NOBIS Austria

YOUNG RESEARCHERS´ DAY

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27. November 2020

Online

NETWORK OF BIOLOGICAL SYSTEMATICS AUSTRIA

Online 2020 NOBIS AUSTRIA 14

NOBIS Young Researchers' Day

14th Annual Meeting of NOBIS Austria

Friday, November 27, 2020

Online

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Online 2020 NOBIS AUSTRIA 14

Dear NOBIS members,

the coronavirus pandemic prevents the 14th meeting of NOBIS Austria from taking place in Graz this year. We therefore arranged an alternative, namely an exclusively online meeting on the afternoon of Friday, November 27th 2020. In order to keep our “virtual” meeting within a manageable time frame, we will follow the example of previous NOBIS Young Researchers’ Days. After an opening keynote delivered by Dr. Alice Laciny (Konrad Lorenz Institute for Evolution and Cognition Research, Klosterneuburg), there will be oral presentations by junior colleagues who compete for the NOBIS awards for the best students’ talks. A final presentation by the awardee of the NOBIS grant, Maximilian Wagner, will conclude the meeting.

Unfortunately, this year’s workshop and poster presentations had to be cancelled under the circumstances. Attendance of and participation in the NOBIS Young Researchers’ Day 2020 is free of charge. Although this year’s meeting will take place online, we hope to have a large audience and the usual active participation, creating a positive and appreciative atmosphere for our invited speaker and junior colleagues.

The goal of NOBIS Austria is to support research in biosystematics, to involve young colleagues in the scientific community, and to foster interdisciplinary communication. This has never been more important than now during a global pandemic that affects every aspect of our lives like and threatens the future of the next generations of scientists. Now more than ever, it is our obligation as scientific community to stand united and support young researchers during these difficult times.

The Nobis Austria Executive Board

Programme

Friday, November 27th 2020

13:00–13:10 Welcome address by **Sabine Agatha**, President of NOBIS Austria

Talks

Chairs: Sabine Agatha & Andreas Kroh

13:10–13:40 **Alice Laciny**: Ants, parasites, and (a lack of) systematics. [Keynote]

Competition for the NOBIS Awards

13:40–13:50 **Noel Orou** et al.: *Messor* sp. n., a new hitherto cryptic harvester ant lineage in the Iberian Peninsula.

13:50–14:00 **David Fröhlich** et al.: Sexual dimorphism in wing venation and cuticular hydrocarbons in the cuckoo wasp *Trichrysis cyanea* (Hymenoptera, Chrysididae).

14:00–14:10 **Silas Bossert** et al.: *Schwarzia* – Overlooked diversity in an Eastern African lineage of cleptoparasitic bees (Apidae, Nomadinae).

14:10–14:20 **Edwin Kniha** et al.: Challenging identification of a sand fly species (Diptera: Psychodidae: Phlebotominae) new to Austria resolved by combining morphological and molecular methods.

14:20–14:30 **Lukas Zangl** et al.: Beyond the barcodes: Mecopteran diversity in Austria.

14:30–14:50 Coffee break

14:50–15:00 **Julian Bibermair** et al.: First modern morphological data on lophopodid Phylactolaemata: Implications for the neuro-muscular ground pattern of the clade.

15:00–15:10 **Sebastian Decker** & Thomas Schwaha: Morphology of the boring: first data on the bryozoan family Penetrantiidae.

15:10–15:20 **Marika Asztalos** et al.: How often do they do it? An in–depth analysis of the hybrid zone of two grass snake species (*Natrix astreptophora*, *N. helvetica*).

15:20–15:30 **Juan Pablo Hurtado Gómez** et al.: Phylogeography of two widely distributed mud turtle species (Kinosternidae: *Kinosternon*), shows contrasting genetic structure patterns and challenges current taxonomy.

Talk by the winner of the NOBIS Grant

15:30–15:40 **Maximilian Wagner**: Exploring the genomic basis of an intertidal fish radiation.

15:40–16:00 Coffee break

16:00 **Elisabeth Haring**: Announcement of the NOBIS Awards and closing words

17:30 General assembly
(WebEx link will be sent by email to registered attendees)

Abstracts

How often do they do it? An in-depth analysis of the hybrid zone of two grass snake species (*Natrix astreptophora*, *N. helvetica*)

Asztalos, M.[1], Ihlow, F.[1], Geniez, P.[2] & Fritz, U.[1]

[1] Museum of Zoology (Museum für Tierkunde), Senckenberg Dresden,
Dresden, Germany; e-mail: marika.asztalos@senckenberg.de
[2] UMR 5175 CEFE, Biogéographie et Ecologie des Vertébrés, EPHE,
PSL Université Recherche, Montpellier, France

NOBIS-Preis-Beitrag

We examined the contact zone of two parapatric species of grass snake in southern France (*Natrix astreptophora* and *N. helvetica*). To this end, we used comprehensive sampling, analyzed mtDNA sequences and microsatellite loci, and built Species Distribution Models for current and past climatic conditions. The contact zone established by the mid-Holocene during range expansions from glacial refuges in the Iberian Peninsula (*N. astreptophora*) and southern or western France (*N. helvetica*). The contact zone represents a narrow bimodal hybrid zone, with steep genetic transition from one taxon to the other and rare hybridization, supporting species status for *N. astreptophora* and *N. helvetica*. Our results suggest that the steepness of the clines is a more robust tool for species delimitation than cline width. In addition, we discovered in western France, beyond the hybrid zone, a remote population of *N. helvetica* with genetic signatures of hybridization with *N. astreptophora*, most likely the result of human-mediated long-distance dispersal. For *N. helvetica*, we identified a southern and a northern population cluster, connected by broad-scale gene flow in a unimodal hybrid zone running across France. This pattern either reflects genetic divergence caused by allopatry in two microrefuges and secondary contact or introgression of foreign alleles into the southern cluster.

First modern morphological data on lophopodid Phylactolaemata: Implications for the neuro-muscular ground pattern of the clade

NOBIS-Preis-Beitrag

Bibermair, J.[1], Wood, T.S.[2] & Schwaha, T.[1]

[1] Department of Evolutionary Biology, University of Vienna, Vienna, Austria; e-mail: Julian.Bibermair@univie.ac.at

[2] Department of Biological Sciences, Wright State University, Dayton, USA

Bryozoans are colonial, mostly marine filter feeders within the lophotrochozoans. Single units of the colony (=zooids) consist of an outer body wall (cystid) and a retractable softbody (polypide) with a ciliated lophophore. The exclussively limnetic Phylactolaemata are regarded as sister taxon to the vast majority of Myolaemata (Stenolaemata, Gymnolaemata). With approx. 70 species, subdivided into six or seven families, the former resemble a rather small group, yet crucial for ground pattern reconstruction. Phalyctolaemate colonial growth patterns range from spherical, including a cluster-like arrangement of the zooids (*Cristatellidae, Lophopodidae, Pectinatellidae*) to branching colonies with serial arranged, often chitinous/ encrusted zooids (*Fredericellidae, Plumatellidae*). Traditional phylogenies considered clustered phylactolaemates as late-branching compared to the early-branching plumatellids/fredericellids. However, recent molecular analyses suggest the clades with clustered colonies to be earlier branching. Especially, lophopodid phylactolaemates are one of the earliest branches among this clade. The morphology of this family remains little investigated but important for a ground pattern reconstruction of the clade. Although, many species and genera were once assigned to the lophopodids, only three genera remain to represent this family. Most available data focus on *Lophopus* and *Lophopodella*, whereas the comparatively new genus *Asajirella* stays rather uninvestigated. *Asajirella* shares similarities with other clustered phylactolaemates like *Pectinatella*, but could also contribute new characters to unify *Lophopodidae* as a family. Consequently, the aim of this study is to provide a morphological analysis of the lophopodid *Asajirella gelatinosa*. More complete analyses of this species date back to the 19th century and emphasize the necessity of newer data on this species. The morphology of *A. gelatinosa* is analysed with histological sections and 3D-reconstruction, as well as immunocytochemical stainings and confocal microscopy for details on the neuro-muscular system. The new data will represent an essential piece for phylactolaemate character evolution and shed more light into the morphological ground pattern of phylactolaemates.

Schwarzia – Overlooked diversity in an Eastern African lineage of cleptoparasitic bees (Apidae, Nomadinae)

NOBIS-Preis-Beitrag

Bossert, S.[1, 2], Copeland, R.S.[2, 3] & Straka, J.[4]

[1] Department of Entomology, Cornell University, Ithaca, USA,
e-mail: sb@2346@cornell.edu
[2] Department of Entomology, National Museum of Natural History,
Smithsonian Institution, Washington DC, USA
[3] ICIPE, International Centre of Insect Physiology and Ecology, Nairobi, Kenya
[4] Department of Zoology, Faculty of Science, Charles University, Prague, Czech Republic

Discovering unexpected biodiversity are the systematic entomologists' Eureka moments. This talk captures one of these moments and tells a story on describing, documenting, and studying species previously unknown to science. I portray the enigmatic African bee genus *Schwarzia* (Apidae, Nomadinae), a thought-to-be monotypic lineage since its description in 2009 and the only representative of its putative tribe Biastini outside the Holarctic region (Eardley, 2009). I show how a chance find led to the discovery of four unknown species of *Schwarzia*, increasing the total number of faunistic records from 5 to 33. With this newly discovered material, I use genomic sequencing of >1,000 ultraconserved elements to estimate phylogenetic relationships within *Schwarzia* and their closest relatives, re-evaluate morphological characters and tribal concepts in light of phylogenetic evidence, and discuss origin and dispersal of the lineage that lead to present-day *Schwarzia* and *Biastes*, its sister-genus. Lastly, I estimate the antiquity of the group using fossil-calibrated MCMC and puzzle on their yet to be discovered hosts.

References

Eardley, C. 2009. First record of the tribe Biastini from the Afrotropical Region (Hymenoptera: Apidae). Zootaxa, 2264, 65–68.

Morphology of the boring: first data on the bryozoan family Penetrantiidae

NOBIS-Preis-Beitrag

Decker, S.[1] & Schwaha, T[1]

[1] Integrative Zoology, Department of Evolutionary Biology, University of Vienna,
Vienna, Austria; e-mail: decker-s@gmx.de

An endolithic lifestyle within mineralized substrates has many advantages and evolved multiple times in various different phyla. This lifestyle also evolved multiple times within the benthic suspension-feeding phylum Bryozoa. All endolithic bryozoans belong to the paraphyletic ctenostome gymnolaemates and colonize predominantly shells of living and dead molluscs. The family Penetrantiidae includes one genus with approximately a dozen species. Based on the presence of an operculum and other morphological characters, the genus *Penetrantia* was debated to be either a ctenostome or a cheilostome bryozoan. The most recent, comparative morphological analysis dates back to the 40ies' of the last century. Consequently, the aim of this study is to analyze the morphology of the genus *Penetrantia* with more modern methods such as confocal laser scanning microscopy combined with immunocytochemistry and serial sections complemented with 3D reconstruction techniques. *Penetrantia* cf. *parva* and *P. concharum* were analyzed in the current investigation. First data on the musculature associated with the operculum and the digestive tract show strong similarities to other ctenostome bryozoans. Together with the lack of cheilostome apomorphic characters, such as vestibular glands, our results show a closer relationship to ctenostome rather than cheilostome bryozoans. Molecular analyses are currently being undertaken to confirm this hypothesis.

Sexual dimorphism in wing venation and cuticular hydrocarbons in the cuckoo wasp *Trichrysis cyanea* (Hymenoptera, Chrysididae)

NOBIS-Preis-Beitrag

Fröhlich, D.[1], Zangl, L.[1], Raspotnig, G.[1] & Koblmüller, S.[1]

[1] Institute of Biology, University of Graz, Graz, Austria; e-mail: david.froehlich@uni-graz.at

Cuckoo wasps (Chrysididae) are a family of Hymenoptera with parasitoid or cleptoparasitic life histories. Although most of them are colorful and shiny little jewels, few species are well investigated and often only little more is known than just the host taxa. We used an integrative approach, employing DNA barcoding, geometric morphometrics, gas chromatography, and mass spectrometry to study intraspecific diversity in one common species of cuckoo wasps, *Trichrysis cyanea*, in eastern Austria. DNA barcodes show that genetic diversity in *T. cyanea* is very low across the study region. Similarly, no geographic clusters are evident in wing shape and venation. Wing shape and venation, however, do show clear differences between the sexes. Females and their wings are not only larger, they also have broader wings with a rather oval shape, while the male wings are tapered towards the end. These differences might be related to behavioral differences between the sexes: Females, when searching for appropriate nesting holes, need to be able to maneuver very precisely, whereas males, when searching for mates, need to be able to efficiently cover large distances. Also, the cuticular hydrocarbon patterns differ between males and females (also in comparisons across several Austrian cuckoo wasp species). In addition, we found quite some variation among the females, which form three distinct chemical clusters. These distinct chemical clusters might be seen as an adaption in the female cuticular hydrocarbon patterns to that of different host taxa, as three genera of Crabronidae and Pompilidae have been reported as hosts of *T. cyanea*. Thus, we propose that these three female chemotypes allow *T. cynaea* females to sneak into the nests of the different host genera.

Phylogeography of two widely distributed mud turtle species (Kinosternidae: *Kinosternon*), shows contrasting genetic structure patterns and challenges current taxonomy

NOBIS-Preis-Beitrag

Hurtado-Gómez, J.P.[1], Vargas-Ramírez, M.[2, 3] & Fritz, U.[1]

[1] Museum of Zoology, Senckenberg Natural History Collections Dresden, Dresden, Germany; e-mail: juan-pablo.hurtado@senckenberg.de
[2] Grupo de Biodiversidad y Conservación Genética, Instituto de Genética, Universidad Nacional de Colombia, Bogota, Colombia
[3] Estación de Biología Tropical Roberto Franco, Universidad Nacional de Colombia, Villavicencio, Meta, Colombia

Mud turtles of the genus *Kinosternon* are distributed throughout most of the American continent. The genus comprises 20 species, most of them with restricted geographic distribution. *Kinosternon leucostomum* and *K. scorpioides* are the two species having the widest distribution. They occur largely sympatrically from southern Mexico to northern Colombia, but the range of *K. leucostomum* extends through the trans-Andean lowlands of Colombia, Ecuador, and Peru, whereas that of *K. scorpioides* extends through the cis-Andean region as far south as Paraguay. To understand their phylogeography, we sequenced three mitochondrial and seven nuclear genes using nearly range wide sampling. Our results show no clear phylogeographic structure for *K. leucostomum*. In contrast, for *K. scorpioides* we found four divergent clades, corresponding to samples from Central America, the Colombian Caribbean region, and two cis-Andean groups. Additionally, our results challenge the current taxonomy regarding the validity of the subspecies of *K. leucostomum*, since there is no genetic structure, and propose a new taxonomic arrangement for the *K. scorpioides* clade.

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Challenging identification of a sand fly species (Diptera: Psychodidae: Phlebotominae) new to Austria resolved by combining morphological and molecular methods

NOBIS-Preis-Beitrag

Kniha, E.[1], Dvořák, V.[2], Obwaller, A.G.[3], Volf, P.[2] & Walochnik, J.[1]

[1] Institute of Specific Prophylaxis and Tropical Medicine, Medical University of Vienna, Vienna, Austria; e-mail: edwin.kniha@meduniwien.ac.at
[2] Department of Parasitology, Faculty of Science, Charles University, Prague, Czech Republic
[3] Federal Ministry of Defence, Division of Science, Research and Development, Vienna, Austria

Phlebotomine sand flies (Diptera: Psychodidae: Phlebotominae) are small hematophagous insects and the vectors of the protozoan parasites *Leishmania* spp., and of bacteria and several arthropod-borne (arbo-) viruses. In Europe, sand flies were considered to be present only in the Mediterranean basin; occurrence north of the Alps was overlooked until *Phlebotomus mascittii* Grassi, 1908, and *Phlebotomus perniciosus* Newstead, 1911, were found in Germany in 1999 and 2001, respectively. During entomological surveys from 2010 to 2013, this species was shown to be present also in four federal states of Eastern Austria. A first report from Slovakia in 2016 and recent new records from Germany show that sand fly distribution in Central European countries is still unresolved. Sand flies in Central Europe are assumed to be remnants of post-glacial recolonization events during the Holocene optima from Mediterranean refugia, which have survived in small, microclimatic areas. Based on this hypothesis, more populations of *Ph. mascittii* as well as other species are expected to be present in Austria. Therefore, entomological surveys were conducted in 2018 and 2019.

New findings of *Ph. mascittii* and a single female specimen of a sand fly species new to Austria were detected at one site in Lower Austria. Female specimens belonging to the respective subgenus are known to be almost undistinguishable at the species level. While morphological identification by two different techniques was limited to the subgenus level, molecular identification by analysis of the barcoding gene *cytochrome c oxidase subunit* 1 showed sequence identity of >99% to reference sequences available at GenBank. However, further analysis revealed unexpected high intraspecific distances between populations of the respective species and low interspecific distances to other species of this subgenus. Thus, a second marker gene, *cytochrome b*, was analysed and haplotype analysis using both genes revealed clustering of the Austrian specimen with individuals from North Macedonia and Greece, indicating a colonization to Central Europe from this area.

This study provides the first finding of a second sand fly species in Austria and the northernmost record so far. Moreover, it reveals insights into the phylogenetic relationships of species within the respective subgenus.

Ants, parasites, and (a lack of) systematics

Laciny, A.[1]

[1] Konrad Lorenz Institute for Evolution and Cognition Research,
Klosterneuburg, Austria; e-mail: alice.laciny@kli.ac.at

As social insects, ants represent extremely interaction-rich biological systems shaped by tightly integrated social structures and constant mutual exchange with a multitude of internal and external environmental factors. Due to this high level of ecological interconnection, ant colonies can harbor a diverse array of parasites and pathogens, many of which are known to interfere with the delicate processes of development and caste differentiation to induce phenotypic changes in their hosts. Such parasitogenic morphologies in ants can shed light on the mechanisms and pathways relevant to host ontogeny, plasticity, and robustness under environmental perturbation, colony-level effects, and caste evolution.

With many of the parasitic organisms affecting ant host morphology having fascinated researchers ever since the 18th century, one would expect them to hold relatively few secrets left to be uncovered today. However, quite contrary to common intuition, research on these enigmatic systems continues to face methodological difficulties, either due to lack of data or vast differences in its interpretation, making comparability across studies challenging. Especially, the poorly resolved taxonomy and phylogeny of the involved hosts and parasites frequently hampers high-quality research and has led to misleading results in the past.

Introducing the examples of ants parasitized by mermithid nematodes and the fungal pathogen *Myrmicinosporidium durum*, I herein wish to highlight some of the obstacles frequently faced by researchers investigating these phenomena. By discussing the shortcomings of common practices and offering possible solutions, I aim to encourage a multidisciplinary approach, combining morphometry, molecular biology, 3D imaging, and biological theory. I further aim to highlight the importance of further taxonomic and phylogenetic studies in the context of parasite-induced host morphology. Implementing such a novel, integrative approach will enable us to draw more sound and meaningful conclusions about these rare and intriguing “natural experiments” and facilitate future research on the subject.

Messor sp. n., a new hitherto cryptic harvester ant lineage in the Iberian Peninsula

NOBIS-Preis-Beitrag

Orou, N.[1], Csősz, S.[2], Arnan, X.[3, 4], Pol, R.[3], Arthofer, W.[4],
Schlick-Steiner, B.[4] & Steiner, F.[4]

[1] Department of Ecology, University of Innsbruck, Innsbruck, Austria;
e-mail: n.orou@gmx.net
[2] MTA-ELTE-MTM Ecology Research Group, Budapest, Hungary
[3] CREAF Centre for Ecological Research and Forestry Applications,
Autonomous University of Barcelona, Spain
[4] University of Innsbruck, Department of Ecology, Innsbruck, Austria

European harvester ants, *Messor* species, are important ecosystem engineers. Diversity of this moderately species-rich genus is mostly concentrated in Mediterranean habitats. There are three species, *Messor barbarus*, *M. bouvieri*, and *M. capitatus* known to often co-occur in the Iberian Peninsula. At a Spanish site, a cluster of nest samples of unknown identity has been found, raising the possibility of emerging either a hybrid lineage or a currently unexplored species in the region. The aim of the study was to test whether the newly recognized cluster is ascribed to a putative hybridization between the synoptically co-occurring *M. barbarus* and *M. capitatus* populations, a form of social hybridogenesis, or it may represent an independent, hitherto undescribed species within this genus. We address this question in an integrative taxonomic fashion combining evidence from microsatellites analyzed via Bayesian cluster analysis, phylogenetic analyses based on mtDNA, and multivariate exploratory and confirmatory analyses of morphometric data. The unidentified *Messor* ants formed a well-separated entity in all these analyses. These results indicate existence of a cryptic species within the genus *Messor*, instead of the formerly hypothesized hybridization and social hybridogenesis.

Exploring the genomic basis of an intertidal fish radiation

Wagner, M.[1, 2], Koblmüller, S.[1], Resl, P.[1] & Svardal, H.[2]

[1] Institute of Biology, University of Graz, Graz, Austria; e-mail: maximilian.wagner@uni-graz.at

[2] Department of Biology, University of Antwerp, Antwerp, Belgium

Clingfishes (Gobiesocidae) are among the few vertebrates on this planet that successfully colonised the harsh conditions of the intertidal zone. Despite their overall low species count (~180), their ecological and morphological diversity is stunning, making clingfishes an ideal study system for comparative eco-evolutionary research. This is also true for the subfamily Lepadogastrinae, which includes seven genera confined to the east Atlantic Ocean and the Mediterranean Sea. However, the phylogenetic relationships among the Lepadogastrinae are poorly resolved (based on mitochondrial 12S and 16S rRNA genes) and hamper future research in this group. We, therefore, aim to disentangle the phylogenetic backbone of the Lepadogastrinae, using short-read whole genome sequencing of at least one member per genus in the subfamily. A high-quality reference genome was sequenced in the course of the *Vertebrate Genomes Project* for the Mediterranean endemic genus *Gouania*. Compared to other Lepadogastrinae, *Gouania* differs greatly in terms of its ecology and morphology. Unlike any other vertebrate species in the Mediterranean, it inhabits life-hostile interstitial space of intertidal Mediterranean pebble beaches. The genus' overall wormlike appearance and morphological truncations (e.g., small body size and eyes; fused anal, dorsal, and caudal fins) are considered adaptations to this "hypogean" interstitial lifestyle. Additionally, *Gouania* harbours a comparatively high species diversity, with recent phylogenetic and taxonomic work confirming the presence of (at least) five valid species (with some species exhibiting quite some geographic population structure). Notably, *Gouania* come in two morphotypes, "slender" and "stout", that convergently evolved in the Eastern Mediterranean as well as the Adriatic Sea and which likely mirror adaptations to certain microhabitats. Altogether, this provides a unique framework to study speciation in marine environments. Based on the above-mentioned phylogenomic framework, exploring and comparing the genomic architecture facilitating these intertidal adaptations (by investigating putative candidate regions; e.g. opsin, hox genes, morphogenes), could be the key to understanding the successful invasion of the intertidal and the further diversification within *Gouania*.

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Beyond the barcodes: Mecopteran diversity in Austria

Zangl. L.[1, 2], Glatzhofer, E.[1], Schmid, R.[1], Randolf, S.[3] & Koblmüller, S.[1]

[1] Institute of Biology, University of Graz, Graz,
Austria; e-mail: Lukas.zangl@uni-graz.at
[2] Universalmuseum Joanneum, Studienzentrum Naturkunde, Graz, Austria
[3] Natural History Museum Vienna, Vienna, Austria

NOBIS-Preis-Beitrag

The holometabolous insect order Mecoptera contains about 600 extant species in nine families distributed across the globe. Among them, the scorpionflies (Panorpidae), the hangingflies (Bittacidae), and the snow scorpionflies (Boreidae) are commonly known for the scorpion stinger-shaped male reproductive organ, their elaborate mating rituals, and their habit of occurring on snowfields, respectively. From Austria, five species of scorpionflies, two species of hangingflies, and two species of snow scorpionflies have been reported so far. In the framework of the Austrian Barcode of Life (ABOL) initiative, we aimed at generating a comprehensive reference DNA barcode database for the Austrian Mecoptera species. However, large phenotypic variability hindering unambiguous morphological species determination was uncovered in snow scorpionflies along with potential cryptic diversity based on DNA barcoding data. Furthermore, cryptic diversity in scorpionflies as well as a lack of recent hangingfly reports from Austria hampered setting up the reference database. Consequently, genomic data was retrieved in order to elucidate cluster relationships in scorpionflies and snow scorpionflies and to make use of museum specimens of hangingflies for the generation of DNA barcodes.

Teilnehmer*innen

Sabine Agatha
sabine.Agatha@sbg.ac.at

Ulrike Aspöck
ulrike.aspoeck@nhm-wien.ac.at

Horst Aspöck
horst.aspoeck@meduniwien.ac.at

Marika Asztalos
marika.asztalos@senckenberg.de

Sonja Bamberger
bambergerson@gmail.com

Björn Berning
b.berning@landesmuseum.at

Julian Bibermair
julian.Bibermair@univie.ac.at

Silas Bossert
silas.bossert@googlemail.com

Sandra Bračun
sandra@nawi-reisen.at

Sebastian Decker
decker-s@gmx.de

Agnes Dellinger
agnes.dellinger@univie.ac.at

Franziska Denner
franziska.denner@gmx.at

Amina Derlic
amina.derlic@students.boku.ac.at

David Fröhlich
david.froehlich@uni-graz.at

Maximilian Ganser
maximilian.Ganser@stud.sbg.ac.at

Santiago Gaviria
santiago.gaviria@gmx.at

Elisabeth Geiser
elisabeth.Geiser@gmx.at

Matthäus Greilhuber
mgreilhuber@gmail.com

Nicole Grunstra
nicolegrunstra@googlemail.com

Christoph Hahn
christoph.hahn@uni-graz.at

Elisabeth Haring
elisabeth.haring@nhm-wien.ac.at

Anna Hawranek
annasophiehawranek@gmail.com

Christoph Hörweg
christoph.hoerweg@nhm-wien.ac.at

Juan Pablo Hurtado-Gómez
juan-pablo.hurtado@senckenberg.de

Mildred Johnson
mildred.johnson@univie.ac.at

Sandra Kirchner
sandra.kirchner@nhm-wien.ac.at

Edwin Kniha
edwin.kniha@meduniwien.ac.at

Stephan Koblmüller
stephan.koblmueller@uni-graz.at

Andreas Kroh
andreas.kroh@nhm-wien.ac.at

Alice Laciny
alice.laciny@kli.ac.at

Julia Lanner
julia.lanner@hotmail.com

Noel Orou
n.orou@gmx.net

Susanne Randolf
susanne.randolf@nhm-wien.ac.at

Simone Raus
simone.raus@gmx.at

Susanne Reier
susanne.reier@nhm-wien.ac.at

Philipp Resl
philipp.resl@uni-graz.at

Ahmed Saadi
ahmed.saadi@univie.at.ac

Helmut Sattmann
helmut.sattmann@nhm-wien.ac.at

Martin Schebeck
martin.schebeck@boku.ac.at

Lisa-Maria Schmidt
lisa-maria.schmidt@nhm-wien.ac.at

Marcia Sittenthaler
marcia.sittenthaler@nhm-wien.ac.at

Anna Sommer
anna.sommer@sbg.ac.at

Bettina Sonntag
bettina.Sonntag@uibk.ac.at

Nikola Szucsich
nikolaus.Szucsich@nhm-wien.ac.at

Tobias Ternus
tobias.Ternus@web.de

Andreas Tribsch
andreas.tribsch@sbg.ac.at

Maximilian Wagner
maximilian.wagner@uni-graz.at

Julia Walochnik
julia.walochnik@meduniwien.ac.at

Birgit Weißenbacher
birgit.weissenbacher@sbg.ac.at

Frank Zachos
frank.zachos@nhm-wien.ac.at

Lukas Zangl
lukas.zangl@uni-graz.at

Robert Zimmermann
robert1.zimmermann@biologie.uni-regensburg.de

Dominique Zimmermann
dominique.zimmermann@nhm-wien.ac.at