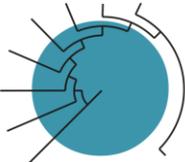




München 2014

N  B I S AUSTRIA 8

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# Crossing Borders

Gastgeber

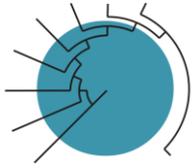
Prof. Gerhard Haszprunar

Zoologische Staatssammlung München



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München 2014

N  B I S AUSTRIA 8

München 2014



**Veranstaltungsort** Zoologische Staatssammlung München

**Organisation** Gerhard Haszprunar

**Vorträge** 15+5 Minuten

**Sprache** Deutsch oder Englisch

**Poster** A0 (Portrait-Format)

**Tagungsbeitrag** NOBIS-Mitglieder: € 10.-; Nicht-Mitglieder: € 30.-

## Programm

**Freitag, 28. November**

Anreise

13.30 Führung durch die Zoologische Staatssammlung München ZSM

15.00-16.30 Generalversammlung (Hörsaal ZSM)

16.30-18.00 Registrierung bzw. 2. Führung

18.30 Verleihung der Ritter-von-Spix-Medaille und Festvortrag

ca. 20.00 "Bayerische Brotzeit"

**Samstag, 29. November**

8.30-9.00 Registrierung

9.00-9.10 Begrüßung durch

Gerhard Haszprunar, Direktor der Zoologischen Staatssammlung

München

Mathias Harzhauser, Präsident von NOBIS Austria

Vortragsprogramm

NOBIS-Preis Beiträge

Chair: Gerhard Haszprunar

9.10-9.30 **Georgopoulou, E.**, Neubauer, T. A., Harzhauser, M., Kroh, A. & Mandic, O.: European freshwater gastropods: major patterns of biodiversity and biogeographical processes.

9.30-9.50 **Hyžný, M.**, Klompaker, A. A. & Portell, R. W.: The ghost shrimp *Glypturus* in space and time: systematics, diversity, taphonomy and (palaeo)-biogeography.

9.50-10.10 **Macek, O.**, Bodner, M., Bartel, D., Szucsich N., Raspotnig, G. & Pass, G.: Uncoiling the diversity of Austrian pill millipedes (Glomerida) using an integrative taxonomic approach.

10.10-10.30 **Sann, M.**, Mayer, C., Niehuis, O., Donath, A., Peters, R. S., Bleidorn, C. & Ohl, M.: A novel target enrichment strategy for phylogenomic analyses of sphecid wasps.

10.30-10.50 **Nebel, C.**, Anderson, G., Gamauf, A., Haring, E., Segelbacher, G., Villers, A. & Zachos, F. E.: Phylogeographic analysis reveals Holarctic homogeneity and a distinct circum-Mediterranean lineage in golden eagles (*Aquila chrysaetos*).

10.50-11.10 Kaffeepause

Vortragsprogramm

Chair: Sabine Agatha

11.10-11.30 **Foissner, W.:** Protist distribution: 100 new neotropic soil ciliates emphasize moderate ciliate endemism.

11.30-11.50 **Neubauer, T. A.,** Harzhauser, M., Kroh, A., Georgopoulou, E. & Mandic, O.: Paleobiogeographic regions for European Neogene freshwater systems: a trend toward increasing provincialism.

11.50-12.30 Poster-Session moderiert durch Julia Walochnik  
(2 Minuten pro Poster)

12.30-14.00 Mittagspause mit Buffet im ZSM

Vortragsprogramm

Chair: Christian Sturmbauer

14.00-14.20 Schneider, K., Koblmüller, S. & **Sefc, K. M.:** Automated tree based screens for hybrid signals in multilocus (AFLP and SNP) datasets.

14.20-14.40 **Jaksch, K.,** Haring, E., Eschner, A. & Fehér, Z.: Treasured genes in museum collections.

14.40-15.00 **Kroh, A.,** Bronstein, O. & Haring, E.: Conflicting genetic signals in the Red Sea collector urchin: Mitochondrial and nuclear markers show different patterns.

15.00-15.20 **Kropf, M.,** Bardy, K., Höhn, M., Thiv, M. & Plenk, K.: Genetic diversity patterns of steppe plants across borders in Central Europe.

15.20-15.50 Pause

Vortragsprogramm

Chair: Luise Kruckenhauser

- 15.50-16.10 **Akkari, N.** & Metscher, B.: Innovative approaches, interactive tools and modern imaging: Pushing boundaries in myriapod taxonomy.
- 16.10-16.30 **Shaverdo, H.**, Toussaint E. F. A. & Balke, M.: *Exocelina* diving beetles: large scale environmental change as a driver for lineage diversification across Melanesia.
- 16.30-16.50 **Zimmermann, D.** & Vilhelmsen, L.: Does the head anatomy of Evanioidea clarify the phylogenetic placement of aculeate wasps?
- 16.50-17.10 **Schratt-Ehrendorfer, L.**: Across the scientific border.
- 
- 17.10 **Aspöck, U.**: Zuerkennung des NOBIS-Preises und Schlussworte
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## Abstracts

## Putative Tintinnid Fossils (Alveolata, Spirotricha, Oligotrichea) are actually Acritarcs

Agatha, S.<sup>1</sup>, Lipps, J. H.<sup>2</sup>, Dolan, J. R.<sup>3</sup> & Dunthorn, M.<sup>4</sup>

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Paleontological studies have greatly contributed to our understanding of the evolution of life. Since ciliates (Alveolata, Ciliophora) rarely possess hard parts such as shells that easily fossilise, the scarcity of fossils hampers evolutionary reconstruction in this large and ecologically important clade of microbial eukaryotes. Tintinnids, a group of loricate (house-forming) planktonic ciliates, are the only group that has a significant fossil record ranging from modern sediments to those dating back to the Mesoproterozoic era. The forms older than Jurassic, however, possess characters that cannot be found in extant ciliates (Lipps *et al.* 2013). This also holds for a recently described fossil *Nassacysta reticulata* (Steevens *et al.* 2014), which deviates distinctly in several respects from tintinnids and ciliates in general. Until future studies have conclusively demonstrated that these organisms are most likely extant orchid seeds or fossilised plant remnants, they are best considered *incertae sedis* and are thus regarded as acritarchs (organic-walled microfossils of unknown biological affinity) or remains of some 'other eukaryotes'. To prevent the publication of uncertain taxa as ciliates, which would distort the interpretation of the early ciliate evolution, experts on extant ciliates should always be included in the review process.

### References

- Lipps, J.H., Stoeck, T., Dunthorn, M. 2013. Fossil tintinnids. In: Dolan, J.R., Montagnes, D.J.S., Agatha, S., Coats, D.W., Stoecker, D.K. (eds.): *Biology and Ecology of Tintinnid Ciliates: Models for Marine Plankton*. Wiley-Blackwell, West Sussex: 186-197.
- Steevens, P., Breuer, P., de Ville de Goyet, F., Marshall, C., Gerrienne, P. 2014. A Givetian tintinnid-like palynomorph from Libya. *Rev. Paleobot. Palynol.*, 203, 3-8.

## Innovative approaches, interactive tools and modern imaging: Pushing boundaries in myriapod taxonomy

Akkari, N.<sup>1</sup> & Metscher, B.<sup>2</sup>

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Morphology-based taxonomy is facing a continuous decline and a lack in human and financial resources. Since the time of Linnaeus approximately 1.9 million species have been described, which accounts for only a moderate fraction of global species diversity. This forces taxonomists to look for alternative methods that could catalyze species descriptions as using modern technologies and embracing other disciplines of biosystematics has become vital. In myriapodology, only a few attempts have been made in this respect, ranging from using next generation molecular sequencing to jumping in the vast world of cybertaxonomy.

The relentless development of the open access has increased the pace of digital publishing and tremendously improved the dissemination of the taxonomic information. However, cybertaxonomic applications in myriapodology have remained limited. Here, we briefly review some state-of-the-art innovative approaches and present 3D models of a new species of genus *Ommatoiulus* (Myriapoda, Diplopoda) using X-ray microtomography to discuss the potential of this non-destructive technique in describing new species of millipedes and other organisms.

## Two cases of cryptic species in Polycladida (Rhabdithophora: Platyhelminthes)

Bahia, J.\* , Padula, V. & Schrödl, M.

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Plathelminthes of the order Polycladida live in all marine environments from coral reefs and rocky shores to soft bottoms in all oceans. Their main characteristic is their simple, flat body with a much ramified intestine. Globally, polycladid diversity is poorly known compared to other marine invertebrate groups. There are around 900 valid Polycladida species, based on characters related to reproductive anatomy, arrangement of eyespots, type and form of pseudotentacles and pharynx (Faubel 1984). Coloration pattern is also used to differentiate species. Their morphological simplicity may, however, camouflage cryptic species, as reported in other marine invertebrate groups (Held & Wägele 2005). Integrative approaches also using molecular species delimitation are efficient for testing traditional taxonomic concepts and revealing hidden species complexes. Integrative studies can thus change regional diversity estimates, essential to species and habitat conservation as well as evaluating biogeographical patterns. One potential species complex is *Thysanozoon brocchii* Risso, 1818. They are reportedly widely distributed with records from Gulf of Naples, Italy (type locality), Brazil, Argentina, and possibly Japan and parts of Africa. Brazilian and Mediterranean specimens studied herein showed differences in the form of dorsal papillae and coloration pattern. However, phylogenetic analysis of 28S rDNA sequences failed to differentiate western and eastern Atlantic populations. One *Thysanozoon* specimen from Northeastern Brazil is distinctive morphologically and molecularly; it may represent an undescribed species. Similar analysis of the *Pseudoceros bicolor* complex confirmed the results of Litvaitis *et al.* (2010). The externally similar *P. rawlinsonae* and *P. bicolor* were reciprocally monophyletic. A new morphotype found in Northeastern Brazil lacks the otherwise characteristic marginal band; it forms a sister group to the *P. bicolor* clade and may represent a new species.

### References

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- Held, C., Wägele, J.W. 2005. Cryptic speciation in the giant Antarctic isopod *Glyptonotus antarcticus* (Isopoda: Valvifera: Chaetiliidae). *Scientia Marina*, 69, 175-181.
- Litvaitis, M.K., Bolaños, D.M., Quiroga, S.Y. 2010. When names are wrong and colours deceive: unraveling the *Pseudoceros bicolor* species complex (Turbellaria: Polycladida). *Journal of Natural History*, 44, 829-845.

## Going further south, an integrative approach to the nudibranch family Tritoniidae (Gastropoda: Heterobranchia)

Berning, M. I.<sup>1</sup>, Joerger, K.<sup>2</sup>, Wilson, N.G.<sup>3</sup>, Schroedl, M.<sup>4</sup>

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Nudibranchia are conspicuous, highly diverse, shell-less marine mollusks with a worldwide distribution. The nudibranch fauna in Antarctic and sub-Antarctic waters may be especially rich, yet species tend to be morphologically variable or, alternatively, complexes of cryptic species may exist. Southern Ocean tritoniids are macroscopic and commonly sampled, but their taxonomy has not yet been well-established. Incomplete morphoanatomical descriptions, unknown ranges of variation, apparently wide distributional ranges of currently valid species, and the lack of molecular data contribute to taxonomic uncertainty. In the Magellanic region, the effects of alternating periods of population decrease, fragmentation or extinction, and subsequent expansion of surviving lineages has hardly been explored. In Antarctica, this complex history supposedly induced the so-called biodiversity pump, which has led to multiple phenotypically similar but ecologically and genetically specialized species. In this work, we explore the species level taxonomy, phylogenetic relationships and geographic distributions of the nudibranch family Tritoniidae, including members with planktonic larvae. During numerous expeditions with e.g. 'RV Polarstern', specimens were observed, documented alive, and fixed for multiple purposes. Specimens were dissected, described anatomically, and compared with type material. Tissue samples were analyzed under a scanning electron microscope or embedded for histological study. DNA from muscle and mantle tissue was extracted and sequenced for mitochondrial and nuclear markers. Preliminary results from our combined approach (i.e. traditional morphological knowledge and molecular data) unraveled three cryptic *Tritonia odhneri* (one in the southern Chilean fiords, one in the northern Chilean fiords, and one in both); and four cryptic *Tritonia challengeriana* (one along the southern Scotia Arc, one in South Chile, one in the eastern Weddell Sea, and one all over the Chilean fiords). The monotypic *Tritoniella* is recovered as a clade in multi-locus analyses, but shows considerable morphological variation. More sensitive genetic markers may be necessary to resolve such highly complex, potentially quite recent diversifications.

## Non allopatric speciation in rock-dwelling gastropods?

Fehér, Z.<sup>1</sup>, Jaksch, K.<sup>2</sup>, Szekeres, M.<sup>3</sup>, Bamberger, S.<sup>4</sup>, Kruckenhauser, L.<sup>5</sup>,  
Sattmann, H.<sup>6</sup> & Haring, E.<sup>7</sup>

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<sup>3</sup> Institute of Plant Biology, Biological Research Center of the Hungarian Academy of Sciences, Temesvári krt. 62, H-6726 Szeged, Hungary; e-mail: szekeres@brc.hu

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Among rock-dwelling gastropods, living on isolated rocky outcrops in topographically complex terrain, there are several genera comprising large numbers of narrow-range, morphologically-distinguishable taxa, providing an excellent system to study different phases of geographic divergence. Earlier it was considered that allopatric speciation is common in rock-dwelling gastropods and that co-occurring congeners are in secondary contact. But the exclusively allopatric origin of these taxa has been recently questioned. *Alopi*a and *Montenegrina* are among the most taxon-rich genera in the subfamily Aloiinae (door-snails). Although most taxa occur alone, there are some rare examples of syntopic and/or parapatric occurrences of congeners. In *Alopi*a, there are six pairs of taxa, which are morphologically identical but reversely coiled (i.e. they are mirror images or so called enantiomorphs). In *Montenegrina*, there are seven pairs of taxa, which differ mainly in the ribbing of the shell (ribbed–unribbed morphs). We have reconstructed the phylogeny of *Alopi*a and *Montenegrina*, based on mitochondrial markers, with the aim of revealing the evolutionary relationships of these parapatric taxon pairs. In some of these taxon pairs the average K2P divergence in mitochondrial COI, 16S, 12S markers was found to be as low as 0–0.5%, indicating their close phylogenetic relationship. This makes us presume that (i) some morphological features, which were considered important in the taxonomy of these groups – namely the ribbing in *Montenegrina* and the shift of the coiling direction in *Alopi*a –, appeared multiple times independently during their phylogenesis, and (ii) these taxon pairs are not in secondary contact but provide examples of non-allopatric speciation in rock-dwelling gastropods. As a next step, we are planning to perform microsatellite analyses to estimate gene-flow and divergence times between *Montenegrina* taxon pairs for better understanding of the development of ribbed–unribbed taxon pairs.

## Protist distribution: 100 new neotropic soil ciliates emphasize moderate ciliate endemism

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I studied 80 soil samples from the neotropics, mainly from Venezuela and some from the Galapagos Islands, using the non-flooded Petri dish method and classic and modern taxonomic tools. I identified about 400 ciliate species of which 120 were undescribed, representing 30 new genera and some new families. These data were compared with similar studies from Namibia (Africa) and Central Europe, showing about 60% species overlap. This and some “flagships” emphasize a moderate ciliate endemism globally and a huge number of undescribed ciliates. The new species are described in a forthcoming monograph.

Supported by the Austrian Science fund, FWF project P 22846-B17.

## Deciphering the *Favella* Cluster – Redescription of the Tintinnid Ciliate *Favella panamensis* Kofoid and Campbell, 1929 (Alveolata, Ciliophora)

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Tintinnid ciliates are unicellular planktonic organisms mainly living in the sea. They are able to build a huge diversity of shells called loricae. Discovered more than 230 years ago, their lorica features are the basis for the entire classification of tintinnids. This, however, poses a problem for several species that display considerable phenotypic plasticity of the loricae. This and the lack of knowledge about their cell features makes the distinction of closely related species difficult. To date, the cell morphology is only known in approximately 30 out of the about one thousand species.

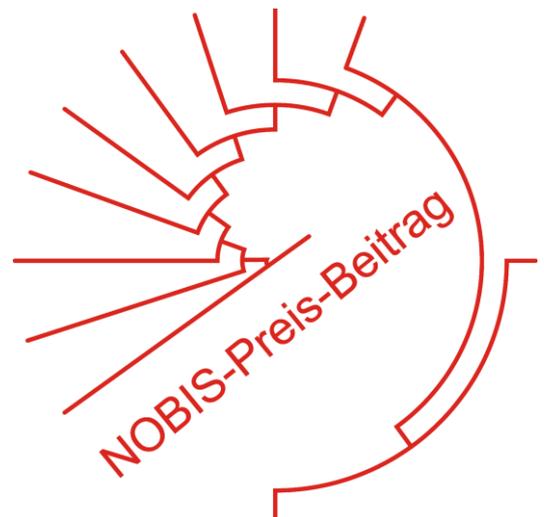
Our specimens of *Favella panamensis* are from the surface waters of the Indian River Lagoon at the Atlantic coast of Florida. Lorica and cell morphology were thoroughly investigated and compared with the very similar *Favella ehrenbergii*, the recently red-described type species. The two species show a 0.11 % divergence in their SSrRNA gene sequences corresponding to two nucleotides, which had been found to indicate different species in the rather closely related hypotrich ciliates. The comparison of the cell morphologies should yield cytological differences supporting the separation of two species; the most promising cell feature of tintinnids is the somatic ciliary pattern. We discovered deviations in the number of ciliary rows, especially of those on the dorsal side, between our Atlantic specimens and *F. ehrenbergii* as described by Kim *et al.* (2010). To verify these differences, we reinvestigated the voucher slide of *F. ehrenbergii* containing cultivated specimens, which were kindly provided by the Natural History Museum of London. Surprisingly, the number of dorsal kineties in the specimens on the voucher slide does not match the re-description. Accordingly, the main distinguishing feature does not exist, and it is still unclear whether the small differences in the SSrRNA, the lorica size, and the number of ciliary rows in the specialised fields are sufficient to keep *Favella panamensis* separate from *F. ehrenbergii*; more detailed studies on the morphology of *F. ehrenbergii* and genes with a higher evolutionary rate (e.g., the ITS 1 and 2 or the D1-D2 region of the LSrRNA) are required for clarification.

## European freshwater gastropods: major patterns of biodiversity and biogeographical processes

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We investigated the biogeography of freshwater gastropods of European lakes. For the first time, we compiled occurrence records for more than 200 gastropod species, as well as data on the limnological and geographical traits (e.g. latitude, longitude, altitude, lake size and depth) for more than 1000 lakes across Europe. Our objectives are to identify biogeographical regions, document species richness and endemism patterns of freshwater mollusks and reveal possible drivers of their distribution. A cluster analysis was conducted in order to estimate the similarity of lake faunas and thus identify biogeographic units. Moreover, regression models were applied to explore the relationships between species richness and lake parameters. Preliminary results reveal two areas with high species richness. The first is located in southeastern Europe and the second in the Baltic Sea region. An increase of endemic species is observed in southern Europe, while central and north European lake faunas are rather homogenous with a clear absence of endemic species. Dendrograms reveal well-defined units for central and northeastern European lake groups. Species distributions are apparently controlled by a combination of historical factors and limnological parameters.



## Morphospace shifts in endemic thermal-spring melanopsids or how an endangered species could lose its species status

Harzhauser, M.<sup>1</sup>, Neubauer, T.A.<sup>1</sup>, Georgopoulou, E.<sup>1</sup>, Wrozyna, C.<sup>2</sup>

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For more than hundred years the thermal spring-fed Lake Pețea near Oradea, Romania, was studied for its highly endemic subfossil and recent fauna and flora. Especially the late Pleistocene and Holocene Melanopsidae of Lake Pețea are one of the most impressive examples for a striking morphologic disparity within a single lineage. Since the first descriptions, 43 species-, subspecies-, variation- and forma-names have been introduced for the enormously rich material that derived from a very small area of only about 4 km<sup>2</sup>. Lake Pețea is already reduced to a muddy pond due to tourism, excessive use of thermal water and low precipitation and all endemics face extinction. Therefore, the endemic "*Melanopsis*" *parreyssii* is severely endangered and is listed on the IUCN Red List of Threatened Species.

Within the current FreshGEN project, this species represented a striking northern outlier in the Holocene *Melanopsis* biogeography, which needs explanation. To reveal the status of this species, a total number of 327 fossil and extant specimens were morphologically analyzed performing an outline-based technique to capture shell shape (Fast Fourier Transform). These analyses documented that subfossil populations of *M. parreyssii* evolved from a smooth fusiform species, which is morphologically identical with extant *Microcolpia acicularis*. The *Melanopsis*-like morphology and the prominent ribbing developed as a mere convergence. The synthesis of old and new data gives a quite detailed picture of the evolutionary mechanisms in Lake Pețea *Microcolpia* during the Holocene. The expanding and successively shifting morphospace, visible as a trend toward stepped and sculptured shells was probably initiated by an environmental crisis. Massive organic input into the small thermal lake limited available habitats and boosted eutrophication. The otherwise biogeographically strange *Melanopsis*-record is now explained by the usual south-eastern European range of *Microcolpia*. Hence, *Microcolpia parreyssii* represents a Pleistocene offshoot of *Microcolpia acicularis*, which became adapted to thermal springs. This result is quite positive from the biogeographer's point of view but may be problematic for the conservation status of this endangered gastropod.

This study is part of the FWF-Project P25365-B25 "Freshwater systems in the Neogene and Quaternary of Europe: Gastropod biodiversity, provinciality, and faunal gradients".

## Fly-fooling flowers: Deceptive pollination in *Ceropegia*

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Floral scents are most important signals in specialized pollination systems. However, little is known about the importance of specific compounds for pollinator attraction. We analyzed floral scent in *Ceropegia* (Apocynaceae, Asclepiadoideae) by gas chromatography coupled to mass spectrometry (GC-MS) to learn more about the compounds emitted by flowers of these plants. *Ceropegia* is characterized by their floral Bauplan of so called pitfall flowers with various trapping devices (e.g. sliding areas, trapping trichomes) to catch, temporarily trap and finally release the pollinator.

In a greenhouse in Bayreuth several species of *Ceropegia* are cultivated, of which *C. denticulate* and *C. sandersonii* are regularly visited/pollinated by kleptoparasitic *Desmometopa* flies. These flies steal food from other animals, generally from predatory arthropods (e.g. spiders), by feeding on haemolymph or other secretions released by their prey items. It is generally believed that *Desmometopa* and other kleptoparasitic flies are attracted to their insect prey items by volatile organic compounds which are set free when a predator devours it. Honey bees are the preferred food source of *Desmometopa* flies and they often can be observed in great numbers when feeding on fluids coating the exterior of honey bees caught by spiders. When honey bees are attacked by a predator (e.g. spider) they extrude their sting and thereby release their alarm pheromone. *Desmometopa* flies may use the thereby released components to find appropriate feeding sites. Indeed, bioassays confirmed that the honey bee alarm pheromone is highly attractive to *Desmometopa*.

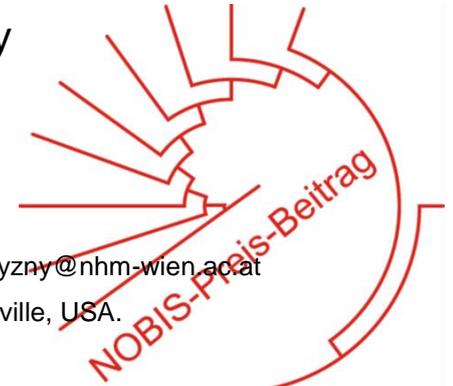
Scent analyses in the *Ceropegia* species pollinated by *Desmometopa* revealed that flowers emit compounds identical to components of the alarm pheromone of honey bees and our study suggests that *Ceropegia* fools flies into pollinating its flowers through food source (e.g. preyed upon honey bees) mimicry.

## The ghost shrimp *Glypturus* in space and time: systematics, diversity, taphonomy and (palaeo)-biogeography

Hyžný, M.<sup>1</sup>, Klompmaker, A. A.<sup>2</sup> & Portell, R. W.<sup>2</sup>

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*Glypturus* is a genus of fossorial heterochelous shrimps (Decapoda: Axiidea: Callianassidae) whose bioturbation is considered a prime example of ecosystem engineering. As these animals are largely soft-bodied, studies on the strongly calcified chelipeds are essential for recognition of the genus in the fossil record as these are the only parts that typically preserve. The presence of spines on the upper margins of the merus and propodus of the major cheliped and on the lower margin of the carpus immediately identifies the genus, whereas the extent of tuberculation on the lateral surfaces of the major propodus is usually important for species-level determination. Based on examination of extensive fossil material, as many as ten species have been recognized (Hyžný & Müller 2012; Hyžný *et al.* 2013; Klompmaker *et al.* in revision); two of which were also supported using bivariate, multivariate and geometric morphometric methods. Morphometric methods suggest that minor chelae are relatively rare to absent compared to major chelae, suggesting a taphonomic bias. *Glypturus* appears to have originated in the Tethyan Realm, with a stratigraphic range reaching back to the middle Eocene (ca. 40 mya). Since then, the genus migrated westwards and eastwards, establishing present-day communities in the Western Atlantic and Indo-West Pacific, each harboring four distinct species. Today, in the presumed area of origin, the genus no longer occurs. An evolutionary trend may be observable in *Glypturus* in that the most tuberculated taxa are Eocene and Oligocene in age, whereas generally less tuberculated taxa are known since the Miocene.

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## Treasured genes in museum collections

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Molecular genetic analyses has become vital in evolutionary biology studies and indispensable in many research projects. Optimally, fresh tissue is collected and analysed, but there are several reasons why it might be not possible to gain fresh material: for example, because the species is rare or extinct, difficult to find or no longer occurring in a particular area. Quite often inaccessibility of distribution areas due to political reasons can also hamper the collecting of specimens. In such cases museum collections are huge treasures, as their collections of specimens also represent a large reservoir of genes. In the present study we tested the usage of museum material for DNA analyses in ethanol conserved molluscs as well as dried shells of snails. For the first task we analysed 72 glasses of the mollusc collection of the Natural History Museum Vienna, comprising 20 different taxa of 4 classes, which were tested with different extraction protocols and PCR primers. The collecting date of the chosen samples ranged from 1877 to 2002. Moreover, we successfully extracted DNA from the mummies that remain in an empty shell of a snail. For this purpose a good working protocol has been established. The dry shells used in these analyses were collected between 1972 and 2006. To test the outcome of the extraction, we amplified and sequenced two short sections of the mitochondrial genome (COI and 16S). In general, our survey of DNA extraction methods from old museum samples yielded very good results and even samples aged about 120 years contained DNA of sufficient quality to isolate the desired sequences. This investigation is a very important step to optimize approaches for DNA analyses of museum material.

## Shedding light on the evolution of an enigmatic fish

### Comparative analyses of cave-dwelling and surface-dwelling populations of *Garra barreimiae*

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Many cave-dwelling vertebrates display the same morphological modifications, such as eye regression and loss of pigmentation. It is still unclear how these regressive traits are genetically determined and whether phenotypic plasticity plays an important role. The cyprinid barb *Garra barreimiae* is endemic to the southeastern Arabian Peninsula, where it inhabits regularly desiccating water bodies. Since a hypogean population with troglomorphic traits is conspecific with the “normally” developed surface population, *Garra barreimiae* seems to be a perfect organism to study the effects of cave life and the origin of troglomorphic characters. Previous genetic analysis of mtDNA (Kruckenhauser *et al.* 2011) revealed that individuals from the cave population are genetically differentiated from the adjacent surface populations. However some individuals from surface populations near the cave entry possess haplotypes characteristic for the cave population. As those individuals mostly display an intermediate phenotype, it is reasonable to assume that hybridization still occurs and that the populations have separated quite recently. In this project we want to answer the question whether and to what extent hybridization between cave and surface populations occurs by analysing microsatellite markers (Kirchner *et al.* 2014). To evaluate the consequences of light exposure during development and crossbreeding between individuals from cave and surface populations we will examine if offspring display different development of eyes and pigmentation in the presence or absence of light. For the first time extensive morphometric and morphological analyses will be conducted with *G. barreimiae*. This will include histology of eye development, various distance measurements and shape analyses. By comparing size and shape of the different species and subspecies of *G. barreimiae* we want to evaluate if status of these species and the subspecies is justified. In order to explain how the current distribution patterns of the species emerged, we will investigate the phylogeography by analysing several mitochondrial and nuclear markers. The combined results shall help to draw a conclusive picture of the evolution of this interesting species and to obtain new insights into mechanisms leading to the transition to troglomorphic life style in general.

## Calibrating the recent blennioid clock: expansion dating in Adriatic black-faced blennies, *Tripterygion delaisi* (Perciformes, Blennioidei, Tripterygiidae)

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DNA substitution rate is an important parameter for understanding molecular evolution and for drawing inferences from population genetic, phylogeographic and phylogenetic studies. Typically, divergence dating based on fossils or ancient vicariant events is employed to calibrate substitution rates. However, there is increasing evidence for a time dependency of the molecular rate of change with the rate decaying from the instantaneous mutation rate in the recent past to the phylogenetic substitution rate (Ho *et al.* 2011), rendering substitution rates inferred from divergence dating based on ancient calibrations inapplicable for estimating recent events. Expansion dating, i.e. inferring substitution rates based on the timing of expansion events, provides an alternative and better way for calibrating the molecular clock over recent time scales. Using mitochondrial control region sequences we infer phylogeographic patterns and historic population size changes of a common littoral marine fish species, the black-faced blenny *Tripterygion delaisi*, from the north-eastern Adriatic Sea. Demographic reconstructions are consistent with recent population expansion, probably triggered by rising sea levels after the last glacial maximum (LGM) (Siddall *et al.* 2003). To estimate a substitution rate for the mitochondrial control region of *T. delaisi*, we place the onset of population growth between the LGM and the warming of surface waters (18,000 to 13,000 years BP) and employ two different approaches: i) a mismatch distribution, and ii) a two-epoch coalescent model of population growth preceded by a constant population size. The substitution rates obtained by these methods are compared with each other. This study is among the first to use expansion dating for estimating substitution rates and the first to provide an estimate for the mitochondrial control region substitution rates in blennioid fishes.

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## Conflicting genetic signals in the Red Sea collector urchin: Mitochondrial and nuclear markers show different patterns

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*Tripneustes gratilla* is one of the most widespread shallow-water echinoids, ranging from the East-Pacific to East Africa and the Red Sea and from the Kermadec Islands (New Zealand) to Japan. Phylogeographic studies performed by several research groups have demonstrated a lack of phylogenetic structure in mtDNA (Lessios *et al.* 2003; Liggins *et al.* 2014). Haplotype sharing between such widely distant localities as the Philippines, Kermadec Island and the Galapagos Islands is suggestive of recent radiation of the species and its high dispersal potential.

*T. gratilla* representatives from the Red Sea are characterized by their sparse interambulacral tuberculation, the proportions of their corona and their distinct coloration patterns, strongly differing from populations in other parts of the species' range. Consequently, a new subspecies was proposed for the Red Sea population: *T. gratilla elatensis* Dafni, 1983. Here we present first genetic data (COI, Bindin) for specimens from the Red Sea, that had not been included to date in phylogeographic studies on *Tripneustes*. In contrast to the expectations raised by the apparent morphological differences, COI data for the Red Sea populations confirm the pattern observed on an ocean-wide scale. Even when using a much longer COI segment than analyzed in previous studies, Red Sea *Tripneustes* fail to be differentiated from Indian Ocean populations, and share haplotypes with specimens from both the Philippines and East Africa. These results would suggest that the observed morphological differences merely represent local variations.

Bindin sequences, however, tell a different story: three clades were found, comprising 1) Red Sea, 2) Indomalayan (Philippines, Guam, Papua New Guinea), and 3) mixed Indo-West-Pacific samples. High levels of bindin differentiation (up to 20%) among these clades suggest ancient radiation, greatly contrasting the COI data. This apparent mismatch of mitochondrial and nuclear DNA data could be indicative of a mitochondrial capture event in the recent past. Independent morphological evidence lends support to this, since in-depth investigations have shown that the differentiation of the Red Sea population is not restricted solely to minor difference in corona proportions and coloration, but is also observed in lantern morphology and tubefeet spicules.

## Genetic diversity patterns of steppe plants across borders in Central Europe

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Basically, we are interested in the phylogeography, performance, and evolution of steppe plants in Central Europe. Therefore, we study a transect across three countries at their absolute northwesternmost distribution limit. We are analysing a set of steppe plants showing similar distributions with more wide-spread continuous occurrences in the Pannonian Basin in Central Hungary compared to the western limit of the Pannonian area in Eastern Austria (i.e. the western range edge of their continuous distribution range) and to the northwesternmost exclave in western Germany (i.e. in Rhineland-Palatinate). Along this edge-transect of increasing peripherality and isolation towards the northwest we, for instance, expect gradually reduced population genetic diversity and performance – being especially decreased within the exclave. In the population genetic part of the project, presented here, we utilise mainly nuclear Amplified Fragment Length Polymorphisms (AFLPs) and chloroplast (cp) DNA sequence data.

In our comparative approach we include *Carex supina* (Cyperaceae), *Oxytropis pilosa* (Fabaceae), and *Poa badensis* (Poaceae), as well as *Linum flavum* (Linaceae) exhibiting a particular situation as this species reaches its absolute westernmost distribution limit not in Rhineland-Palatinate, but in the Swabian Jura in Baden-Württemberg. However, the latter study region also represents an exclave far from its continuous distribution range allowing the same hypotheses. Across the national borders each of the three study regions is represented by four populations.

In our currently available AFLP analyses, we mainly found overall low genetic diversity values, and genetic structuring basically followed a vicariance pattern, i.e. reflecting the borders across the three study regions as expected. With respect to the westernmost exclave a clear vicariance pattern was also demonstrated by the *Linum flavum* cpDNA haplotype analysis. However, in all study species we observed strongly varying levels of cpDNA sequence diversity possibly due to differing life history traits. Therefore, when interpreting genetic structure and diversity patterns at the distribution range limit, the importance of the species' ecological properties and biogeographic histories is exemplified by our results.

## Paraphyly and budding speciation in the hairy snail *Trochulus hispidus* (Pulmonata, Hygromiidae)

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Delimitation of species is often complicated by discordance of morphological and genetic data. This may be caused by the existence of cryptic or polymorphic species. The latter case is particularly true for certain snail species showing an exceptionally high intraspecific genetic diversity. The present investigation deals with the *Trochulus hispidus* complex, which has a complicated taxonomy. Our analyses of the COI sequence revealed that individuals showing a *T. hispidus* phenotype are distributed in nine highly differentiated mitochondrial clades (showing p-distances up to 19%). The results of a parallel morphometric investigation (Duda *et al.* 2014) did not reveal any differentiation between these clades, although the overall variability is quite high. The phylogenetic analyses based on 12S, 16S and COI sequences show that the *T. hispidus* complex is paraphyletic with respect to several other morphologically well-defined *Trochulus* species (*T. clandestinus*, *T. villosus*, *T. villosulus* and *T. striolatus*), which form well-supported monophyletic groups. The nc marker sequence (5.8S–ITS2–28S) shows only a clear separation of *T. o. oreinos* and *T. o. scheerpeltzi*, and a weakly supported separation of *T. clandestinus*, whereas all other species and the clades of the *T. hispidus* complex appear within one homogeneous group. The paraphyly of the *T. hispidus* complex reflects its complicated history, which was probably driven by geographic isolation in different glacial refugia and budding speciation. At our present state of knowledge, it cannot be excluded that several cryptic species are embedded within the *T. hispidus* complex. However, the lack of morphological differentiation of the *T. hispidus* mitochondrial clades does not provide any hints in this direction. Thus, we currently do not recommend any taxonomic changes. The results of the current investigation exemplify the challenges and potentials of barcoding in highly diverse species such as *T. hispidus*.

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## SEM atlas of the sea spiders (Pycnogonida) of the Mediterranean Sea: common littoral species

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In this scanning EM atlas (see also Lehmann *et al.* 2014) 21 medio- and infralittoral pycnogonid species from 5 families are analysed: Ammotheidae (9 species), Callipallenidae (5 species), Endeidae (2 species), Phoxichilidiidae (3 species), and Pycnogonidae (2 species). The material was mainly taken from Mediterranean pycnogonid collections housed in the Bavarian State Collection of Zoology. Additional material was collected during field trips. Altogether the material was obtained from six different locations: Banyuls-sur-Mer (France), Tavolara Island (Italy), Elba Island (Italy), Giglio Island (Italy), Brucoli (Sicily Island, Italy), and Istria Peninsula (Croatia). The animals were studied in detail with a scanning electron microscope (SEM). Additionally series of light microscopic pictures were made to generate extended depth of field pictures of whole animals. The observed features are compared with previous literature.

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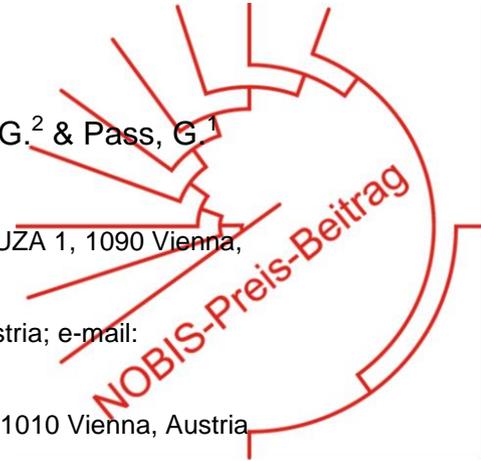
## Uncoiling the diversity of Austrian pill millipedes (Glomerida) using an integrative taxonomic approach

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Glomerida or pill millipedes (Diplopoda, Myriapoda) are known for their conspicuous defensive strategies: they curl up, thus forming a perfectly sealed ball and release sticky defensive secretions from dorsomedian glandular pores, which contain various alkaloids. Pill millipedes show a mainly holarctic distribution and more than 280 species from 34 genera have hitherto been described. Many species are conspicuously colored, and variations in coloration resulted in the description of many subspecies and varieties of questionable validity. In Austria, we have records of numerous varieties for 20 species, representing a well-suited basis to (i) test DNA-barcoding for its capability to delimit both species, as well as intraspecific clades, and (ii) introduce a novel dataset relying on the chemical composition of glomerid defensive secretions.

This study is an interdisciplinary taxonomic project within the ABOL initiative (*Austrian Barcode of Life*). The demand of ABOL to combine as many approaches as possible in studies on biodiversity is reached by the combination of two approaches, both novel to glomerids: DNA-barcoding based on Non-Destructive-DNA-Extraction (NDE) together with chemosystematics. The most important milestones of our study are: (i) the establishment of specific primer-cocktails for DNA-barcoding of pill millipedes, a group where nearly no data is currently available, (ii) clusters obtained by analysing COI barcodes are congruent with additionally generated 28S sequences, and (iii) chemically, pill millipedes show specific combinations of glomerin, homoglomerin, and an assumingly oxygenated homoglomerin in their defense secretions. The latter compound was discovered in the defensive secretion of *Haploglomeris multistriata* and is novel for the entire animal kingdom. Establishing our combined approach for pill millipedes, we are not only eager to put systematics on a more solid basis, but likewise to reveal more secrets of these fascinating “experts of defence”.

## Morphology of the first zoeal stage of the spotted bumblebee shrimp *Gnathophyllum elegans* (Risso, 1816) (Decapoda: Caridea: Gnathophyllidae) studied with light microscopy and scanning EM.

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The morphology of the first stage zoea of *Gnathophyllum elegans* raised in the laboratory is illustrated and analysed in detail with light and scanning electron microscopy for the first time. Larvae were obtained from an ovigerous female, caught in shallow waters west of the isle of Šolta (43°23'00''N, 16°13'47''O), Croatia. Selected features of carapace, antennae, mouthparts and telson are presented here (for details, see Meyer *et al.* 2014). Differential diagnosis between *G. elegans* and *G. americanum* Guérin-Méneville, 1855 the only other *Gnathophyllum* species with available zoea description (Bruce 1986) shows distinct differences in seta patterns of the studied organs. Hence both species can be clearly distinguished by larval morphology. The systematic position of the genus *Gnathophyllum* is under question since Bruce (1986) discovered strong similarities between the larvae of *G. americanum* and different representatives of the subfamily of the Pontoniinae. Comparison of our results with the partner shrimp *Periclimenes amethysteus* Risso, 1827, also studied with the scanning EM (Geiselbrecht & Melzer 2009), shows several common features, hence supporting the need for further comparative analyses of zoea larvae of Gnathophyllidae, Hymenoceridae and Pontoniinae.

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## Phylogeographic analysis reveals Holarctic homogeneity and a distinct circum-Mediterranean lineage in golden eagles (*Aquila chrysaetos*)

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We analysed 250+ feather and tissue samples from golden eagles (*Aquila chrysaetos*) across their distribution range from Europe through mainland Asia and Japan to North America with respect to diversity and structuring of DNA sequences of the mitochondrial control region. By including specimens from museum collections we not only covered a huge geographic area but also a time range going back to 1817, enabling us to assess whether persecution and habitat loss have left a signature in the Golden eagles' genetic diversity. Similar to other large birds of prey (bearded vultures, white-tailed sea eagles, saker falcons) the golden eagle exhibits two distinct mtDNA haplogroups. Interestingly, however, and in contrast to the other raptors, these two lineages did not show a west-east pattern, but instead there was a parapatric distribution with one haplogroup being confined to the Mediterranean and adjacent regions (up north to the Alps), and the other covering the whole remaining Holarctic. The homogeneity across this vast area (at least for North America we would have expected a separate lineage) is further highlighted by three haplotypes with a surprisingly disjunct distribution: the first was found in the Alps, central Asia and Japan; the second in Japan and Fennoscandia; and the third in central Asia and North America. The North American continent is dominated by a single most frequent haplotype, but our sampling outside Europe is limited (perhaps with the exception of Japan) so that definitive conclusions are precluded at this point. Apart from the phylogeographic analysis we introduce a new sliding-window approach to analysing genetic diversity through time without having to arbitrarily define separate time windows and also taking into account the problem of data autocorrelation.

## Paleobiogeographic regions for European Neogene freshwater systems: a trend toward increasing provincialism

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We present for the first time an outline of a paleobiogeographic framework for European Neogene freshwater systems. Presence-absence data of gastropods from freshwater systems of the four time slices Early Miocene, Middle Miocene, Late Miocene, and Pliocene, representing data from over 2,700 localities, were analyzed with cluster analyses. These revealed a generally high degree of provincialism for the Neogene freshwater systems and promoted the definition of biogeographic regions, dominions, and provinces. The delimitations are based on the results of the cluster analyses, the degree of endemism, and geographical coherence.

For the Early Miocene a relatively low degree of provincialism is shown by the data, supporting the distinction of three biogeographic regions. The Middle Miocene in turn demonstrates high-level provincialism, coinciding with the development of many endemic freshwater systems on the Dinarian-Anatolian Island and in Central Europe. Six regions could be defined. The retreat of the Central Paratethys and development of the huge Lake Pannon in the beginning of the Late Miocene largely shaped faunal evolution and the paleobiogeography of freshwater biota in general. Additionally, the formation of the 'Lago-mare' environment after the Messinian Salinity Crisis as well as the development of numerous lakes in Western Europe promoted biogeographic division. Six biogeographic regions, three of which could be subdivided into altogether seven dominions, were distinguished. With the extinction of Lake Pannon and the decline of western European and Mediterranean faunas at the Miocene-Pliocene boundary, biodiversity hotspots shifted toward eastern and southeastern Europe. For the Pliocene four biogeographic regions, five dominions, and four provinces could be defined.

The main factor underlying the proposed classification and faunal differences in general is the varied existence of large, long-lived lakes. Because of their extensive duration they crucially influenced family-level composition, differences of the relative species richnesses per biogeographic unit, and a rising rate of endemism. This pattern is reflected in the continuing continentalization of Europe linked to the Alpidic Orogenesis. Additionally, the retreat of the Paratethys Sea and its isolation from the Mediterranean promoted the evolution of endemic faunas in surrounding freshwater systems. Direct descendants like long-lived Lake Pannon, Lake Dacia or Lake Slavonia persisted over several millions of years and promoted the evolution of highly diverse and endemic faunas.

## Crossing the borders of orders: head anatomy of *Coniopteryx pygmaea* (Insecta: Neuroptera: Coniopterygidae) and convergent miniaturization effects in insects

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*Coniopteryx pygmaea* Enderlein, 1906 with a body length of 1.5 mm is one of the smallest known lacewings. Several miniaturization effects were recognized in the course of the investigation of its head anatomy.

In many insect orders miniaturized forms evolved independently from larger ancestors. Structural, physiological and physical constraints lead to convergent modifications in the head anatomy: In the brain a certain number of neurons are required to retain sensory, motor and humoral control. Thus the relative size of the brain is increased (Beutel & Haas 1998). It occupies any available space in the head capsule and loses its dumbbell-shaped form, which probably represents the ground plan condition in Ectognatha (Beutel *et al.* 2005). As the size of the head also limits the size of the compound eyes, number and length of ommatidia and the diameter of the facets are reduced (Fischer *et al.* 2014). Further, in miniaturized insects diffusion is largely sufficient for the distribution of haemolymph and oxygen, which leads to a simplification of the circulatory and tracheal system. In most studied specimens miniaturization does not affect the total number of muscles but it does result in a smaller number of muscle subunits and muscle fibers (Polilov & Beutel 2009).

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## A novel target enrichment strategy for phylogenomic analyses of sphecid wasps

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Sphecid wasps are a morphologically and behaviorally heterogeneous group of aculeate Hymenoptera and comprise about 10,000 described species. Together with the species-rich bees (Anthophila), they form a well-supported monophyletic group named Apoidea. To understand the phylogeny and evolution of Apoidea, we compiled a taxonomic sampling for molecular phylogenetic analyses that includes all major extant lineages of sphecid wasps as well as selected bees and outgroup taxa.

We aim to conduct a phylogenomic analysis that is based on a target DNA enrichment approach for Illumina multiplexed Next Generation Sequencing. Annotated genomes of a set of reference species as well as 24 transcript libraries of Crabronidae and Sphecidae from the 1KITE project ([www.1kite.org](http://www.1kite.org)) were used to detect a total of 5,537 single-copy orthologous protein-coding genes. Based on the *Nasonia vitripennis* gene models, the aligned transcript sequences were spliced into 25,016 coding exons. Of these, only gap-free multiple nucleotide sequence alignments that contain a nucleotide sequence from at least one representative of the 24 sphecid wasps from the 1KITE project were used to search for potential DNA target regions. Target regions of 240bp in length were tiled into 120-bp-long baits with a new bait every 20bp. Finally, using a clustering approach, bait-binding sequences were clustered into groups that differ less than 6% from each other. This was used to generate artificial bait sequences that exhibit the smallest possible maximum distance to any sequence in a given sequence cluster. We designed 73,719 artificial baits to capture 486 coding exons. Initial results based on analyzing 16 test species revealed that artificial baits highly successfully enrich the target DNA of both closely and distantly related Hymenoptera. To shed light on the evolutionary history of sphecid wasps, we intend to study 192 of 301 currently recognized sphecid wasp genera. Thus, it should be feasible to reconstruct the phylogenomic relationships of the major lineages within the apoid wasps.

## Automated tree based screens for hybrid signals in multilocus (AFLP and SNP) datasets

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Hybridization has undoubtedly contributed to the generation of biological diversity, yet to fully assess its importance, means to identify hybrid taxa are needed. Seehausen (2004) proposed an intuitive approach to the detection of hybrid taxa in multi-locus nuclear trees. The homoplasy excess test (HET) reveals signals of excess homoplasy, which results from the presence of a hybrid taxon and one or more of its parental lineages in a phylogenetic tree. While HETs have successfully been used to detect hybridization in several AFLP studies (e.g. Schliewen and Klee 2004, Egger *et al.* 2007, Larsen *et al.* 2010), a more widespread employment of the test has probably been hampered by the effort involved in manually preparing input for and parsing output of large numbers of phylogenetic analyses. We introduce a new computer program (HExT), which automatically carries out all steps of the HET. Moreover, using datasets including known hybrids, we demonstrate that the test can also be employed with SNP markers and that our software is able to handle the large (~10,000 loci) datasets resulting from next generation sequencing projects.

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## Across the scientific border

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In recent years I have also paid attention to aspects of botany outside of pure science. It turned out, that the engagement of scientists in and outside of universities for the protection of Austrian's landscapes and natural treasures is continually decreasing in recent years. This tendency is contrary to the continuous worsening of the native biospheres conditions. The question is discussed how members of NOBIS can counteract this trend at least to a certain degree.

## Treehoppers (Hemiptera, Membracidae) of Panguana (Peru). A close look on strange shapes

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The ecological field station Panguana in the Amazon lowland of Peru was founded more than 40 years ago. Within the past years the research station was expanded and is run by Juliane Diller (ZSM). Since 2011 it is protected by law as an ACP (área de conservación privada). It is located in the department Huánuco at the river Lullapichis (= Yullapichis) in about 260 m altitude. There are many different habitats, partly dense rainforests, low hills, little creeks, swamps with palm trees and pastures. Panguana has a very rich fauna and is frequently called „hotspot of biodiversity” (Diller & Burmeister 2007, Schönitzer & Feuerabendt 2014).

We investigate the external morphology and species composition of the treehoppers of Panguana. Most treehoppers were caught with a handnet. Some species can be collected quite frequently like *Notocera spinidora*, *Antonae guttipes* and *Cyphonia clavata*. Others like *Cladonota apicalis* and *Heteronotus albospinosus* were only collected once, despite of a series of collection trips. Only four specimens of *Membracis foliafasciata* were found in Panguana, whereas large series were collected in the surroundings of the nearby city Pucallpa. Due to scattered literature and the great number of species determination of the Membracidae is not easy; however the website by Deitz & Wallace (2014) is extremely helpful. Up to now we have determined more than 20 species, but there are certainly many more. In this poster we illustrate some specimens with 3D-SEM pictures. The following species are illustrated: *Cyphonia clavigera*, *C. clavata*, *Notocera spinidora*, *Trichaetipyga junipenna* aff. and *Antonae guttipes*.

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## *Exocelina* diving beetles: large scale environmental change as a driver for lineage diversification across Melanesia

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*Exocelina* Broun, 1886 is a genus of diving beetles (Dytiscidae), with a striking heterogeneity of species richness across Melanesian islands. At present, it includes 118 valid species. Fifteen species occur in Australia and New Zealand, 65 species in New Guinea, 36 species in New Caledonia, one species in China and one species in Hawaii. These small predators are diverse morphologically and show large range of ecological adaptation. Most species, especially in New Guinea and New Caledonia, inhabit low-order streams and habitats associated with wider mountain streams. But there are species in truly stagnant water (pond, pools and puddles) as well as stygobionts. New Guinea, as a core of the biodiversity of the genus, is a central part of our research. Extensive fieldwork and taxonomic investigation reveals constantly the existence of new species in the island. Lately, we have described 24 new species and have more than 70 additional new species under study now - with a predicted total of 300 New Guinean species. Special attention is given to creating of intrageneric structure of the genus and key to species.

Australia, New Caledonia and New Guinea have very different geological histories. Using a comprehensive sampling of the genus, we investigated the origin and tempo of diversification in the archipelago. We used molecular phylogenetics in combination with likelihood methods of macroevolutionary pattern inference to study the faith of colonizers on islands of different geology, age and distance from the source. Our results reveal that the discrepancies in diversity observed between Australia, New Caledonia and New Guinea are likely accounted for by the availability of new ecological niches fostered by large-scale abiotic shifts. With a recent Miocenic orogeny that created plenty of new habitats in both horizontal and vertical dimension, New Guinea has provided the setting for an accelerated recent diversification. Australian and New Caledonian fauna is older, and the longer diversification there apparently resulted in more even rates of diversification but higher morphological diversity.

## ABOL – DNA-Barcoding and the Inventory of the Biodiversity of Austria

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Austria is a hotspot of biodiversity, both from the number of observable biotopes, as well as species numbers. Many correlated factors causally influenced the formation of this diversity, which still is poorly explored to date. The “Austrian Barcode of Life”-Initiative (ABOL) aims to generate DNA-Barcodes from all Austrian species of animals, plants, and fungi.

DNA-Barcoding generates sections of standardized DNA-sequences, which due to their species-specificity can be used as molecular characters to identify species. DNA-Barcoding opens a wide spectrum of possibilities, spanning from the discovery of new species, to the identification of eggs, larva and organismal remains. Applicability is manifold, e.g. in conservation, criminalistics, pest control or food inspection. In recently evolved species and species with unusual variation the method reaches its limits. But even in such cases it is a catalyst for exciting scientific questions, which foster a number of exciting new insights.

## Does the head anatomy of Evanioidea clarify the phylogenetic placement of aculeate wasps?

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The phylogenetic relationships of Hymenoptera are well resolved and many clades well supported, but some problematic areas remain. One of the latter is the position of the aculeate wasps, including such well known insects as hornets, bees and ants. Traditionally, they have been regarded as the sister group of the Ichneumonoidea (e. g. Rasnitsyn 1988), one of the largest parasitic wasp taxa. In a new hypothesis (Sharkey *et al.* 2012), the Aculeata are placed as the sister group of the Evanioidea, a comparatively small and heterogenous assemblage comprising parasitoids of wood-living insects (Aulacidae), bee nest 'cuckoos' (Gasteruptiidae), and cockroach egg capsule predators (Evaniidae). The Aculeata-Evanioidea relationship is moderately supported by molecular data, but not by any known morphological character. The aim of this project is to address this hypothesis by exploring the internal head anatomy.

Hitherto three characters relevant in the described context could be recognized: 1. a structure in the inner skeleton of the insect head, which is present in Evanioidea and Aculeata, but also, though slightly modified, in Ichneumonoidea; 2. a muscle of the salivarial system, which is present in Evanioidea and Aculeata, but is also described for a very basal hymenopteran; and 3. a gland of the digestive system, which is common in Aculeata and is newly found (solely) in the family Evaniidae. The characters and their conflicts are discussed.

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