

12. Jahrestagung von NOBIS Austria



Bozen - Naturmuseum Südtirol
22.-23. November 2018

NATURMUSEUM SÜDTIROL
MUSEO SCIENZE NATURALI ALTO ADIGE
MUSEUM NATÖRA SÜDTIROL

BIODIVERSITY CENTER



NETWORK OF BIOLOGICAL SYSTEMATICS AUSTRIA

Bozen 2018



12. Jahrestagung von NOBIS Austria

Gastgeber:

Dr. David Gruber

Direktor des Naturmuseums Südtirol (Museo di Scienze Naturali dell'Alto Adige)

Bozen, Italien



Impressum: NOBIS Austria, c/o Naturhistorisches Museum Wien, Burgring 7, 1010 Wien

Bozen 2018



Auf Einladung von Dr. David Gruber und unter Mitwirkung von PD Dr. Evelyn Kustatscher findet die diesjährige Jahrestagung von NOBIS Austria im Naturmuseum Südtirol (Museo di Scienze Naturali dell'Alto Adige) in Bozen, Italien, statt. Die Tagung ist somit eine Gemeinschaftsveranstaltung und beinhaltet Führungen durch die Sammlung des Naturmuseums Südtirol und die Möglichkeit zum Besuch des Südtiroler Archäologiemuseums, wo der berühmte „Ötzi“ zu besichtigen ist.

Das Naturmuseum Südtirol bietet in seiner Dauerausstellung einen biologisch-kulturgeschichtlichen Streifzug durch eine der vielfältigsten Regionen Europas und veranschaulicht die Entstehung und das Erscheinungsbild der einzigartigen Südtiroler Berg- und Tal-Landschaften mit ihren Lebensräumen. Schwerpunkte der museumseigenen Forschung und der Sammlungen sind die Fachbereiche Erdwissenschaften, Botanik und Zoologie.

Programmübersicht

Donnerstag, 22. November

ab 15.00 Registrierung im Naturmuseum Südtirol (Bindergasse 1/Via dei Bottai 1)
16.00 s.t. Führung durchs Naturmuseum Südtirol (max. 30 TeilnehmerInnen)
17.00 s.t. Führung durchs Naturmuseum Südtirol (max. 30 TeilnehmerInnen)
Icebreaker im Naturmuseum Südtirol bis 18:00, danach Abendessen im Weißen Rössl/Cavallino Bianco (Bindergasse 6/Via dei Bottai 6)
Freier Eintritt in Südtiroler Archäologiemuseum am Donnerstag und Freitag mit Namensschild der Tagung und/oder ausgedruckter Bestätigung!

Freitag, 23. November

9.00–9.10 Begrüßung im Naturmuseum Südtirol
9.10–17.45 Vorträge, Poster-Präsentationen und NOBIS-Preis-Verleihung

Vorträge 15+5 Minuten
Sprache Englisch
Beitrag NOBIS-Mitglieder: € 20.-; Nicht-Mitglieder: € 40.-
Zahlung NOBIS Austria
IBAN: AT622011128822667900,
BIC: GIBAATWW
oder bei der Registrierung

Bozen 2018



Programm

Freitag, 23. November 2018

8.30–9.00 Registrierung

9.00–9.10 Begrüßung durch
David Gruber, Direktor des Naturmuseums Südtirol
Sabine Agatha, Präsidentin von NOBIS Austria

Vortragsprogramm
NOBIS-Preis Beiträge
Chair: Sabine Agatha

9.10–9.30 **Susanne Reier** et al.: New insights into the occurrence of the genus *Pomphorhynchus* Monticelli, 1905 (Acanthocephala) in Austria.

9.30–9.50 **Lisa-Maria Schmidt** et al.: Linking the ecological species concept with systematics of trochid gastropods in the Northern Adriatic Sea.

9.50–10.10 **Paul Wolf** et al.: Phylogeny of the Eurasian Jay (*Garrulus glandarius*) based on mitochondrial marker sequences.

10.10–10.40 Kaffeepause

Vortragsprogramm
NOBIS-Preis und weitere Beiträge
Chair: Ulrike Aspöck

10.40–11.00 **Michael Gruber** & Sabine Agatha: A new type of somatic kinetid and cortical network in the model tintinnid *Schmidingerella meunieri* and a scenario of character evolution (Alveolata, Ciliophora, Spirotricha).

11.00–11.20 **Herbert Wagner**: Integrative taxonomy and evolution of the cryptic pavement ants of the *Tetramorium caespitum* complex (Hymenoptera: Formicidae).

- 11.20–11.40 **Martin Hahn** et al.: Species, species, species: adaptive radiation in a genus of freshwater bacteria.
- 11.40–12.00 **Sabine Agatha** et al.: Phylogenetic significance of ultrastructural features in the planktonic freshwater ciliate *Limnostrombidium viride* (Alveolata, Ciliophora, Oligotrichida).
- 12.00–13.20 Mittagspause

Vortragsprogramm

Chair: Andreas Tribsch

- 13.20–13.40 **Wilhelm Foissner**: Follow micro-organisms MacArthur's and Wilson's equilibrium theory of island biogeography?
- 13.40–14.00 **Hannes Schuler** et al.: The microbial community of *Cacopsylla* spp. (Hemiptera: Psyllidae).
- 14.00–14.20 **Helena Shaverdo** & Michael Balke: Study of Copelatinae (Coleoptera: Dytiscidae) of Australasia.
- 14.20–14.40 **Elisabeth Geiser**: How many animal species are living in Austria? Update after 20 years.
- 14.40–15.00 **Andreas Kroh** & Omri Bronstein: Arbaciid mitogenomes revisited (Echinodermata: Echinoidea) – how transcriptomic data help to improve gene annotation.
- 15.00–15.50 Kaffeepause und Poster session moderiert von Andreas Tribsch (5 Minute pro Poster)

Bozen 2018



Vortragsprogramm

Chair: Frank Zachos

15.50–16.10 **Stephan Koblmüller** et al.: Of fish and parasites: the *Lates* puzzle.

16.10–16.30 **Maximilian Wagner** et al.: Mediterranean river blennies – diversity and conservation.

16.30–16.50 **Nicole Grunstra** et al.: Humans as inverted bats: A comparative approach to the obstetric conundrum.

16.50–17.20 Vortrag der Gewinnerin des NOBIS-Stipendiums

Anne-Sarah Ganske & Nesrine Akkari: Phylogenetic analyses of a challenging centipede taxon – What do morphology and molecules tell us about the evolutionary history of the genus *Lithobius* Leach, 1814 (Arthropoda, Myriapoda)?

17.20 **Elisabeth Haring**: Zuerkennung der NOBIS-Preise und Schlussworte.

Bozen 2018



Abstracts

Phylogenetic significance of ultrastructural features in the planktonic freshwater ciliate *Limnostrombidium viride* (Alveolata, Ciliophora, Oligotrichida)

Agatha, S.¹, Stockmann, N.² & Bardele, C.F.²

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Limnostrombidium viride (Stein, 1867) Krainer, 1995 is a mixotrophic oligotrichid ciliate and might be abundant in the pelagial of Eurasian and Antarctic freshwater lakes. The first transmission and scanning electron microscopical studies in combination with freeze-fracture technology disclosed some of its important morphological and ultrastructural features. (I) The left of the paired basal bodies in the horizontal ciliary row have associated conspicuous club-shaped cilia with perhaps sensory function. (II) The ciliated endoral membrane delimits the peristome on the right side. It is proximally covered by a cytoplasmic fold and distally by multiple membranous layers. Thus, this ciliary structure is entirely covered and probably not any longer strongly involved in food capture; yet, its associated microtubules might be important in stabilising the peristome and cytopharynx. (III) A horizontal ring-canal with supposed osmoregulatory function occurs instead of a common contractile vacuole. (IV) The extrusive nature of the trichites is not only observed in electron micrographs, but the attachment sites of these organelles also display a rosette of “8+1”-particles in the P-face of freeze-fracture replicas as typical for ciliate extrusomes. (V) The neof ormation organelle is a permanent subsurface tube in which the oral ciliature of the daughter’s cell forms. The phylogenetic significance of these structures is discussed. The work of SA was financially supported by the Austrian Science Fund FWF Project 28790.

Species delimitation in an Austrian endemic land snail: The case of *Trochulus oreinos* (Pulmonata: Hygromiidae)

Bamberger, S.^{1*}, Tribsch, A.², Duda, M.³, Macek, O.¹,
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*Trochulus oreinos** is an Austrian endemic land snail species occurring in the Northeastern Calcareous Alps at high elevations. Within *T. oreinos*, two morphologically highly similar subspecies have been distinguished: The westerly distributed subspecies *T. o. scheerpeltzi* is characterized by a groove beneath the shell keel, whereas the eastern *T. o. oreinos* features an additional penial fold. First molecular genetic analyses of mitochondrial (*COI*, *16S*, *12S*) as well as nuclear marker sequences (*ITS2*) indicated a high genetic divergence between the subspecies. A clear geographic break was found within the potential contact zone, the Haller Mauern mountain range (Ennstal Alps). Samples of all western sites were part of the clade representing *T. o. scheerpeltzi* and almost all samples from the eastern sites clustered with *T. o. oreinos*. However, within two sampling sites of the eastern Haller Mauern, a few individuals possessed a *COI* sequence matching the *T. o. oreinos* clade, whereas at the *ITS2* locus they were heterozygous possessing the alleles of both taxa. Based on these striking results, indicating historical and/or ongoing hybridization, no decision could be made on whether to consider the two taxa as separate species. Therefore, we used Amplified Fragment Length Polymorphism (AFLP), a DNA fingerprinting technique, to investigate the extent of gene flow between the two subspecies within the Haller Mauern contact zone. The AFLP results of 200 individuals confirmed a clear separation of the two taxa congruent with the mitochondrial data. Although they occur on the same mountain range without any physical barrier, no indication of ongoing gene flow between the two taxa was found.

*In the revision of the family Hygromiidae, Neiber et al. (2017) suggested the genus name *Noricella* for *T. oreinos*.

Follow micro-organisms MacArthur's and Wilson's equilibrium theory of island biogeography?

Foissner, W.

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In our 2016 meeting, I reported on "Dispersal of ciliated protozoa: lessons from a 4-year-experiment with environmental mesocosms". The experiment was performed in three plastic containers filled with tap water and pieces of broken glass: 1.5 l, surface area 468 cm²; 6 l, 875 cm²; 12 l, 1500 cm². The containers were placed on the south of a roof garden with vegetables and were investigated monthly.

Altogether, only 20 ciliate species were observed at 25 sampling occasions during April 2009 and October 2012: 14 species in the 1.5 l container, 11 in the 6 l container, and 9 in the 12 l container. This was opposite the expectation, viz., the widely accepted Mac Arthur's and Wilson's (AW) theory of island biogeography, i.e., that the number of species increases with area size. When I asked the audience for an explanation, only one colleague gave a rather harsh comment, viz., that my analysis was wrong because based only on ciliates while the AW theory requires the investigation of many groups of organisms in a certain area. She suggested me to attend her university lecture on ecology. However, I could not remember to have seen an investigation of this kind. Indeed, her suggestion was nonsense as you can see in the book of AW and many textbooks on ecology.

Mac Arthur and Wilson (1967) noticed in their book that some data do not or only partially fit their theory. They explained this with special ecological conditions. However, later several studies questioned AW, e.g., Dickerson and Robinson (1985), who performed a similar experiment as I did, using ciliates and some algae. They state: "Contrary to the MacArthur-Wilson prediction, small microcosms had significantly higher species richness than large microcosms." They showed that habitat quality and/or species diversity appear to be more important than area size. In this context, we should remember AW: "Differences in the ecology among islands can distort the area-diversity curve because such differences do occur over short distances in many parts of the world; area alone cannot be assumed in any particular case to be a precise predictor of species diversity". Unfortunately, this does not help my data because the containers were virtually identical and side by side except for the amount of water and surface area. Thus, the island theory of AW is questioned for micro-organisms. Supported by the FWF, Project 26846-B17.

References

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Phylogenetic analyses of a challenging centipede taxon – What do morphology and molecules tell us about the evolutionary history of the genus *Lithobius* Leach, 1814 (Arthropoda, Myriapoda)?

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The Palearctic genus *Lithobius* Leach, 1814 includes more than 500 described taxa. A previous morphological study suggested *Lithobius* as a non-monophyletic taxon; yet, rigorous phylogenetic analyses to answer questions on the species interrelationships within the genus are lacking. In fact, the subdivision of the genus *Lithobius* into eight “subgenera” is based on taxonomic characters without any evidence of the monophyly of these groupings. This study represents the first attempt to understand the phylogeny of *Lithobius*, based on data from morphological and molecular investigations.

The species sampling focused on European *Lithobius* species collected in Austria, Finland, Hungary, Romania, Spain, and UK. The extensive study of the morphology of the peristomatic structures, the mandibles and the first maxillae, using scanning electron microscopy, revealed eight new characters for lithobiid phylogeny. These new characters together with eleven more characters from internal head structures and 43 characters from external structures (in total 62 chars.) were coded for 33 *Lithobius* species and four other representatives of Lithobiidae. For the genetic characterisation, sequences of the mitochondrial loci COI and 16S rRNA, and the nuclear locus 28S rRNA have been acquired from 44 *Lithobius* species and eight other lithobiid genera.

The resulting morphological matrix and the sequence data were used for phylogenetic analyses, using the optimality criteria maximum parsimony and maximum likelihood, with representatives of Henicopidae (sister group to Lithobiidae) and Scutigera as outgroups. The resulting cladograms support the monophyly of Lithobiidae and reflect the genus *Lithobius* as paraphyletic. Furthermore, the “subgenera” of *Lithobius* are resolved non-monophyletic, except for *Sigibus* under parsimony, using morphological data only. As a next step, mapping the morphological characters on a molecular tree and analysing both data sets as a concatenated file will help to understand certain species interrelationships and relationships to allied lithobiid genera – addressing some questions on the evolutionary history of the genus.

How many animal species are living in Austria? Update after 20 years

Geiser, E.

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Geiser (1998) estimated 45,870 species of animals to occur in Austria. This number is a result of summing up published species lists with extrapolation from species numbers in groups where knowledge is insufficient. An update after 20 years is justified by more and better evaluated species lists resulting from various research activities, and better consolidated species numbers from Germany, which were used as the basis for extrapolation. As the new and better verified outcome 54,125 animal species are reported for Austria. Insects alone count for 40,000 species (Geiser 2018).

This augmentation by 18% or 8,255 species is first and foremost due to better knowledge. The Checklist Series of the Academy of Science, the ABOL Project, the 3rd edition of the FAA (Fauna Aquatica Austriaca) and several monographic studies contribute to well-grounded species numbers in much more groups than 1998.

There is a considerable amount of species of which only few individuals are known from Austria. Some of them are known only by a single specimen preserved in museum collections. Others were not recorded in Austria for more than 50 years. A part of these species is really rare, but often they likewise are difficult to observe, to catch and to identify.

Keep in mind, that the increase in recorded species numbers from Austria masks a serious problem: It is not that the pressure on biodiversity decreased, to the contrary. The biomass of insects diminished by 75% during the past decades, even in protected habitats. This decline entails many side effects, to mention exemplarily the dependence of reproduction of birds and bats, as well as of the pollination of plants on insects. Therefore, it is necessary to keep in mind that this pleasant high number of animal species in Austria includes an increasing number of endangered species.

References

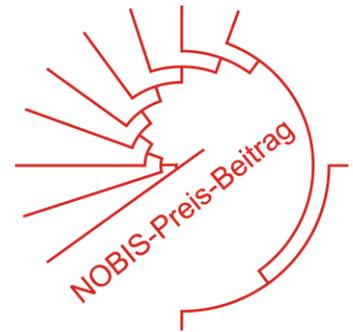
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Geiser, E. 2018 (in press). How many animal species are living in Austria? Update after 20 years. *Acta ZooBot Austria*, 155.

A new type of somatic kinetid and cortical network in the model tintinnid *Schmidingerella meunieri* and a scenario of character evolution (Alveolata, Ciliophora, Spirotricha)

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The Oligotrichea are characteristic plankton ciliates mainly in marine habitats, comprising the oligotrichids and choreotrichids (~1,200 species). Molecular phylogenies of this group are incongruent with morphological data because they reveal several unresolved branches, unexpected relationships, and non-monophylies; possibly, the lack of some genera and families in the gene trees also influences the topologies. In the outgroup taxa (euplotids and hypotrichs) and the oligotrichids, the somatic ciliary rows consist of paired basal bodies with cilia only at the anterior basal bodies, whereas the choreotrichids demonstrate four types of somatic kinetids, namely, paired basal bodies with cilia (i) only at the anterior basal bodies, (ii) at both basal bodies, (iii) only at the posterior basal bodies, or at single basal bodies; combinations of three types might even co-occur in a single species. In the “Kinetid Transformation Hypothesis”, the evolution of these kinetid types had been reconstructed and used for characterising choreotrichid families. Yet, support from ultrastructural data is lacking, except for some anecdotal findings. The present integrative approach thus combines taxonomic, molecular, and new ultrastructural data, providing insights into the fibrillar associates of the somatic kinetids in the loricate choreotrichid *Schmidingerella meunieri* (Kofoid & Campbell, 1929) Agatha & Strüder-Kypke, 2014, a suitable model organism for marine tintinnids. Ultrathin sections of cryofixed cells reveal a totally new kinetid type for ciliates: beyond the three common associates (kinetodesmal fibril, postciliary ribbon, transverse ribbon), it is characterised by three conspicuous microtubular ribbons which form a dense network in the cortex of the anterior cell portion. The data corroborate the “Kinetid Transformation Hypothesis” for a certain group of tintinnids. The evolutionary constraints which might have fostered the development of such conspicuous structures are discussed. Perhaps, the introduction of these additional fibrillar associates of the somatic kinetids is correlated with changes in the function of the somatic cilia or the need for an increase in cell rigidity. The study was financially supported by the Austrian Science Fund (Project P 28790).

Humans as inverted bats: A comparative approach to the obstetric conundrum

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The narrow human birth canal evolved in response to multiple opposing selective forces on the pelvis. These factors cannot be sufficiently disentangled in humans because of the limited range of relevant variation. We outline a comparative strategy to study the evolution of human childbirth and to test existing hypotheses in primates and other mammals. We combine a literature review with comparative analyses of neonatal and female body and brain mass, using three existing datasets. We also present images of bony pelvises of a diverse sample of taxa. Bats, certain non-human primates, seals, and most ungulates, including whales, have much larger relative neonatal masses than humans, and they all differ in anatomical adaptations for childbirth. Bats, as a group, are particularly interesting in this context as they give birth to the relatively largest neonates, and their pelvis is highly dimorphic: whereas males have a fused pubic symphysis, females exhibit a large pubic gap that is bridged by a ligament. The demands on the widened and vulnerable pelvic floor in bats are likely relaxed by aerial locomotion and roosting head-down. Parturition has constituted a strong selective force in many non-human placentals. We illustrated how the demands on pelvic morphology resulting from locomotion, pelvic floor stability, birth, and perhaps also erectile function in males have been traded off differently in mammals, depending on their locomotion and environment. Exploiting the power of a comparative approach, we present new hypotheses and research directions for resolving the obstetric conundrum in humans.

Species, species, species: adaptive radiation in a genus of freshwater bacteria

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The genus *Polynucleobacter* (Burkholderiaceae, Betaproteobacteria, Bacteria) comprises bacteria with two distinct lifestyles, obligate endosymbionts of ciliates and free-living planktonic strains (Hahn et al. 2016a). Comparative genome analyses suggested that the endosymbiotic members of the genus represent derived stages undergoing degenerative genome evolution. Planktonic *Polynucleobacter* spp. show an ubiquitous and cosmopolitan distribution in standing freshwater systems and contribute at least in acidic, humic-rich lakes and ponds large fractions of total bacterial cell numbers (up to 60% of bacterioplankton). The environmental success and the wide geographical and ecological distribution of the genus can mainly be attributed to subgroup C (aka PnecC) of the genus. Surprisingly, the ecological diversity of this taxon is contrasted by a rather low sequence diversity of the 16S rRNA gene (> 99% sequence similarity) of strains affiliated with this subgroup (Hahn et al. 2016b). Analyses of >100 genomes of PnecC strains revealed an enormous genomic diversity within the taxon, which is strongly contrasting the small divergence of the ribosomal genes (Hoetzing and Hahn 2017). Ecophysiological investigations and cultivation-independent surveys on environmental distribution of taxa suggested niche separation among taxa including in some cases complete ecological isolation of taxa. Estimations suggest that subcluster PnecC harbours > 100 species.

References

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“Now and then” – Comparison of historic and current data on tintinnid (Alveolata, Ciliophora) communities in the East Pacific

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Among planktonic ciliates, only tintinnids build loricae, which are the only feature complex for taxonomy and classification in the about 1,000 species. Since identification keys to the species do not exist, the outstanding monographs of Kofoid and Campbell (1929, 1939) as well as the compilation by Zhang et al. (2012) have to be used. But, species identification by means of these monographs is hampered by (i) the lack of descriptions for most species, (ii) numerous subjective synonymizations and thus changes in species limitations, (iii) illustrations often showing subjective synonyms, and (iv) the frequent lack of measurements (Kofoid and Campbell 1929) or uncritical compilations of literature data often without the original ones (Zhang et al. 2012). Therefore, exclusively original species descriptions were used for determination in the present study on tintinnids from three stations on a transect from oceanic to coastal waters in the Northeast Pacific. Based on comprehensive morphometric analyses and micrographic documentation, 99 morphospecies, 31 genera, and 10 families were recorded representing about 1/10 of the extant tintinnid species and nearly 50% of the extant genera. The majority of coastal tintinnids have agglutinated loricae with adhered foreign particles, while most oceanic forms have hyaline loricae without particles. This trend emerged also in the present study with a restriction of the genera *Tintinnopsis* and *Stenosemella* to neritic waters and a much higher percentage of hyaline taxa in open waters; only *Codonella* occurred also in open waters. In the light of climate change, the species composition shall be compared to the tintinnid community in the eastern tropical Pacific assessed by Kofoid and Campbell more than a century ago. The project was funded by the Federal Institute for Geosciences and Natural Resources of Germany.

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Of fish and parasites: the *Lates* puzzle

Koblmüller, S.¹, Schögl, C.A.¹, Kmentová, N.^{2,3,4}, Zangl, L.¹, Van Steenberge, M.^{4,5,6}, Lorber, C.J.¹, Artois, T.³, Muterezi Bukinga, F.⁷, Mulimbwa N'sibula, T.⁷, Muzumani Risasi, D.⁷, Masilya Mulungula, P.⁷, Gelnar, M.² & Vanhove, M.P.M.^{2,3,4,8}

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Lates perches of the genus *Lates* (Latidae) include both marine and freshwater species and these have a strikingly disjunct distribution range. Four species of *Lates* occur in coastal areas and estuaries of the Indo-Pacific region, but not along the African coast. The remaining seven *Lates* species inhabit large African freshwater systems, in particularly large rivers and some large lakes. Even though many *Lates* species are important food and game fish, next to nothing is known about phylogenetic relationships within the genus. First phylogenetic data of African *Lates* perches and their monogenean parasites (family Diplectanidae) provide evidence that the four endemic Lake Tanganyika species constitute a monophylum, contrary to what has been previously suggested based on morphological data. Pairwise genetic distances among *Lates* species are surprisingly low, indicating either recent divergence or low mutation rates. Continuous morphological variation and shallow divergence among parasites from geographically isolated host species indicate that, quite atypical for monogeneans, only one diplectanid species is parasitizing *Lates* across different African basins.

Arbaciid mitogenomes revisited (Echinodermata: Echinoidea) – how transcriptomic data help to improve gene annotation

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Currently available complete mitochondrial genome (mitogenome) sequence data is highly biased towards commercially exploited echinoids. Phylogenetic inference based on complete mitogenomes performs much better than analyses based on single markers, but the biased taxon sampling of currently available mitogenome sequences, undermines the efforts to achieve a robust phylogenetic inference. At present, 86% (n=44) of published echinoid mitogenomes sequences are of species from the order Camarodonta. Only two are available for spatangoids and diadematoids (each), and only one for each of the genera *Arbacia* and *Glyptocidaris*. The latter are identified as immediate sister-taxa to camarodonts by cladistic analyses based on morphology. The phylogenetic placement of *Arbacia* (based on complete mitochondrial data) fluctuates depending on the taxon set included in the analysis and sequence data used. Published in 1996, the mitogenome of *A. lixula* was one of the earliest echinoid mitogenomes, thus having very little available data for evaluating potential sequence errors. Here, we present novel complete mitogenome sequences assembled from publicly available transcriptomic data of two independent *A. lixula* specimens, and a partial mitogenome (missing three tRNAs) of *Arbacia punctulata*. The novel assemblies corroborate the earlier published *A. lixula* mitogenome sequence and increase taxon sampling in that poorly represented part of the echinoid tree. Usage of transcriptomic data to recover mitogenomes involves more effort than assembly from whole genomic short read data, but offers insights into mitochondrial transcription and has implications for mitogenome annotation. Mapping of raw reads on the novel mitogenomes shows the placement of the poly(A)-tails at the 3' end of the transcripts, indicating positions of stop codons. Comparison with echinoid mitogenome annotations documented in GenBank indicates that annotation for NADH dehydrogenase subunit 4 (ND4) is erroneous in all published echinoid mitogenomes. Position of the poly(A)-tails suggests that the present notion of a 10-bp-overlap between ND4 and tRNA-His is incorrect and that ND4 is terminated by an incomplete stop codon that is completed by polyadenylation. Funding by the Austrian Science Fund (FWF): project P29508-B25 is gratefully acknowledged.

Phylogenetic analyses of the Goshawk *Accipiter [gentilis]* superspecies using mitochondrial DNA sequences

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† During the final work on this study Anita Gamauf sadly passed away. We dedicate this work to her memory.

The Northern goshawk *Accipiter gentilis* is a medium-sized bird of prey inhabiting boreal and temperate forests. It has a Holarctic distribution with ten recognized subspecies following del Hoyo and Collar (2014). Traditionally, it has been placed within the *Accipiter [gentilis]* superspecies, together with Henst's goshawk *Accipiter henstii*, the Black sparrowhawk *Accipiter melanoleucus* and Meyer's goshawk *Accipiter meyerianus* (Amadon 1966). While those four taxa are geographically separated from each other, hence referred to as allospecies, phylogenetic relationships are still unknown.

In the present study, we performed phylogenetic analyses on the *Accipiter [gentilis]* superspecies, including all recognised subspecies of all four allospecies, using partial sequences of two marker sequences of the mitochondrial genome, the *control region* and the *cytochrome B* gene.

We found a major split of *A. gentilis* into two reciprocally monophyletic groups, a Nearctic clade (3 subspecies) and a Palearctic clade (7 subspecies). *Accipiter meyerianus* nested within the clade together with Palearctic *A. gentilis*; therefore, *A. gentilis* appears to be paraphyletic. Although comprising seven subspecies distributed from the Atlantic coast in Western Europe continuously to Eastern Siberia, we found a strong genetic homogeneity within Palearctic *A. gentilis*. Individuals of *A. henstii* and *A. melanoleucus* form distinct clades. Relationships between the four clades could not be resolved without uncertainty. We discuss phylogenetic and taxonomic implications.

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The Caribbean Sea – pathway and barrier at the same time?

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The Caribbean Sea provides an excellent framework for evolutionary biologists because of the well known oceanographic and geological history. Research on oribatid mites (Acari, Oribatida) makes no exception. The majority of Oribatida can be found in terrestrial habitats, only a few, e.g. the Selenoribatidae (Ameronothroidea), inhabit marine associated habitats. All selenoribatid species are exclusively found in the littoral zone of subtropical and tropical coasts. These mites are air-breathing organisms and can survive in habitats subject to daily tidal inundation. Selenoribatidae dwell in algae growing on sandy and rocky substrates, on mangrove roots, or on man-made structures and were sampled on Bermuda, in Central and North America, and on several Caribbean islands (Antilles, Bahamas). Oribatid mites are considered poor dispersers, due to their small size, the lack of any phoretic adaptation, the fact that they are not able to fly or swim actively, etc. However, ocean currents and/or anthropogenic transport may facilitate long distance dispersal in these taxa. This study is the first to examine the biodiversity, the biogeography, and the ecology of species belonging to two selenoribatid genera (*Carinozetes* and *Thalassozetes*). Species delimitation methods were employed to obtain a first estimate of species diversity based on mitochondrial COI sequences, and comparison of phylogenetic patterns among species within these two genera unveiled strikingly different biogeographic patterns; island endemics on the one hand, and widespread species on the other. Thus, the Caribbean Sea seems to provide both – a pathway and a barrier for closely related species within the genera *Carinozetes* and *Thalassozetes*.

New insights into the occurrence of the genus *Pomphorhynchus* Monticelli, 1905 (Acanthocephala) in Austria

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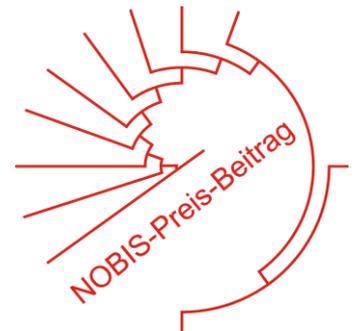
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The genus *Pomphorhynchus* Monticelli, 1905 belongs to the phylum Acanthocephala and represents obligate endoparasites infesting mostly freshwater fish. The morphological similarities of the species *Pomphorhynchus laevis* (Müller, 1776) and *Pomphorhynchus tereticollis* (Rudolphi, 1809) led to a considerably high level of misidentifications in former times, associated with false conclusions regarding their distribution in Europe. Less is known about the status of the genus in Austria. In the course of the last survey on Acanthocephala in Austria 30 years ago, *P. laevis* was the only representative of the genus in Austrian waters. In recent studies, a high diversity of genetic lineages was detected in *Pomphorhynchus*, contrasting with the morphological similarities between species. In the present study, we performed a survey of *Pomphorhynchus* sp. in fish derived from Austrian waters. It is the first survey in Austria, using an integrative taxonomic approach with a combination of morphological and molecular genetic methods. Our results revealed the occurrence of three species of the genus *Pomphorhynchus* in Austria: *P. laevis*, *P. tereticollis*, and *Pomphorhynchus bosniacus* Kiskároly and Čanković, 1967. While *P. bosniacus* was the predominant species in the Danube, *P. laevis* was recorded exclusively in Styria. *Pomphorhynchus tereticollis* occurred mainly in rivers of Styria, and additionally, we found one individual in the Danube River. These results are the first evidence of the occurrence of *P. bosniacus* and *P. tereticollis* in Austria. Combining our results with published DNA sequences, a high intraspecific diversity in *P. bosniacus* was observed, suggesting that the species has a long history in Middle and Central Europe and probably was repeatedly misidentified as *P. laevis* in former times. The same applies to *P. tereticollis*. The sparse morphological characters available for taxonomic assignment together with a high intraspecific variability in *Pomphorhynchus* leads to a high risk of misidentification. Our study highlighted the importance of using integrative taxonomical methods for reliable identification of *Pomphorhynchus* species.

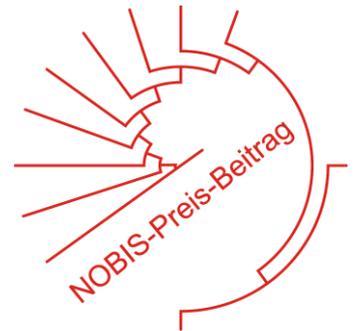
Linking the ecological species concept with systematics of trochid gastropods in the Northern Adriatic Sea

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The genera *Gibbula*, *Phorcus*, and *Steromphala* represent a clade of marine gastropods of the family Trochidae (Vetigastropoda). About 25 species of these genera live along rocky coasts of the Mediterranean Sea and the Atlantic Ocean feeding on biofilms on rocks and seagrass leaves. The use of DNA-barcoding, shell morphometrics, and radula morphology improved species delineation sufficiently to put the ecological species concept to the test. Although some of these closely related species occur in sympatry, little is known about their ecological niche differentiation. Abiotic parameters such as exposure to wave action, air and temperature, as well as biotic factors like predation and different reproductive strategies are potential key factors for this and may result in different vertical distribution patterns of these snails in the intertidal and shallow sublittoral zones.

Preliminary observations indicate different depth preferences when two or more species of these genera co-occur. To quantify this observation, snails were collected at several sites along transects from the midwater line to about 4 m depth in Rovinj and on the Brijuni Islands, Croatia.

The specimens were identified by their shell, with additional DNA-barcoding to aid species identification, especially of juvenile specimens. Ten species were identified by this integrative approach. The results show that, although the depth ranges of the species may overlap, the structure of the trochid species assemblages change from shallow to deep habitats. *Phorcus turbinatus* and *P. articulatus* dominate along the waterline and are replaced by *Steromphala* species in the upper sublittoral. *Steromphala varia* and *Clanculus* spp. occur predominantly in the deepest parts of the studied depth range.

Adaptations to crop-collecting in the digestive tract of bees (Hymenoptera: Anthophila)

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While most bees carry pollen externally by means of certain structures on legs or the abdomen, some follow the strategy of transporting pollen internally. In that case, the pollen is swallowed, stored in a crop inside the metasoma and regurgitated at the nest. Crop-collecting is accomplished by Hylaeinae – represented by the genus *Hylaeus* (masked bees) in Europe – and the Australian Euryglossinae, both belonging to the family Colletidae. Although in masked bees internal pollen storage is proven and illustrated, data in literature about the exact anatomy of the organs involved is diverging. Also, *Xylocopa* and *Ceratina* (carpenter bees) are described to facultatively transport the pollen inside the body in a crop; however, this phenomenon is poorly studied. As carpenter bees belong to the family Apidae, it has to be assumed that crop-collecting evolved at least twice independently.

The study aims at investigating the digestive tract of obligate and facultative crop-collectors, as well as outgroups, by means of microCT scans, to detect all involved structures and adaptations for internal pollen storage. Furthermore, a comparison between masked bees and carpenter bees shall clarify if the involved structures are similar or if obligate crop-collectors possess more complex adaptations.

The microbial community of *Cacopsylla* spp. (Hemiptera: Psyllidae)

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Phytoplasmas are pathogens that are responsible for a large number of plant diseases of different economically important plant species. Apple proliferation (AP) is a severe disease of apple trees caused by the phytoplasma '*Candidatus Phytoplasma mali*'. AP phytoplasma is causing proliferation of auxiliary shoots, decreased size and low quality of the fruit and is therefore responsible for vast economic losses.

In nature phytoplasmas are primarily transmitted by plant sap feeding insects. Psyllids of the genus *Cacopsylla* are the main vectors of '*Ca. P. mali*'. Although, more than 15 species are known to occur in apple orchards, just two – *Cacopsylla picta* and *Cacopsylla melanoneura* – are able to acquire and transmit phytoplasma. Knowledge on the factors influencing vector capacity in psyllids is currently limited. One important aspect that is potentially influencing the acquisition and transmission of phytoplasma is the microbial community of the insects.

Here, we present a high-throughput metagenomic analysis of the 16S rRNA of 12 different *Cacopsylla* species. All species share two endosymbionts: The primary endosymbiont *Carsonella* and a secondary – yet undescribed – symbiont. Fine-scale analysis, however, show that all species harbour a unique strain of both endosymbionts, highlighting a long co-evolutionary history of the two symbionts with their hosts. Moreover several individuals of different species are infected additionally by the endosymbionts *Rickettsia*, *Wolbachia*, *Arsenophonus*, and *Spiroplasma*. We discuss the role of the microbial community on the fitness of their hosts and their potential impact on phytoplasma transmission.

Study of Copelatinae (Coleoptera: Dytiscidae) of Australasia

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The presentation is aimed to report the results of our completed study on the genus *Exocelina* Broun, 1886 in New Guinea and introduce our new project on the genus *Copelatus* Erichson, 1832. These two genera are the most species rich within the diving beetle subfamily Copelatinae and are the only representatives in Australasia - a biogeographical realm, which is limited to the eastern part of the Indonesian Archipelago, New Guinea, Australia, New Zealand, and several Pacific island groups. In this region, *Exocelina* is represented by 180 species, with 125 New Guinea species as the core of genus biodiversity, whilst only 35 *Copelatus* species are known from the realm, and only 13 species from New Guinea. Our knowledge on New Guinea *Exocelina* has been evidently enriched due to our project, in which we revealed and described 84 species and four subspecies new for science and created a species-group structure of the genus that includes 24 species groups. In addition, we inferred that the genus originated in Australia 20–15 million years ago and twice colonised New Guinea approximately 10–5 million years ago. However, only one of the colonisations was very successful, resulting in a radiation of more than 120 species. We also showed that the main reason for this amazing species diversity (60% of dytiscid fauna of the island) is the geological evolution of the island. New Guinea, with its intensive volcanic activity, rapid rising of the new lands, and other complex geological processes, was a “cradle of biodiversity” for the genus providing a species richness and establishing a high local endemism that is not older than the present-day landmass. The gained knowledge we intend to apply in our new study of the closely related genus *Copelatus*, the largest and one of the most taxonomically and phylogenetically enigmatic diving beetle groups. Based on our preliminary investigations of this genus, we assume more than 80 new species in Australasia. Based on morphological and molecular data, we will propose a new preliminary supraspecific classification of the genus, which is aimed to replace the old one and could be a solid base for further work on the genus representatives from the other regions. Also, using these data, we will carry out a phylogenetic analysis of Australasian *Copelatus* and build the dataset needed to reconstruct the biogeographical evolution of this diverse circumtropical insect group and bring new information on biogeography of Australasia in general and new data on insular insect radiations.

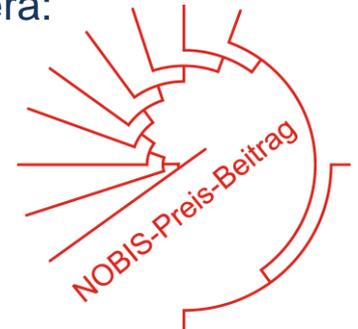
Bozen 2018



Integrative taxonomy and evolution of the cryptic pavement ants of the *Tetramorium caespitum* complex (Hymenoptera: Formicidae)

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Ants (Formicidae) are one of the best-studied groups of insects. However, since ants contain many morphologically cryptic species, even in Europe species delimitation is incomplete. The species level is the base for most biological studies; research often only makes sense if the study organism is correctly determined at the species level. A recent study suggested the presence of at least eight western Palearctic species in the genus *Tetramorium*, but did not analyse nuclear DNA or draw formal taxonomic conclusions. Within this PhD project, using 1,428 nest samples in an in-depth integrative taxonomy approach, I revised the European species of the *Tetramorium caespitum* complex (until 2017 known as *Tetramorium caespitum/impurum* complex) and addressed research questions to the evolution of cryptic species itself. Our team established a reduced representation library of nuclear DNA markers based on amplified fragment-length polymorphism (AFLP) PCR products. The yielded set of anonymous nuclear loci revealed too little interspecific variability and thus I switched to AFLP. Unsupervised analyses provided independent species hypotheses based on molecular and morphological disciplines. Integrative taxonomy suggested the presence of ten clearly distinguishable European species differing in mitochondrial DNA, nuclear DNA, morphology of workers and males, and ecology. The observed mitochondrial-nuclear discordances result most likely from peripatric speciation, historical introgression, and recent hybridization. Morphological-nuclear discordances are caused by error rates in discriminant analyses and thus by morphological cryptic species. Nuclear DNA reveals that the *Tetramorium caespitum* complex is a monophylum and thus contradicts previous mitochondrial DNA findings. The morphological similarity of species correlates positively with phylogenetics, so there is a loss of morphological similarity over evolutionary time, which indicates that cryptic species evolved by stasis and not by convergence. Species-specific morphological adaptations to ecological niches are exceptions. I interpret the cryptic species in this complex as a result of stasis due to stabilizing selection and consider the worker morphology of the species complex as an adaptive solution for various environments.

Mediterranean river blennies – diversity and conservation

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The blenniid fish genus *Salaria* Forsskål, 1775 is characterized by a peculiar evolutionary history. *Salaria* not only includes two marine species with a pan-Mediterranean distribution, but also the only freshwater blennies in Europe. Highly isolated and patchily distributed across the Mediterranean basin (and outside), three distinct freshwater species are currently being recognized: *Salaria fluviatilis* (Asso, 1801), *S. economidisi* Kottelat, 2004, and *S. atlantica* Doadrio, Perea & Yahyaoui 2011. In previous studies, however, it has been suggested that several additional yet unrecognized species might be present within the freshwater clade of *Salaria*. In the light of potential cryptic diversity and already extirpated populations, such as on Cyprus, the necessity to gain adequate knowledge and understanding of the underlying evolutionary relationships among populations is fundamentally important, particularly with regard to conservation actions that involve re-introductions in areas where freshwater blennies have gone extinct in recent years. Here, we summarize preliminary results concerning the overall phylogeography and diversity of freshwater blennies around the Mediterranean Sea and highlight urgent needs and measures for conserving these charismatic, but highly threatened fishes.

Phylogeny of the Eurasian Jay (*Garrulus glandarius*) based on mitochondrial marker sequences

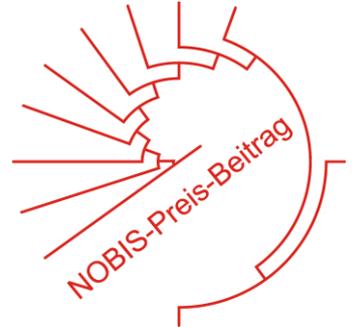
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The Eurasian Jay (*Garrulus glandarius*) is a corvid bird with an extensive distribution covering the wooded areas of the Palearctic and the northern Oriental region. The species exhibits a complex geographic pattern of morphological variation. The major checklist authorities currently recognise between 34 and 40 different subspecies (Clements et al. 2018; Gill and Donsker 2018) that are variably arranged in five to eight groups. The phylogeny of the Jay was investigated based on samples of 91 birds from the entire distribution range. Altogether we covered 24 subspecies representing the eight proposed morphological subspecies groups, as well as the two closely related species *Garrulus lanceolatus* and *Garrulus lidthi*. Fresh muscle and liver tissues as well as foot pads from museum specimens were utilised to obtain 1,300 bp sequences of the mitochondrial control region. The constructed phylogenetic tree revealed a division into five main lineages within *G. glandarius*: (1) a Japanese “*japonicus* group”, (2) a Southeast Asian group, (3) *taivanus* (Taiwan), (4) a “*brandtii* group”, and (5) a Western group, which is further subdivided. The Southeast Asian group unifies the morphologically distinct “*bispecularis*” and “*leucotis*” groups, contrary to the recently proposed treatment of each of these groups as separate species. The Western group is composed of four subclades corresponding to the morphological “*atricapillus* group” from the Near East, the “*cervicalis* group” from North Africa, the European “*glandarius* group” as well as the insular subspecies *glaszneri* from Cyprus. Of the numerous subspecies described from across Europe (*glandarius* group) only *G. g. cretorum* from Crete proved to be slightly distinct from the nominate form.

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Barcoding Austria's scorpionflies: unexpected cryptic diversity

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Scorpionflies (Mecoptera, Panorpidae) are a rather species-poor family of winged insects. Five species, *Panorpa alpina*, *P. cognata*, *P. communis*, *P. germanica*, and *P. vulgaris* are reported for Austria. First DNA-barcodes of these species, generated in the framework of the ABOL (Austrian Barcode of Life; www.abol.ac.at) initiative, however, cluster into seven distinct mitochondrial lineages. *Panorpa communis* samples fall in two distinct lineages that are resolved as paraphyletic with respect to *P. vulgaris*. Similar results were found in *P. alpina*, for which two very divergent mitochondrial lineages were recovered. Whether these additional *P. communis* and *P. alpina* lineages indeed represent distinct species, shall be clarified by means of morphological/morphometric and nuclear multi-locus data.

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