A DECADE OF DIVERSITY

10. Jahrestagung von NOBIS Austria

Linz - Schlossmuseum und Biologiezentrum
2.-3. Dezember 2016

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Linz 2016 NOBIS AUSTRIA 10

A decade of diversity

Die Kick off-Tagung von NOBIS Austria im Linzer Schlossmuseum im Dezember 2007 war ein wunderbares Fest und der Anfang einer Erfolgsgeschichte! Mit der 10. Jahrestagung kehren wir gerne an diesen Ort zurück. Die Tagung wird gemeinsam von NOBIS Austria und dem Biologiezentrum des Oberösterreichischen Landesmuseums veranstaltet.

Das Tagungsmotto „*A decade of diversity*“ soll auf die Vielzahl und Verschiedenartigkeit der Präsentationen hinweisen, welche die TeilnehmerInnen der Jahrestagungen während der letzten 10 Jahre zu sehen, hören und lesen bekamen.

Programm

Freitag, 2. Dezember

16.00	Führung durch die Ausstellung „Flechten – Farbe, Gift & Medizin“ im Biologiezentrum (J.-W.-Klein-Str. 73, 4040 Linz/Dornach)
ab 17.00	Icebreaker im Biologiezentrum
17.00-20.00	Registrierung
ab 20.00	Abendessen im Gasthaus Lindbauer (Linke Brückenstr. 2, 4040 Linz)

Samstag, 3. Dezember

9.00	Begrüßung im Festsaal des Schlossmuseums Linz (Schlossberg 1, 4020 Linz)
9.10-17.10	Vorträge, Posterpräsentation und NOBIS-Preis Verleihung

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

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Samstag 3. Dezember

8.30-9.00 Registrierung

9.00-9.10 Begrüßung
Mathias Harzhauser, Präsident von NOBIS Austria

Vortragsprogramm

NOBIS-Preis Beiträge

Chair: **Stephan Koblmüller**

9.10-9.30 **Sonja Bamberger** et al.: Testing gene flow between the subspecies of *Trochulus oreinos* in their supposed contact zone.

9.30-9.50 **Arthur Pichler**: Morphological diversity and variation of a nuclear marker sequence in the endemic Arabian barb *Garra barreimiae* [Teleostei: Cyprinidae].

9.50-10.10 **Denise Grau** & Cathrin Pfaff: Baby squirrels and the middle ear of secrets.

10.10-10.30 Kaffeepause

NOBIS-Preis Beiträge

Chair: **Björn Berning**

10.30-10.50 **Susanne Reier** et al.: DNA barcoding as a tool for species identification in fish-parasitizing Acanthocephala of Austria.

10.50-11.10 **Philipp Resl** et al.: Studying substrate associations of lichens with phylogenetic comparative methods and comparative genomics.

11.10-11.30 **Maximilian Wagner** & Stephan Koblmüller: The genus *Gouania*: a thus far unrecognized radiation of cryptobenthic fish in the Mediterranean Sea.

11.30-11.50 **Omri Bronstein** et al.: The urchin doesn't fall far from the tree… in most cases – exploring speciation at the edge of distribution

11.50-12.10 **Vortrag der Gewinnerin des NOBIS Austria DNA-Barcoding Grant**

Franziska Bergmeier et al.: Barcoding the unknown: deep-sea Solenogastres (Mollusca) from the Sea of Okhotsk (Russia).

12.10-13.10 Mittagessen

Chair: **Andreas Kroh**

13.10-13.30 **Thomas Schwaha**: The peculiar life cycle of the ctenstome bryozoan *Pherusella* cf. *brevituba* from the Mediterranean Sea**.**

13.30-13.50 **Fernando Fernández-Mendoza** et al.: A phylogenetic insight into the diversification of black-fruited *Caloplaca* in Eurasia (*Pyrenodesmia*, Teloschistaceae).

13.50-14.10 **Demetra Rakosy** et al.: The evolution of imperfect mimicry in sexually deceptive orchids.

14.10-14.30 **Gerhard Haszprunar** et al.: Barcoding in Bavaria: state of the art and next steps.

14.30-15.20 Kaffeepause und Poster

Chair: **Ulrike Aspöck**

15.20-15.40 **Anneke van Heteren**: The problematics of comparing present and past diversity.

15.40-16.00 **Frank Zachos**: Why springtails and the platypus are not primitive – Tree thinking and the “primitive lineage fallacy”.

16.00-16.20 **Hannes Schuler** & Jeffrey Feder: Der Endosymbiont *Wolbachia* als möglicher Faktor in der Evolution amerikanischer Kirschfruchtfliegen.

16.20-16.40 **Sabine Agatha** et al.: Best practice in description and documentation of ciliate biodiversity (Alveolata, Ciliophora).

16.40-17.00 **Wilhelm Foissner**: Dispersal of ciliated protozoa: lessons from a 4-year-experiment with environmental micro- and mesocosms.

17.00-17.10 **Elisabeth Haring**: Zuerkennung des NOBIS-Preises und Schlussworte

17.10-18.00 **Mitgliederversammlung**

Abstracts

Best Practice in Description and Documentation of Ciliate Biodiversity (Alveolata, Ciliophora)

Agatha, S.[1], Warren, A.[2], Patterson, D.J.[3], Montagnes, D.J.S.[4], Dunthorn, M.[5], Clamp, J.C.[6] & Aescht, E.[7]

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Ciliates (Ciliophora) are unicellular eukaryotes affiliated with the Alveolata. The nomenclature of these organisms and other heterotrophic protists is governed by the International Code of Zoological Nomenclature (ICZN) that also established minimal standards for documenting newly described species, such as by the deposition of type specimens in permanently curated repositories. Only since permanently stained material had become available, types could also be deposited in ciliates. Concerning molecular analyses, specifically, gene sequencing, there are, however, no formal standards for their application in identification or description of ciliate species. During a workshop of the International Research Coordination Network for Biodiversity of Ciliates (IRCN-BC), which is jointly funded by the NSF and NSFC, specific recommendations for best practice in the observation and documentation of ciliate biodiversity had been compiled for integrative approaches combining taxonomic, molecular, and ecologic investigations. Furthermore, the establishment of a firm online base of high-quality primary data is promoted which facilitates and encourages as information resource modern, integrative research into the biodiversity of ciliates.

Supported by FWF Project P28790.

Testing gene flow between the subspecies of *Trochulus oreinos* in their supposed contact zone

NOBIS-Preis-Beitrag

Bamberger, S.[1], Tribsch, A.[2], Duda, M.[3], Macek, O.[1,4],
Affenzeller, M.[2], Haring, E.[1,3], Sattmann, H.[3] & Kruckenhauser, L.[1]

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Trochulus oreinos is an endemic land snail species occurring in the NE Austrian Alps at high elevations. Two morphological highly similar subspecies (*T. o. scheerpeltzi, T. o. oreinos*) have been distinguished (comp. Klemm 1974). Genetic analyses of the nuclear marker sequence *ITS2* (*internal transcribed spacer 2*) as well as mitochondrial marker sequences (*cytochrome c oxidase subunit 1* (*COI*), *16S rRNA gene, 12S rRNA gene)* indicated a high genetic divergence between the two taxa (Duda *et al.* 2011). Analysing a large sample in the potential contact zone at Haller Mauern, a clear phylogeographic break was found: All western samples were part of the clade representing *T. o. scheerpeltzi*, while all eastern samples clustered with *T. o. oreinos*. However, within the sampling sites of the eastern Haller Mauern, a few individuals possessed a *COI* sequence matching the *T. o. oreinos* clade, while at the *ITS2* locus they were heterozygous possessing the alleles of both taxa. Based on these results that suggest historical and/or ongoing hybridization, no decision could be made on whether to consider the two taxa as separate species. Therefore, in a next step, the amount of gene flow between the two subspecies of *T. oreinos* within the Haller Mauern contact zone was investigated using Amplified Fragment Length Polymorphisms (AFLPs), a DNA fingerprinting technique. 200 individuals including samples from the whole distribution range were investigated. The AFLP results verified a clear geographical separation of the two taxa, congruent with the mitochondrial data. Although they occur on the same mountain range without a physical barrier and only about 7000m apart from each other no indication of ongoing gene flow between the two taxa was found. The results of the AFLP analysis will also bring further insights into the glacial refugia of the two subspecies.

Klemm, W. 1974. Die Verbreitung der rezenten Land-Gehäuse-Schnecken in Österreich. Denkschriften der Österreichischen Akademie der Wissenschaften (mathematisch-naturwissenschaftliche Klasse). 117, 1-503.

Duda, M., Sattmann, H., Haring, E., Bartel, D., Winkler, H., Harl, J., Kruckenhauser, L. 2011. Genetic differentiation and shell morphology of *Trochulus oreinos* (Wagner, 1915) and *T. hispidus* (Linnaeus, 1758) (Pulmonata: Hygromiida) in the Northeastern Alps. Journal of Molluscan Studies, 77(1), 30–40.

Barcoding the unknown: deep-sea Solenogastres (Mollusca) from the Sea of Okhotsk (Russia)

Bergmeier, F.S.[1], Ostermair, L.[1], Brandt, A.[2], Haszprunar, G.[1,3] & Jörger, K.M.[1,3]

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The 'SokhoBio Expedition' set out in 2015 to explore the deep-sea benthos of the Sea of Okhotsk (Russia, Northwest Pacific). During the cruise, the bathyal Kuril Basin of the Sea of Okhotsk was sampled at twelve different stations using a variety of gear. Among the samples were more than 100 specimens of Solenogastres. This small clade of aplacophoran worm-molluscs forms an important component of the deep-sea fauna, and could contribute to a better understanding of the biological interactions and distributional patterns in deep-sea organisms. However, Solenogastres often remain unidentified due to their time-consuming and challenging taxonomy, requiring a complex set of morphological and anatomical characters. In an effort to elucidate solenogaster diversity in the Kuril Basin, we pursued an integrative taxonomic approach combining molecular barcoding with imaging methods (e.g., light and scanning electron microscopy, anatomical 3D-reconstructions derived from histological serial sections). Due to the low amplification success with standard barcoding primers, we designed and established a set of solenogaster specific 16S rRNA primers. The obtained combination of characters allows for robust species delineation and a characterization of the species diversity found in bathyal depths of the Sea of Okhotsk. We compare our results with the solenogaster diversity of the Kuril-Kamchatka trench and its adjacent abyssal plain (sampled during the 'Kuril-Kamchatka Biodiversity Studies – KuramBio Expedition'), which are connected with the semi-enclosed Kuril Basin via two bathyal straits. The Solenogastres collected during this cruise represent diverse lineages, however with little faunal overlap in comparison to the Sea of Okhotsk. Our integrative taxonomic approach leads to an immense boost in the hitherto little explored diversity of Solenogastres in the Far Eastern Seas. Additionally, the obtained barcodes can facilitate future identification of Solenogastres and hopefully help transform this neglected taxon into a clade more accessible for biogeographical and ecological studies.

Seasonal growth patterns of the sea grass *Cymodocea nodosa* and patterns of its epiphyte diversity in relation to water depth in the northern Adriatic Sea

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The Neptune grass, *Cymodocea nodosa*, is found in shallow sandy habitat in the Mediterranean Sea and some regions in the eastern Atlantic, where meadows formed by this seagrass species provide an important habitat for epiphytic organisms. Yet, only little is known about factors determining the diversity of epiphytes on *C. nodosa*. In this study, growth patterns of *C. nodosa* and patterns of epiphytic diversity were studied during a seasonal cycle in the northern Adriatic Sea. A total of 52 shoots were analyzed per month in 1.5 m and 5 m water depth. In general, throughout the observation period seagrass biomass and shoot density was higher at 1.5 m water depth, with highest biomass and shoot density in July in both depths. Estimates of epiphyte diversity revealed significant differences throughout the season, with generally higher diversity at 1.5 m depth. Autotrophic organisms dominated all months in both depths, particularly at 1.5 m. Total epiphytic coverage increased with leaf-age. However, the number of heterotrophic epiphytes tended to decrease with leaf-age, indicating that they are outcompeted for space by autotrophic epiphytes. This becomes further evident from detailed analyses of the epiphyte positions along the leaves, with heterotrophs mainly found in the basal region (the younger part of the leaf) and autotrophs dominating the apical region (the older part of the leaf).

The urchin doesn't fall far from the tree… in most cases – exploring speciation at the edge of distribution

NOBIS-Preis-Beitrag

Bronstein, O.[1,2,3], Kroh, A.[2], Däubl, B.[3], Liggins, L.[4] & Haring, E.[3]

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Sea urchins of the genus *Tripneustes* are some of the most abundant and common shallow-water echinoids. Of all *Tripneustes* species, *T. gratilla* is the most wide-spread, ranging from the East-Pacific to East Africa and the Red Sea (RS) and from the Kermadec Islands (New Zealand) to Japan. *T. gratilla* is unique in being one of the most commercially valued echinoderms as well as an ecological keystone species in many tropical regions. As such, its populations are being increasingly manipulated by humans for economic and environmental reasons. However, a recent discovery, combining molecular (mitochondrial and nuclear), morphological and ecological evidence demonstrated that RS *Tripneustes* comprise a completely distinct clade of *Tripneustes*, endemic to the RS. Using a novel molecular genetic approach to diagnose and interpret unique sequence features generally excluded from traditional alignment-based analyses, in combination with newly discovered fossil material, we were able to provide independent evidence for the distinction of the RS *Tripneustes* lineage. We argue that mitochondrial capture, as demonstrated in the RS *Tripneustes* populations, may account for many of the discrepancies between genealogies derived from mitochondrial vs. nuclear markers, masking the true extent of species diversity. Thus, *T. gratilla* may consequently manifest a complex of cryptic species containing highly localized endemic species at the edges of its presumed range. Such unrecognized endemics within commercially exploited species are putting them at risk of extinction since replenishment of stocks by re-settlement of larvae from other regions is impossible. In order to re-assess the geographic ranges of cryptic species within *T. gratilla* and their interaction we analyzed novel material from four remote localities; Sri Lanka, at the center of the species distribution and Hawaii, South Africa and Kermadec Islands, at the edge of its distribution, and compare the results with our previously gathered data from the RS, Western Indian Ocean and the Philippines. We demonstrate further cryptic speciation in *T. gratilla* and provide an updated phylogeny of this species complex. The discovery that *Tripneustes* is genetically much more diverse than expected and may contain endemic species, possibly restricted to single island groups or basins, may inform the development of effective conservation plans and provide support for their inclusion in national and international Red Lists.

A phylogenetic insight into the diversification of black-fruited *Caloplaca* in Eurasia (*Pyrenodesmia*, Teloschistaceae)

Fernández-Mendoza, F.[1], Rabensteiner, J.[1], Kopun, T.[1], Muggia, L.[2], Gaya, E.[3], Mayrhofer, H.[1] & Grube, M.[1]

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The lichen genus *Pyrenodesmia* in the strict sense (Arup *et al.* 2013) comprises a phylogenetically coherent group of species within the wider genus *Caloplaca*, sharing the lack of anthraquinones and the presence of dark brown to black acetone insoluble pigments as diagnostic characters. The taxon, being widespread across the northern hemisphere, shows an exceptionally high morphological and genetic diversity in the Mediterranean and Irano-Turanian regions of Eurasia.

Previous studies have found a striking lack of congruence between phylogenetic reconstructions and morphology-based species concepts (Frolov *et al.* 2016). Under the current paradigm of phylogenetic species delimitation, this incongruence would result in the proposition of multiple new taxa based on the estimated phylogeny. These 'cryptic' species concepts (Crespo & Pérez-Ortega 2010) are often narrow and dataset-dependent. Moreover, they may overlook both the permeability of species boundaries, and whether the phylogeny represents the history of the genomic regions that contribute to reproductive isolation or local adaptation. One solution to these limitations is to develop phylogenies using large portions of the genome.

In this study, we present the results of a series of phylogenetic and phylogenomic surveys carried out on the *Pyrenodesmia* group to discuss the factors underlying the high genetic and morphological diversity of the group.

Arup U, Søchting U, Frödén P (2013) A new taxonomy of the family Teloschistaceae. Nordic J. Bot., 31, 016-083.

Crespo A, Pérez-Ortega S (2010) Cryptic species and species pairs in lichens: A discussion on the relationship between molecular phylogenies and morphological characters. An. Jardín Bot. Madrid, 66, 71-81.

Frolov I, Vondrák J, Fernández-Mendoza F *et al.* (2016) Three new, seemingly-cryptic species in the lichen genus *Caloplaca* (Teloschistaceae) distinguished in two-phase phenotype evaluation. Ann. Bot. Fennici, 53, 243-262.

Dispersal of ciliated protozoa: lessons from a 4-year-experiment with environmental micro-and mesocosms

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Still, there is a widespread believe that microscopic organisms have cosmopolitan distribution because they are easily spread by, e.g., air and water. Presently, two dispersal models are discussed; viz., cosmopolitanism vs. moderate endemicity (~ 1/3 of species). Current research clearly favours the moderate endemicity model ranging from bacteria to rotifers. However, the reasons for the restricted distribution remain unclear. Several have been discussed over the years, viz., dispersal by air and water, animals, the lack of extinction, and the low weight of the resting cysts. The last reason has been disproved by Foissner (2011). But what happens with the other reasons?

This question can be tested by environmental micro- and mesocosms. Thus, I performed a 4-year-experiment using a microcosmos with 1.5 l water and two mesocosms with 6 litre and 12 litre water. The containers were placed on the south of a roof garden with vegetables. Each container was investigated monthly. As the early data showed few species and considerable extinction, I performed two kinds of controls: centrifuged container water was used as culture medium for a variety of ciliates and a chemical water analysis at end of the experiment.

Altogether, only 20 ciliate species were observed at the 25 sampling occasions: 14 in the 1.5 l microcosm, 11 in the 6 l, and 9 in 12 l mesocosms. The cumulative species number showed that the minimal areal was reached after 14 to 19 samples. Most of the species found are terricole or semiterricole, and all can produce resting cysts. Most are bacteria feeders but do not feed on cyanobacteria. The observations show repeated extinction and recolonization of the ciliate fauna. Air dispersal was dominant but low because only 20 species developed visible populations at the 25 sampling occasions. As many cyanobacteria developed, I supposed that they produced substances restricting ciliate growth. However, this was disproved by the controls mentioned above. Dispersal by animals was also observed, viz., once I saw a raven cleaning a piece of bread in the 6 l container followed by a ciliate bloom. Masses of cyanobacteria, various algae, rotifers (*Phialina roseola*), and biting midges developed frequently; especially, the insect larvae fed on the accumulating mud destroying cyst reservoirs. Island biogeography suggests the larger the area the more species. The opposite occurred in my experiment. Supported by the FWF, Project 26325-B16.

Baby Squirrels and the Middle Ear of Secrets

NOBIS-Preis-Beitrag

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This project focuses on the ontogenetic development of the middle ear region in juvenile specimens of the red squirrel, *Sciurus vulgaris,* with an age between three and twelve weeks. Here the development of the bony septa within the epitympanic recess and the tympanic cavity of the middle ear region were investigated. The goal of this study was to determine the distribution of the septa during the ontogeny of the species and the respective consequences in terms of phylogeny. In order to answer phylogenetic questions within rodents, teeth became the main focus of investigations (e.g. Maridet 2011; Martin 1992). However, as rodents often have similar diets, anatomical convergences are to be expected (Samuel 2009). To overcome this important issue new methods were developed that did focus on the highly conservative anatomy of the ear region. The 'septal compass' was invented to map different types and patterns of bony septa and, therefore, allowing septa to reveal their phylogenetic signal (Pfaff 2015). In rodents, septa of varying amounts in both the epitympanic recess and tympanic cavity are present, dividing these structures into segments or diverticula. Anatomical investigations of teeth were made to dissolve systematic questions in extant and extinct rodents (e.g. Maridet 2011; Martin 1992). This talk will not only discuss what ontogeny can tell us about phylogenetic signals in the ear region of the red squirrel, but will also focus on the question how to obtain juvenile organisms for scientific studies.

Maridet, O. et al. 2011. New Discoveries of Glirids and Eomyids (Mammalia, Rodentia) in the Early Miocene of the Junggar Basin (Northern Xinjiang Province, China). Swiss Journal of Palaeontology, 130(2), 315-23.

Martin, T. 1992. Schmelzmikrostruktur in den Inzisiven Alt-Und Neuweltlicher Hystricognather Nagetiere. Laboratoire de paléontologie des vertébrés de l'Ecole pratique des hautes études.

Pfaff, C., Martin, T., Ruf, I. 2015. 'Septal Compass' and 'septal Formula': A New Method for Phylogenetic Investigations of the Middle Ear Region in the Squirrel-Related Clade (Rodentia: Mammalia). Organisms Diversity & Evolution, 15(4), 721-30.

Samuel, J.X. 2009. Cranial Morphology and Dietary Habits of Rodents. Zoological Journal of the Linnean Society, 156(4), 864-888.

Barcoding in Bavaria: state of the art and next steps

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Barcoding activities at the Zoologische Staatssammlung München (http://barcoding-zsm.de) already started in 2009 with the scope of the project "Barcoding Fauna Bavarica" (www.faunabavarica.de) funded by the Bavarian State Ministry of Science. In 2012 the German Barcode of Life (GBOL: www.gbol.org) started being a concerted effort of six large German natural history museums financed by the German Federal Ministry of Science. Both projects are currently financed until end of 2018. In both cases the first goal was to establish a barcode reference library for the Bavarian resp. German fauna, and we currently have about 18.000 species with sufficient background, i.e. several samples and taken analyses. Data releases so far published concern herpetology and fish, Myriapoda, Lepidoptera, Coleoptera, apoidean Hymenoptera, Heteroptera, Orthoptera, Neuropterida (see www.faunabavarica.de → publications), several more are "in the pipeline". More recently, we have focused on specific applied projects, such as forensics, food control, customs necessities, pest control, or biodiversity monitoring in the National Park Bayerischer Wald. With the introduction of Next Generation Sequencing (NGS) technology new applications have become available: First, environmental barcoding enables to monitor in particular freshwater (aim) species in ponds or lakes (e.g. crest newts, invasive gobies or fish otter) with high sensitivity, and we currently try to extend this application to creeks and rivers. Moreover, we are part of the Global Malaise Trap Program (http://globalmalaise.org) and currently test, how far pre-sorting of the multi-species samples does raise the identification success (Moriniere et al. 2016). The same is true for soil samples and other types of mixed samples.

Last but not least our "youngsters" have founded a service company (AIM: www.aimethods-lab.com), which will provide help with barcoding technology to all those citizens or offices, who don´t have direct access to sequencing facilities. Indeed, we are coming close to offer "DNA-barcoding as a reliable, cost-effective, and accessible method of species identification" (Hebert et al. 2003).

Hebert, P.D.N., Cywinska, A., Ball, S.L., deWaard, J.R. 2003. Biological identifications through DNA barcodes. Proc . R. Soc. Lond. B, 270, 313-321.

Morinière, J., de Araujo, B.C., Lam, A.W., Hausmann, A., Balke, M., Schmidt, S., Hendrich, L., Doczkal, D., Fartmann, B., Arvidsson, S., Haszprunar, G. 2016. Species identification in Malaise trap samples by DNA barcoding based on NGS technologies and a scoring matrix. PLoS ONE, 11(5), e0155497 (14 pp).

Genetische Diversität der rückläufigen Blaurackenpopulation *Coracias garrulus* in Österreich

Kadletz, K.[1,2], Nebel, C.[1], Gamauf, A.[1], Haring, E.[1], Tiefenbach, M.[3], Sackl, P.[4], Winkler, H.C.[5] & Zachos, F.E.[1]

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Aufgrund weitreichender Habitatverluste schrumpfte die österreichische Blaurackenpopulation *Coracias garrulus* rasant von ca. 270 Paaren in den 1950er Jahren auf zwei Brutpaare und acht Nichtbrüter im Jahr 2016. Dieses isolierte Vorkommen liegt etwa 250 km von der nächstgelegenen Population in Ungarn entfernt. Da seit 2002 Nestlinge und Altvögel beringt werden, ist bekannt, dass immer dieselben Individuen nach Österreich zurückkehren. Eine Vermischung mit anderen Populationen wurde nie beobachtet; es gibt hingegen Belege für die Verpaarung nah verwandter Vögel in der österreichischen Brutpopulation. Bislang wurden keine Untersuchungen über die genetische Variabilität dieser Population durchgeführt, aber aufgrund der geringen Populationsgröße in Österreich und fehlender oder im besten Fall geringer Immigration aus anderen Populationen erscheint eine genetische Verarmung wahrscheinlich, was die Frage nach einer bestehenden bzw. zu erwartenden Inzuchtdepression aufwirft. Ziel dieser Untersuchung ist es, die genetische Variabilität der isolierten österreichischen Blaurackenpopulation zu bestimmen. Dazu werden Blutproben von Nestlingen aus den vergangenen Jahren mit historischen Museumsproben verglichen, die aus einer Zeit stammen, als die Blauracke in Österreich noch weit verbreitet war. Zusätzlich werden auch Proben aus anderen Teilen des europäischen Verbreitungsgebietes inkludiert. Das Ergebnis soll helfen, potentielle Spenderpopulationen für eine mögliche Supplementierung mithilfe von Nestlingen zu ermitteln, um die genetische Diversität zu erhöhen ("genetic rescue"). Erste auf mitochondrialen DNA-Sequenzen basierende Ergebnisse bestätigen eine kontinuierliche Abnahme der genetischen Variabilität während der letzten 135 Jahre in Österreich. Die gegenwärtige österreichische Population ist im untersuchten genetischen Marker völlig monomorph. Da es sich bei mitochondrialer DNA um ein rein maternal vererbtes Genom handelt, sind derzeit keine Rückschlüsse auf Inzucht und Inzuchtdepression möglich. Nukleäre, extrem variable Mikrosatellitenloci sollen für weitere Untersuchungen verwendet werden, um den Grad der Inzucht und das Verwandtschaftsverhältnis der noch lebenden Individuen zu klären.

Barcoding of wild bees using the Illumina technology

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We applied a DNA barcoding method incorporating next generation sequencing to identify wild bees improving the description of biodiversity data of Vienna. The barcoding region (COI) is used to determine species, which is especially interesting for groups of difficult identification such as bees. This gene was amplified in a two PCR step with primers elongated with Illumina adapters allowing the preparation of libraries that can be sequenced in this platform.

The method described here is applied to estimate wild bees´ biodiversity in Vienna. More specifically we aim to identify possible cryptic species, verify circumscription of species, and identify species that have recently migrated into the city or have not yet been identified. We investigate currently captured wild bees in comparison to historical collections from the Natural History museum of Vienna.

With our approach we will contribute for the creation of a reference database that can be used to identify wild bees from Vienna and compare current with historical diversity. Moreover, the application of a high throughput method it is possible to collect and process large amounts of data so also the barcoding of large sample sizes for biodiversity studies is feasible.

Extracting the flooded! First genetic insights into the biodiversity and biogeography of intertidal oribatid mites from the Caribbean

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

Morphological diversity and variation of a nuclear marker sequence in the endemic Arabian barb *Garra barreimiae* [Teleostei: Cyprinidae]

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The cyprinid fish *Garra barreimiae* Fowler & Steinitz, 1956 is endemic to the northern Oman and the United Arab Emirates. Based on DNA sequences of the mitochondrial control region (*CR*) and the cytochrome c oxydase subunit I (*COI*) at least four different clades (named West clade, Central clade, North clade and East clade) with genetic distances ranging between 6% and 10% in *COI* have recently been identified (Kirchner et al., unpublished data) and, moreover, *G. barreimiae* did not appear to be monophyletic in the phylogenetic trees, indicating the possibility of cryptic species.

The goal of the present study was to clarify, if morphological differences between the mitochondrial clades can be found and if nuclear clades of the *RAG-1* gene can be distinguished. Morphological characteristics of *G. barreimiae* are very variable, but the West clade can be clearly distinguished from the other clades by its higher number of gill rakers on the lower limb of the first gill arch with 15-17 versus 10-14 in the other clades. Furthermore, the West clade has one intermediate vertebra, while most specimens of the other clades have two. Another striking difference is found in the number of the branched pelvic fin rays. West clade specimens mostly have seven, while the specimens of the other clades usually have eight. The analysis of the nuclear gene *RAG-1* yielded three distinct but closely related clades: West clade and North clade, which are congruent with the mt clades, and Central-East clade, which consists of the mt Central clade and East clade. *G. barreimiae* does not form a monophylum as *G. rufa* forms a clade with the Central-East clade. It is indicated that the West clade is a distinct species equivalent to *G. barreimiae* and maybe also *G. b. shawkahensis*. The other clades are not clearly distinguishable based on the applied morphological methods, but genetic differences indicate cryptic species.

Fowler HW and Steinitz H. 1956. Fishes from Cyprus, Iran, Iraq, Israel and Oman. Bulletin of the Research Council of Israel 5B: 262–289.

The evolution of imperfect mimicry in sexually deceptive orchids

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Mimicry involves the accurate imitation of signals which carry a functional importance to a common receiver. The mimic thereby gains a fitness advantage by identifying with its model. Some of the most unusual examples of mimicry can be found in orchids. Sexually deceptive orchids for instance mimic the olfactory, visual and tactile cues emitted by receptive hymenopteran females. Successful pollination is ensured by luring mate searching males into performing copulation attempts with the flowers. By hijacking the female sexual communication system, these orchids have established a species specific relationship with their pollinators. In order to maintain this relationship theory predicts that female mimicry is subjected to a high level of accuracy. However many sexually deceptive orchids are characterized by an imperfect mimicry of their models which translates into unusually high levels of floral trait variation. Here we present results from several of our studies which have focused on quantifying floral trait variation and on elucidating the mechanisms which drive it. By integrating bioassays, chemical analyses and 3D geometric morphometrics we found that the evolution of floral traits can be shaped by different mechanisms, depending on their level of specificity. Even more, components of floral traits which functionally interact with pollinators are subjected to different selection pressures than those which do not. Patterns and amounts of floral trait variation are thereby shaped by the dynamic interaction between pollinator-mediated selection and drift, acting against a complex geographic background. This interaction has been driving imperfect mimicry in components of floral traits which do not functionally interact with pollinators, while those components which functionally guide pollinators to the reproductive parts of the flowers are far more accurate. We discuss the implications of selective mimicry for reproductive isolation and diversification in sexually deceptive orchids and beyond.

DNA barcoding as a tool for species identification in fish-parasitizing Acanthocephala of Austria

NOBIS-Preis-Beitrag

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DNA sequences as molecular genetic markers are widely used, but have been rarely applied in the phylum Acanthocephala. Especially in small sized and sparsely investigated parasitic phyla DNA barcoding as a tool for species identification gains increasing importance. The purpose of this study was to survey fish-parasitizing Acanthocephala from Austria by morphological and molecular genetic identification to contribute reference sequences to the Austrian Barcode of Life data base.

154 individuals representing 36 fish species were examined from various rivers in Austria. In the 39 fish infested with helminths, altogether 309 individuals of Acanthocephala were found. A section of the mitochondrial (mt) *cytochrome oxidase subunit 1* gene (COI) was amplified by PCR and sequenced. In addition, morphological identification was conducted by different staining, light microscopy, scanning electron microscopy and confocal laser scanning microscopy. Three genera of Acanthocephala were found: *Pomphorhynchus* (Monticelli 1905), *Acanthocephalus* (Koehlreuther 1771) and *Echinorhynchus* (Zoega in Müller 1776), all belonging to the class Palaeacanthocephala. The specimens assigned morphologically to the genus *Echinorhynchus* could not be determined to species level as the proboscis was not fully everted. They all belong to one mt lineage which is not yet represented in GenBank. Concerning *Acanthocephalus*, all individuals were assigned to *Acanthocephalus lucii* based on the shape of the hook plates and the length of the hooks on the proboscis. This classification is in accordance with the genetic results. Three species of *Pomphorhynchus* could be discriminated: *P. tereticollis*, *P. laevis* and a third one that could not be assigned to any described taxon. Genetic distances between the DNA barcoding sequences of the individuals analysed and sequences of *Pomphorhynchus* in GenBank confirmed the assignment of the former two species, while the third mt lineage is not represented in GenBank. Its genetic p distance to *P. laevis* is 10.2%.

This pilot study shows the importance of combining morphological and genetic characteristics to establish reliable reference sequences in GenBank that will allow correct species identification in future analyses.

Studying substrate associations of lichens with phylogenetic comparative methods and comparative genomics

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Lichen symbioses colonize a wide array of organic and non-organic substrates. Although the symbiotic association of heterotrophic fungi with autotrophic algae should potentially lead to substrate independence it has long been recognized that many lichen species exhibit strikingly narrow substrate preferences. However, substrate associations of lichen-forming fungi are seldom placed in an evolutionary context and hypotheses explaining them are poorly developed. We studied substrate preferences and their evolutionary consequences in a group of lichen-forming fungi that live in close physical contact with very different substrates in a two step approach: First, we analyzed substrate affinity and ecological strategy of species in a comprehensive phylogenetic comparative framework. We performed ancestral state estimations, speciation rate and character correlation analyses on a set of phylogenetic trees, to better understand phylogenetic distribution, history and consequences of different substrate associations.

Informed by our phylogenetic results we sequenced, assembled and annotated seven lichen-forming fungal genomes and transcriptomes. In a comparative genomic framework we searched for signatures related to long-lasting substrate use in carbohydrate active enzymes (CAYzymes) and gene ontology (GO) term patterns in orthologous gene sets. Our results reveal high levels of substrate-related niche conservatism with possibly extreme consequences. The long-term symbiotic association of heterotrophic fungi with autotrophic algae in lichens impacts the substrate component of the ecological niche of the fungal partner. We hypothesize that this creates limits but also new opportunities for the evolution of lichen-forming fungi and we will give examples of how lichens colonizing different substrates handle these.

Feeding preferences of four closely related *Hylaeus*-species (*Dentigera*) on an abandoned train station in Vienna

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Hylaeus (mask bees) is a genus of solitary bees, consisting of 47 species in Central Europe. Four morphologically similar species of the subgenus *Dentigera*, *H. brevicornis*, *H. gredleri*, *H. imparilis* and *H. intermedius*, are still challenging to distinguish and a critical review including DNA analysis will be necessary for a clear definition. In contrast to other non-parasitic solitary bees, females of *Hylaeus* have no exterior scopa for collecting pollen, but the pollen is swallowed and transported in the crop. Whereas most Central European *Hylaeus* species are deemed to be polylectic (collecting pollen from two or more plant families), three of them are known to be oligolectic (collecting pollen from one single plant family or genus). However, there is still uncertainty about the pollen preferences of mask bees because the bees also visit flowers to drink nectar and the analysis of the crop content requires time-consuming dissections.

The presented master thesis is designed to fill this gap. By analyzing the pollen it aims to investigate whether the four *Dentigera* species are oligolectic or polylectic, whether they differ in their feeding preference in a certain study area, and whether the composition of collected pollen changes spatially and temporally. Furthermore, DNA barcodes and possibly a morphometric analysis of head structures will enable a more reliable identification.

Field work is carried out on the premises of the former Northern train station in Vienna. The collected specimens are dissected by cutting off the abdomen. The pollen is removed from the crop to be analyzed under a light microscope. Of each individual one leg is cut off, stored in 96% ethanol, and sent to a laboratory for genetic analysis. The data from DNA and pollen analysis might be complemented by morphometry, for which an adequate methodical approach has yet to be developed.

A final synthesis of the results shall clarify if there are ecological, genetic or morphological differences between the four investigated *Dentigera* species.

Der Endosymbiont *Wolbachia* als möglicher Faktor in der Evolution amerikanischer Kirschfruchtfliegen

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Mikroorganismen spielen eine bedeutende Rolle in der Ökologie und Evolution von Insekten. Das weltweit am weitesten verbreitete Bakterium ist *Wolbachia*. Dieser Endosymbiont befällt eine Vielzahl unterschiedlicher Insektenarten. Eine Infektion kann für den Wirten entscheidende Konsequenzen haben: *Wolbachia* kann die Reproduktion des Wirten beeinflussen, ihn aber auch vor Viren und Parasiten schützen. Somit verschaffen diese Bakterien ihren Trägern einen Fitnessvorteil und ihnen selbst eine schnelle vertikale Verbreitung innerhalb einer Population. Darüber hinaus kann *Wolbachia* eine zytoplasmatische Inkompatibilität zwischen infizierten und nicht-infizierten Populationen hervorrufen. Dies kann zu einer postzygotischen Isolation führen und dadurch zum Artbildungsprozess beitragen.

Fruchtfliegen der Gattung *Rhagoletis* sind ökonomisch bedeutende Schädlinge im Obstbau. Die Apfelfruchtfliege *Rhagoletis pomonella* ist ein Modellorganismus für die sympatrische Artbildung: Eine Population der natürlich auf Weißdorn vorkommenden Art wechselte ihre Wirtspflanze und adaptierte sich an den Apfel. Innerhalb weniger Generationen entwickelte sich diese zu einer neuen Wirtsrasse, die sich genetisch wie auch ökologisch von der Ursprungspopulation unterscheidet. Im Gegensatz dazu entwickelten sich die nordamerikanischen Kirschfruchtfliegen *Rhagoletis cingulata* und *Rhagoletis indifferens* durch klassische allopatrische Artbildung.

In diesem Vortrag präsentiere ich die Vielfalt von *Wolbachia* in unterschiedlichen Populationen von *R. cingulata* und *R. indifferens* in den USA und Mexiko, vergleiche den Infektionsstatus mit der genetischen Struktur deren Wirten und die mögliche Auswirkung dieses Endosymbionten auf die Artbildung von Kirschfruchtfliegen.

The peculiar life cycle of the ctenstome bryozoan *Pherusella* cf. *brevituba* from the Mediterranean Sea

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Bryozoans are colonial benthic filter-feeders that predominantly inhabit marine environments. Most common and known are the calcified forms – the Stenolaemata and gymnolaemate Cheilostomata. The uncalcified Ctenostomata are a lesser-known and small group of approximately 300 species. The genus *Pherusella* comprises three described species, *P. tubulosa*, *P brevituba* and *P. flabellaris*. *P. brevituba* was originally described from the Pacific and forms large and commonly large, erect colonies. Over 10 years ago, *P. brevituba* was recorded as invasive species growing on *Posidonia* in the Mediterranean Sea. However, the colonies were always small and showed no erect growth at all. In the past years, samples were collected regularly from the Northern Adriatic. Colonies are quite abundant and mostly do not exceed colony sizes of 4-6 zooids. The ancestrula is easily identified in these colonies by remains of the two cuticular valves of the larvae. Larvae are easily detectable in colonies even with just two zooids. These are brooded within the maternal zooid and become lecithotrophic pseudo-cyphonautes larvae. When the larvae hatch, they swim for a short duration and settle again on *Posidonia* blades again. Colonies were so far not encountered on any other substrate. Consequently, the life cycle of this species is quite peculiar with only small colonies that immediately start to reproduce sexually. Future studies will focus on the morphology of this species as well as try to find out whether this is an undescribed species or not.

The problematics of comparing present and past diversity

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Although there are numerous ways of measuring diversity in the present, which can be confusing, these are all relatively straightforward and often directly measurable rather than having to be estimated. Assessing diversity of past ecological systems is often much more cumbersome.

Firstly, diversity cannot be measured directly, but has to be estimated from (sub)fossil remains. Due to preservation bias and taphonomy, these rarely reflect the actual number and distribution of species.

Secondly, the species concept is even more problematic in extinct taxa than it already is in extant taxa. More than 20 different species concepts have been proposed over time (Groves 2004). For example, the biological species concept uses the interbreeding criterion to determine whether populations are distinct species, which is difficult to determine in fossils, and the genetic species concept states that species are distinguishable by a certain degree of genetic distance, which is problematic, because DNA is often not preserved in fossils.

Here, I will illustrate these problems using the family Ursidae, in particular comparing cave bears (*Ursus spelaeus*) and Asiatic black bears (*Ursus thibetanus*). Neither genetic analyses nor morphological analyses use comparable criteria for determining species in these taxa (van Heteren 2012). Even in a relatively small family and only looking back several ten thousands of years, the problems associated with assessing diversity are already pronounced. In larger families and going back further in time, these problems become more pronounced to the point where it becomes difficult to accurately assess diversity all together. This has major influences on our capability to assess recent changes in diversity on which our conservation programs are based. Possible solutions include close collaborations between biologists and palaeontologists to ensure diversity is assessed using comparable methods on all time scales and sufficient funding for palaeontology to allow accurate reconstructions of past biodiversity.

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The genus *Gouania*: a thus far unrecognized radiation of cryptobenthic fish in the Mediterranean Sea

NOBIS-Preis-Beitrag

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We report a hitherto unknown radiation of cryptobenthic shallow-water fish from the Mediterranean Sea. *Gouania willdenowi* (Risso 1810), the sole representative of the monotypic clingfish genus *Gouania*, is endemic to the Mediterranean Sea where it lives a very cryptic and secretive life in the interstices of pebble beaches. With its wormlike body and small eyes it is perfectly adapted to this extreme environment. Because of a reduced swim bladder and a very patchy distribution of suitable habitats, adult *G. willdenowi* are very weak active dispersers and dispersal likely happens passively during the pelagic larval phase. Despite being quite common in pebble beaches throughout the Mediterranean, hardly anything is known about its biology, behaviour, phylogeny or taxonomy. Preliminary analyses based on mitochondrial and nuclear DNA, as well as overall morphology of *G. willdenowi* across large parts of the Mediterranean basin gained unexpected results concerning its diversity. Molecular data suggest that the genus *Gouania* represents a thus far unrecognized radiation, comprising several fairly divergent species that likely radiated around 5 million years ago, right after the Messinian Salinity Crisis, when the Mediterranean basin was refilled via the Strait of Gibraltar. Moreover, whereas little diversity is seen in the western Mediterranean basin, independently evolved syntopic species pairs (consisting of a gracile, elongate morph and a more stocky morph) are found throughout the eastern basin (including the Adriatic Sea). Apparently, the extremely low active dispersal ability of adults implies that dispersal – even over short distances – happens exclusively via larval drift with water currents and that populations/species remain trapped in particular circulation systems. The eastern basin (including the Adriatic Sea) with its numerous island is characterized by complex local circulation systems particularly facilitates the evolution of locally confined species in the clingfish genus *Gouania*. To conclude, the radiation of *Gouania* represents a promising model system for studying rapid radiation and the independent origin of ecomorphologically similar species pairs, and the role of water currents for driving diversification in the marine environment.

Timing and host plant associations in the evolution of the weevil tribe Apionini (Apioninae, Brentidae, Curculionoidea, Coleoptera) indicate an ancient co-diversification pattern of beetles and flowering plants

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Host plant shifts of insects can lead to a burst of diversification driven by their arrival in a new adaptive zone. In this context, our study aims to explore timing and patterns in the evolution of the weevil tribe Apionini (Brentidae, Curculionoidea, Coleoptera), particularly in relation to affiliations with their host plants. The classification of Apionini is difficult because of their relatively uniform appearance. Most taxa live mono- or oligophagously on members of Asteraceae or Fabaceae, but many are associated with other plant families, like Lamiaceae, Malvaceae and Polygonaceae. However, a comprehensive hypothesis of the phylogenetic relationships within the tribe Apionini is still missing. In the present study, we reconstructed trees and estimated divergence times among tribes. These results were further used to reconstruct the ancestral host plant use in Apionini weevils and to infer if the divergence timing of putative subtribes corresponds with the occurrence and radiation of their specific host plant groups. Phylogenetic analyses confirm the monophyly of most subtribes, with the exceptions of Oxystomatina, Kalcapiina and Aspidapiina. The subtribe Aplemonina is inferred to be sister to all remaining Apionini. Divergence time estimates indicate the first occurrence of Apionini in the Upper Cretaceous and a simultaneous occurrence of several families of flowering plants and the occupation by Apionini weevil herbivores. These conspicuous coincidences support either an ancient co-diversification scenario or an escalating diversification in weevils induced by the radiation of flowering plants.

Why springtails and the platypus are not primitive – Tree thinking and the “primitive lineage fallacy”

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The biological, including evolutionary and phylogenetic, literature teems with expressions like higher and lower, or more and less primitive, organisms and taxa, although these terms do not carry any biological meaning but only betray pre- or unscientific anthropocentrism. Closely connected with this misconception is the pitfall of falsely reading phylogenetic trees as ladders of progress from left to right, usually with humans on the far right. As a consequence, taxa depicted on the left are those that are less diverse or perceived as less “advanced” than their allegedly more “progressed” sister taxa on the right side of the tree. This has been called the primitive lineage fallacy, and its roots lie in the idea of a great chain of being, or *scala naturae*, according to which all living beings (along with inanimate objects like minerals) can be arranged in a continuous ladder from “low” to “high”, with humans and supernatural beings (angels etc.) and ultimately God at the top. This metaphysical notion goes back to antiquity and was particularly prominent in the age of Enlightenment, including in biologists like Bonnet and Lamarck. However, as has repeatedly been shown it still lurks beneath the surface in our modern interpretations of evolutionary trees and processes.

This talk aims at sensitizing the listeners to the problem by showing how most of us (including the presenter) are prone to a false interpretation of phylogenetic trees. There simply are no basal or primitive extant taxa, there is no main trunk and no side branches in the Tree of Life, and consequently taxa cannot branch *off* but only branch into equivalent sister groups. Purging our language from such misconceptions goes a long way towards embracing tree thinking and an evolutionary biology that is truly unbiased and free of unwarranted anthropocentrism.

Which and how many species of gudgeons (genus *Gobio*) are there in the Austrian Danube system? Insights from molecular data

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Gudgeons of the genus *Gobio* are small elongate bottom-dwelling cyprinid fishes that are found in rivers and lakes throughout Eurasia. The genus includes numerous, often very closely related species, several of which have been described only recently. It is still not clear which *Gobio* species inhabit(s) the Austrian Danube system. Some sources state that the Austrian gudgeons are *G. gobio* whereas others suggest them to be *G. obtusirostris*, with a potential hybrid zone between the two species in the upper Danube. To clarify the status of the gudgeons in the Austrian Danube system, we sequenced two mitochondrial (COI & D-Loop) and one nuclear (RPS7) gene of the Austrian gudgeons and analysed them together with previously published *Gobio* sequences from throughout Europe. Our analyses showed that based on molecular data Austrian gudgeons cannot be assigned to a single valid species, but rather represent a mixture of three different species/lineages. *G. gobio, G. obtusirostris* ad a lineage mainly distributed in the Balkans. Interestingly, and quite unexpected, this hybrid swarm is not confined to a particular geographic region but seems to be found throughout the (eastern) Austrian Danube system. Genetic distances among and within the major mitochondrial lineages indicate that they have diverged about one million years ago, survived the Pleistocene glaciations in separate refugia and came into secondary contact only recently (most likely after the last glacial maximum).

Hidden treasures within? The use and performance of head anatomical characters for the reconstruction of insect phylogeny

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In recent years several phylogenetic analyses of insect taxa have been performed with a focus on the exploration of head anatomical characters. The study of internal anatomy offers a wide range of characters but requires cost- and time-consuming methods. While light microscopy is mostly sufficient to investigate external anatomy, complex methods as microCT or histological sectioning are necessary to study the musculature, nervous system, glands and digestive tract.

At the same time internal anatomy comprises character systems in which structural and functional constraints limit morphological change. This can make them more conservative in a phylogenetic context and thus valuable for the resolution of older splitting events. The use and performance of different kinds of characters in phylogenetic analyses is compared and discussed.

“Non-solitary” behaviour in selecting species of solitary bees for a crowd-funded DNA-barcoding project

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Hosting about 690 species of Apiformes, Austria can call itself a bee-rich country. Aiming for a complete record of the Austrian biodiversity by DNA-barcoding, ABOL likewise wants to cover all species of bees. Crowd funding by the initiative “Mutter Erde” allows for a first start, funding the generation of DNA-barcodes from 75 species of solitary bees. The focus of our project lies on species which utilise but a certain plant taxon as pollen source, so called oligolectic bees, as well as on species with a limited distribution in Austria. These two restrictions firstly allowed us to adjust the number of species to the given fund, and secondly provided enough potential to be communicated to the public.

Our budget plan considers not only lab and sequencing, but likewise costs for field work, preparation, identification by experts, the imaging of specimens for BOLD, and communication of the results to the public.

Our project is closely linked and coordinated with the University of Natural Resources and Life Sciences (BOKU) where another project on DNA-barcoding of Viennese bees is carried out simultaneously.

Altogether our study aims to test current hypotheses of species delimitation, to provide a basis for monitoring species by molecular approaches, and last but not least to boost the public esteem for biodiversity and conservation biology.

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