

NOBIS Austria

YOUNG RESEARCHERS' DAY 2017

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1 December 2017

Department of Botany and Biodiversity Research, Vienna

NETWORK OF BIOLOGICAL SYSTEMATICS AUSTRIA

NOBIS Young Researchers' Day 2017

Join the network!

The 2nd NOBIS Young Researchers' Day strives to attract young members of the scientific community, who usually depend on temporary, third-party funded projects. NOBIS intends to provide a platform for information exchange and networking, especially, during these early stages of a scientific career. The keynote by Gerald M. Schneeweiss on the "phylogeny and evolution of the non-photosynthetic parasitic broomrapes (Orobanchaceae)" will provide a glimpse into the strange world of plants gone astray.

In contrast to earlier meetings NOBIS Austria now, for the first time, offers two awards: one for Master and one for PhD students. Each winner will be awarded with 300 Euro each and three years of free NOBIS Austria memberships. Young scientists present the results of their recently completed or nearly finished scientific projects and compete for the two NOBIS Awards. Based on the quality of the research and the presentations during the NOBIS Young Researchers' Day, the winners are selected by a jury composed of established members from different fields of life and earths sciences and announced at the end of the meeting. Additionally, the best poster is elected by public vote and awarded with three years of free NOBIS Austria membership.

NOBIS Young Researchers' Day 2017 – Overview

Venue: Department of Botany and Biodiversity Research, Rennweg 14, 1030 Vienna

Thursday, November 30th

- 15.00 Guided Tour “Die Geologisch Paläontologische Sammlung des Naturhistorischen Museums” (A. Kroh, meeting point: Burgring 7, 1010 Vienna, side entrance Naturhistorisches Museum; duration: 45 minutes)
- 17.30 Einblick in die Röntgentomographische Forschung am Rennweg (Y. Städler, meeting point: entrance Department of Botany and Biodiversity Research, Rennweg 14, 1030 Vienna)
- 18.30 – 22.00 Icebreaker in the Department of Botany and Biodiversity Research, Rennweg 14, 1030 Vienna)
- 18.30 – 20.00 Registration

Friday, December 1st

- 9.00 – 9.30 Registration
- 9.30 – 17.10 Talks, Poster Presentations and NOBIS Awards

Talks 15 + 5 minutes

Poster A0 portrait format, 3 minutes presentation with one Power Point slide (graphical abstract, no animations)

Language English

Fees 10 € contribution (coffee breaks and lunch included)

Payment at the registration desk

Programme
Friday, December 1st

9.00 – 9.30 Registration

Introduction

9.30 – 9.10 Welcome

Konrad Fiedler, Head of the Department of Botany and Biodiversity Research

Sabine Agatha, President of NOBIS Austria

9.40 – 10.10 Keynote **Gerald Schneeweiss**: The phylogeny and evolution of the non-photosynthetic parasitic broomrapes (Orobanchaceae)

10.10 – 10.30 **Christoph Hahn**: The hyperdiverse fish-parasite genus *Gyrodactylus* – barcoding challenges and genomic insights into the evolution of selected species

10.30 – 11.00 Coffee break

NOBIS Award: Master Students

Chair: **Frank Zachos**

11.00 – 11.20 **Hannah Schmidbauer**: A comparative study on the nervous system of Syllidae (Annelida: Phyllodocida)

11.20 – 11.40 **Maximilian Wagner**: Cryptic diversity in pebble beaches: Rapid speciation and convergent evolution in the genus *Gouania* (Gobiesocidae)

11.40 – 12.00 **Lukas Zangl**: Up for surprises – the story of Austria's gudgeons

12.00 – 12.20 **Sabine Schoder**: The *Hylaeus brevicornis* group revisited – an integrative approach to delimit four closely related species of masked bees (Hymenoptera: Apidae)

12.20 – 13.30 Lunch break (buffet)

NOBIS Award: PhD Students

Chair: **Julia Walochnik**

- 13.30 – 13.50 **Andrea Lienhard:** Mites of the Caribbean! The biodiversity and biogeography of intertidal Oribatida (Acari)
- 13.50 – 14.10 **Alice Laciny:** Caste evolution and characterization in “exploding” ants
- 14.10 – 14.30 **Anne-Sarah Ganske:** On the significance of morphological characters of head structures for the systematics of the centipede genus *Lithobius* (Myriapoda)
- 14.30 – 14.50 **Martin Schebeck:** RAD Sequencing helps to unravel the phylogeography of the spruce bark beetle *Pityogenes chalcographus* (L.)
- 14.50 – 15.10 **Umilaela Arifin:** Revisiting phylogeny of *Huia* Yang, 1991 (Amphibia: Ranidae) reveals unexpected *Huia* diversity and taxa new to science: case study Sumatra, Indonesia

15.10 – 15.40 Coffee break

15.40 – 16.10 Poster session, Chair: Stephan Koblmüller

Closing Session

- 16.10 – 16.30 **Agnes Dellinger:** Floral trait convergence and functional differentiation in accordance with pollinator shifts in Merianieae (Melastomataceae)
- 16.30 – 16.50 **Andreas Kroh:** Phylogeny & evolution of edible sea urchins
- 16.50 – 17.10 **Sabine Agatha:** Handing over of the NOBIS Award and closing words

Abstracts

Revisiting phylogeny of *Huia* Yang, 1991 (Amphibia: Ranidae)
reveals unexpected *Huia* diversity and taxa new to science:
case study Sumatra, Indonesia

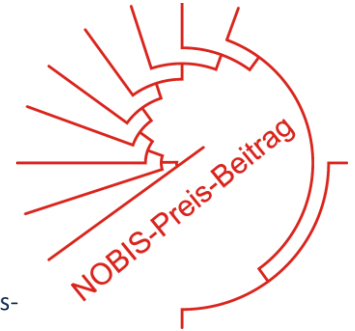
Arifin, U.¹, Smart, U.², Hertwig, S.³, Smith, E.², Iskandar, D.T.⁴ & Haas, A.¹

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The systematics and phylogenetic position of the Asian frogs of the genus *Huia* has been unstable through time and has not been resolved convincingly. Currently, five valid species (*H. cavitympanum*, *H. masonii*, *H. sumatrana*, *H. modigliani*, and *H. melasma*) are known under this genus. All of them are associated with cascading, clear streams and possess gastromyzophorous tadpoles, although larval forms of the last two species are still unknown. In extensive fieldwork, we compiled broad samples from Sumatra and Java including the hitherto most comprehensive taxon sample of *Huia*. We analysed DNA markers (mtDNA: *12S*, *16S*, *COI*, *Cyt-b*, and nucDNA: *Rag1*, *Tyr*, *POMC*; total length 5,112 bps) from *Huia* and taxa that are believed to be close relatives (*i. e.*, *Amolops*, *Meristogenys*, and other riparian ranids) in order to solve current phylogenetic uncertainties. Confirming the previous hypotheses, *Huia* species did not form a monophyletic group because the type species (*H. cavitympanum*) was more closely related to *Meristogenys* from Borneo than the other species in *Huia*. Our analysis discovered that the genus *Huia* is more diverse than previously thought with two new candidate species from Sumatra and Java. Furthermore, we could show the existence of another well-delimited genus from Sumatra that possess gastromyzophorous larva, but is clearly distinct from *Huia*. Thus, taxonomic amendment is indeed necessary to resolve the paraphyly of *Huia* among ranids with gastromyzophorous tadpoles. This study is yet another example of previously underestimated Southeast Asian frog diversity.

Floral trait convergence and functional differentiation in accordance with pollinator shifts in Meranieae (Melastomataceae)

Dellinger, A.S.¹, Artuso, S.², Fernández-Fernández, D.³, Penneys, D.S.⁴, Michelangeli, F.A.⁵, Alvear, M.⁶, Almeda, F.⁶ & Schönenberger, J.¹

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Flowers are integrated structures with organs co-functioning to achieve pollinator attraction and pollen transfer and recurring trait convergence in association with specific functional pollinator groups is known as pollination syndromes. Despite overall integration, floral organs carry different functions in pollination and thus underlie different selective pressures, particularly apparent in the comparison of closely related taxa whose pollinators have shifted from one functional group to another.

Our study focuses on the Neotropical tribe Meranieae (Melastomataceae) as a model system for the study of pollinator mediated selection on floral traits. The Meranieae are characterized by repeated independent shifts from bee to hummingbird/bat/rodent, and passerine pollination. We combine qualitative trait mapping with a modern micro-CT 3D-geometric morphometric assessment of flowers across 60 Meranieae species. Our goal is (i) to challenge the concept of pollination syndromes and evaluate its applicability in Meranieae and (ii) to pinpoint functional trait differentiation in pollen transfer mechanisms between the different pollination systems.

We find support for the concept of pollination syndromes in the Meranieae with convergence in floral shape and function in relation to the different pollinators. Particularly strongly affected floral traits include reward type, stamen appendage shape, thecal wall structure as well as size of the staminal pore, all of which are related to different pollen expulsion mechanisms. Furthermore, geometric morphometric analyses of 3D landmark data highlight changes in patterns of floral integration, with changes of corolla function associated with shifts from bee to bird pollination, and a loss in function of stamen appendages as triggers of pollen expulsion mechanisms in hummingbird pollinated species.

Comparative developmental staging of cichlid species from the three Great East African Lakes

Dreo, B., Gallaun, J., Singh, P. & Sturmbauer, C.

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Cichlid fish research has increasingly focused on the development and the underlying gene networks of the feeding apparatus, which is an important basis for ecological divergence and speciation (Fryer & Iles 1972). Yet, little is known about the timing of the crucial steps in chondrogenesis and skeletogenesis during craniofacial development, particularly across the major cichlid fish radiations in Africa. We examine 12 mouthbrooding haplochromines from Lakes Tanganyika, Malawi, and Victoria adapted to corresponding trophic niches, to identify intra- and inter-specific differences in oral and pharyngeal jaw development. We established a larval staging timeline to compare larval development across species from the point of hatching to the end of post-embryonic development (stage 26). To quantify differences in ossification we carried out bone/cartilage staining, and measured area of bony and cartilaginous tissue in the oral and pharyngeal jaws. Additionally, 2D geometric morphometrics analysis of jaw elements was conducted. Preliminary results show a decreasing larval period duration in species from Lake Tanganyika to Lake Malawi to Lake Victoria. Our analysis indicates that Lake Victoria species are pre-mature in terms of craniofacial development at stage 26, when the yolk-sac is absorbed, and the larvae are released from the mother's mouth, compared to the Lake Malawi and Tanganyika species. This means that Lake Malawi and even more dramatically, Lake Tanganyika species, continue larval development to a more mature stage, probably due to larger yolk mass, before becoming independent. The markers to define the end of the larval period should therefore be distinguished from the markers for larval craniofacial skeletogenesis.

References

Fryer, G., Iles, T.D., 1972. *The Cichlid Fishes of the Great Lakes of Africa, their Biology and Distribution*. Oliver and Boyd, Edinburgh.

Evaluating information content of molecular phylogenies in tintinnid ciliates (Alveolata, Ciliophora, Choreotrichia)

Ganser, M. & Agatha, S.

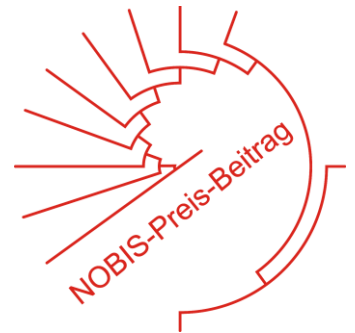
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Molecular phylogenies based on different rDNA loci are an important tool for inferring relationships. Especially in tintinnid ciliates with their artificial, lorica-based classification, gene sequence analyses provide the most comprehensive insight into genealogies. While taxon diagnoses in ciliates comprise morphological characters, autapomorphies in genetic data, *i. e.*, signature nucleotide positions, are usually not determined. Likewise, the quality of the historical signal contained in the alignments is not examined prior to establishing the phylogenetic trees in tintinnids. Therefore, two different methods were applied for assessing the phylogenetic content of sequence data of choreotrichid ciliates and specifically of the order Tintinnida. They allowed distinguishing historical (molecular synapomorphies) from non-historical signals (molecular homoplasies) in sequences of ribosomal RNA genes obtained from GenBank. First, a phylogenetic network was computed, visualizing the dataset and characterizing consistent and conflicting information. Secondly, a split spectrum analysis was applied for identifying the number and quality of the nucleotide positions responsible for the statistical support of tree nodes. The results demonstrate the potential as well as the limitations of the presently used molecular markers for resolving the relationships of certain tintinnid groups. They also indicate accidental sequence resemblance which can cause high support values in tree calculations, but are actually the result of long-branch artefacts. The implementation of these methods might also reveal apomorphies in the sequence data usable for characterizing particular tintinnid clusters in the phylogenies. This study is supported by the Austrian Science Fund (FWF Project I 3268).

On the significance of morphological characters of head structures for the systematics of the centipede genus *Lithobius* (Myriapoda)

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Traditional taxonomic characters are with no doubt insufficient to draw an overview of the species-interrelationships within the centipede genus *Lithobius* Leach, 1814 (> 500 spp.) and its systematic position within the Lithobiidae. Previous research demonstrated that cuticular structures of the mouth and the preoral chamber bear phylogenetically useful information (e. g., Edgecombe *et al.* 2002; Koch & Edgecombe 2008). In the present study, we explore the microanatomy of the peristomatic structures (epipharynx, hypopharynx), the mandibles, and the first maxillae of 32 species of four lithobiid genera: *Lithobius* (29 spp.), *Eupolybothrus* Verhoeff, 1907 (1 sp.), *Neolithobius* Stuxberg, 1875 (1 sp.), and *Disphaerobius* Attems, 1926 (1 sp.) with scanning electron microscopy (SEM) and microcomputed tomography (μ CT). Eight characters from the peristomatic structures have now been defined and further characters are checked from the gnathal edge of the mandible and the coxal projection of the first maxillae. The present morphological research, which will be supplemented with molecular analyses, underlines the phylogenetic significance of the head structures for the phylogeny of genus *Lithobius*.

References

- Edgecombe, G.D., Giribet, G., Wheeler, W.C. 2002. Phylogeny of Henicopidae (Chilopoda: Lithobiomorpha): A combined analysis of morphology and five molecular loci, *Systematic Entomology*, 27, 31–64.
- Koch, M., Edgecombe, G.D. 2008. The peristomatic structures of lithobiomorpha (Myriapoda, Chilopoda): Comparative morphology and phylogenese significance, *Journal of Morphology*, 269, 153–174.

Morphology of *Tintinnopsis everta* (Alveolata, Ciliophora, Spirotricha) suggests homology of posterior and second dorsal kinety

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Molecular and preliminary cladistic analyses strongly indicate that the current lorica-based classification of the tintinnid ciliates is artificial. To fully understand the phylogeny and ecology of tintinnid ciliates (Alveolata, Ciliophora, Spirotricha), knowledge on their cell features is urgently required beyond the lorica characteristics. *Tintinnopsis everta* was discovered in the Kiel Bay by Laackmann in 1908 and lives in the plankton of marine and brackish coastal waters. The species is redescribed from the east coast of the USA based on live observation, protargol-stained material, scanning electron microscopy, and genetic analyses. It falls into the large group of tintinnids with the most complex somatic ciliary pattern (with a right, left, and lateral ciliary field as well as ventral, dorsal and posterior kineties), but demonstrates some unique features: the posterior kinety is left of the left ciliary field (vs. below the left or lateral ciliary fields) and the distance between the ciliary fields and the collar membranelles is extraordinarily wide. Its unique position and dikinetidal structure with cilia associated only with the posterior basal bodies suggest a homology of the posterior kinety with the second (left) dorsal kinety. Congruent with the morphological findings, the species is consistently placed among the tintinnids with the complex ciliary pattern in the gene trees, but its closed relatives could not reliably be determined as the species' placement differs somewhat between the Bayesian Inference, Maximum Likelihood, Maximum Parsimony, and Neighbor Joining analyses and is not well supported. The study was financially supported by the Austrian Science Fund (Project P 28790).

The hyperdiverse fish-parasite genus *Gyrodactylus* – barcoding challenges and genomic insights into the evolution of selected species

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The genus *Gyrodactylus* (Monogenea, Platyhelminthes) contains an estimated number of 20,000 species worldwide, with only little over 400 formally described to date. These fish ectoparasites are characterized by high host specificity and a unique assemblage of reproductive features (hyperviviparity, progenesis). Taxonomy is traditionally based on host species and the morphology of the hook apparatus, which they use to attach to their hosts. Due to morphological conservatism, cryptic diversity may be assumed to be common in this taxon, but further systematic molecular investigations are hampered by the lack of reliable generic barcoding primers for the genus. In the course of the ABOL (Austrian Barcode of Life) initiative we are working towards establishing primers and efficient protocols to ultimately reveal and characterize *Gyrodactylus* diversity on fish species in Austria and worldwide. Arguably the best-studied gyrodactylid on the planet is *Gyrodactylus salaris*, a notorious pathogen of European salmonids, infecting host species as diverse as Atlantic salmon, Arctic charr, rainbow trout and European grayling. Despite decades of research, however, the complex evolutionary history of the species is still surprisingly poorly understood and especially the lack of phylogenetic resolution with respect to isolates from the latter host species (*Gyrodactylus thymalli*) fuels debates about the taxonomic status of these lineages, despite some evidence for host specificity mediated pre-zygotic reproductive isolation. Based on whole-genome sequencing (WGS) data obtained for multiple lineages of *G. salaris* and *G. thymalli*, we inferred fully resolved phylogenetic relationships that are incongruent with previous results, including mitochondrial markers. The dataset includes isolates obtained from five salmonid host species and we used the population-level data to scan the gyrodactylid genomes for regions of increased divergence, sometimes called ‘genomic islands of speciation’, and key genes under positive selection, between the evolutionary lineages infecting different host species.

And then there were four – hidden genetic diversity within the cyprinid freshwater fish *Garra barreimiae* from Oman

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The North of the Sultanate of Oman is characterized by the Al Hajar Mountains, which consist of anticlinal folds of limestone and dolomites. It is a harsh and arid environment with high mountain peaks and many wadis, which occasionally dry out. Only some of the bigger ones carry water permanently. These water bodies are inhabited by the cyprinid *Garra barreimiae*, which is endemic to the northern Oman and the UAE. Within this species, three subspecies have been described: *G. b. barreimiae* Fowler & Steinitz, 1956, *G. b. shawkahensis* Banister & Clarke, 1977, and *G. b. gallagheri* Krupp, 1988. The latter has been lifted to species status recently. In the present phylogeographic study, we investigated the species' genetic diversity using mitochondrial (CR, *COI*, *Cytb*) and nuclear (microsatellite) markers. The analyses based on mt data display a high genetic diversity, resulting in four well-defined clades. This is also supported by the microsatellite data, which highlights substructuring within the clades. These clades have different geographic distributions which are in accordance with the drainage systems of the Al Hajar Mountains. Between these clades the genetic distances are high and in the range of those between *G. barreimiae* and the closely related *Garra rufa*. A recent study showed that these groups are morphologically variable and only few meristic characters separate the West clade from the others (Pichler *et al.*, submitted). While the West clade comprises samples of both subspecies *G. b. barreimiae* as well as *G. b. shawkahensis*, the remaining three clades correspond to not yet described taxa. Our results clearly show cryptic variability within *G. barreimiae* and will help to decipher the taxons' historic background. Consequently, as *G. barreimiae* is not monophyletic according to our results, this study depicts the necessity for a revision of this group from Oman, which should cover the three newly discovered clades and establish them as species.

Phylogeny & evolution of edible sea urchins

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Sea urchins of the order Camarodonta evolved roughly 100 Million years ago in the mid-Cretaceous Period. For a long time, they encompassed mainly small and often rare forms occurring in the carbonate deposits of the European shelf. Only in the Late Eocene, approximately 40 Million years ago, after the Paleocene/Eocene Thermal Maximum Event (the most extreme global warming event known to date), camarodont echinoids experienced massive radiation. Within a comparatively short time span of about 10 million years all of the modern camarodont families evolved, as did many of the modern camarodont genera. This radiation coincides with the rise of modern-type scleractinian coral reefs. Indeed, many of the camarodonts existing today are associated with reefal environments.

Modern camarodont echinoids are important components of diverse marine environments, largely due to their extensive ecological impact. Some researchers consider echinoids to be the single most important group of consumers to live in shallow marine habitats, ultimately controlling the structure and function of a wide range of marine communities including kelp forests, seagrass beds and coral reef ecosystems. They are intensively used in scientific studies on reproduction and development and serve as model organisms in classroom education. Human interest, however, is not limited to scientific aspects of camarodonts – their reproductive organs are considered a delicacy and camarodont sea urchins are heavily exploited by a multimillion-dollar fisheries industry.

A new research project (FWF P29508-B25), sponsored by the Austrian Science Fund (FWF) aims to decipher the origin and evolutionary history of camarodont sea urchins. In order to achieve this goal, genetic information at the genome level, will be combined with an in depth morphological analysis. Phylogenomic methods will provide significantly more genetic data than currently available, allowing for more robust results. The first occurrences of camarodont sea urchins in the geological record (*i. e.*, fossils) will be used to infer minimum ages of individual groups within camarodonts. Cladistic morphological analysis will be used to create a joint phylogenetic tree for extant and extinct camarodonts.

A large amount of sequence data alone, however, is insufficient to infer robust and accurate phylogenetic trees – as the problem often lays in sorting and matching the relevant sequences among the different samples to facilitate meaningful comparisons. Within the proposed project, specific portions of the genome will be targeted and enriched in order to improve the capture success of orthologous sequences.

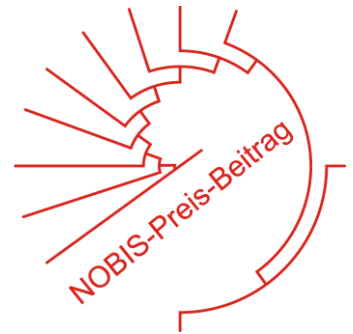
Caste evolution and characterization in “exploding” ants

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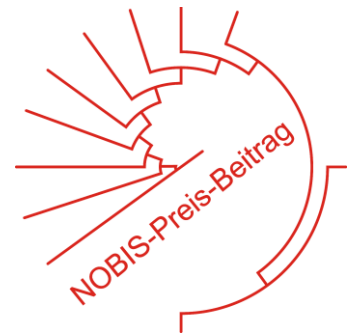
Based on molecular and morphological data, the systematic relationships within the ant subfamily Formicinae in general and the tribe Camponotini in particular have been subject to major changes in the past few years. This diverse and widespread tribe is particularly known for the occurrence of specialized castes within certain clades. Especially, the phragmotic major workers of the newly resurrected genus *Colobopsis* show a broad range of caste-specific morphological adaptations. The evolution and characterization of these strikingly altered castes has been a matter of scientific dispute for decades and most studies on the subject lack extensive morphometric data and statistical analysis. By combining morphometry, microCT and multivariate statistics, we aim to characterize the different castes of the genus *Colobopsis* and its relatives. This work is set within the framework of the multidisciplinary WWTF project “Voluntary self-sacrifice in exploding ants: a mechanism to defend coevolved microbiomes?” – The project focusses on the ecology and evolution of the extraordinary Southeast-Asian *Colobopsis cylindrica* (COCY) group, which has evolved a unique defensive behaviour: In territorial combat, they sacrifice themselves by rupturing their integument to release the sticky and irritant contents of their hypertrophied mandibular glands. The COCY group largely consists of undescribed species with unresolved phylogeny – a question addressed within the project by a combined approach of DNA barcoding and morphometric analysis.

In addition, studies on COCY ants have led to the discovery of several morphologically aberrant mermithogynes – intercaste specimens infected by parasitic nematodes. The study of these parasite-induced morphological changes and the underlying developmental paths can provide valuable insight into phenotypic integration, plasticity, developmental modularity, and the evolution of novel castes.

Mites of the Caribbean! The biodiversity and biogeography of intertidal Oribatida (Acari)

Lienhard, A., Pfingstl, T. & Koblmüller, S.

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Only a few taxa of the mostly terrestrial oribatid mites inhabit marine associated habitats. The majority of these taxa belong to the superfamily Ameronothroidea. These mites are air-breathing organisms and can survive in habitats subject to daily tidal inundation. The ameronothroid families Selenoribatidae and Fortuyniidae have a transoceanic distribution but are restricted to the intertidal zone of subtropical and tropical coasts. So far, genetic data on Caribbean intertidal Oribatida have been lacking. Here, we present a preliminary phylogeny, based on mitochondrial and nuclear DNA, of species belonging to six selenoribatid and three fortuyniid genera from Central and North America and from several Caribbean islands (Antilles, Bahamas), collected from algae samples growing on sandy and rocky substrates, on mangrove roots, or on man-made structures. Species delimitation methods were employed to obtain a first estimate of species diversity based on mitochondrial COI sequences. Additionally, phylogeographic patterns were compared and found to be strikingly different among several taxa.

RAD Sequencing helps to unravel the phylogeography of the spruce bark beetle *Pityogenes chalcographus* (L.)

Schebeck, M.^{1*}, Dowle, E.J.², Avtzis, D.N.³, Bertheau, C.⁴, Schuler, H.¹, Feder, J.L.⁵, Ragland, G.J.² & Stauffer, C.¹

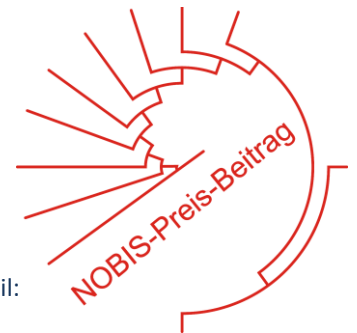
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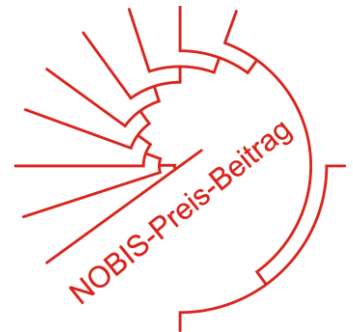
Present distribution and genetic structure of organisms were shaped by past climatic oscillations, *e. g.*, changes in temperature during the Pleistocene. During the last glacial maximum Europe was covered by a thick ice shield in northern regions and high elevation areas, and survival was only possible in glacial refugia. The spruce bark beetle, *Pityogenes chalcographus* (L.), is an insect with a life cycle closely associated with its main host tree Norway spruce. It is hypothesized that both species shared the same glacial refugia. Postglacial warming led to a range expansion and recolonization of Europe.

We reassessed the glacial and postglacial history of *P. chalcographus* by studying individuals from a huge part of the beetle's range. We applied ddRADSeq to disentangle the present genetic population structure and to infer glacial and postglacial processes. We confirmed and re-evaluated three glacial refugia in the Apennine-Dinaric region, in the Carpathian Mountains and in the Russian plain. Present genetic structure was strongly influenced by secondary contact during warm periods and the insect's reproductive and dispersal behavior. Population structure analyses revealed a high level of gene flow across populations leading to a shallow genetic structure and a low level of population differentiation.

A comparative study on the nervous system of Syllidae (Annelida: Phyllodocida)

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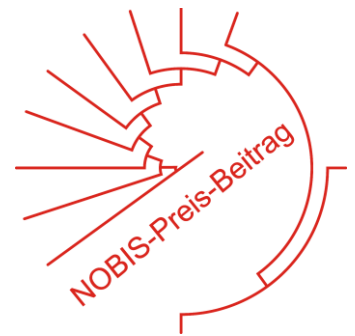
Syllidae are a diverse family of annelids within the order Phyllodocida. They are distributed worldwide in a variety of marine habitats. Even though the family comprises a vast number of species and thus forms an important part of marine diversity, their evolutionary relationship to other annelid families remains uncertain. Confocal laser scanning microscopy (CLSM) and immunocytochemical staining offer the opportunity to produce data on the three-dimensional architecture of the nervous system of small animals. So far little data is available on syllid nervous systems and additional information could yield insight into their relationships to other Phyllodocida. The focus of this study is to describe the complete nervous system of five selected species from two subfamilies with immunocytochemistry, CLSM and histological methods. Three of the species (*Syllis garciai*, *S. tyrrhena* and *Plakosyllis brevipes*) belong to the subfamily Syllinae and two (*Prosphaerosyllis marmarae* and *Sphaerosyllis taylori*) to the subfamily Exogoninae. Special attention is given to differences and similarities between subfamilies and species and the evaluation of novel neuromorphological characters. Many analysed features of the nervous system are similar in both subfamilies, such as the number of ventral, segmental and longitudinal nerves, the brain, the innervation of appendages and the stomatogastric nervous system. These features are possibly part of the ground pattern in Syllidae. In both species of Exogoninae the somata of the brain form a pair of dorsal lobes, which may be an autapomorphy of the subfamily Exogoninae, but data on more species is necessary to confirm this assumption. Several other features are species specific and not consistent within one subfamily. At present too little data on other families within the Phyllodocida is available to draw conclusions on the position of Syllidae in regard to other phyllodocid families. However, the present results are the first detailed study for future comparisons of families of the Phyllodocida concerning systematic and phylogenetic relationships.

The *Hylaeus brevicornis* group revisited – an integrative approach to delimit four closely related species of masked bees (Hymenoptera: Apidae)

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Hylaeus (masked bees) is a genus of solitary bees, consisting of 47 species in Central Europe. Four morphologically similar species of the subgenus *Dentigera*, *Hylaeus brevicornis* Nylander, 1852, *Hylaeus gredleri* Förster, 1871, *Hylaeus intermedius* Förster, 1871, and *Hylaeus imparilis* Förster, 1871, were studied in order to search for differences in ecology and morphology. To clarify their still ambiguous relatedness, pollen analyses of the crop content, as well as molecular and morphometric analyses were carried out. The specimens were collected on the area of the former Nordbahnhof in Vienna, where the species syntopically occur.

Females of *Hylaeus* do not have an exterior scopa, but the pollen is swallowed and transported in a crop. The females were dissected by cutting off and opening the metasoma to study the crop content. Pollen analyses showed that the four investigated *Hylaeus* species are generally polylectic, collecting pollen of different plant families. They do have preferences for plants with small florescence like Apiaceae, Brassicaceae and Crassulaceae, depending on availability, though. Between the species no significant differences in pollen composition could be detected.

One leg of each individual was cut off and stored in 96% ethanol for molecular analyses. Results gained from DNA barcoding largely agreed with previous studies and supported the determination on basis of morphology. While *H. brevicornis*, *H. imparilis*, and *H. gredleri* were proven to be monophyletic, "*H. intermedius*" in the present sense turned out to be polyphyletic, consisting of at least two distinct species in this sample. Differences between the species were also recovered by morphometric measurements of head structures. However, large intraspecific size variation, especially in *H. gredleri* and *H. intermedius*, complicate a reliable determination of females on basis of morphology. This problem should be revisited in the light of a two-species-hypothesis of *H. intermedius*.

Cryptic diversity in pebble beaches: Rapid speciation and convergent evolution in the genus *Gouania* (Gobiesocidae)

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Gouania willdenowi (Risso, 1810), the sole representative of the monotypic clingfish genus *Gouania*, is endemic to the Mediterranean Sea, where it lives a very cryptic and secretive life in the interstices of pebble beaches. With its wormlike body and small eyes it is perfectly adapted to this extreme environment. Because of a reduced swim bladder and a very patchy distribution of suitable habitats, adult *G. willdenowi* are very weak active dispersers and dispersal likely happens passively during the pelagic larval phase. Despite being quite common in pebble beaches throughout the Mediterranean, hardly anything is known about its biology, behaviour, phylogeny or taxonomy.

DNA-barcoding, species tree analysis (*BEAST) including nine nuclear and one mitochondrial marker, as well as geometric morphometric analyses and MicroCT imaging across the whole Mediterranean Sea, yielded unexpected results regarding the evolutionary history of this genus. Molecular data suggests that the genus *Gouania* underwent a thus far unrecognized radiation into several fairly divergent species that started around 1.5–4 million years ago, after the Messinian Salinity Crisis. Moreover, whereas little diversity is seen in the western Mediterranean basin, convergently evolved syntopic species pairs (consisting of a gracile, elongate morph and a stockier morph) are found throughout the eastern basin (including the Adriatic Sea). Apparently, the extremely low active dispersal ability of adults implies that dispersal – even over short distances – happens exclusively via larval drift with water currents and that populations/species remain trapped in particular circulation systems. The eastern basin (including the Adriatic Sea) with its numerous islands is characterized by complex local circulation systems that might drive the evolution of locally confined species in the clingfish genus *Gouania*. To conclude, the radiation of *Gouania* represents a promising model system for studying rapid radiation and the independent origin of eco-morphologically similar species pairs, and the role of water currents for driving diversification in the marine environment.

Barcoding Austria's damselflies and dragonflies – From the first steps to flying high

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The order Odonata, consisting of the suborders Anisoptera (dragonflies) and Zygoptera (damselflies), is one of the oldest groups of winged insects and originated more than 300 Million years ago. Even though the number of recognized species is fairly small compared to other groups of insects (both on a global and local scale), they are very important flagship taxa and bioindicators for conservation management and ecological project planning, as they are comparatively well-known and appreciated by the non-scientific society. To barcode the close to 80 different species of damsel- and dragonflies reported for Austria, the University of Graz, within the framework of ABOL (Austrian Barcode of Life), and the Museum of Natural History Vienna, within an ABOL associated project "Dragonflies in Vienna: DNA-Barcoding and survey, with focus on FFH-species *Cordulegaster heros* and *Leucorrhinia pectoralis*", have joined forces. New sets of Odonata-specific primers have been designed, a large number of species (and specimens) has already been collected, and the first DNA-barcodes have been generated. However, this is just the beginning and lots of effort (and enthusiasm) will be put into collecting and sequencing specimens of all species from throughout Austria to finally be able to provide a complete DNA-barcode reference data base for Austrian damsel- and dragonflies.

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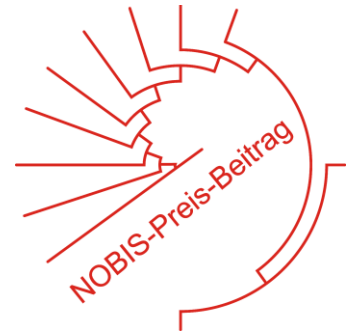
Up for surprises – the story of Austria's gudgeons

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Gudgeons (subfamily Gobioninae) are a group of ecologically and morphologically diverse small cyprinid fishes that is distributed throughout Eurasia. Only two genera, *Gobio* and *Romanogobio*, both of which comprise bottom-dwelling, mainly riverine species are native to Europe. Although taxonomy and systematics of *Gobio* and *Romanogobio* in general have been the matter of a long-standing debate, the number and identity of gudgeon species native to Austria has been thought to be well known. Two species, *G. gobio* and *G. obtusirostris* have been reported for Austria, with a potential hybrid zone in the upper Danube. Phylogenetic and phylogeographic analysis of mitochondrial COI and control region sequences, as well as nuclear ribosomal protein S7 sequences, however, shows that the proposed hybrid zone is not restricted to the upper Danube, but spans large parts of the Austrian Danube system (upper Danube, Rába, and Mur systems). Moreover, our data show that also a third lineage, closely related to species from the southern Balkan, contributed to the gene pool of Austrian *Gobio*. Patterns of intra-lineage genetic diversity indicate that the distinct *Gobio* lineages expanded their distribution recently (most likely post-glacially) to come into secondary contact and hybridize in the Danube system.

Additionally, three species of the genus *Romanogobio*, namely *R. kesslerii*, *R. uranoscopus*, and *R. vladkovi*, have been assumed to occur in Austria. However, our DNA-barcoding data show that (i) the Upper Mur River is inhabited by a thus far unknown *Romanogobio* species (also supported by morphological data) and (ii) the fish previously believed to be *R. kesslerii* is in fact *R. banaticus*.

Phylogeny, morphology and pollen preferences of five Austrian species in the *Colletes succinctus* group (Hymenoptera: Apidae)

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Colletes Latreille, 1802 is a solitary bee genus with almost worldwide distribution (except Australia). The common name “polyester bees” derives from a characteristic cellophane nest lining produced by the Dufour gland and applied with the tongue (Westrich 1990). This study focuses on the *Colletes succinctus* group, which is problematic in regard to species delimitation. In Austria five species of this group fly from late summer to autumn, with one generation per year. Regarding their pollen preferences, they are classified as either polylectic, pseudo-oligolectic, or oligolectic (Müller & Kuhlmann 2008; Teppner & Brosch 2015). The oligolectic behaviour and habitat preferences were sometimes used for identification of females, which are difficult to separate by morphology. We will perform morphological studies (morphometry, analyses of genitalia and microstructures by scanning electron microscopy) in order to find so far unrecognized characteristics and to determine whether the species can be safely differentiated. Specimens collected in September and October 2017 in Vienna, Lower Austria, and Burgenland as well as those from the collection of the Natural History Museum Vienna will be sorted to species level based on morphology and DNA-barcoding. In addition, the bee-collected pollen will be analysed to determine how plant-specific the species are within a small geographic range. We thereby aim to develop a better understanding of phylogeny, morphology and pollen preferences of eastern-Austrian members of the *Colletes succinctus* group.

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Genetic structure of cheetah populations through genome-wide ddRAD sequencing

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The cheetah (*Acinonyx jubatus*) consists of five subspecies, of which four are distributed over Africa, but only one critically endangered population (*A. j. venaticus*) exists in Asia and is present in Iran (Charruau, 2011). Due to short divergence times between some of the subspecies, there have been discussions launched by the IUCN Cat Specialist Group (<http://www.catsg.org>) recently to collapse cheetahs into only two subspecies. This makes a re-evaluation of the phylogeographic structure on a larger scale necessary, and currently the Research Institute of Wildlife Ecology (FIWI), Vetmeduni Vienna, is the only institute with a sample set of not only global, but also historic samples, which makes this re-evaluation of population structure possible. Based on previous studies, our hypothesis is that the two southern subspecies, *A. j. jubatus* and *A. j. raineyii*, will not show large population differentiation, but we expect long-term divergence between the other three cheetah subspecies, specifically between Asia and Africa. Our goal is to clarify the population structure of *A. jubatus* and its subspecies, not only for recent populations and their distribution, but also historically. For this, 96 individuals covering the historic distribution of cheetahs will be re-evaluated by ddRAD, double digest restriction-site associated DNA sequencing, (IGA Technologies, Udine, Italy). The samples mainly originate from a historic sample set, collected by Léna Godsall Bottriell and Paul Bottriell from the Rex Foundation, UK, and their DNA was extracted in the cleanroom-laboratory at FIWI via a modified Rohland *et al.* (2010) aDNA protocol. Additionally, some fresh tissue samples were extracted with the Qiagen DNeasy Kit. Through ddRAD, a genome wide set of SNPs will be received. This method is particularly suitable for our project, as it will most likely provide a large set of markers (min. 20,000 SNPs), which ensures for population parameters to be estimated more precisely (Davey, 2011) than previously. The R package Adegenet (Jombart, 2008) will be used for calculating and graphically displaying summary statistics, as well as population structure via principal component analysis (PCA) and discriminant analysis of principal components (DPCA). In addition, we will use Bayesian analysis to detect population structure and admixture using the software fastStructure (Raj *et al.*, 2014). Finally, Bayescan will be used to screen for loci under potential selection, which will provide information on adaptive polymorphisms. Further demographic analyses will investigate population size changes over time. The results of this project will have a high impact on the current conservation and management strategies of endangered cheetah populations in Africa and Asia.

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