

EGGENBURG 2015

N B I S AUSTRIA 9

Biosystematics from Past to Present

Gastgeber

Dr. Johannes Tuzar

Direktor des Krahuletz Museums



EGGENBURG 2015

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Biosystematics from Past to Present

Auf Einladung von Dr. Johannes Tuzar, Mag. Gerhard Dafert und Prof. Fritz Steininger, findet die diesjährige Jahrestagung von NOBIS Austria im Festsaal des Rathauses in Eggenburg statt. Die Tagung ist eine Gemeinschaftsveranstaltung mit der Krahuletz-Gesellschaft und dem Krahuletz-Museum.

Das Tagungsmotto "*Biosystematics from Past to Present*" ist eine Anspielung auf den starken paläontologischen Schwerpunkt des Krahuletz-Museums. Darüber hinaus forschen viele Mitglieder von NOBIS in Projekten, in denen die historische Komponente wesentlich dazu beiträgt, rezente Verbreitungsmuster oder genetische Eigentümlichkeiten zu erklären.

Programm

Freitag 27. November

- 16.00 Führung durch das Krahuletz-Museum (Krahuletzplatz 1)
- 17.30 Icebreaker im Krahuletz-Museum
- 17.30-20.00 Registrierung
- 20.00 Abendessen im Stadthotel Oppitz (Kremserstraße 8)

Samstag 28. November

- 9.00 Begrüßung im Festsaal im Rathaus (Kremserstraße 3)
- 9.10-17.20 Vorträge, Posterpräsentation und NOBIS-Preis Verleihung

Vorträge 15+5 Minuten

Sprache Deutsch oder Englisch

Beitrag NOBIS-Mitglieder: € 10.-; Nicht-Mitglieder: € 30.-

Zahlung NOBIS Austria

IBAN: AT622011128822667900

BIC: GIBAATWW

oder bei der Registrierung

Samstag, 28. November

8.30-9.00 Registrierung

9.00-9.10 Begrüßung durch
Johannes Tuzar, Direktor des Krahuletz Museums
Mathias Harzhauser, Präsident von NOBIS Austria

Vortragsprogramm

NOBIS-Preis Beiträge

Chair: **Jürgen Kriwet**

9.10-9.30 **Susanne Affenzeller:** Morphometric approaches to species delineation and characterisation in the trochid Genus *Gibbula* (Gastropoda).

9.30-9.50 **Elisabeth Georgopoulou et al.:** From Past to Present: What do fossil snails tell us about the evolution of European aquatic hotspots?

9.50-10.10 **Katharina Jaksch et al.:** Exploring speciation in the rock-dwelling land snail genus *Montenegrina*.

10.10-10.30 **Rebecca Thom et al.:** Mouthpart morphology of the waterlouse *Asellus aquaticus* and the common woodlouse *Porcellio scaber* (Crustacea: Peracarida: Isopoda).

10.30-10.50 **Vanessa Düster:** Similar body size, variable proboscis length – comparison of mouthpart morphology of two euglossine bee species (Hymenoptera, Apidae, Euglossini).

10.50-11.20 Kaffeepause

11.20-12.30 Poster-Session moderiert durch **Björn Berning**
5 Minuten pro Poster

12.30-14.00 Mittagspause im Stadthotel Eggenburg (Kremserstraße 8)

Vortragsprogramm

Chair: **Sabine Agatha**

14.00-14.20 **Omri Bronstein** et al.: Genes do lie! Mitochondrial capture masking the Red Sea collector urchin, *Tripneustes gratilla*, true identity.

14.20-14.40 **Michael Duda** & Katharina Jaksch: Penis sections as an additional tool for differentiation of *Helicopsis* from Eastern Austria and adjacent areas (Gastropoda: Eupulmonata: Hygromiidae).

14.40-15.00 **Elisabeth Geiser**: Don't underestimate the small stuff – what subfossil insect fragments can tell us.

15.00-15.20 **Josef Greimler** (Reich et al.): Changes in the distribution of *Gentianella austriaca* and *G. praecox* on the century scale.

15.20-15.50 Pause

Vortragsprogramm

Chair: **Matthias Kropf**

- 15.50-16.10 **Nikolaus Szucsich** et al.: ABOL –infrastructural demands, scientific challenges, and benefits of the aim to inventorize the biodiversity of Austria.
- 16.10-16.30 **Mathias Harzhauser** & Thomas A. Neubauer: The presence is not the key to the past – self-fulfilling prophecies in taxonomy.
- 16.30-16.50 **Björn Berning**: Über die Evolution einer synthetischen Theorie.

Vortrag des Gewinners des **NOBIS-Stipendiums**

- 16.50-17.20 **Gerald Auer** & Werner Piller: Ultrastructure of coralline red algae – a potential tool for phylogeny and taxonomy.
- 17.20 **Elisabeth Haring**: Zuerkennung des NOBIS-Preises und Schlussworte



- 1: Museum (Krahuletzplatz 1)
- 2: Stadthotel Oppitz (Kremserstraße 8)
- 3: Festsaal im Rathaus (Kremserstraße 3)

Homepage <http://www.nobis-austria.at/>

Kontakt Mathias Harzhauser (mathias.harzhauser@nhm-wien.ac.at)

Abstracts

Morphometric approaches to species delineation and characterisation in the trochid Genus *Gibbula* (Gastropoda)

Affenzeller Susanne¹

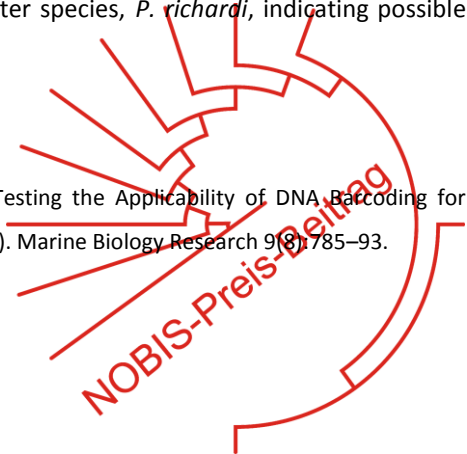
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The trochid genus *Gibbula* (Gastropoda, Mollusca) is abundant and diverse in the Mediterranean Sea, but poses problems in species identification and delineation. This is due to high variability in shell form, vague original descriptions and missing or unspecific type material. In recent studies (Barco et al. 2013) COI barcoding yielded good results. In the present study geometric shell morphometric methods were used as a tool for species delineation. With the help of standardized shell photographs and landmarks most of eight species from Croatia and Crete present in this sample, which were identified through CO1 barcoding, could be delineated. Both lateral and ventral views proved important to include all relevant identification characters. *Gibbula divaricata* and *G. varia* cannot be distinguished with the barcoding approach, but are separable in the geometric morphometric analysis. Other species are well separated in the CO1 gene tree but show overlaps with others in the geometric morphometric approach. Therefore, a dual method approach is the best way to identify *Gibbula* species.

The putative sister genus *Phorcus* renders *Gibbula* paraphyletic in the molecular analysis. However their shell morphometrics set these species well apart from *Gibbula* species in most analyses. *Phorcus mutabilis* shows two morphotypes from Crete and Croatia respectively. One individual of *P. mutabilis* is unequivocally identified by CO1 barcoding but clearly shows the shell morphology of its sister species, *P. richardi*, indicating possible hybridisation or incomplete lineage sorting.

References

Barco, A., Evans, J., Schembri, P.J., Taviani, M., and Oliverio, M. 2013. Testing the Applicability of DNA Barcoding for Mediterranean Species of Top-Shells (Gastropoda, Trochidae, *Gibbula* S. L.). *Marine Biology Research* 9(8): 785–93.



Comparison of cell division patterns in the tintinnid genera *Favella* and *Schmidingerella* (Alveolata, Ciliophora, Spirotricha)

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The classification of tintinnid ciliates is mainly based on lorica features, which are influenced by intrinsic and extrinsic factors and often display a huge intraspecific variability and interspecific similarity; hence, the loricae are mostly of low taxonomic value. This assumption is supported by cladistic analyses of the few cytologically studied species and genetic phylogenies. The evolutionary development of the somatic ciliary pattern has, however, shown to mirror rather well the topology of the gene trees (Agatha & Strüder-Kypke 2013), and there are some further cell features that might be of taxonomic significance. Since differences in cell division patterns are used to characterise genera and families in the related hypotrich ciliates (e.g., Berger 2011), ontogenesis was investigated in two tintinnid species that were previously supposed to be congeneric owing to very similar loricae; now, they belong to the distantly related genera *Favella* Jörgensen, 1924 (Family Ptychocylididae Kofoid & Campbell, 1929) and *Schmidingerella* Agatha & Strüder-Kypke, 2012 (Family Rhabdonellidae Kofoid & Campbell, 1929). *Favella panamensis* and *Schmidingerella arcuata* were collected at the east coast of the USA.

The analysis of protargol-impregnated dividing specimens, which clearly show the ciliary pattern as well as the nuclear apparatus (somatic macronucleus nodules and generative micronuclei), revealed differences in (i) the timing of the macronucleus cycle and the elongation and kinetid duplication in the somatic kineties, (ii) the length of the ventral kinety fragments in proter and opisthe, (iii) the orientation of the interphase macronucleus nodules, and (iv) the position of the oral primordium in very early dividers. The study was financially supported by the FWF (Austrian Science Foundation; Project P20461-B17).

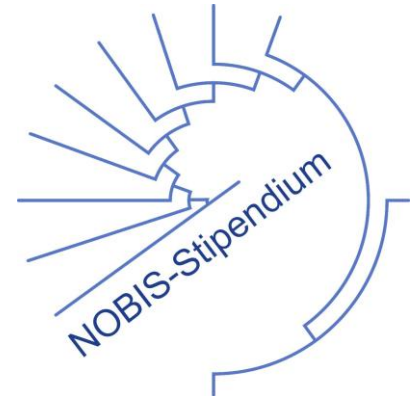
References

- Agatha S. & Strüder-Kypke M.C. (2013): Systematics and evolution of tintinnid ciliates. In: Dolan J.R., Montagnes D.J.S., Agatha S., Coats W.D. & Stoecker D.K. (eds.): The Biology and Ecology of Tintinnid Ciliates: Models for Marine Plankton. Wiley-Blackwell: 42–84.
- Berger H. (2011): Monograph of the Gonostomatidae and Kahliellidae (Ciliophora, Hypotricha). Springer Dordrecht.

Ultrastructure of coralline red algae – a potential tool for phylogeny and taxonomy

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Coralline red algae (order Corallinacea, Sporolithacea) are heavily calcifying marine macrophytic algae. Their global occurrence, role as important ecosystem engineers, and potential climate recorders, makes them prime subjects for both fossil and recent ecological and climatological studies. The taxonomic classification of corallines, however, mainly focuses on the soft tissue anatomy of their reproductive cavities, the conceptacles, secondary connections between filaments cells (i.e. secondary pit connections or cell fusions) and the existence of genicula. While a working morphological taxonomy using these features exists, molecular studies (Bitter et al., 2011) suggest that except the presence of uniporate or multiporate conceptacles none of the features used are distinct for specific families, creating often paraphyletic and polyphyletic morphological clades.

The present study aims to analyze the shape of crystallites formed within the polysaccharide matrix of the coralline cell wall as a taxon specific morphological tool. To achieve this we apply scanning electron microscope analysis of both the calcite crystallites deposited within the walls of epithelial cells, meristem cells and the vegetative thallus. The analysis focuses on global sample set of different coralline taxa belonging to the genera *Phymatolithon*, *Lithothamnion*, *Lithophyllum*, *Titanoderma*, *Porolithon*, *Hydrolithon*, *Neogoniolithon*, *Mastophora*, *Sporolithon* and *Spongites*.

Results show, that formed calcite crystallites have distinct genus specific shapes. Based on their association with the polysaccharide matrix of the cell walls, these epithelial crystals can thus be used as a taxonomic tool on at least a generic level. Additionally the previously described calcified cell wall types also allow a differentiation of the investigated genera. The calcite ultrastructure thus provides powerful morphological criteria for the classification of calcareous red algae. A comparison with recent molecular genetic analysis of coralline specimens reveals a fit of the observed ultrastructure morphology with the phylogenetic tree based molecular data of extant coralline red algae, bridging the gap between phylogeny based on molecular versus morphological characters.

Morphological convergences in the inner ear of marsupial Diprotodontia and placental mammals

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The membranous labyrinth of all jawed vertebrates consists of the anterior semicircular (ASC), posterior semicircular canal (PSC), and lateral semicircular canals (LSC) and is located within the bony labyrinth of the skull. The semicircular canals are filled with endolymph, which, upon turning acceleration of the head moves the sensory hair cells and thus sends signals to the brain. This mechanism is crucial for orientation in the three-dimensional space. It is well established that the inner ear comprises valuable functional and phylogenetic information (Gunz et al., 2012). Size and alignment of the three semicircular canals, e.g., are closely linked to the mode of movement of the head and hence the mode of locomotion of the investigated species (Pfaff et al. 2015). We were able to perform exact comparisons of the bony labyrinths of the specimens by employing non-invasive high resolution micro-CT scanning of skulls and subsequent 3D reconstruction of the inner ear region.

Here, we analysed the bony labyrinth of several members of the marsupial order Diprotodontia because of their diversity in locomotion modes (arboreal, fossorial, gliding, hopping and subterranean) (Phillips, 2007) and compared our findings with the bony labyrinth of placentals with similar locomotion modes. The goal of this study is to identify extrinsic convergent traits in the two sister groups within a phylogenetic framework. The detailed examination of functional and phylogenetic traits of the inner ear has great potential to elucidate evolutionary and developmental patterns of pouched and unpouched mammals.

References

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- Pfaff, Cathrin et al., 2015, Bony labyrinth morphometry indicates locomotor adaptations in the squirrel-related clade (Rodentia, Mammalia). *Proceedings of the Royal Society B* 282: 20150744.
- Phillips, M. J. et al., 2007. Family-level relationships among the Australasian marsupial “herbivores” (Diprotodontia: Koala, wombats, kangaroos and possums). *Molecular Phylogenetics and Evolution*, Volume 46, issue 2, 594–605

Über die Evolution einer synthetischen Theorie

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Um 1950 herum wurden die bis dahin weitgehend getrennt voneinander betrachteten und bearbeiteten Gebiete der Biologie, Genetik, Paläontologie und Systematik zur Synthetischen Evolutionstheorie zusammengefasst, welche die Entwicklung des Lebens auf der Erde hinreichend erklären sollte. Obwohl dieser Schritt eindeutig zum Verständnis der Evolution beitrug, wurde ein wirkliches Zusammenkommen aller Wissenschaftsrichtungen lange Zeit hauptsächlich durch die unzureichenden Kenntnisse auf dem Gebiet der Genetik behindert.

Natürlich sind wir auch heute noch weit davon entfernt, die komplexen Abläufe im Inneren unserer Zellen oder während der Ontogenese zu verstehen. Allerdings hat eine bahnbrechende Erkenntnis Ende des 20. Jahrhunderts dafür gesorgt, dass die verschiedenen Bereiche zusammenwachsen: extrem konservative Genabschnitte, die sogenannten Hox-Gene, steuern in der Entwicklung des befruchteten Eis hin zum vielzelligen Organismus die Bildung der wichtigsten Körperabschnitte und Organstrukturen. Diese Gene finden sich in allen Tieren in äußerst gering abgewandelter Struktur und haben in allen Gruppen die gleichen oder zumindest ähnliche Aufgaben. Das heißt, die Genetik kann nun die Entwicklungsbiologie eines Organismus erklären, wobei entwicklungsbiologische Abläufe und Ergebnisse ebenso aus dem Fossilbericht ersichtlich sind, so dass man mit paläontologischen Funden nicht nur systematische Verwandtschaftsverhältnisse rekonstruieren, sondern auch detailliert auf genetische Prozesse und Veränderungen im Verlauf der Evolution schließen kann. Einige Beispiele hierfür werden in diesem Vortrag dargelegt.

Genes do lie! Mitochondrial capture masking the Red Sea collector urchin, *Tripneustes gratilla*, true identity

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Tripneustes gratilla is one of the most widespread Indo-Pacific shallow-water echinoids, ranging from the East-Pacific to East Africa and the Red Sea and from the Kermadec Islands to Japan. Phylogeographic studies of *Tripneustes* have demonstrated a lack of phylogenetic structure in mitochondrial DNA (mtDNA) (Lessios et al. 2003). Haplotype sharing between widely distant localities as the Philippines, Kermadec Island and the Galapagos Islands is suggestive of recent radiation and high dispersal potential. In the Red Sea (RS) *T. gratilla* representatives are morphologically well differentiated from populations in other parts of the species' range. Consequently, a separate subspecies was proposed for the RS population: *T. gratilla elatensis* Dafni, 1983. Yet, RS *Tripneustes* have never been studied and illustrated in a modern way and no data is available on the southwards extension of *T. g. elatensis*. Here we present a re-evaluation of the taxonomic status of *T. g. elatensis*, utilising both morphological and molecular markers and introduce the first phylogenetic reconstruction based on genetic data for *Tripneustes* from this region. We found that *T. g. elatensis* could be distinguished from *T. gratilla* based on both morphological and molecular markers and propose to assign the RS *Tripneustes* as a separate species. However, in contrast to the expectations raised by the apparent morphological differences, we found that RS *Tripneustes* are not differentiated based on mtDNA data from the Indian Ocean populations and share haplotypes with both Philippines and East African populations. Nonetheless, adding the nuclear DNA (nDNA) marker Bindin gene and samples from widely distant populations to the analysis, contradicted the mtDNA data and supported of the morphological evidence. The Bindin sequences depicted three clades: RS, Indomalayan (Philippines, Guam, Papua New Guinea), and a mixed Indo-West-Pacific clade. High levels of differentiation in Bindin sequences among these clades suggest ancient radiation, greatly contrasting the mtDNA data. This apparent mismatch of mt- and nDNA implies a mitochondrial capture event in the recent past.

Only true pelagics mix: Comparative phylogeography of deepwater Bathybatini cichlids from Lake Tanganyika

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Allopatric speciation is thought to be the predominant mode of speciation in East Africa's spectacular lacustrine cichlid radiations, and indeed most cichlid species investigated thus far do show high levels of geographic population differentiation. This is particularly true for stenotopic littoral taxa. Only little is known about the population genetic structure of benthopelagic and pelagic cichlids, although it is widely assumed that these taxa form large panmictic populations. Here we present preliminary phylogeographic data for four highly mobile piscivorous species of the Lake Tanganyika deepwater cichlid tribe Bathybatini, all of which are prime targets of artisanal fisheries. Despite their old evolutionary age, which would have allowed for the accumulation of high genetic diversity, all species investigated show only very little intraspecific divergence and little genetic diversity, indicative for a fairly recent genetic bottleneck. Particularly low levels of diversity and a recent north/south divergence are observed in the benthopelagic species *Bathybates graueri* and *Hemibates stenosoma*, whereas the truly pelagic species *B. fasciatus* and *B. leo* exhibit somewhat higher levels of genetic diversity and no indication for population genetic structuring across the entire lake. Our findings indicate that (effective) population sizes in these taxa, especially the benthopelagic species, appear to be smaller than previously assumed and that only truly pelagic species constitute panmictic populations across the entire lake.

Penis sections as an additional tool for differentiation of *Helicopsis* from Eastern Austria and adjacent areas (Gastropoda: Eupulmonata: Hygromiidae)

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New research on east Austrian taxa of the genus *Helicopsis* (Gastropoda: Eupulmonata: Hygromiidae) show that these taxa – *H. s. striata* (O. F. MÜLLER 1774), *H. s. hungarica* (SOOS & WAGNER, 1935) and *H. s. austriaca* GITTENBERGER 1969 – are well separated by mitochondrial markers and also show a different phylogeographic background and evolutionary history.

Nevertheless, morphological traits clearly delimitating the taxa were still missing. Concerning shell morphology and superficial genital morphology only a separation by trend was possible. Yet, detailed sections of the penis papillae of the three taxa allowed distinguishing them and brought clear results and concordant to their genetic separation.

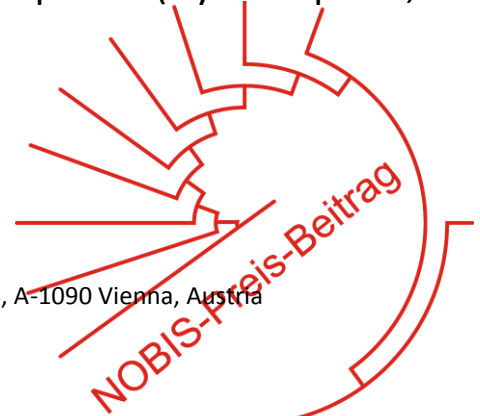
The seminal duct of *H. s. striata* is surrounded by two penial plicae on which a third one is situated adjacent. The inner side of the spongy body of *H. s. hungarica* is characterized by numerous little folds. *H. s. austriaca* on the other side shows no consistent pattern of inner penis structures. The penis papilla is very often open or grown together with the penis sheet and the seminal duct is often not connected with the spongy body.

These new findings – together with molecular genetic and conchological data - now allow to separate the three taxa unambiguously and to confirm information on their unconnected distribution ranges. Additionally they give a final justification for the reevaluation of *H. s. austriaca* and *H. s. hungarica* to species level.

Similar body size, variable proboscis length – comparison of mouthpart morphology of two euglossine bee species (Hymenoptera, Apidae, Euglossini)

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Euglossa is the most species rich genus within the Euglossini and attracts the attention of many scientists because of their bright shiny and colorful appearance. There is still little known about the nectar feeding behavior, although their proboscides have extreme lengths. This study compares the mouthpart morphology of *Euglossa imperialis* with *Euglossa championi*. The lightmicroscopic and section electron microscopic (SEM) observations of the proboscis of two species within one genus that have almost the same body size but differ significantly in proboscis length show only the distal parts being clearly elongated in *E. imperialis*. Galeae, labial palps and glossa, forming the proboscis are almost double sized in *E. imperialis*, whereas the basal mouthparts are of same size. The glossa and glossal tip region are double the size in *E. imperialis*, the flabellum is larger but not twice as long. Broad and distant hairs at the apical region and thin adjacent microtrichia in the basal region are similar in both species. The total number of sensilla on the glossa of *E. imperialis* is greater, but not twice the number; the relative number and distribution is similar in both species. *Euglossa championi* is able to take up nectar faster than *E. imperialis*. *E. imperialis* has a longer proboscis and is able to take up twice as much volume with one lapping cycle, whereas the number of licking cycles per second is alike, but the time needed on one flower is greater for *E. imperialis*. The morphometric comparison should allow conclusions of allometric relation and the consequences for an extremely elongated proboscis as an adaptation to nectar uptake. This study refers to the assumption that the extremely elongated proboscis of *E. imperialis* is an adaptation to long tubed flowers as alternative food source for stepping aside in the same habitat. Flower handling time, corolla depth of visited flowers and nectar gain should allow discussion about costs and benefits of an extremely elongated proboscis.

References

Düster J.V. 2015. Similar body size, variable proboscis length – comparison of mouthpart morphology of two euglossine bee species (Hymenoptera, Apidae, Euglossini). Master's thesis, University of Vienna.

New Information on Eocene Antarctic Chondrichthyan diversity

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Eocene Antarctic sediments comprise one of the most diverse fossil fish faunas of the Southern Hemisphere to date. At the end of the Eocene, almost all elasmobranchs (sharks, skates and rays) disappeared from Antarctic waters and the modern Antarctic elasmobranch fauna conversely is extremely impoverished including only few skates. The main faunal elements of the Southern Ocean, nowadays, are ice-fishes, notothenioids, which are perfectly adapted to freezing temperatures of the Antarctic waters. The reason for these diversity and taxonomic content shifts still are ambiguous. In the Eocene 24 shark, ray and skate species in 15 families inhabited the waters surrounding the Antarctic continent. Isolated elasmobranch teeth are the most abundant remains. Here, we present new information about the Eocene chondrichthyan faunas based on newly collected material. The distribution of chondrichthyan remains is very heterogeneous throughout the sediment sections. In all studied assemblages ranging from the middle to the late Eocene (Lutetian – Priabonian), the dominant shark species is *Striatolamia macrota*, an extinct sandtiger shark. It also is evident that the diversity of chondrichthyans was low in the lower part of the sections TELMs 1-3 (Late Thanetian – Middle Ypresian), while the highest occur in the middle part of the section (TELMs 4-5; Middle to Late Ypresian). According to the existing literature chondrichthyans seemingly disappeared in the upper parts of the section (TELM 6; Lutetian) and no remains of cartilaginous fishes have been found in TELM 7 (Bartonian – Early Priabonian) up to now. The absence of chondrichthyan fishes thus might not be directly related to the onset of Antarctic glaciation. Our new material, however, indicates that chondrichthyans gradually decreased. This deterioration essentially correlates largely with decreasing surface water temperature and the disappearance of chondrichthyans from Antarctic waters, seemingly is related to reduced shelf areas and sub-zero water temperatures due to ice-shield formations on the Antarctic continent.

Occurrence simulations of rock-dwelling gastropods (Mollusca: Gastropoda) infer competitive exclusion and high niche similarity below the genus level

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Rock-dwelling gastropods contribute substantially to the species diversity of karst areas of the Mediterranean Basin. This group is characterized by low capability of active dispersal, considerable morphological diversity, high proportion of narrow-range endemic and/or sporadically distributed taxa. Their phylogeny is little known and it is intensely debated how, and to what extent, adaptive and non-adaptive mechanisms contribute to their evolution. Our objective was to find evidence for altered niche preferences within rock-dwelling gastropods at different stages of their phylogeny. We used Balkan taxa as study system with main focus on *Montenegrina*, a genus of known phylogeny, which is therefore suitable for comparisons of intra-generic lineages. We tested whether or not there is any niche differentiation beyond macroclimatic requirements. To this end, we compared the ratio of simulated and observed co-occurrences of different *Montenegrina* species, supra-specific *Montenegrina* lineages, and also of *Montenegrina* and other rock-dwelling snail genera where distributions are simulated assuming random distribution and independence across taxa. At the genus level and above, simulated and observed co-occurrences have not differed significantly. In contrast, we observed less than expected co-occurrences between *Montenegrina* species and lineages, indicating that (mostly allopatric) distribution of *Montenegrina* species results not only from random chance. We propose the lack of niche differentiation as the most likely explanation for the hindrance of congener co-occurrences.

Ontogeny of the brown banded bamboo shark (*Chiloscyllium punctatum*, Müller & Henle, 1838) and the development of jaws

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Chiloscyllium punctatum (Müller and Henle, 1838), the brown banded bamboo shark, belongs to the Orectolobiformes, which is a basal order in the superorder of Galeomorphii. It is a small species of benthic, oviparous sharks, similar to *Scyliorhinus canicula* (Linnaeus, 1758), a well-studied carcharhiniform shark (Compagno, 2001). Both species are bred in captivity all around the world but nowadays the bamboo shark gets more and more prominent in science for studying evolution. Due to its basal position inside the modern galeomorph sharks it presumably is a better model organism to study issues as jaw or tooth evolution (Harahush et al., 2007). This project aims at answering questions concerning the jaw and tooth development of this species. It was shown that the development of cat- and bamboo sharks proceed in similar ways and certain key characteristics, as the appearance of gill filaments or the formation of the fins, can be compared (Ballard et al., 1993; Harahush et al., 2007). Hence staging of the embryonic development was conducted starting with a late pharyngula stage following the protocol established for *S. canicula*. At this stage outer gill filaments are still gaining in length and the embryos bear a hatching gland on their forehead, which is important for the opening of the fissure in the egg later on (Ballard et al., 1993). The overall adult body shape is present from stage 30 on and pigmentation starts at stage 31. Formation of the jaw presumably starts at stage 28 and the main developmental steps concerning the differentiation of the jaw elements occur between stages 29 and 31. Tooth development starts slightly lagged at stage 30. Both teeth and jaw mineralize at stage 31 and mineralization of the jaw holds on during growth of the jaw apparatus in the adult organism. Analysing the growth pattern with a thin-plate splines analysis showed that the palatoquadratum as well as Meckel's cartilage, as two counter parts, develop synchronously and seem to be dependent on each other. The teeth grow in an alternate tooth patterning and equate each other in morphology throughout the whole jaw as well as through ontogeny.

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Palaeoecology and diversity of Miocene sharks and rays (Chondrichthyes, Elasmobranchii) of the Paratethys

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The palaeogeographic development of Austria was affected by the raising Alps, which separated the Paratethys north of this developing mountains. This sea existed in the Miocene (23.03–5.33 Ma) with a diverse shark and ray fauna. The Paratethys gradually silted up from the West to the East during the proceeding orogenesis. Only a brackish lake remained during the Pannonian, which finally disappeared about 7 Ma years ago. Previous studies showed significant differences in the diversity of molluscs (Harzhauser et al. 2003) and echinoderms (Kroh 2007) during the early to middle Miocene transition of the Paratethys in Austria, mostly driven by fluctuations in the climate. Using these studies as a catalyst, an investigation was conducted to evaluate whether elasmobranchians from this time period were also affected by extrinsic factors such as sea level or climatic changes. Even though there was a serious climatic change between the Eggenburgian (20.4–18.4 Ma) and the Ottnangian (18.4–17 Ma), the main focus of this project is the diversity change from the early to middle Miocene which correlates with middle Miocene climatic optimum. In the present study, a total of 1128 isolated teeth housed in the collection of the University of Vienna were analysed. These teeth represent 11 different shark and myliobatiform genera and were derived from 26 localities. In a first step, the sampling effort (rarefaction analysis) and the alpha diversity were established for both the early and middle Miocene. Subsequently, the beta diversity using the Margalef Index between the early and the middle Miocene was established to identify diversity fluctuations across this boundary. Our results show that elasmobranchian diversity did not change dramatically during the studied time interval ranging from the early Miocene to the Badenian (16 – 12.7 Ma) indicating that chondrichthyan fishes are less sensitive to sea level and temperature changes than molluscs and echinoderms. Nevertheless, this analysis only used large taxa and more work is warranted also considering small taxa.

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Difficulties in assessing the global distribution of a model organism – the biogeography of *Favella panamensis* (Alveolata, Ciliophora)

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Accurate circumscriptions and determinations of species are essential for biodiversity and biogeography assessments; traditionally, the morphospecies concept was employed. Tintinnid ciliates are exceptional as – in contrast to the vast majority of ciliates – the whole taxonomy and classification of the more than one thousand marine planktonic species are almost exclusively based on characteristics of their vase-shaped loricae (houses). Because it is relatively easy to collect, preserve, examine, and classify, the lorica has allowed the accumulation of invaluable diversity and distribution data for more than two centuries. However, lorica-based taxonomy is problematic because of the high intraspecific variability and interspecific similarity of the loricae; so, the species limitations are currently unknown. Besides misidentifications, the diversity and geographic ranges perceived are especially affected by revisionary taxonomic treatises differing in their species circumscriptions from the original descriptions due to synonymisation (range of morphologic features became wider) and splitting (range of features became smaller) of species. Despite these difficulties, Montagnes (2013) suggested the tintinnid genus *Favella* as a model for planktonic ciliates. In the present study on the biogeography of *Favella panamensis*, the species records from about one hundred of taxonomical and ecological studies were classified according to their quality: (i) reliable records from the type and neotype localities mentioned in the original description and authoritative redescription; (ii) more or less reliable records supported by descriptions, measurements, and/or illustrations that fit the original description and redescription; and (iii) unsubstantiated records (mostly simple species lists) based on uncertain identifications. The comparison of the data provided by substantiated records with the original description revealed false positive and negative identifications. Since currently the species circumscriptions are uncertain, the usage of the original descriptions or authoritative redescriptions for the identification of tintinnid ciliates is strongly recommended. Only later, when the cell features and barcodes of the morphotypes are known, we might be able to perform justified synonymisations.

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Don't underestimate the small stuff – what subfossil insect fragments can tell us

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Subfossil fragments of insects are often found in peat bogs and lake sediments, which provide ideal conditions for preservation - lack of oxygen and low pH-value. Beetles are more robust than most of the other insects, therefore they are abundant in such subfossil assemblages. These fragments provide a deep insight into the environmental conditions in former times. I will demonstrate this by means of three examples from the post-glacial period, the Holocene.

Example (1): Beetle fragments are used for quantitative estimation of paleotemperatures

From the Unteraar-Glacier in Berner Alps (Switzerland) parts of a Cyperaceae fen peat were eroded from the glacier bed. These organic sediment clasts contained more than 5000 insect fragments. The Institute of Geology of the University of Bern got the funding for a comprehensive scientific project, these fragments were provisionally identified and then specialists were invited for further identifications. I got 150 fragments, most of them were elytrae of reed-beetles (Chrysomelidae, Donaciinae). With the Mutual Climatic Range Method an assessment was possible of the average, max and min temperature 3800 years ago at this site.

Example (2): Beetle fragments assist plant identification better than palynology

From the Glacier Pasterze 8100 years old clasts of a peat bog were eroded. With palynological methods it was possible to identify the plant genus *Senecio*, but not the species. The samples did also contain fragments of the Chrysomelid *Oreina cacaliae*. This beetle feeds exclusively on *Senecio fuchsii* and *Adenostyles alliariae*. No *Adenostyles* pollen was found in the clasts, therefore the *Senecio* pollen must have originated from *Senecio fuchsii*.

Example (3): Insect fragments support archaeological research

Blattella germanica in a house => effective heating system in winter time.

Dung beetle fragments indicate about details in keeping livestock.

Sitophilus granarius => grain storage site.

Bruchus rufimanus => *Vicia faba* was cultivated and stored.

Therefore: Don't underestimate the small stuff and the systematicists who identify it!

From Past to Present: What do fossil snails tell us about the evolution of European aquatic hotspots?

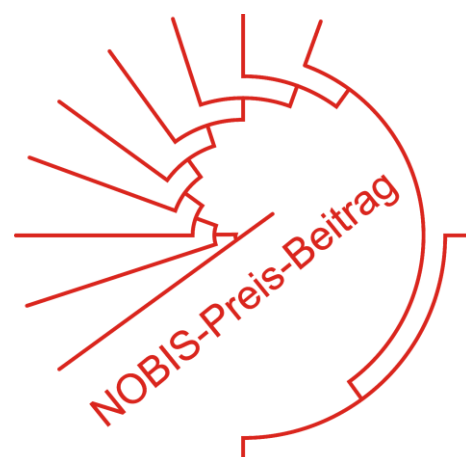
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Understanding the distribution of continental aquatic species richness hotspots across the planet is a challenging task. While in present-day Europe only two such cradles of biodiversity exist (Lake Ohrid on the Balkans and the Caspian Sea), a great variety of shifting mega-hotspots with striking numbers of species (e.g. Lake Pannon with 605 species) and endemism developed in a series of long-lived lakes during the Neogene. However, the mechanisms responsible for the existence of aquatic biodiversity hotspots throughout the Neogene and Quaternary remained unknown.

Using a comprehensive dataset of ca. 1300 Miocene to Recent aquatic systems, we show that the existence and evolution of such hotspots in inland-water systems are tightly linked to the geodynamic history of the European continent. As a rule, the rise of aquatic hotspots of Europe is related to the formation of long-lived lakes and isolation of inland basins or marine embayments. Their individual faunal evolution is related to warm climates and lake surface area. Accordingly, the demise of hotspots is linked to the extinction of such aquatic systems. The Quaternary icehouse climate and extensive glaciations triggered a severe decline of lacustrine gastropod diversity across Europe and Neogene mega-hotspots disappeared. The Recent distribution pattern of lacustrine gastropods is a very young phenomenon, shaped after the Last Glacial Maximum (ca. 19 kyr BP) and subsequent formation of postglacial lakes, while hotspots are related to long-lived lakes in preglacially formed, permanently subsiding geological basins.



The presence is not the key to the past – self-fulfilling prophecies in taxonomy

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As paleontologists we are pleased to see that the fossil record is increasingly integrated by zoologists to understand modern biogeographic patterns and to link their phylogenetic trees to geological time. First occurrences of taxa as fossils are a valuable hint for a minimum age and may be used to calibrate molecular clock data. Aside from many methodological problems in interpreting such molecular clock data correctly, a quite blunt problem may be introduced by the subjective taxonomic opinion of the researcher. Although most of us will consider this a bromide, we want to present examples of how the expectation of a researcher, with knowledge based on modern taxa and their distribution, influences the taxonomic, paleobiogeographic and paleoecological conclusions in the fossil record – which then, unsurprisingly, matches exactly the predicted patterns.

One example considers Eocene continental molluscs from the Arabian peninsula. Depending on different working experience, two groups of taxonomists independently working with the material documented either their ancestor-descendant relation with modern Africa faunas or, in harsh contrast, with those of Socotra, fitting to the timing of the paleogeographic separation of this island from the Arabian mainland. Both opposing views would be quite influential for the interpretation of the evolution of such emblematic genera like *Achatina*. The much more logical approach to compare these faunas with coeval 35-million year old Tethyan ones, leads to completely different results.

The second example considers paleo(bio)geographic misconceptions from illogical projections of modern distribution patterns into the past. Eggenburg, as venue for this NOBIS-meeting, is famous for its tropical early Miocene mollusc faunas, which are mentioned in numerous publications as proof for immigration from the Indian Ocean, simply because they bear some genera now restricted to the Indo-West-Pacific. In fact, they document a wide Tethyan distribution, which became increasingly restricted by the global Neogene cooling and the formation of land bridges. Similarly, the interpolation of ecological requirements – e.g. adaptation to brackish water systems – of modern assemblages into the geological past may be misleading, as these assemblages went through various bottlenecks, which might have forced them into much narrower niches.

Exploring speciation in the rock-dwelling land snail genus

Montenegrina

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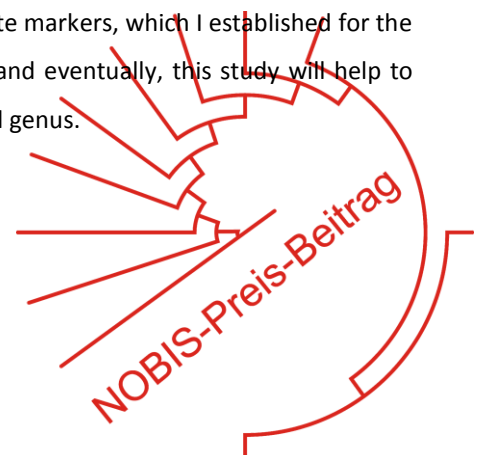
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Montenegrina is one of the taxon-richest genera of rock-dwelling gastropods comprising more than 90 described taxa. It has a very restricted and - compared to the size of the genus - rather small distribution range in the southern Balkan Peninsula. The morphological diversity in *Montenegrina* is high and most of the taxa consist of one or a few populations only. Living on isolated rocky outcrops, the snails have a low dispersal activity which results in a very patchy distribution. This led to the assumption that rock-dwelling gastropods mainly evolve by allopatric speciation and that co-occurring taxa therefore must be in secondary contact. Hence, we would assume that such co-occurring taxa are genetically differentiated. Several taxon-pairs (subspecies) are known that occur sympatrically, but are easily distinguishable by their morphology and a few taxon-pairs differ even exclusively in their ribbing (e.g. ribbed vs. smooth).

First phylogenetic results (mitochondrial genes: COI, 16S, 12S) show a low genetic distance between these taxon-pairs, which led us to the hypothesis that they could be in the first phase of sympatric speciation. To test this assumption we reconstructed the phylogeny of this genus with multi-locus molecular analyses. In future analyses we will complement the results with morphometric and ecological data. Furthermore, I will assess gene flow and trace population genetic structures with the help of microsatellite markers, which I established for the first time in clausiliids. Finally, the genus *Montenegrina* will be revised and eventually, this study will help to answer fundamental questions of speciation in this highly diverse clausilid genus.



Reduced ossification in the dentary bone of notothenioid ice-fishes (Teleostei: Perciformes)

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Notothenioidei is a monophyletic suborder within the Perciformes comprising 134 species. Their distribution is limited to the Southern Hemisphere and they dominate the Antarctic fish fauna (Eastman et al. 2014). These fishes do not possess a gas bladder and are characterized by reduced bony material (Eastman et al. 2014). Most members of this suborder have a predominantly benthic lifestyle. Although this is the plesiomorphic pattern, some more derived species manage to remain in the water column during their ontogenesis or even throughout their entire life. Since their gas bladder is reduced, among other highly derived adaptations (e.g., lack of haemoglobin in Channichthyidae), the key to remaining in the water column lies in weight reduction through decreased ossification (Eastman 1993). Eastman et al. (2014) showed that all Antarctic notothenioids as well as the non-Antarctic notothenioid Eleginopsidae share the trait of a very light skeleton weighing $\leq 2\%$ of the body mass (Eastman et al. 2014). Modifications include the ossification pattern resulting in spongy bones and persisting cartilage in the skull and appendicular skeleton. The aim of this study is to analyse the ossification pattern of the lower jaws in notothenioid fishes, which was not included in the study of Eastman et al. (2014). The jaw-design is a functional characteristic and important in terms of nourishment implying that reduction of ossification is not present in the lower jaw for maintaining solid structures. The left dentary bone of four selected notothenioids and one gadid, *Gadus morhua*, representing the outgroup were scanned with a micro-CT (SkyScan 1173) and the data gathered was used for 3D reconstruction with the software package Amira (version 5.4.1) as well as for a colour coded density analysis with the software package CT Analyser (version 1.14.4.1). These 3D reconstructions allowed measuring the mean thickness of the compact bony material, while the density analysis displays the proceeding reduction of bony material in respect to whether the specimens are benthic or adapted to a life within the water column. Both methods indicate a correlation between lifestyle and reduction of bony material. The more decreasing ossification can be observed, the more the species are adapted to being semi-pelagic or pelagic.

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To see and to be seen – A closer look into the evolution of a blind fish

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The cyprinid *Garra barreimiae* is endemic to the southeastern Arabian Peninsula, where it inhabits regularly desiccating water bodies. Since a hypogean population with troglomorphic traits (loss of eyes/pigmentation) is conspecific with the “normally” developed surface population, *G. barreimiae* seems to be a perfect organism to study the effects of cave life and the origin of troglomorphic characters.

Previous genetic analysis (Kruckenhauser et al. 2011) showed that specimens from the cave population are genetically differentiated from the adjacent surface populations. Few surface individuals were found, which exhibit haplotypes characteristic for the cave population and most of these display an intermediate phenotype. This indicates a quite recent separation of the cave population from the surface populations. For a better understanding of the evolution and the maintenance of the troglomorphic phenotype it is crucial to know if and to what extent gene flow between the cave and surface populations occurs. For this purpose, we will investigate individuals from three different cave localities, including individuals with an intermediate phenotype, as well as several surrounding surface populations with 19 variable microsatellite markers, which were designed and established especially for *G. barreimiae* in a previous study (Kirchner et al. 2014). The results of the present study will deliver the basis for interpreting the recent population genetic history of the species, detect hybridisation and evaluate genetic variability within the species in general.

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How many fish species are hidden under the taxon *G. barreimiae*?

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Garra barreimiae is an endemic species in the southeastern Arabian Peninsula (Hajar Mountains) where it is abundant in the south of the United Arab Emirates and northern Oman. So far, three subspecies have been described: *Garra barreimiae barreimiae* Fowler & Steinitz (1956) can be found throughout the northern Oman, *G. b. gallagheri* Krupp (1988) only at one location (Wadi Bani Khalid, northern Oman) and *G. b. shawkahensis* Banister & Clarke (1977) in the north of the United Arab Emirates. Populations of the species *G. barreimiae* inhabit rivulets or surface water bodies in wadis as well as the artificially constructed falaj water pipeline systems. One hypogean population displaying a troglomorphic phenotype lives in the Al Hoota cave. First phylogeographic analyses of *G. barreimiae* were carried out by Kruckenhauser et al. (2011). The genetic differentiation between different epigeal populations and the hypogean population was investigated. They revealed that certain populations belong to a very distant lineage. In the present study we present a comprehensive phylogeographic data set, based on a 750 bp fragment of the mitochondrial control region and 350 individuals, on the genus *Garra* in Oman. At least four different mitochondrial lineages, with distances in the COI sequence up to 10 % can be identified. These lineages have a clear geographic pattern following the water drainage systems. The pattern is not always congruent with the described subspecies. Moreover, comparison with GenBank data questions the monophyly of the species.

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The Rapunzel tintinnid – Redescription of *Tintinnopsis subacuta*

Jørgensen, 1899 (Alveolata, Ciliophora, Spirotricha)

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Tintinnids contribute distinctly to the microbial biomass in the marine plankton. Since the species have specific requirements concerning physico-chemical conditions and food items, reliable identification is indispensable for assessing their role in the food web. About one thousand extant tintinnid species are known, whose descriptions are exclusively based on the features of their loricae (houses); merely in about 30 species, cell characteristics have been studied. Since lorica shape and size are affected by environmental conditions and might show a polymorphism in the cell cycle, the tintinnid classification is artificial. Investigations of the cell, especially of the ciliary pattern and nuclear apparatus (generative micronuclei and somatic macronucleus nodules) are, however, supposed to provide features for a natural classification; these characters are revealed by protargol (silver proteinate) staining.

Tintinnopsis subacuta was collected from surface waters of the Indiana River at the Atlantic coast of Florida (USA) and stained with protargol. Cell and lorica morphology were investigated under a compound microscope at up to 1250x magnification. The lorica is 55–119 μm , on average 79 μm long and consists of a cylindrical collar about 34 μm across and a subspherical bowl about 45 μm wide. The lorica wall has agglutinated mainly mineral particles. The contracted cell measures $30 \times 28 \mu\text{m}$ and is attached to the bottom of the lorica by a contractile peduncle. The somatic ciliary pattern is of the most complex type, i.e., it comprises a ventral, dorsal, and posterior kinety as well as a right, left, and lateral ciliary field. The ventral kinety has associated an extraordinary ciliary tuft of cell length that extends outside the lorica posteriorly, resembling the golden hair let down from the tower by Rapunzel; *T. subacuta* is unique in this respect. The right and left ciliary fields are composed of about 11 ciliary rows each, the lateral field consists of invariably 15 rows. While the majority of tintinnids have only two macronucleus nodules, *T. subacuta* has 4–34, on average 14 nodules.

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From genes to means: Morphology and molecular phylogeny of four distinct mitochondrial clades of *Garra barreimiae* (Teleostei: Cyprinidae)

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The cyprinid fish *Garra barreimiae* is endemic to the northern Oman and the United Arab Emirates where it lives in rivulets, wadis and artificial falaj systems. *Garra barreimiae* has a long body with a flat underside and features an adhesive disk on the lower lip. The snout is often tuberculated. Specimens have a standard length of up to 6 cm and are variably coloured from dark grey to brown. *Garra barreimiae* has been categorized as vulnerable by the International Union for Conservation of Nature (IUCN). Currently, three subspecies have been described: *Garra barreimiae barreimiae* (Fowler & Steinitz, 1956), *Garra barreimiae gallagheri* (Krupp, 1988) and *Garra barreimiae shawkahensis* (Banister & Clarke, 1977) which have slightly different morphological features. *Garra barreimiae barreimiae* has 7 branched dorsal rays and 11-14 gill rakers on the lower limb of the first gill arch differing from 8 branched rays in *Garra barreimiae gallagheri*. *Garra barreimiae shawkahensis* generally resembles the nominate subspecies but has 15-18 gill rakers.

Based on the mitochondrial control region at least 4 different clades, which follow a biogeographic pattern around the omanese Hajar mountains, have recently been identified (Kirchner et al., unpublished data). Their distribution does not reflect the differentiation of the subspecies. The genetic distances between the clades ranges between 6 and 10 % in a fragment of the mt COI gene. Comparison with GenBank data questions the monophyly of the species. The current investigation is the first attempt for a comprehensive morphological analysis of *G. barreimiae* to evaluate whether morphological differences between the genetic clades can be found. This will be done by using traditional morphometric and meristic methods. In addition nuclear DNA sequences (e.g. Rag-1, ITS) will be utilized to provide a phylogenetic tree to examine their evolutionary relationships.

Consequences of past climate changes on ecology, fitness and population genetics of *Saponaria pumila*, an Alpine perennial cushion plant

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The “central-marginal model” in evolutionary biology states that populations which occur in marginal areas of a species’ distribution range display lower levels of genetic and phenotypic variation and are more prone to extinction than populations which are situated in the central areas (Lewontin R.C.1974, Vucetich et al, 2003)). However, climate driven range dynamics can also influence the genetic structure among the populations of a species. Former studies (Tribsch et al, 2002) indicate that *Saponaria pumila* might have survived the last glacial period of the Holocene in refugia on the Eastern outlines of the Austrian Alps and recolonized the mountain range in the following interglacial period. According to the “leading-edge-hypothesis” this process is followed by a decrease of genetic diversity (Hewitt 1993, 2000). The aim of our study is to find out if this genetic depauperation has an effect on the morphology and fertility of *S. pumila*. We also want to test if there are ecological niche gradients within the distribution area (central-marginal, east-west and within the altitudinal range) and if they can also be linked to the genetic structure. We approached these questions by an even sampling of populations covering the two major distribution areas in the Austrian Alps and applied AFLP fingerprinting combined with investigations about ecological habitat preferences via vegetation relevés, soil analysis and measuring different morphological and fitness parameters. The analysis of the genetic data so far supports a combination of both evolutionary models.

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Changes in the distribution of *Gentianella austriaca* and *G. praecox* on the century scale

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Gentianella austriaca and *G. praecox* are two biennial taxa that have become rare in some regions of Austria. For a better understanding of the reasons for these changes in the distribution we have evaluated all available herbarium samples covering a sampling history of nearly 200 years. We have preferred this more labor-intensive approach because the often diffuse information in floristic literature renders herbaria the only reliable source of more precise information on the historical distribution of taxa. Herbaria are greatly acknowledged for many purposes of plant systematics, biogeography, and recently for an increasing number of studies also as archives providing ancient DNA.

Yet their power is still under-estimated for answering ecology-related questions. The sampled data open windows into various time segments that can be related to data on historical land use, climate, etc. The sampled data per se give some insights into collection history: e.g., high collection activities in earlier times for exchange and commercial purposes changing with periods of low floristic activities due to economic or political crisis, paradigmatic shifts etc. The occasional lack of precise information on sampling sites provides some challenge with old collections. There are, however, ways to get a reasonable estimate on the sampling site in those cases. Keeping the error on the site coordinates as small as possible is crucial for relating sampling data to other data, e.g., land use data.

So far following the mere changing distribution patterns gives a clear picture of regional losses of populations, of hot spots of local extinction. At present we relate the distribution data to current (SINUS) and historical data on land use (Franzisco-Josephinische Landesaufnahme = Dritte Landesaufnahme, a mapping project covering the territory of Habsburg Monarchy). We expect that the knowledge gained from this will help to predict future performance of these species that have become rare in many regions.

Do fixatives influence histochemical tests in tintinnid loricae (Alveolata, Ciliophora, Spirotricha, Tintinnina)?

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Tintinnids are extraordinary marine planktonic ciliates as they form vase-shaped loricae (houses). Additionally, they are intermittently highly abundant ($\sim 10^4$ cells litre⁻¹) and have a considerable grazing impact on the nano- and microplankton (up to 62% of the primary production). For assessing their precise role in ecological and geochemical processes, also knowledge about the chemical lorica composition is indispensable. After cell death, the lorica sediments; both during its sedimentation and in the benthic deposition, bacteria might decompose the hyaline loricae or the lorica matrix in agglutinated loricae, contributing to the recycling of the nutrients. The chemical lorica composition does not only determine which bacteria might be involved in the decomposition, but also influences the degradation rate; hence, it has an impact on the fossilization probability. Additionally, the chemical composition might be of taxonomical significance. Actually, it has been investigated since the 1880s in about 24 out of the 75 genera. Owing to its impressive resistance against strong alkaline solutions, the studies suggested a chitinous or keratinaceous nature of the lorica forming material. The most comprehensive recent study clearly indicated proteins in the lorica material (Agatha & Simon, 2012); yet the usage of exclusively preserved material could have prevented the detection of further substances as well as the staining and enzymatic digestion in some species.

Therefore, common fixatives (formaldehyde, Bouin's and Lugol's solution, mercuric chloride plus osmium tetroxide) were tested for their effects on four histochemical reactions detecting polysaccharides, proteins, and lipids. For the first time, loricae of the tintinnid *Schmidingerella meunieri* were analysed. The preservatives did not influence the staining properties of the species' loricae which contain proteins with the amino acid tyrosine and possibly some lipids; polysaccharides could again not be detected. An identification of the extraordinarily resistant proteins is now needed. Deviations in the lorica wall structure of *S. meunieri* found in the present study were ascribed to different growth phases of the cultures used, although an influence of extrinsic factors could not be excluded.

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ABOL – infrastructural demands, scientific challenges, and benefits of the aim to inventorize the biodiversity of Austria

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The approaches to biodiversity are as manifold as the multitude of species. A standardized approach to biodiversity thus can constitute an anchor point for all different applications of biodiversity data. The latter include not only scientific fields like ecology, evolutionary biology, systematics and phylogeography, but likewise monitoring approaches, as well as applied fields like forensics, customs control, and food control.

DNA barcoding meets all demands of such a standardized approach to biodiversity. It uses a fragment of the genome as a genetic signature of species. Based on collections it holds all aspects of an integrative approach. As an open-access initiative it is open to all applications.

ABOL, the Austrian Barcode of Life-initiative aims at providing DNA barcodes for all species of animals, plants and fungi from Austria. Most importantly, the initiative will constitute a platform for people dealing with all aspects of biodiversity. Thus, it hopefully will stimulate studies, which will help to understand past and present causes for the rich biodiversity of Austria.

Mouthpart morphology of the waterlouse *Asellus aquaticus* and the common woodlouse *Porcellio scaber* (Crustacea: Peracarida: Isopoda)

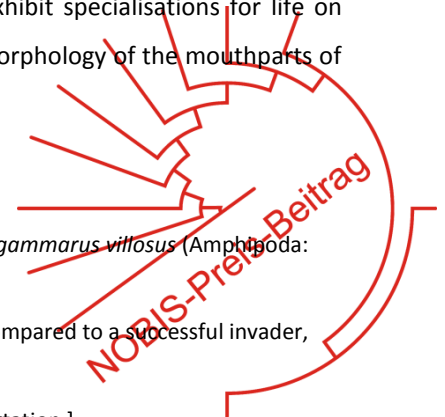
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Isopoda (Malacostraca: Peracarida) are a very diverse taxon of Crustacea including marine, freshwater and even fully terrestrial species. *Asellus aquaticus* is a freshwater isopod living in slowly flowing streams, lakes, ponds and even in drinking water systems in Germany (Mayer, M. 2013). Traditionally, *A. aquaticus* has been addressed to be omnivorous and assigned to the functional feeding group of shredders. Studies on freshwater amphipods performed by Mayer G. et al. (2008, 2009) revealed that, despite common opinions, amphipods actually have highly specialised mouthparts reflecting diverse feeding habits. We therefore investigated the mouthparts of *A. aquaticus* using SEM techniques and compared them to those of different, specialised isopod and amphipod species. Mouthpart morphology indicates that the animal is not capable of proper grinding of leaf litter but rather seems to use its mouthparts for ingesting detritus and for removing fungi and algae from litter surfaces. Setae on the different mouthparts vary in size and shape suggesting that they are able to hold back specific particles and to transport different kinds of food particles to the mouth. Very little work has been done on the mouthparts of isopods so far, but the situation in *A. aquaticus* appears plesiomorphic compared to that of the land-living Oniscidea. For better comparisons we also investigated the mouthparts of the common woodlouse *Porcellio scaber*. In this species, the whole mouth area keeps up a liquid-filled extraoral cavity, mainly enclosed by the shovel-like maxillipeds. In particular the mandibles exhibit specialisations for life on land. Further investigations on the feeding mechanism and on the functional morphology of the mouthparts of other land-living isopods remain to be done.

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Reinvestigation of the phylogenetic relationship of glirids using the ‘septal compass’ and ‘septal formula’

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The middle ear of several groups of mammals can be divided into the dorsally lying epitympanic recess and the ventrally lying tympanic cavity. In rodents, both the epitympanic recess and the tympanic cavity are additionally divided into several chambers by bony septa (e.g., Cox & Hautier, 2015). For comparative analyses, the ‘septal compass’ and ‘septal formula’ were invented as a new method for phylogenetic investigations of the middle ear in the squirrel-related clade (sciurids, glirids, and aplodontids). As the combinations of septa are specific to species, genus and even family levels, conclusions on the phylogenetic relationships can be drawn between the investigated species (Pfaff et al., 2015). While many taxa of the squirrel-related clade are characterized by septa in the epitympanic recess, glirids were assumed not to show any septa in this region. However, a reinvestigation revealed that some glirids do indeed have at least one septum inside the epitympanic recess.

Here, we reanalyse the morphology of the middle ear region of almost all genera of extant glirids and also extinct species. A new phylogenetic tree will be suggested for glirids, followed by a discussion on how the unique middle ear region of *Glirulus japonicus* might be a special kind of gliridae.

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