lineages are deeply divergent from other European G. fossarum and further increase the number of MOTUs in this species complex. Several sampling locations and catchment areas harbour more than one MOTU and more than one of the major clades. In contrast, genetic diversity within MOTUs is generally low. The genetic patterns suggest the existence of relict, phylogenetically diverse MOTUs within the eastern Alpine region, with individual populations subject to strong genetic drift. Increasing frequencies of hot drought-associated (near-)desiccation events are expected to increase environmental pressure on these populations and possibly trigger lineage- or clade-specific responses.

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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. Imagines emerge in late fall and are active during the winter, when they are occasionally observed wandering on top of the snow. Most of their time, however, is spent hidden in moss pads, where they feed on the mosses and deposit their eggs. Two species of Boreidae have been recorded in Austria, Boreus westwoodi and B. hyemalis, 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 the present study, we extended the previous sampling effort in order to investigate the geographic pattern of mtDNA lineage diversity in southern and eastern Austria. In addition to collecting genetic data, we also used GC-MS (gas chromatography – mass spectrometry) to examine the composition of cuticular lipids. 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 substantial genetic and chemical diversity, which were, however, only weakly correlated with each other. The phylogeographic signal in the mtDNA data was blurred by sympatric occurrences of divergent genetic lineages and haplotype sharing between sampling locations. Even within the same mtDNA lineage, local genetic diversity was high at several of the sampling locations. Opposite to expectations based on life history and abundances, the genetic data suggest large effective population sizes and considerable degrees of population connectivity. Chemical patterns of cuticular compounds do not mirror mtDNA-based structure, such that the detected MOTUs remain cryptic in terms of both morphology and cuticular compound composition.

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Gudgeons of the genus *Gobio* in Austria and Croatia, and their monogenean parasites: the mystery of their diversity [Talk]

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Fishes of the genus Gobio (Gobionidae) are known for their wide distribution; they can be found in different freshwater habitats throughout Eurasia. Gobio species show great phenotypic similarity, but also considerable intraspecific morphological variability, which, coupled with unresolved taxonomic issues and high levels of genetic diversity (fueled by hybridisation events), makes them an interesting subject of research. Previous research (Zangl et al. 2020) on Austrian Gobio identified a large hybrid zone between G. gobio and G. obtusirostris and also uncovered a lineage clustering with south-eastern European Gobio species, that spans large parts of Austria. In the present study we extended the sampling to additional parts of the Danube system, with a particular focus on Croatia, to explore the species diversity and phylogeography of Gobio across a larger part of the Danube region by means of DNA barcoding (sequencing of the 5'-end of the mitochondrial COI gene). In addition, gudgeons were screened for ecto-parasites of the genus Gyrodactylus (Platyhelminthes: Monogenea), and the ribosomal ITS region of individual parasites was sequenced. The preliminary results show the presence of yet another mitochondrial Gobio lineage in Croatia, closely related to several south-eastern Gobio species. Gyrodactylus were found in 91.7 % of the sampled Gobio populations in Austria (n=11) and 61.5 % in Croatia (n=8). We identified several distinct genetic lineages (presumably species) of Gyrodactylus on both Austrian and Croatian gudgeons, with no clear phylogeographic pattern becoming apparent as of yet. However, phylogenetic inference including other European species strongly indicates that Gyrodactylus colonised gudgeons in the Danube system at least twice independently.

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Parallel genomic signals in an interstitial clingfish radiation [Talk]

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Assessing the predictability of evolution in the biological world remains one of the most fascinating fields in evolutionary biology. Indeed, parallelism (or convergence) resulting in similar forms and functions of distinct populations or species is ubiquitously observed across the tree of life and is one of the profound types of evidence of natural selection. We investigated the extent of parallel morphological and genomic evolution in "slender" and "stout" ecotypes of the genus *Gouania*, an endemic interstitial clingfish genus from the Mediterranean Sea. Allopatric species pairs show a high extent of morphological parallelism which reflect adaptations to diverging intertidal gravel microhabitats. Compared to their stout counterparts, slender *Gouania* tend to show an increased body flexibility (by increased number of vertebrae), smaller eyes and a generally compressed head shape. Additionally, based on whole genome re-sequencing data, we explored genome wide signals of parallel evolution and found promising candidate regions associated with divergent *Gouania* phenotypes.

A single list of the world's species – background information and results of a recent large-scale survey [Talk]

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Over the last few years, a newly formed initiative, the Global Species List Working Group (GSLWG), has been working on principles and infrastructure to establish a governance system for a single list of the world's species. While particularly the Catalogue of Life (COL) has done great work when it comes to listing, there are still different global lists for various taxa, and there is no completely standardised and transparent process to decide which partial lists are included in the global list and why, i.e. which criteria they must meet. The GSLWG is the result of a scientific debate triggered by a controversial publication and subsequent commentaries. It unites researchers and stakeholders from both sides of the argument, and is now working in close collaboration with COL. In 2020, the foundational article of the project was published, highlighting, among other things, that any global list to be accepted by the larger community must be based on science and free from non-taxonomic interference; be transparent in its composition and not constrain academic freedom; have traceable and archived content; and include appropriate recognition of contributors. A topical collection of papers in 2021 further elaborated on many of these points. However, we had not yet interacted with the taxonomic (and other) communities to include their opinions and suggestions. A large survey (with more than 1,100 valid responses) that was sent out to various networks and societies, including NOBIS Austria, was recently carried out to close this gap. It has yielded great support for the project and further insights into what the community considers relevant and what not. In my presentation, I will give background information and more detailed results of the survey, which we consider an important step towards a single global and truly authoritative list of the world's species.

Changes in the wild bee communities over 100 years in relation to land-use: A case study in a protected steppe habitat in Eastern Austria [Talk]

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The wild bee community of the sand steppe habitat in "Oberweiden", a 120-hectare large protected area in eastern Austria, was surveyed in the years 2018 and 2019, complemented with historical bee data from literature and databases from over 100 years, and analyzed in relation to changes in the landscape using historical aerial photographs since the 1960ies. In total, 310 bee species representing 41 genera were recorded in the area until now, with the oldest records dating back to the year 1882. Across the two periods with approximately complete samples (1931–1966 vs. 2001–2021) 283 species were recorded, with an overlap of 82 species, while 164 species occurred only in the time period 1931-1966, and 37 species only in the later one. We observe a disproportionally high decline of steppe and sand associated species, and a distinct shift from species nesting in the ground to species nesting above ground. The area covered with woods, specifically areas characterized by medium and sparse wood cover, increased from 1966 to 2018, while the total area covered with grassland and fallows decreased slightly between 1966 and 1994 and stayed equal afterwards. The impact of possible drivers (e. g., management of the area) is discussed in the light of the observed changes.

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Graz 2022

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N B I S B I 6

Graz 2022

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