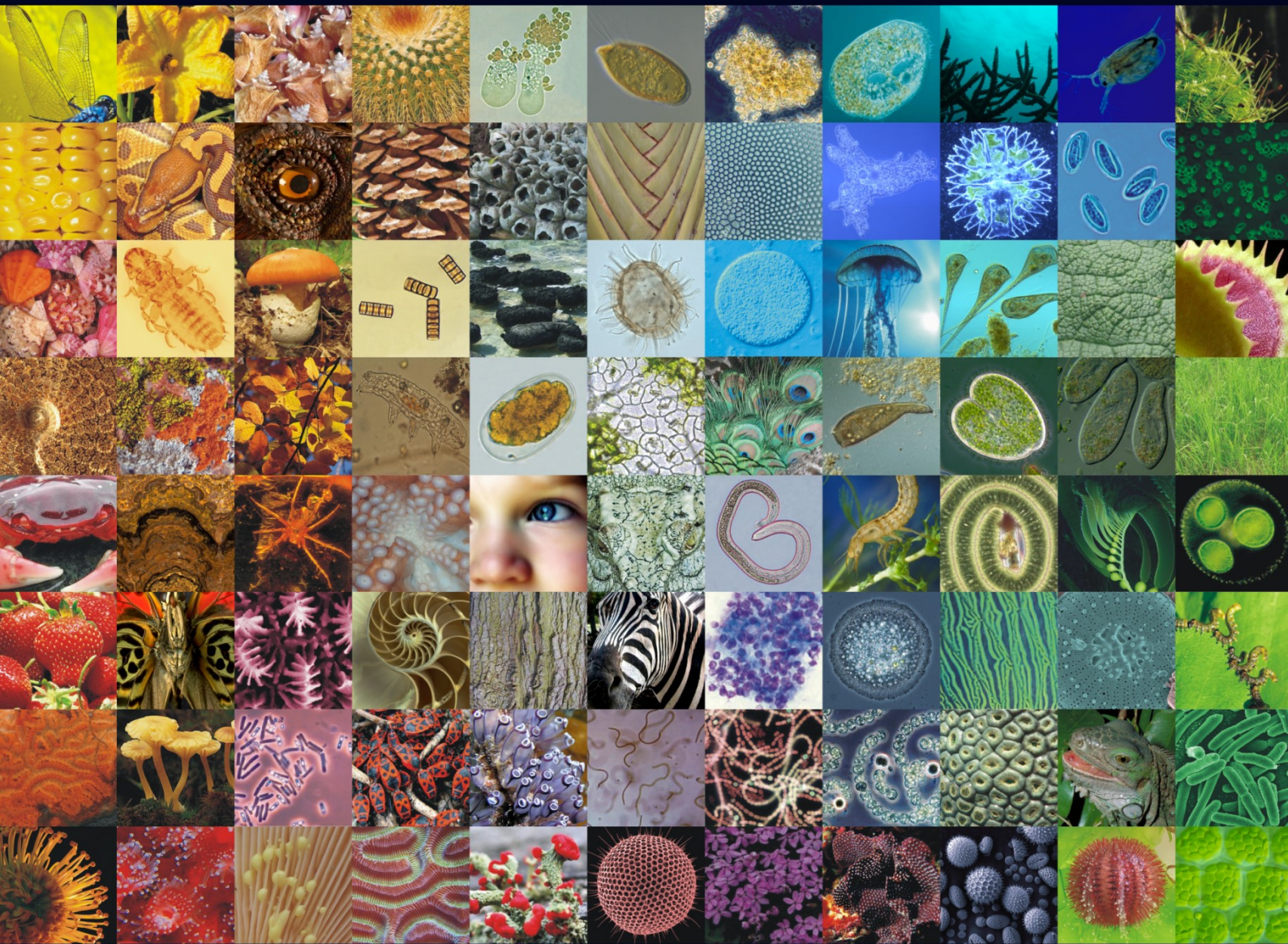


13. Jahrestagung von NOBIS Austria



Haus der Natur Salzburg
28.-29. November 2019



NETWORK OF BIOLOGICAL SYSTEMATICS AUSTRIA

13. Jahrestagung von NOBIS Austria

Gastgeber:

Haus der Natur

Salzburg, Österreich



Die Jahrestagung von NOBIS Austria findet dieses Jahr im Haus der Natur in Salzburg statt. Das Haus der Natur vereint ein breites Spektrum an Sammlungen, mit besonderem Augenmerk auf das Bundesland Salzburg. Seine Dauerausstellungen sprechen regionale, aber auch überregionale Themen an und bieten einen reichen Bilderbogen der Natur- und Kulturgeschichte der Region. Neben den Ausstellungsbereichen beherbergt das Haus der Natur wissenschaftliche Sammlungen von großer regionaler Bedeutung. NOBIS Austria ist mit der diesjährigen Jahrestagung nun bereits zum zweiten Mal seit Gründung der Gesellschaft im Haus der Natur zu Gast – die Präsidentin spricht dem gesamten Team vom Haus der Natur im Namen des Vorstandes und aller Mitglieder herzlichen Dank für die Gastfreundschaft aus und hofft auf viele weitere Jahre produktiver Zusammenarbeit.

Programmübersicht

Donnerstag, 28. November 2019

- 13.00–17.00 Nomenklatur-Workshop für Mitglieder von NOBIS Austria
von Dr. Andreas Kroh, NHMW (Ort: Univ. Salzburg, NAWI,
Hellbrunnerstrasse 34, Raum HS 431) Anmeldung erforderlich!
- 18.00–19.30 Icebreaker im Haus der Natur (Museumsplatz 5, 5020 Salzburg)
- ca. 20.00 Gemeinsames Abendessen in L'Osteria Salzburg (Dreifaltigkeitsgasse 10)

Freitag, 29. November 2019

- 8.30–9.00 Registrierung
- 9.00–9.05 Begrüßung
- 9.10–17.30 Vorträge, Poster-Präsentationen und NOBIS-Preis-Verleihung

- Vorträge** 12+3 Minuten
- Poster** 3 Minuten Kurzvorstellung mit grafischer Zusammenfassung
- Sprache** Englisch
- Beitrag** NOBIS-Mitglieder: € 20.-; Nicht-Mitglieder: € 50.-
- Zahlung** NOBIS Austria
IBAN: AT622011128822667900
BIC: GIBAATWW
oder bei der Registrierung

Programm

Freitag, 29. November 2019

- 8.30–9.00 Registrierung
- 9.00–9.05 Begrüßung durch
Robert Lindner, Sammlungsleiter und Dir. Stv. vom Haus der Natur
Sabine Agatha, Präsidentin von NOBIS Austria

Vortragsprogramm
NOBIS-Preis Beiträge (MSc)
Chair: Sabine Agatha

- 9.05–9.20 **Sebastian Decker** et al.: Life cycle and morphology of an undescribed bryozoan species from the Mediterranean Sea.
- 9.20–9.35 **Nikolaus Helmer** et al.: More leaves on the phylogenetic tree of Scaphopoda (Mollusca).
- 9.35–9.50 **Tobias Ternus** et al.: Phylogeography and morphological variation of freshwater spring snails (*Bythinella*), along a west – east transect in Austria.
- 9.50–10.05 **Tim Langnitschke** et al.: Bats have big babies too: Obstetric adaptations in the pelves of small flying mammals.
- 10.05–10.20 **Silvester Bartsch** et al.: A novel decomposition of global and local aspects of hominid cranial shape.

Poster session

Chair: Thomas Schwaha

- 10.50–11.20 Kaffeepause

Vortragsprogramm

NOBIS-Preis (PhD) und weitere Beiträge

Chair: Maximilian Ganser

- 11.20–11.35 **Sonja Bamberger** & Bernhard Hausdorf: One (un)like the other?
Species delimitation in the Cretan *Albinaria cretensis* complex
(Gastropoda, Clausiliidae).
- 11.35–11.50 **Susanne Affenzeller**: Pigments, colours and patterns – The
contribution of eumelanin and pheomelanin to molluscan shell
ornamentation.
- 11.50–12.05 **Clemens Maylandt** et al.: Genetic, morphological and cytological
diversity of the widespread steppe plant *Astragalus onobrychis*
(Fabaceae).
- 12.05–12.20 **Maximilian Wagner** et al.: Adriatic currents and the population
structure of the triplefin blenny *Tripterygion tripteronotus*.
- 12.20–14.00 Mittagspause

Vortragsprogramm

Chair: Bettina Sonntag

- 14.00–14.15 **Christoph Hahn** et al.: Resolving the deep evolutionary history of
vertebrate parasitism in flatworms – genomic insights from the
Monogenea.
- 14.15–14.30 **Maarten Vanhove**: Exploring the use of mitogenomics as a potential
solution for barcoding problems in a set of non-model flatworms.
- 14.30–14.45 **Maximilian Ganser** et al.: DeSigNate: A user-friendly tool to detect
signature nucleotides for taxon diagnoses.

14.45–15.00 **Wilhelm Foissner** et al.: *Pycnothrix monocystoides* Schubotz, 1908, a unique, intestinal ciliate from the African endemic *Procavia capensis* (Felsendachs): Morphology and evolution.

15.00–15.15 **Thomas Pröschold** et al.: An integrative approach sheds new light onto the systematics and ecology of the widespread ciliate genus *Coleps* (Ciliophora, Prostomatea).

15.15–15.45 Kaffeepause

Vortragsprogramm
Chair: Nicole Grunstra

15.45–16.00 **Andreas Kroh** & Omri Bronstein: Conservation of mitochondrial genome gene order in echinoids.

16.00–16.15 **Thomas Schwaha**: Welcome to the club: the puzzle of deep sea clavoporid bryozoans.

16.15–16.30 **Dominique Zimmermann** et al.: Morphological adaptations to the use of a new nest substrate in the pollen wasp genus *Quartinia* (Masarinae, Vespidae).

16.30–16.45 **Nikol Kmentová** et al.: Lates perches and their parasite fauna in Lake Tanganyika.

16.45–17.00 **Stephan Koblmüller** et al.: The color puzzle: resolving the relationships among color variants of the Lake Tanganyika cichlid genus *Tropheus*.

17.00 Verleihung der NOBIS-Preise und Schlussworte.

Poster session

Freitag, 29. November 2019, 10.20–10.50

Chair: Thomas Schwaha

Sabine Agatha & Ronja Rüdel: The significance of the lorica matrix for inferring tintinnid phylogeny (Alveolata, Ciliophora, Spirotricha).

Felicitas Flemming et al.: Systematics of symbioses: challenges and potential solutions from the ciliate *Paramecium bursaria* and its intracellular algae.

Michael Gruber & Sabine Agatha: Tintinnid's first top model: Ultrastructural insights into the oral ciliature of *Schmidingerella meunieri* (Alveolata, Ciliophora).

Sabine Schoder et al.: ABOL BioBlitz 2019 – a community-based initiative, making biodiversity expertise available to society.

Hannah Schubert et al.: DNA barcoding of the spring snails (Hydrobiidae) from the Kalkalpen National Park.

Bettina Sonntag et al.: The story of a tiny symbiont-bearing *Cyrtolophosis* (Ciliophora, Colpodea) living in lake plankton – a showcase of a facultative endosymbiosis with green algae?

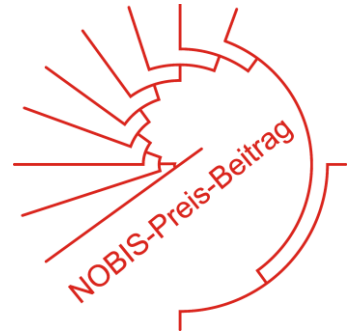
Christian Spanner et al.: Diagnostic PCR for the identification of endosymbiotic green algae in *Paramecium bursaria* (Ciliophora, Oligohymenophorea).

Abstracts

Pigments, colours and patterns – The contribution of eumelanin and pheomelanin to molluscan shell ornamentation

Affenzeller, S.

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Some of the most beautiful works of art built by nature are colourful mollusc shells. Not only is molluscan shell pigmentation important for the value of these shells, but is also still used in many cases for species identification. In recent years, interest into the pigments behind these patterns increased. One commonly mentioned pigment for many dark geometric patterns is melanin. But, a lot of techniques for melanin identification have to be adapted to be usable with often difficult molluscan tissues and shell material. A newly developed method allows mass spectrometric testing of melanin pigmentation in 13 different mollusc species. Evidence for eumelanin could be found in three conchiferan classes: *Nautilus pompilius* (Cephalopoda), *Mytilus edulis* (Bivalvia), *Clanculus pharaonius*, and *Steromphala adriatica* (Gastropoda). Both eumelanin and pheomelanin were detected in the gastropod *Cepaea nemoralis*. To further test the involvement of eumelanin and pheomelanin in shell pigmentation, *C. nemoralis* was used as a model organism to test the quantitative expression levels of genes known to be involved in melanin synthesis in insects and mammals in shell producing mantle tissue. It was found that *Tyrosinase* and *Tyrosinase Related Protein* are well expressed all over the mantle tissue, but show no differential expression in band building mantle tissue. This finding leads to the conclusion that both types of melanin seem to be involved in shell colouration, but not band patterning, of this gastropod shell. A surprisingly large number of other bivalve and gastropod species tested for melanin show similar geometric patterns that could not be verified as eumelanin with currently no indication of a known pigment being responsible for these colourations.

The significance of the lorica matrix for inferring tintinnid phylogeny (Alveolata, Ciliophora, Spirotricha)

Agatha, S. & Rüdel, R.

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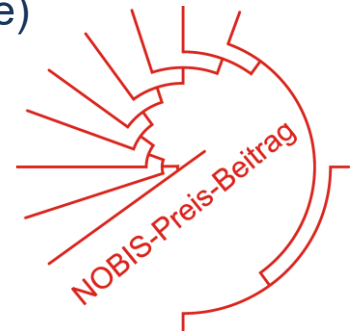
Tintinnid taxonomy and classification base almost exclusively on lorica features. Four major types of tintinnid lorica structures are distinguished: entirely hyaline loricae; entirely agglutinated and hard loricae; entirely agglutinated and soft loricae; and loricae composed of an agglutinated bowl and a hyaline collar. Molecular phylogenies and cladistic analyses of the cell features indicated that the lorica structures are unsuitable for inferring relationships and thus for establishing a natural tintinnid classification. Yet, the material excreted by the cell to form the wall in hyaline loricae or the matrix in agglutinated loricae/lorica portions is supposed to possess some significance in hypothesising relationships. Therefore, the ultrastructure of the lorica walls was investigated by electron microscopy in about twenty taxa, and the own findings were supplemented by literature data. The lorica walls emerged to represent currently nine types: monolaminar and compact; monolaminar with alveoli and a smooth surface; monolaminar with alveoli and surface ridges; trilaminar and compact; trilaminar with an alveolar middle layer; trilaminar with a tubular middle layer; trilaminar with large alveoli in the middle layer and minute ones in the inner and outer layers; tubular; and possibly fibrillar. The mapping of these character states on the gene tree provides support for some branches and hypothesises relationships in currently unresolved parts of the molecular tintinnid phylogeny.

Financially supported by the Austrian Science Fund (FWF) projects P28790-B29 and I3268-B29.

One (un)like the other? Species delimitation in the Cretan *Albinaria cretensis* complex (Gastropoda, Clausiliidae)

Bamberger, S. & Hausdorf, B.

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Delimiting species in radiations is notoriously difficult because of incomplete lineage sorting and introgression between incipient species. Next generation sequencing of genome-wide markers may help to overcome these problems. The door snail genus *Albinaria* VEST, 1867 from the Eastern Mediterranean is one of the most species-rich land snail genera. We studied the radiation of the *Albinaria cretensis*-complex on Crete. So far, species delimitation within this complex was based exclusively on shell characters. Competing classifications list 5–9 species with up to 18 additional subspecies (e.g., Nordsieck 2004, 2017; Welter-Schultes 2010). Several of the morphologically delimited species proved to be polyphyletic in a mitochondrial gene tree. We successfully generated double digest Restriction Associated DNA sequencing (ddRADseq) data for 53 *Albinaria* populations. We reconstructed the phylogeny of the *Albinaria cretensis*-complex based on these data and compared the results of several approaches for delimiting species (Structure, Gaussian clustering, etc.) with the classifications based on morphological data. In addition, we evaluated whether the differentiation between allopatric taxa can be explained by isolation by distance using a novel test. As a result, the status of several species could be confirmed, for example, *A. sphakiota* and *A. sublamellosa*. In addition, cases of hybridisation and introgression were verified as already suggested based on morphology.

References

- Nordsieck, H. 2004. *Albinaria cretensis* group: definition of the species and subspecies, with the description of new taxa (Gastropoda, Pulmonata, Clausiliidae). *Basteria*, 68, 51–70.
- Nordsieck, H. 2017. New species taxa of the genus *Albinaria* Vest (Gastropoda, Stylommatophora, Clausiliidae) in Crete. *Conchylia*, 48/1–2, 9–30.
- Welter-Schultes, F.W. 2010. Revision of the genus *Albinaria* in Crete (Greece): presence of geographically variable monotypic and polytypic species (Gastropoda: Clausiliidae). *Arch. Molluskenkd.*, 139, 143–245.

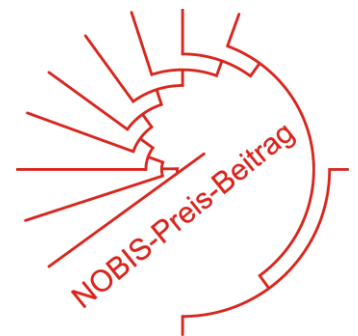
A novel decomposition of global and local aspects of hominid cranial shape

Bartsch, S.J.¹, Grunstra, N.D.S.^{1,2,3} & Mitteroecker, P.^{1,2}

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The cranium is a highly functional and adaptive morphological complex in vertebrates: It protects and houses the brain, sensory organs, and the masticatory apparatus. Individual cranial bones need to form an integrated whole in order to facilitate these functions throughout development and into adulthood, in spite of the considerable changes in cranial shape taking place during ontogeny in many vertebrates. The aim of the present study was to explore how the relative contribution of individual cranial bones to overall cranial shape changes during development.

To this end, we used a novel decomposition of cranial shape into a 'global' shape component, which captures the *outline shape* of the cranium without any regard for the delineation of individual bones, and a 'local' shape component, which captures only the relative contributions of the individual bones to overall shape (we call this *residual shape*). To see how stable these patterns are across closely related species, we compared chimpanzees (*Pan troglodytes*) and humans (*Homo sapiens*).

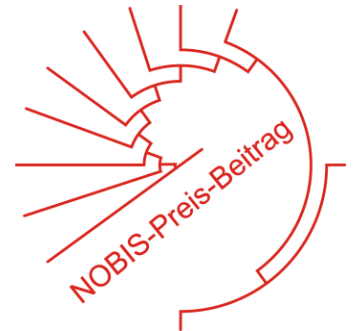
Using a geometric morphometric approach, we measured a set of 93 midsagittal landmarks in 3D on 84 CT scans of *P. troglodytes* and *H. sapiens* crania of different postnatal age stages. Principal component analysis (PCA) of outline shape clearly showed species differences (PC1) as well as ontogenetic trajectories (PC2), which were similar for humans and chimpanzees. By contrast, a PCA of residual shape showed no ontogenetic trend within either species and interspecific differences were less pronounced, although they remained statistically significant ($p < 0.001$).

Ontogenetic cranial shape changes after birth, as well as cranial shape differences between humans and chimpanzees, are thus accrued globally rather than locally. We found that the relative extent to which individual bones realize overall cranial shape (i.e. residual shape) arises prenatally and remains largely stable postnatally. We also found evidence that the cranial outline is more canalized during development than individual bones, which may suggest that it is functionally more relevant than residual shape.

Life cycle and morphology of an undescribed bryozoan species from the Mediterranean Sea

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The epiphytic community on the endemic seagrass *Posidonia oceanica* from the Mediterranean Sea is well studied, but still harbors some little investigated epiphytic bryozoans. From the ctenostome family Pherusellidae only *Pherusella tubulosa* was reported as a member of the Mediterranean fauna that inhabits several species of algae and the rhizome of *P. oceanica*. In 2004, small colonies inhabiting the leaves of *P. oceanica* in Sicilian waters were identified as *Pherusella brevituba*, a species originally described from the Eastern Pacific. First findings of a similar species in the Northern Adriatic Sea with always small colonies, called into question the species identity of the Mediterranean population. The aim of this study was to generate data on the life history, colonial development, and reproduction of the Mediterranean population of this *Pherusella* species. In addition, the morphology of zooids was also studied in more detail owing to the complete lack of data gathered with modern techniques on the family.

Numerous characters such as the colony pattern, colony size, and life cycle altogether with its specific habitat and distribution range indicate that the species under examination is in fact an undescribed species of the genus *Pherusella*. This study constitutes one of the first long time observations of the lifecycle and colonial growth of a ctenostome bryozoan, including additional morphological data about the neuro-muscular system of an otherwise incompletely known group of bryozoans.

Systematics of symbioses: challenges and potential solutions from the ciliate *Paramecium bursaria* and its intracellular algae

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Symbiotic systems occur all over the tree of life and encompass a huge diversity of organisms. We use the ciliate *Paramecium* as model host to address questions regarding molecular, ecological, and evolutionary consequences of endosymbiosis. Paramecia can harbor diverse symbionts including bacteria, fungi and even other eukaryotes: we focus on algal endosymbionts of *Paramecium*. Two species are known to harbor photobionts, the common *Paramecium bursaria* and the extremely rare *Paramecium chlorelligerum*. The intracellular green algae belong to the genera *Chlorella*, *Micractinium* or *Meyerella*, the most commonly found symbionts. We are interested in changes of swimming behavior as reaction to light stimuli, depending on the photobiont's presence, and aim to correlate observed phenotypic differences to genotypic ones. The first step is a definite identification of both organisms – host as well as photobiont. Both being unicellular eukaryotes, a molecular characterization protocol tailored to the “systematics of symbioses” has to be established for DNA-isolation and gene amplification considering the challenges of limited cell numbers, cell wall lysis and mixed template DNA. A secondary algal symbiont creates further confusion in identifying the photobionts. Additive, *Chlorella* and *Micractinium* are known to possess unpredictable intron insertions. A hidden sibling species complex of five to six syngens also obscures the molecular characterization of *P. bursaria*. Addressing these challenges, we improved our DNA extraction and used a combination of different markers including the SSU rRNA, ITS, and mitochondrial COI gene. Our multiple-marker approach provides promising preliminary molecular characterizations of both host and photobiont for all tested strains. SSU rRNA gene and ITS successfully identified the host as *P. bursaria*. Data analysis regarding potential syngen affiliation based on COI sequences is still ongoing. Molecular characterization according to the algal symbiont's SSU rRNA and ITS sequence data revealed preliminary identification as *Chlorella variabilis* in three and *Micractinium conductrix* in the other five strains. The secondary symbiont associates to *Choricystis*-like algae. Data of the completed molecular analyses will be used to identify the involved species and syngens. Further, we will compare the similarities and differences among host and symbiont strains. These phylogenetic analyses will answer the question to which extent genotypic variation contributes to the observed differences in the symbiosis' phenotypes in our system.

Pycnothrix monocystoides Schubotz, 1908, a unique, intestinal ciliate from the African endemic *Procavia capensis* (Felsendachs): Morphology and evolution

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³ Department of Molecular and Cellular Biology, University of Guelph, Guelph, ON, Canada;
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⁴ Department of Zoology, University of British Columbia, Vancouver, V6T 1Z4, BC, Canada (†)

1. We re-investigated *Pycnothrix monocystoides* SCHUBOTZ, 1908 using protargol impregnation, electron microscopy, and molecular biology.

2. *Pycnothrix* is a unique, up to 5 mm long intestinal ciliate with about 2 million cilia and many cytostomes (POLYPHARYNGY) in the oral furrow (vestibulum) that extends on both sides of the cell.

3. Both walls of the furrow are covered by adoral membranelle-like polymerizations.

4. Right of the furrow and of the cytostomes there are small ciliary fields very likely homologous to the “dorsal brush” present in the free-living Litostomateans.

5. The molecular investigations show *Pycnothrix* as sister to *Balantidium* and endemic Australian intestinal ciliates.

6. We propose that the common ancestor had both an oral furrow and a special ciliary field both similar to that found in *Balantidium*.

7. We speculate that the big size and the polypharyngy evolved by multiple fission of a *Balantidium*-like ancestor.

DeSigNate: A user-friendly tool to detect signature nucleotides for taxon diagnoses

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Currently, taxon diagnoses are mainly restricted to morphological characters, whereas molecular characters have only infrequently been added in integrative taxonomic approaches. The inclusion of molecular characters into taxon diagnoses is hampered by both problems in standardization as well as the lack of efficient and user-friendly tools.

DeSigNate is a novel tool that detects signature nucleotides in a sequence alignment, which are diagnostic for the taxon of interest. An intuitive web application guides the user through the analysis process in three simple steps comprising (1) the upload of input data, (2) the specification of search parameters, and (3) the taxon selection. Then, the underlying algorithm uses so-called nucleotide vectors for calculating metrics for each position in the alignment. These metrics are subsequently analysed to detect candidate nucleotides and to rank them according to their diagnostic relevance. The results clearly display the ranking and the classification of the signature nucleotide positions. Furthermore, the positions can be assigned to conserved or variable sequence regions by entropy calculations based on the alignment. The aim is to facilitate the integration of signature nucleotides as molecular characters for complementing taxon diagnoses and thus to enable taxon delimitation and identification in various applications.

The study is financially supported by the Austrian Science Fund (FWF projects I3268-B29 and P29859).

Tintinnid's first top model: Ultrastructural insights into the oral ciliature of *Schmidingerella meunieri* (Alveolata, Ciliophora)

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The Oligotrichea are mainly marine planktonic ciliates with a globular or obconical cell shape and an apically located zone of ciliary fans (membranelles) employed in both locomotion and feeding. Their closest relatives, the hypotrichs, are dorsoventrally flattened benthic ciliates crawling on the substrate by means of their ventral ciliary bristles (cirri). For feeding, they use their ventrally located C-shaped zone of membranelles. In contrast to the oligotrichids, which still possess the ancestral C-shaped membranellar zone, the choreotrichids have the membranelles arranged in a circle. Some aloricate choreotrichids obtained the ability to jump obviously only by means of their membranelles, and the about 1,000 tintinnid species (loricate choreotrichids) are attached inside a cumbersome lorica. Accordingly, the membranellar zone changed its position, function, and shape during the evolution of the Oligotrichea likely with effects on its ultrastructure, i.e., the links between the basal bodies of a membranelle and the links between the membranelles in the zone. For a comparative study on the oral ciliature, ultrastructural data from hypotrichs are available in the literature, whereas information is insufficient concerning the Oligotrichea. *Schmidingerella meunieri* (Kofoid & Campbell, 1929) Agatha & Strüder-Kypke, 2014 was chosen here as tintinnid representative because it has been investigated in various, primarily ecological respects, making it a suitable model organism. The findings on *S. meunieri* are the first detailed ones on tintinnid ciliates and Oligotrichea in general. Thus, the current analysis focused on the detection of apomorphies by comparing the situation in *S. meunieri* with that in the hypotrich outgroup. Beyond some plesiomorphies, supposedly derived character states are actually discovered. However, more data are required from other tintinnids, aloricate choreotrichids, and oligotrichids for placing the apomorphies correctly in the cladograms and on the gene trees.

The study was financially supported by the Austrian Science Fund (FWF Project P28790-B29).

Resolving the deep evolutionary history of vertebrate parasitism in flatworms – genomic insights from the Monogenea

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² Research Group Zoology: Biodiversity and Toxicology, Centre for Environmental Sciences, Hasselt University, Diepenbeek, Belgium

The Neodermata (Platyhelminthes) are a highly diverse assemblage of obligate parasitic flatworms, comprising Cestoda (tapeworms), Monogenea, and Trematoda (flukes), many of biomedical, veterinary and economic importance. Together, they span an impressive range of hosts and parasitic lifestyles. Despite decades of research, however, the relationships between the main parasitic lineages remain contentious. Recent work has sought to resolve the controversy by means of phylogenomic inference, but particularly Monogenea remain vastly underrepresented in these datasets, despite their importance and ubiquity. With their simple, direct life cycles, monogeneans are key for understanding the shift towards obligate parasitism of vertebrates, the evolutionary history of ecto- and endoparasitism, and the emergence of complex life cycles in Neodermata.

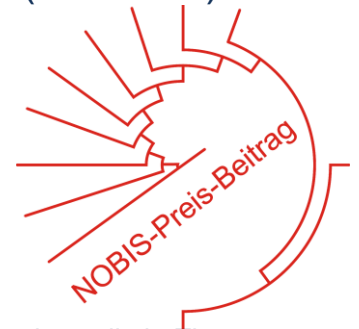
We will give an overview on and present first results from the project “Deep Evolutionary Genomics of Monogenea”, which has recently been funded by the FWF and represents a large international collaborative effort currently supported by a consortium of Monogenea experts from 15 countries and 17 research institutions. The project aims, by means of extensive taxon sampling and cutting edge bioinformatic/phylogenomic methods, to: (i) elucidate the phylogenetic position of the Monogenea and thus the origins of vertebrate parasitism within Platyhelminthes, (ii) infer the interrelationships of Monogenea and test hypotheses of deep evolutionary host-parasite interactions, and (iii) identify genomic features associated with the diverse parasitic life history strategies employed by the Monogenea, and Neodermata in general.

More leaves on the phylogenetic tree of Scaphopoda (Mollusca)

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Despite the global marine distribution, the taxon Scaphopoda is notoriously understudied. The evolutionary position of this infaunal group within the molluscs is as disputed as the internal systematics. The greatest diversity of scaphopod species is recorded from depths below 200 m and tropical shallow water habitats. Diagnoses of the 576 recent species are mostly based on shell characters. Only in some cases, the description is supplemented by radula features (Steiner & Kabat 2004). Scaphopod systematics was investigated in several morphological studies based on softbody characters. Although the subtaxa Dentaliida and Gadilida are well defined, the validity of many family and genus-rank taxa remains unresolved (Reynolds 2002). Molecular phylogenetic studies suffered from limited taxon sampling and agreed with the morphological studies on a robust support for Dentaliida and Gadilida only (Steiner & Reynolds 2003, Reynolds & Steiner 2008).

The present study is based on mostly Indo-Pacific dentaliid specimens from the National Museum of Natural History, Paris. Nuclear marker sequences (18S rRNA, 28S rRNA) and mitochondrial markers (16S rRNA, cytochrome c oxidase subunit 1) were analysed with the aim to improve our knowledge on the phylogenetic signal of these markers and to gain new insights into the poorly studied phylogeny of this group.

The preliminary trees are better resolved than those in preceding studies. Major taxa like Dentaliida, Gadilida, Entalimorpha, and Gadilimorpha are also well supported. However, monophyly of family-level taxa and most genera with more than two species in the dataset (e.g., *Dentalium* and *Antalis*) is not supported. This indicates that shell shape and sculpture, even if supplemented by radula morphology, are too homoplastic and, thus, not sufficient for diagnosing taxa at genus and higher levels.

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Lates perches and their parasite fauna in Lake Tanganyika

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Lake Tanganyika is a biodiversity hotspot with exceptional species richness and levels of endemism. Given the global importance of the lake in the field of evolutionary biology, the understudied status of its parasitological fauna is surprising. Hitherto, a total of 51 species of parasitic flatworms have been described in Lake Tanganyika. Although the most famous group within the lake's fish fauna are cichlids, the pelagic zone is dominated by endemic species of sardines (Clupeidae) and lates perches (Latidae). Our surveys revealed the presence of a single monogenean parasite (Diplectanidae) infecting three out of the four species of lates perches in the lake. This diversity is surpassed by the six recently recovered species of digeneans (Cryptogonomidae). Three out of the four reported parasitic genera are new to science. The comparatively low host-specificity in some of these parasites is probably an adaptation to the sympatric occurrence and low population densities of latid predators in the open water realm. Moreover, conspecificity of the monogenean species recovered from lates perches endemic to Lake Tanganyika and the widespread Nile perch, *Lates niloticus*, supports a recent invasion of this fish family in the lake. Unlike the recovered digeneans, which belong to an exclusively freshwater clade, the phylogenetic position of the monogenean parasite corresponds with the marine origin of the host family, given the sister-group relationship with a species infecting the Asian lineage of lates perches. This discrepancy might be explained by the difference in the parasites' life strategies. Our study highlights the importance of a multidisciplinary approach to reveal the diversification processes involved in this host-parasite system.

The color puzzle: resolving the relationships among color variants of the Lake Tanganyika cichlid genus *Tropheus*

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With >120 mostly allopatrically distributed color morphs, the stenotopic rock-dwelling Lake Tanganyika cichlid genus *Tropheus* is undoubtedly one of the most spectacular examples of geographic color variation in vertebrates. Yet, to date, *Tropheus* comprises only four valid species, mainly because overall morphology appears to be quite conserved across most populations and color morphs. However, genetic (and to some extent also morphological) analyses indicate the presence of additional diversity that is not reflected by currently recognized species. Here, we present by far the most comprehensive attempt to disentangle the phylogenetic relationships among *Tropheus* species using a genome-scale dataset obtained by anchored hybrid enrichment, AFLPs, mtDNA sequences, and morphological data. We find evidence for i) the presence of several additional *Tropheus* species, some of which appear to be confined to fairly narrow stretches of shoreline, ii) complex patterns of haplotype sharing/gene flow among (sometimes geographically-distant) populations/species, and iii) signatures of hybridization contributing to the origin of novel phenotypes. Moreover, this study provides a robust phylogenetic framework for analyzing the factors and processes underlying the evolution of new color morphs in this rapid radiation.

Conservation of mitochondrial genome gene order in echinoids

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Extant echinoids are subdivided into two major groups, the cidaroids, with a single, often massive primary spine per plate, and the euechinoids, with numerous primary spines per plate. Based on their fossil record our understanding of the phylogeny of the Echinoidea suggests that the two groups diverged in Late Palaeozoic. The oldest known cidaroid is Permian (Roadian–Capitanian) in age, placing the divergence of the two groups at least 268.8 million years before present. Recent research suggests that a large-scale reorganization of echinoid gene regulatory networks occurred prior to the divergence of cidaroids and euechinoids.

Here, we present 13 new complete echinoid mitochondrial genomes including, for the first time, four complete and fully annotated genomes of the order Cidaroida assembled from next-generation sequence (NGS) data. Results of our phylogenetic analysis provide strong support for the basal placement of cidaroids among the Echinoidea. Despite the long divergence time of cidaroids, echinoid mitochondrial genomes are surprisingly conservative, showing no gene rearrangements. This observed stability of echinoid mitochondrial genome is in stark contrast to the situation observed in other echinoderm groups, particularly ophiuroids, which show multiple mitochondrial genome rearrangements in different subclades.

Deviations from the standard echinoid mitochondrial gene order had apparently been previously reported for some stronglylocentrotid echinoids. Closer inspection of the published sequence data and alignment to well-supported, high-coverage mitogenomes assemblies of closely related species, however, showed evidence of assembly errors, including an incomplete annotation of the ND4 gene in the previously reported sequences. Re-assembly of the original raw data using read trimming and improved assembly pipelines proved that the previously reported deviant stronglylocentrotid gene order was indeed only an artefact based on misassembly.

Camarodont echinoids are the best sampled group in terms of echinoid mitochondrial genomes. Phylogenetic analyses of complete echinoid mitochondrial genome sequences overcome many problems observed in the analysis of single short marker sequences and produce well-supported trees.

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Bats have big babies too: Obstetric adaptations in the pelves of small flying mammals

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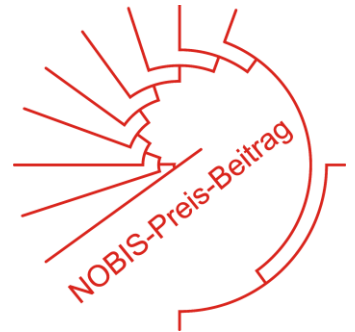
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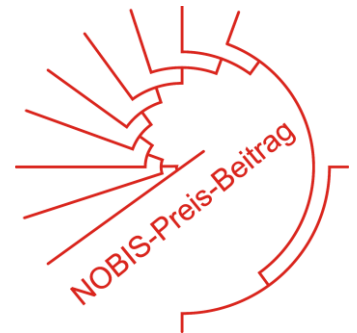


Human childbirth is difficult compared to parturition in other mammals. This is mainly due to a very tight fetopelvic fit: humans have very large neonates relative to the size of their bony pelvis. Indeed, obstructed labor is not infrequent, and thus a longstanding question in anthropology concerns the failure to evolve a larger, more spacious birth canal. We draw on the pelvic and reproductive biology of bats (Chiroptera) as a comparative ‘model’ for better understanding this particular human evolutionary question. Bats give birth to neonates that make up 10–40% of maternal mass (human babies weigh ~6% of maternal mass). In order to accommodate such large young, females of all bat species inspected to date lack a pubic symphysis but instead possess a pubic ‘gap’ spanned by a hyper-flexible ligament, which enables birth of the large fetus. We hypothesized that the selection pressure acting to constrain the size and flexibility of the human birth canal is not present in bats due to their volant mode of locomotion and particular roosting behaviour, and that bats are therefore free to respond to obstetric selection and increase their pubic gap in proportion to the size of their neonate. To test this prediction, we conducted a morphometric study of pelvic size on 245 specimens pertaining to 103 bat species and collected mean adult and neonatal body masses from the literature for a subsample of 65 species. Pubic gap size relative to body size was positively associated with absolute neonatal body mass across bats, but lacked a correlation with relative neonatal body mass (as a percentage of maternal mass). Nevertheless, male bats rarely show a pubic gap, resulting in strong pelvic sexual dimorphism, which is evidence for sex-specific selection in female bats related to obstetrical demands. We discuss these findings in the context of bat ecology and measurement error.

Genetic, morphological and cytological diversity of the widespread steppe plant *Astragalus onobrychis* (Fabaceae)

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The name *Astragalus onobrychis* is applied to a heterogeneous, abundant and widespread steppe plant, which occurs in dry to semi dry grasslands from the Western Alps to the Altai Mountains. The Eurasian steppes occupy a significant portion of the worldwide land surface and their biota have been affected by specific past range dynamics driven by ice ages-related climatic fluctuations. These dynamic alterations in conditions during the Pleistocene triggered reticulate evolution and whole genome duplication events in *A. onobrychis* (Závěská et al. 2019). This led to a remarkable diversity of genotypes, morphotypes and cytotypes, which is impressively underlined by the existence of about 45 synonyms for *A. onobrychis*. Most of their loci classici were sampled for this study and were further complemented by surrounding populations. An integrative approach, which combines a complementary array of morphometry, plastid DNA sequencing, RAD sequencing and flow cytometry, was used to infer the relationships within this complex group. To date, four ploidy levels were found, that is, diploids in the Balkans and the Western Pontic Plains, tetraploids in the Balkans, Apennines, Carpathians and Eastern Alps, hexaploids along the Black Sea coast and octoploids within in the Alps, the Pannonian Basin, the Carpathians and the Pontic Plains eastwards extending to the Altai Mountains. According to the molecular analyses, all octoploids are allopolyploids, whereas the tetraploid and hexaploid populations appear to have resulted from autopolyploidisation. The genepools encountered in *A. onobrychis*, which have their origins in the Caucasian Area, could be assigned to specific geographic regions. The morphological investigations revealed seven main groups: (1) diploids in the southern Balkans, (2) diploids in the western Balkans, (3) diploids in the western Pontic area, (4) tetraploids from the Balkans, Apennines, Carpathians and Eastern Alps, (5) hexaploids along the Black Sea Coast, (6) octoploids in the Alps, and (7) octoploids in the Pannonian Basin, Carpathians and Pontic Plains. In summary, the results uncovered a complex evolutionary history and strongly suggest that a thorough taxonomical revision of the *A. onobrychis* group is urgently needed.

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An integrative approach sheds new light onto the systematics and ecology of the widespread ciliate genus *Coleps* (Ciliophora, Prostomatea)

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Species of the genus *Coleps* are one of the most common planktonic ciliates in Lake Mondsee (Austria) and Lake Zurich (Switzerland). Based on morphology, three mixotrophic species of *Coleps* were found: *Coleps hirtus viridis*, *Coleps spetai* and one species with different morphological features, which does not match the described species. *Coleps hirtus hirtus*, a species without endosymbiotic green algae, has been observed in different depths of Lake Mondsee and Lake Zurich. The aim of the study was to detect the phenotypic plasticity and the genetic variability of different *Coleps* specimens newly isolated from the plankton and available strains from culture collections. We used an integrative approach for comparison of the *Coleps* isolates. To study these strains, the following procedure was developed: (i) cultivation in suitable culture medium, (ii) detection of the morphological variability under different culture conditions by light microscopy alive and stained with protargol and silver nitrate, and (iii) sequencing of SSU and ITS rDNA including secondary structures. The *Coleps* strains showed a high phenotypic plasticity and low genetic variability. *Coleps* is common in both lakes over the whole year in different depths and high throughput sequencing has revealed that only one genotype is present in both lakes despite the different life style (mixotrophic with green algal endosymbionts or heterotrophic without algae). Based on these results, the species concept of the genus *Coleps* needs to be revised.

The study is funded by the Austrian Science Fund (FWF): projects P28333-B25 and I2238-B25.

ABOL BioBlitz 2019 – a community-based initiative, making biodiversity expertise available to society

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Biodiversity Days (*Tage der Artenvielfalt*) are among the most important events in Austria where the multiplicity of species and their importance is conveyed to interested people. This year, the organizers of these events supported the involvement of the initiative Austrian Barcode of Life (ABOL) in their event, allowing ABOL to carry out its own small project: the ABOL BioBlitz'. In this projects, ABOL offered to generate DNA barcodes from organisms collected by the participants of the Biodiversity Days. Altogether, about 1,800 tissue samples from six different Biodiversity Days throughout Austria were sent to the Canadian Center for DNA Barcoding (CCDB), with a main focus on various insect groups like Coleoptera, Hymenoptera, Diptera, Hemiptera, and Lepidoptera. The gained DNA barcodes do their bits in building up a reference database, which finally will allow for determining all species of animals, plants and fungi from Austria. The ABOL BioBlitz thus again points at the invaluable importance of biodiversity expertise held by private citizens. The currently ongoing biodiversity loss implies an increasing importance of biodiversity knowledge. Open access data on biodiversity thus becomes an utterly important societal goal. The public outreach achieved through the ABOL BioBlitz will help to increase the awareness of biodiversity research and environmental protection in the society.

DNA barcoding of the spring snails (Hydrobiidae) from the Kalkalpen National Park

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The Kalkalpen National Park, situated in Upper Austria and comprising about 209 km², contains more than 800 springs (Stadler 2017). The international importance of this park is, from the perspective of nature conservation directives, highly significant (European nature reserve Natura 2000, recognized wetland of the Ramsar convention). For the protection of the local endemics, the national park bears absolute responsibility.

So far, two endemic spring snails (Hydrobiidae), which were described based on morphological and anatomical examination, are found in the Kalkalpen National Park and its close surroundings: *Belgrandiella aulaei* and *Bythiospeum nocki* (Haase et al. 2000). Apart from that, the knowledge of the Hydrobiidae in the national park is incomplete.

In the current study, the spring snails of the Kalkalpen National Park will be investigated in more detail. Snails have been collected from more than 50 springs and are examined by morphological determination, photographic documentation and genetic analysis by DNA barcoding. The data will be compared with hydrobiid sequences from the ABOL Mollusca project. Until now, more than 60 individuals of the genus *Bythinella* (Moquin-Tandon, 1856) from 19 different springs were thoroughly investigated. The results suggest the occurrence of a single species: *B. conica*.

The investigation of hydrobiids is especially desirable, as several species are threatened (for example by construction works for drinking water production or by grazing) and as they are important for water quality assessment. Species identification by DNA barcoding will help to generate a better knowledge of the species distribution, and hence provides the basis to protect unique species of Hydrobiidae from extinction.

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Welcome to the club: the puzzle of deep sea clavoporid bryozoans

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Bryozoans are a phylum of aquatic, colonial suspension-feeders that occur in freshwater as well as marine environments. In the latter, they are present in various habitats including the deep sea. Among the non-calcified ctenostome bryozoans, several families are known from depths exceeding 1.000 m, with the record being over 7,000 m. Clavoporid ctenostomes are a family of club-shaped bryozoans that have a stalk consisting of non-feeding, polymorphic zooids, which attach the colony to the substrate, and a capitulum, which contains the feeding autozooids. Currently, only six species from five genera are described for this family that each differ in their proportions. Last year, I received a large amount of deep sea clavoporids from New Zealand that were collected over the past 40 years. Preliminary analysis of the material shows that none of the encountered specimens fit to any past description and that probably all of the material represent new species and even genera. Individual colonies show a high variation of the following characters: 1) stalk composition, 2) stalk-capitulum ratio, 3) attachment rhizoids, 4) capitulum structure, and 5) budding zones. The high heterogeneity of each individual colony hampers species description, particularly with the obvious lack of knowledge of the biology of this family. In this presentation, I will give an overview on the diversity of clavoporid ctenostomes and the problems arising with their taxonomic assignment and description.

The story of a tiny symbiont-bearing *Cyrtolophosis* (Ciliophora, Colpodea) living in lake plankton – a showcase of a facultative endosymbiosis with green algae?

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In plankton of several Austrian and Swiss lakes, we subsequently detected a symbiont-bearing *Cyrtolophosis* species of app. 20×10 µm in size. The morphological characters of the ciliate as well as the SSU rDNA sequence almost match available descriptions and molecular sequences of *Cyrtolophosis mucicola*. The algae belong to the newly described green algal species *Carolibrandtia ciliaticola* and only few individuals (up to 15) are found in one ciliate cell simply because there is no space for more. Similar to *C. mucicola*, individual green *Cyrtolophosis* often live in mucous colonies consisting of long hyaline tubes. In culture, in the mucus of these tubes many green algae (former symbionts that escaped from dead ciliates?) are incorporated. Under unfavourable conditions, the green *Cyrtolophosis* form resting cysts still containing algal symbionts. In lakes, the green *Cyrtolophosis* occurs from the onset of the spring bloom through November and is one of the predominant ciliate species in the euphotic zone (up to several thousand individuals per litre). Overall, our results now raise the question if the green *Cyrtolophosis* is a new species or if the acquisition of green algal symbionts was an evolutionary adaptation to environmental habitat conditions.

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Diagnostic PCR for the identification of endosymbiotic green algae in *Paramecium bursaria* (Ciliophora, Oligohymenophorea)

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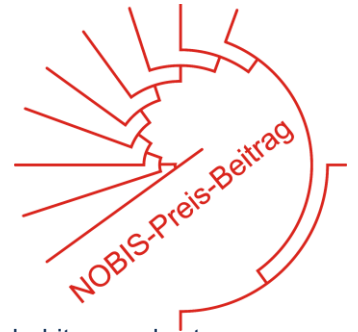
Paramecium bursaria is one of the single-celled model organisms for studying endosymbiosis among ciliates and green algae. Most strains of *P. bursaria* bear either *Chlorella variabilis* or *Micractinium conductrix* as endosymbionts. Both algal genera are unicellular green algae characterized by cup-shaped chloroplasts containing a single pyrenoid and reproduction of autospores. Due to their size and only few morphological characteristics, these green algae are very difficult to discriminate by microscopy. Moreover, it is difficult and time-consuming to cultivate the endosymbionts. Therefore, we developed a diagnostic PCR method for their identification. For comparative studies, we collected about fifty strains of *P. bursaria* from all over the world (new strains and commonly used laboratory strains). For the diagnostic PCR, we designed specific primers for *C. variabilis* and *M. conductrix* and used Chlorellaceae-specific primers for strains, in cases where the species-specific PCRs failed. The genetic variability among the endosymbionts was compared by sequencing of the ITS-2-region using different phylogenetic methods. Most strains of *P. bursaria* bear the two known species as endosymbionts. The distribution of *C. variabilis* and *M. conductrix* neither correlates to the geographical origin of *P. bursaria* nor to the syngens (subspecies) of *P. bursaria*.

The study is funded by the Austrian Science Fund (FWF): P28333-B25.

Phylogeography and morphological variation of freshwater spring snails (*Bythinella*), along a west – east transect in Austria

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The small and dioecious spring snails of the genus *Bythinella* Moquin-Tandon, 1856 inhabit groundwater and caves, but typically are endemic to cold springs. They are spread from northern Germany to Sicily and from Spain to Turkey. At the present time, more than 83 allopatric occurring species and subspecies are classified. Nevertheless, it is not certain that these previously described species are distinct since their morphologic characteristics display a wide variation.

The aim of this study is to gain insights into the phylogenetics and the morphologic variation of the central European *Bythinella* species *Bythinella austriaca* (Frauenfeld, 1857) and *Bythinella conica* (Clessin, 1910) in Austria. The research is based on an integrated approach combining genetics and morphology. For the study, 100 specimens from 25 locations along a west–east transect in Austria were examined. The molecular investigation was done by using DNA sequences of the mitochondrial cytochrome oxidase subunit I (COI) gene from the specimens to delimit the species. Additionally, the ribosomal internal transcribed spacer 2 region (ITS2) was investigated to search for further variation that is congruent to the ones from the COI analysis. The morphometrical analysis based on Landmarks was performed to compare the overall shell shape and to check for characteristics that show comparable patterns to the genetic analysis.

The molecular analysis, however, revealed a clear separation of *Bythinella conica* located in the west and *Bythinella austriaca* located in the east of Austria. Even though the separation is not a strict vertical one, it roughly follows the Hochkar mountain ridge. The morphological features are still being processed. So far, the analysis did not show a distinct pattern. Instead, these morphologic characteristics are linked to the prevailing abiotic parameters at the spring.

Exploring the use of mitogenomics as a potential solution for barcoding problems in a set of non-model flatworms

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Monogenean flatworms are the main ectoparasites of fishes. Gyrodactylidea and Dactylogyridea are probably the most species-rich monogenean taxa, with representatives that can be harmful fish pathogens, especially in intensive aquaculture conditions or after anthropogenic co-introduction outside of their native range. A limitation when studying them, however, is the small number of genetic markers available for these flatworms. The need for additional and higher-resolution markers is especially apparent when studying processes on a recent timescale, such as population genetics, phylogeography or barcoding. At the moment, a small set of established mitochondrial gene fragments constitutes the most variable markers available for such purposes, with advantages like the lack of recombination, the high rate of molecular evolution ... In addition, these mitochondrial sequences also served in flatworm systematics on a higher, macro-evolutionary scale. The high (amino acid) sequence variability within the mitochondrial genomes of monogeneans (and other flatworms) has, however, hampered the availability of universal barcoding primers, rendering even Sanger sequencing-based barcoding a challenge in these animals (Vanhove et al. 2013). With this in mind, we intend to initiate a mitogenomic approach of primer development to capture the most variable mitochondrial regions. We here present the first mitogenomic data on African monogeneans based on Illumina technology (Vanhove et al. 2018). Specimens were collected from cichlid and clariid hosts in the framework of ongoing work on invasive species in Congolese aquaculture and fisheries. Hitherto, we mostly explored questions on phylogenetic position and gene order. We will highlight some future research avenues for these understudied monogeneans and some problems keeping mitogenomic data on these animals scarce.

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Adriatic currents and the population structure of the triplefin blenny *Tripterygion tripteronotus*

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Population structure and connectivity of marine organisms are shaped by isolation by distance and/or isolation by resistance, the latter for instance determined by oceanographic barriers. In particular, ocean currents can have a large influence on planktonic larval dispersal, which is also the major form of dispersal for many large benthic animals. In the present study, we address the effects of the hydrodynamic properties of the Adriatic Sea on the population structure of a small, benthic fish, the triplefin blenny *Tripterygion tripteronotus*, a common inhabitant of the shallow rocky littoral. The Adriatic Sea is divided into three major sub-basins, the northern, central and southern Adriatic, which correspond to recognized biogeographic regions and are connected through a cyclonic basin-wide surface circulation. Seasonally changing re-circulation gyres are embedded within each of the three sub-basins and a fourth cyclonic gyre exists in the very northern part of the Adriatic between the Istrian peninsula and the Po river delta. In most previous studies, the sparse sampling of Adriatic populations did not allow to distinguish between effects of geographic distance and effects of dispersal barriers (gyre boundaries) on population structure. Here, we collected mtDNA sequences from *T. tripteronotus* populations sampled at intervals of <5–90 km along the Croatian coast and detected a significant correlation between population differentiation and the Adriatic gyres. The most pronounced differentiation occurred between the central and northern sub-basin, while weaker differentiation between the two northern gyres might be associated with shorter divergence times after post-glacial recolonization of the desiccated northern sub-basin. Lagrangian simulations of particle drift revealed that the observed structure cannot simply be explained by passive planktonic drift, but suggest additional roles for larval swimming behavior or differential settlement success. Within gyres, connectivity among populations was high and independent of geographic distance. Lacking comparable studies from the region, it currently remains open whether the detected phylogeographic pattern is shared across Adriatic species with similar ecologies and life histories.

Morphological adaptations to the use of a new nest substrate in the pollen wasp genus *Quartinia* (Masarinae, Vespidae)

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Pollen wasps are a monophyletic lineage of Vespidae, most obviously united by the provisioning of the larvae with pollen. The most species-diverse genus *Quartinia* comprises the desert dwellers within the pollen wasps and exhibits several adaptations to this habitat, as a unique nesting biology. While other pollen wasp genera nest in muddy soil or rigid sand or use these kinds of substrates to build aerial earthen cells (Gess 1996), all representatives of the genus *Quartinia* observed until now construct their nests in habitats with loose sand (Mauss & Müller 2016). A silky excretion is applied on the inner surface of the burrow, stabilizing the walls. Representatives of the genus *Quartinia* and of other pollen wasp taxa were studied comparatively to recognise the structures correlated with this behaviour. This way we could identify a hitherto unknown maxillary gland, as well as a process of the galea that likely serves the formation of the silky threads from the gland excretion. The newly found structures are key adaptations of the genus *Quartinia* that allowed it to inhabit new habitats and likely facilitated the species diversity of this genus.

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