



Programme & Abstracts

online from 22-25 February 2021

**hosted by:
Micah Dunthorn & Nadine Grauper
Eukaryotic Microbiology
University of Duisburg-Essen**

Dear DGP 2021 participants,

Welcome to the 40. Tagung der Deutschen Gesellschaft für Protozoologie.

As we presented at last year's meeting, our plans for this year were to meet at the Wyndham Garden Hotel in Mettmann, visit the Neanderthal Museum, and party at the Road Stop Restaurant. While we cannot have these personal interactions, this online meeting was designed to primarily provide an opportunity for students and junior researchers to present their recent work.

This year's meeting is free for students and junior researchers. The Deutsche Gesellschaft für Protozoologie still needs funds to provide future opportunities and meetings. So please become an active member of the society.

During the first day of the conference, Dr. Andrea Burfeid-Castellanos (Department of Phycology, University of Duisburg-Essen) will teach the Digital Microscopy Workshop. During the following days, 125 registered participants will learn from two keynote lectures, the Karl-Gottlieb-Grell Award Winner lecture, 21 contributed talks from students and junior researchers, and 24 posters from researchers at all levels.

The meeting Zoom link, as well as the password to access the posters, will be sent by email before the start of the meeting. Please download and install the Zoom application on your computer so that you can easily navigate between the main room and the breakout rooms of your choice. Breakout rooms will be available after the sessions to meet the speakers, and the posters will be presented in their own rooms during the poster session. Information about navigating breakout rooms can be found here: <https://support.zoom.us/hc/en-us/articles/115005769646-Participating-in-breakout-rooms>.

We thank Corey Holt (University of British Columbia) for designing the meeting's logo.

kind regards,
DGP 2021 Organizing Team

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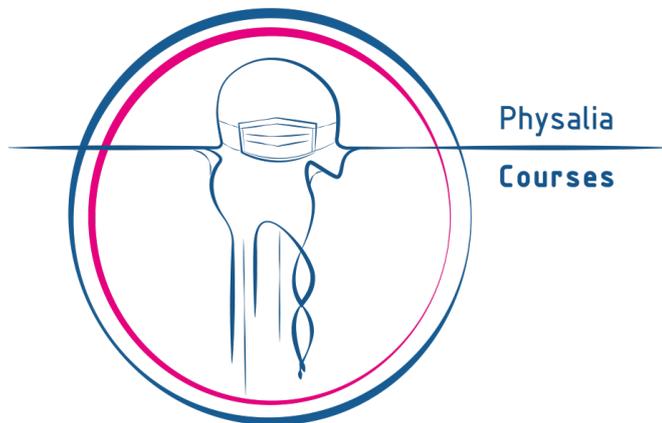
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Funders

Prizes for best talks and posters by students and junior researchers are provided by:



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Programme Overview

	Monday 22 February	Tuesday 23 February	Wednesday 24 February	Thursday 25 February
08:50-09:00		welcome address		
09:00-9:45		keynote lecture: Sonja Rueckert	Karl-Gottlieb-Grell award lecture: Quentin Blandenier	keynote lecture: Peter Vďačný
9:45-10:30		session 1: Amoebae	session 3: Ecology & Feeding	session 5: Genomics & Transcriptomics
10:30-11:00	Digital Microscopy Workshop	coffee break / breakout rooms to meet speakers	coffee break / breakout rooms to meet speakers	coffee break / breakout rooms to meet speakers
11:00-12:30		session 2: Metabarcoding & Metagenomics	session 4: Posters breakout rooms to meet presenters	session 6: Ecology & Choanoflagellates & Ciliates
12:30-13:00		coffee break / breakout rooms to meet speakers		coffee break / breakout rooms to meet speakers
14:00-16:00				membership meeting & talk/poster awards

Meeting Programme

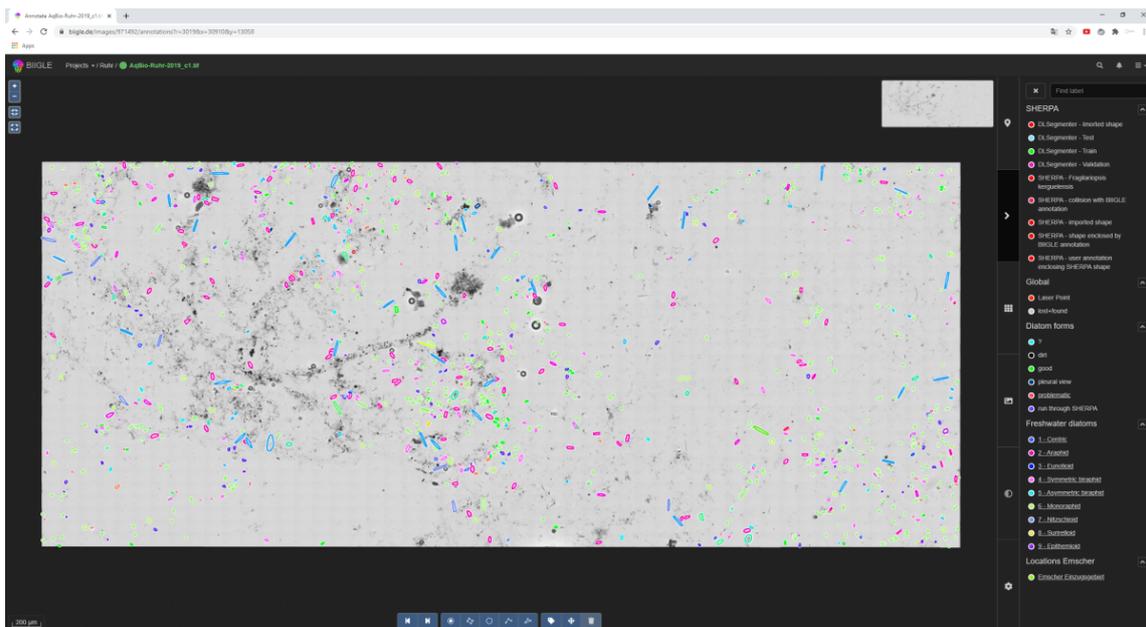
Monday, 22 February

Digital Microscopy Workshop

10:00-14:00

Andrea Burfeid-Castellanos (University of Duisburg-Essen, Germany)

The focus of this workshop will be on digital light microscopy, based on taxonomy and ecology of diatoms. Using your own computer from the comfort of your home you will familiarize yourself with Biigle 2.0 web-based software, make use of the measurement and annotation tools to identify diatoms from the Ruhr and make two collaborative inventories. You will compare and harmonize identifications using the LARGO* tool. Finally, the resulting and curated inventories will be downloaded to show the process from start to finish. The workshop schedule contains introducing lectures, the annotation of 1-2 diatom slides and a final discussion of the use and future of digital microscopy in both taxonomy and ecology of microscopic organisms. Questions about own images are welcome. This online workshop requires the use of a computer. No further software is necessary. Two digital slides will be provided.



Tuesday, 23 February

08:50-09:00 **Welcome address**

Keynote Lecture

09:00-09:45 **Sonja Rueckert** (Edinburgh Napier University, United Kingdom)
Gregarines on the symbiotic spectrum: a glimpse into the evolution of parasitism in the Apicomplexa

Session 1: Amoebae

09:45-10:00 **Sophie Erb** (University of Neuchâtel, Switzerland)
Use of spatially aware models in palaeoecology: application to water table depth reconstruction using testate amoebae in peatlands

10:00-10:15 **Rubén González-Miguéns** (Real Jardín Botánico de Madrid, Spain)
Solving the morphology puzzle by an integrative taxonomy in genus Arcella (Arcellinida, Lobosea, Amoebozoa)

10:15-10:30 **Carmen Soler-Zamora** (Real Jardín Botánico de Madrid, Spain)
Arcellinida testate amoebae as climate miner's canaries in Southern Spain

10:30-11:00 **coffee break / breakout rooms to meet speakers**

Session 2: Metabarcoding & Metagenomics

- 11:00-11:15 **Christopher A. Hempel** (University of Guelph, Canada)
Comparing total RNA sequencing and metagenomics pipelines for multi-domain taxonomic profiling: implications for ecological assessments
- 11:15-11:30 **Alexandra Rybarski** (University of Cologne, Germany)
High diversity and the adaptation of aquatic protists to extreme conditions in the Atacama Desert
- 11:30-11:45 **Manon Hohlfeld** (University of Cologne, Germany)
Vertical distribution patterns of benthic protists in the deep sea influenced by sedimented macroalgae
- 11:45-12:00 **Maximilian H. Ganser** (University of Salzburg, Austria)
Genetic diversity in marine planktonic ciliates (Ciliophora, Alveolata) suggests distinct geographical patterns - data from Chinese and European coastal waters
- 12:00-12:15 **Estelle P. Bruni** (University of Neuchâtel, Switzerland)
Seasonal variation of soil protists along elevation gradients in the Alps (Switzerland) and the Sierra Nevada (Spain)
- 12:15-12:30 **Shuyin Huang** (University of the Ryukyus, Japan)
Soil protist beta diversity patterns and their drivers along an elevation gradient on Mt. Taisetsu, Hokkaido, Japan
- 12:30-13:00 **breakout rooms to meet speakers**

Wednesday, 24 February

Karl-Gottlieb-Grell Award Winner Lecture

09:00-09:45 **Quentin Blandenier** (University of Neuchâtel, Neuchâtel, Switzerland)
Karl-Gottlieb-Grell Award winner for outstanding PhD dissertation in protistology
Exploration and characterization of Amoebozoa diversity and investigation of their diversity patterns at regional and global scales

Session 3: Ecology & Feeding

09:45-10:00 **Nathalie Amacker** (Utrecht University, The Netherlands)
Describing protist feeding patterns to assess their ecological functions

10:00-10:15 **Jannika Moyer** (University of Cologne, Germany)
Revealing the role of carbohydrate-active enzymes in microbial protoplast feeders by transcriptome-informed cell biology

10:15-10:30 **Mario Aigner** (University of Innsbruck, Austria)
Feeding of fish larvae on ciliates

10:30-11:00 **coffee break / breakout rooms to meet speakers**

Session 4: Posters

11:00-13:00 **breakout rooms to meet individual poster presenters**

Thursday, 25 February

Keynote Lecture

09:00-09:45 **Peter Vďačný** (Comenius University, Slovakia)
Phylogeny of the ciliate SAL supercluster (Alveolata: Ciliophora)

Session 5: Genomics & Transcriptomics

09:45-10:00 **Agnes K. M. Weiner** (Smith College, United States of America)
Using single-cell transcriptomics to study genome traits, population genetics and symbioses in Arcellinida

10:00-10:15 **Jennifer V. Gerbracht** (University of Cologne, Germany)
De novo assembly and computational analysis of two viridiraptorid transcriptomes highlight the potential of free-living protists as a resource for enzyme discovery

10:15-10:30 **Andreas Suthaus** (University of Cologne, Germany)
Expanding knowledge on the biodiversity, ecological adaptations and distribution of vampire amoebae (Vampyrellida, Rhizaria)

10:30-11:00 **coffee break / breakout rooms to meet speakers**

Session 6: Ecology & Choanoflagellates & Ciliates

- 11:00-11:15 **Megan Gross** (University of Kaiserslautern, Germany)
Effects of different simulated upwelling intensities on protistan plankton structures in the Peruvian Humboldt current system
- 11:15-11:30 **Sven Katzenmeier** (University of Kaiserslautern, Germany)
Community response of protistan plankton and their mediated carbon flow to eddies
- 11:30-11:45 **Sabine Schiwitza** (University of Cologne, Germany)
Underestimated species richness of nudiform choanoflagellates?
- 11:45-12:00 **Maksim Melekhin** (Saint Petersburg State University, Russia)
Inheritance of mating types in Paramecium calkinsi
- 12:00-12:15 **Zhishuai Qu** (University of Kaiserslautern, Germany)
Gastronautidae Deroux, 1994 and Trithigmostoma Jankowski, 1967: evolutionary links among cyrtophorian ciliates (Protista, Ciliophora, Phyllopharyngea)
- 12:15-12:30 **Eubomír Rajter** (University of Duisburg-Essen, Germany)
Ciliate SSU-rRNA reference alignments for phylogenetic placement
- 12:30-13:00 **breakout rooms to meet speakers**

Membership Meeting & Talk/Poster Awards

14:00-16:00

Invited Talks

Gregarines on the symbiotic spectrum: a glimpse into the evolution of parasitism in the Apicomplexa

Sonja Rueckert (Animal and Plant Science Research Group, Biosciences, Edinburgh Napier University, Edinburgh, United Kingdom)

The phylum Apicomplexa is known to contain only obligate parasites, which is probably true for many of the more than 6.000 known species. Gregarine apicomplexans seem to represent an important transition step from closely related free-living photosynthetic (e.g. *Chromera*, *Vitrella*), or predatory (e.g. *Colpodella*) lineages to obligate, intracellular parasites (e.g. *Plasmodium*, *Toxoplasma*). Even though they are always referred to as parasites, it is currently disputed what lifestyle the gregarines have due to their unique position within the apicomplexans, which will be discussed with a view on the past, present and future.

Phylogeny of the ciliate SAL supercluster (Alveolata: Ciliophora)

Peter Vďačný (Department of Zoology, Comenius University, Bratislava, Slovakia)

Ciliates represent a highly diverse phylum comprising a dozen of major lineages that altogether account for about 8,000 to 40,000 species. Although the main ciliate clades are morphologically and genetically well-defined, their relationships are left almost completely unresolved in 18S rRNA gene phylogenies. The first transcriptome analyses united three morphologically and ecologically highly dissimilar ciliate classes, Spirotrichea, Armophorea, and Litostomatea, into the so-called SAL supercluster. Subsequent phylogenomic inferences and 18S rRNA gene phylogenies suggested that five species-poor groups might belong to the SAL supercluster as well: cariacotrichids, odontostomatids, caenomorphids, muranothrichids, and parablepharismids. The inclusion of these orphan lineages caused chaos in the SAL classification, and ultrastructural, conjugation, and ontogenetic data, which could cast some light on their classification, are still very limited. Moreover, the available ontogenetic and conjugation data about the three main and species-rich SAL groups conflict with multi-gene trees. Either many specific ultrastructural, ontogenetic, and conjugation features were present in the common ancestor of the SAL supercluster and lost in the class Spirotrichea, or multiple outstanding features evolved independently in the classes Armophorea and Litostomatea. During the keynote lecture, the morphology, ontogenesis, and conjugation of the SAL supercluster will be introduced and discussed in the context of molecular phylogenies, and some future directions in the SAL classification framework will be proposed.

Karl-Gottlieb-Grell Award winner (for outstanding PhD dissertation in protistology)

Exploration and characterization of Amoebozoa diversity and investigation of their diversity patterns at regional and global scales

Quentin Blandenier (Laboratory of Soil Biodiversity, Institute of Biology, University of Neuchâtel, Neuchâtel, Switzerland; Real Jardín Botánico, Madrid, Spain)

The world eukaryotic diversity is dominated by (mostly) single-celled organisms referred to as protists. Among them, the Amoebozoa are one of the most numerous, diverse and characteristic groups in soil, thus playing important roles in ecosystem functioning. However, their study has been impeded by the difficulty in detecting them and the lack of stable morphological traits in most groups. Nevertheless, some amoebozoans such as the Hyalospheniformes (Arcellinida) are characterized by a self-constructed test (i.e. shell) which facilitates their identification, and are then considered as a suitable model group for investigating diversity patterns of repartition. The recent development of DNA barcoding has helped considerably taxonomic identification, whereas metabarcoding has allowed revealing microbial community composition without observational and cultivation biases. These methods have proved efficient for several microbial groups, but only few studies have been designed for Amoebozoa and available protocols are still rather scarce. The aims of my thesis were then to 1) improve and develop molecular methods to study the amoebozoan diversity and ecology, 2) estimate their taxonomic and functional diversity in the soil, 3) improve the taxonomic and phylogenetic frame for this diversity in order to build a sound basis for further research and 4) characterize the ecological drivers which are likely to influence microbial diversity at local and global scales. We first identified a new molecular marker to survey arcellinids taxa, which proved to be efficient for discriminating closely-related taxa and simultaneously investigating deep relationships among distant taxa. In addition, we also adapted a metabarcoding protocol with specific COI primers to survey the diversity within the genus *Nebela* at a fine taxonomical resolution. Then, we isolated, cultivated and described the first member of a deep-branching environmental clade of Amoebozoa. This amoeba, one of the smallest amoeboid species described, presents a unique life cycle with an alternation of phagotrophic active trophozoites and osmotrophic fungi-like ramifications. Its presence has been pervasively reported in many soil metabarcoding studies, but this organism had never been characterized. By contrast, Hyalospheniformes are known since the works of Ehrenberg in the 19th century. However, their diversity at the species level remains poorly characterized. Indeed, we showed that the iconic testate amoeba species *Nebela militaris* did not belong to genus *Nebela* but branched as a separate entity in the Hyalospheniformes tree. Therefore, we erected the new genus *Alabasta* for this species. In addition, we demonstrated that Hyalospheniformes diversity had been greatly underestimated. Indeed, our morphological and molecular results have revealed the presence for several species within the genera *Apodera*, *Alocodera* and *Padaungiella*. This new diversity has implications on microbial biogeography as *Apodera* *vas* and *Alocodera* *cockaynei* were previously considered as two non-cosmopolite species with very broad geographical ranges and large ecological tolerances. Furthermore, we showed that the situation was

far more complex, suggesting the existence of narrow local endemisms and ecological specialists, similarly to genera *Hyalosphenia* and *Nebela*. Finally, we explored the diversity patterns of the genus *Nebela* along an elevation gradient. We observed a decrease of abundance and diversity in high elevation corresponding to a typical mid-domain effect. Our study also revealed several unknown phylotypes restricted to the higher elevation that seemed to present competitive exclusion with the generalist taxa from lower elevation. In conclusion, this thesis highlights that molecular methods associated to robust morphological observations are efficient to reveal and describe the diversity of Amoebozoa. Furthermore, these microbial organisms display biogeographical and macroecological patterns similarly to animals, plants and fungi, when all groups are studied at the same taxonomical rank, i.e. species level.

Contributed Talks

Feeding of fish larvae on ciliates

Mario Aigner (Research Department for Limnology, University of Innsbruck, Austria), **Josef Wanzenböck** (Research Department for Limnology, University of Innsbruck, Austria), **Ulrike Scheffel** (Research Department for Limnology, University of Innsbruck, Austria), **Bettina Sonntag** (Research Department for Limnology, University of Innsbruck, Austria)

Fish larvae are known to feed on bulk 'plankton' during and after yolk sac resorption. In order to test if ciliates were one of their first food sources, we investigated whether predacious *Coregonus* fish larvae were able to feed on widespread ciliates such as *Paramecium bursaria* and *Coleps hirtus*. Fish larvae of an age of 5 - 12 (still partly having their yolk sac) and 26 - 75 days (yolk bag already completely resorbed) were experimentally tested. Therefore over 8 h, the fish larvae were fed with ciliate densities up to 20 ind. ml⁻¹ in triplicates against a control. Lugol-stained ciliates were counted during the experiments to investigate the feeding impact by the fish larvae. Additionally, under the epifluorescence microscope, the direct uptake of the protists by the fish larvae was verified from DAPI-stained ciliates by checking their presence both in the whole fish larva and after dissection of the intestine. Fish larvae of both ages consumed a significant proportion of *P. bursaria* but not *C. hirtus*.

Describing protist feeding patterns to assess their ecological functions

Nathalie Amacker (Environmental Biology, Utrecht University, Utrecht, The Netherlands), Jie Hu (Environmental Biology, Utrecht University, Utrecht, The Netherlands), Zhilei Gao (Environmental Biology, Utrecht University, Utrecht, The Netherlands), George Kowalchuk (Environmental Biology, Utrecht University, Utrecht, The Netherlands) Alexandre Jousset (Environmental Biology, Utrecht University, Utrecht, The Netherlands) Stefan Geisen (Wageningen Research and University, Wageningen, The Netherlands)

Microbes are recognized as essential determinants of plant health and growth. Many bacteria and fungi with plant-beneficial traits have been identified as promising alternatives for agrochemicals, but applications have been only marginally successful. To tackle challenges of this research line, we advocate to include another group of microbial organisms: the free-living heterotrophic protists. As major consumers of plant root-associated bacteria, protists strongly impact their community composition and activity. As such, protists could offer new opportunities to engineer the plant microbiome. We still need, however, to understand how the predation by various protist species affects bacterial communities. Indeed, considering the huge genetic diversity of protists, we expect an equivalently big diversity in their impact as predators. To investigate the feeding patterns of protists, we selected eight well-characterized isolates covering major phylogenetic lineages found in the rhizosphere, including amoeboid and flagellate morphotypes. We studied their ability to grow on twenty rhizobacterial isolates displaying a range of plant-beneficial traits via a plate assay. We calculated feeding related variables for each protist isolate in order to describe and compare their feeding pattern. We hypothesised that protist isolates with similar feeding range would induce similar changes in more complex bacterial communities. We therefore investigated in a soil microcosm how bacterial community composition changed when exposed to these same protists. While each protist species showed a certain degree of specificity in their feeding range and effect on the soil bacterial community composition, some protist isolates showed similar feeding range reflected in both the plate assay and the soil microcosm. The two *Cercomonas* sp., for instance, grouped together with the most similar feeding range and induced significant increase/decrease of similar bacterial genera in the soil. We argue that identifying the feeding range of protist isolates is essential to assess their ecological importance and potential application.

Seasonal variation of soil protists along elevation gradients in the Alps (Switzerland) and the Sierra Nevada (Spain)

Estelle P. Bruni (Laboratory of Soil Biodiversity, Faculty of Science, University of Neuchâtel, Neuchâtel, Switzerland), Juan Lorite (Department of Botany, University of Granada, Granada, Spain), Julio Peñas (Department of Botany, University of Granada, Granada, Spain), Pascal Vittoz (Institute of Earth Surface Dynamics, University of Lausanne, Lausanne, Switzerland) Guillaume Lentendu (Laboratory of Soil Biodiversity, Faculty of Science, University of Neuchâtel, Neuchâtel, Switzerland), Edward A.D. Mitchell (Laboratory of Soil Biodiversity, Faculty of Science, University of Neuchâtel, Neuchâtel Switzerland)

Despite playing essential roles in soil ecosystems, little is known about the temporal variability of soil micro-eukaryotes. However, when carrying environmental DNA surveys along climatic gradients (elevation or latitudinal), seasonal dynamics may bias the geographical patterns as all sites will not be at the same phenological stage. Repeated sampling campaigns across seasons would allow overcoming this bias but this is often logistically or financially challenging. As part of a study of soil protists along elevation gradients at the global scale, we therefore aimed to assess the magnitude of this potential bias. We compared the temporal pattern of soil protist communities along five elevation gradients in two distinct mountain regions, the Alps (Switzerland) and the Sierra Nevada (Spain), using V4 18S rDNA HTS of Eukaryotes. Bulk soil samples were collected in contrasted habitats (i.e., forests and open grasslands). Each plot was sampled twice (i.e., spring and summer). Additionally, bioclimatic variables and basic soil characteristics were measured in order to test which factors best explained the structure of soil protists community. Soil protist alpha diversity was significantly higher in the Alps than in the Sierra Nevada in both seasons. Beta diversity analyses showed that habitat type and geographic region induced significant changes in community composition in contrary to seasonality. Our data suggest that soil protists diversity and community patterns vary more in relation to habitat heterogeneity, macroclimate, and likely biogeographical patterns than season and, thus, that a single sampling campaign will suffice to cover their diversity.

Use of spatially aware models in palaeoecology: application to water table depth reconstruction using testate amoebae in peatlands

Sophie Erb (Laboratory of Soil Biodiversity, University of Neuchâtel, Neuchâtel, Switzerland; Institute of Statistics, University of Neuchâtel, Neuchâtel, Switzerland), Matthieu Mulot (Laboratory of Soil Biodiversity, University of Neuchâtel, Neuchâtel, Switzerland), Alina Matei (Institute of Statistics, University of Neuchâtel, Neuchâtel, Switzerland), Edward Mitchell (Laboratory of Soil Biodiversity, University of Neuchâtel, Neuchâtel, Switzerland; Botanical Garden of Neuchâtel, Neuchâtel, Switzerland)

Peatlands are ecosystems characterized by a high water table, close to the surface, inducing a low decomposition rate and thus accumulation of dead organic matter (carbon sink function). Fluctuations of the water table affect this carbon sink function and also influence the composition of microbial communities, among which testate amoebae (TA). Therefore it is possible, using methods called ‘transfer functions’, to model the relationship between TA community composition and Water Table Depth (WTD). As TA shells are preserved in the peat after the organism’s death, one can extract TA from peat, and then infer past WTD from fossil TA communities using transfer functions. However, transfer functions developed over the last decades rely on assumptions that are not always valid. The emergence of new relevant mathematical models and additional knowledge on TA distribution and biogeography led us to investigate more appropriate methods. Thus, we tested basic general models such as Multiple Linear Regression (MLR) and Lasso regression and more advanced models, which take into account the spatial distribution, namely Geographically Weighted Regression (GWR) and Geographically Weighted Lasso (GWL). We applied these models on a large compiled Pan-European dataset previously used for reconstruction with classical methods by Amesbury et al. 2016 and compared the performance of our models with theirs. Results are significantly better with our models, even with the basic MLR, which is surprising. Also, GWR and GWL were applied with two types of spatial distance: geographical and bioclimatic. We expected bioclimatic distance to provide better information about the (dis)similarity of sites and to allow better predictions, but the models with geographical distance were actually the most efficient overall. These results suggest that taking spatial distribution into account might improve models in TA-based (and more broadly protists-based) ecological study. Finally, it calls for bringing more modern mathematical tools in ecology as substantial improvements can be expected.

Genetic diversity in marine planktonic ciliates (Ciliophora, Alveolata) suggests distinct geographical patterns - data from Chinese and European coastal waters

Maximilian H. Ganser (Department of Biosciences, University of Salzburg, Salzburg, Austria), Dominik Forster (Department of Ecology, Technische Universität Kaiserslautern, Kaiserslautern, Germany), Thorsten Stoeck (Department of Ecology, Technische Universität Kaiserslautern, Kaiserslautern, Germany) Weiwei Liu (South China Sea Institute of Oceanology, Chinese Academy of Sciences, Guangzhou, China) Xiaofeng Lin (College of the Environment and Ecology, Xiamen University, Xiamen, China), Sabine Agatha (Department of Biosciences, University of Salzburg, Salzburg, Austria)

Unravelling geographic distribution patterns of planktonic protists is a central goal in marine microbial ecology. Using a novel combination of recently developed phylogenetic and network analyses on a V4 18S rDNA metabarcoding dataset, the genetic diversity of marine planktonic ciliate communities in Chinese and European coastal waters was analysed. This approach provides an unprecedented perspective accomplished by a very fine resolution down to single nucleotides within operational taxonomic units (Swarm OTUs). The majority of OTUs (87%) exclusively contained sequences of either Chinese or European origin, whereas OTUs containing sequences from both regions were those with the most (84%) reads. Phylogenetic analyses of OTUs revealed genetically distinct Chinese and European clades within the same taxa that were further substantiated by signature nucleotides (= identical nucleotide polymorphisms). Network analyses uncovered further significant geographic patterns in OTUs comprised of sequences from both regions. Within these OTUs, sequences preferably clustered together with sequences from the same region indicating an ongoing speciation process. Our detailed analyses propose geographic distribution patterns in protists that might be the result of historic and ongoing effective dispersal. The discovery of these patterns generated on different time scales suggests that a cosmopolitan distribution in marine planktonic ciliates is much rarer than previously postulated. The study was financially supported by the FWF project I3268 given to SA and the NSFC project 3161101359 given to XL. DF was supported by a postdoctoral research grant of the Carl Zeiss Foundation.

De novo assembly and computational analysis of two viridiraptorid transcriptomes highlight the potential of free-living protists as a resource for enzyme discovery

Jennifer V. Gerbracht (Institute for Zoology, University of Cologne, Cologne, Germany), Sebastian Hess (Institute for Zoology, University of Cologne, Cologne, Germany)

Across the tree of life, for only a fraction of species genomic or transcriptomic data are available. The exploration of uncharacterised genomes leads to the discovery of novel genes and proteins as well as extending the knowledge about the fundamental biology, ecology and evolution of species. A lack of high-throughput genetic data is particularly pronounced for microbial eukaryotes or protists. Here, we present de novo transcriptome assemblies generated from short read RNA-seq data of the algivorous protoplast feeders *Orciraptor agilis* and *Viridiraptor invadens* (Viridiraptoridae, Cercozoa). In absence of reference genomes, we employed a detailed workflow for generating high-quality de novo transcriptomes and compared the performance of different assembly software. The specialised feeding strategy of viridiraptorid flagellates involves the recognition and local dissolution of the algal cell wall. Performing comparative transcriptomics across different life history stages of the viridiraptorids yielded functional clusters of differentially expressed genes. Among these we have identified carbohydrate-active enzymes (CAZymes) which could potentially be involved in binding and attacking the prey. We further identify homologues of these CAZymes in a recently published database of diverse eukaryotic high-throughput data to assess the evolutionary patterns of certain enzyme families. This analysis reveals that fungal and bacterial enzymes have been relatively well characterised, while information about the presence and diversity of such enzymes in protists is extremely scarce. Furthermore, we demonstrate that the CAZyme repertoire of *Orciraptor agilis* strongly differs from that of its closest known relative, *Viridiraptor invadens*. Our findings emphasise the potential of protists for enzyme discovery and highlight the knowledge gap that exists regarding the diversity of CAZymes. Bridging this gap could give valuable insights into the feeding ecology of protists as well as facilitate our understanding of biomass degradation, including potential biotechnological applications.

Solving the morphology puzzle by an integrative taxonomy in genus *Arcella* (Arcellinida, Lobosea, Amoebozoa)

Rubén González-Miguéns (Department of Mycology, Real Jardín Botánico (RJB-CSIC), Madrid, Spain), Carmen Soler-Zamora (Department of Mycology, Real Jardín Botánico (RJB-CSIC), Madrid, Spain), Milcho Todorov (Institute of Biodiversity and Ecosystem Research, Bulgarian Academy of Sciences, Sofia, Bulgaria), Mar Villar-de Pablo (Department of Mycology, Real Jardín Botánico (RJB-CSIC), Madrid, Spain) Antonio Guillén (independent researcher, Spain), Enrique Lara (Department of Mycology, Real Jardín Botánico (RJB-CSIC), Madrid, Spain)

The characterization and classification of the biodiversity into evolutionary coherent units is essential in biology. Species are the basic taxonomic unit on which all disciplines in life sciences are based upon; however, they are often matter for discussion, especially in protists where a unified consensus on species concepts is still lacking. To correctly delimit a species, it is necessary to characterize a group of organisms with an independent evolutionary history which can be characterized by integrating morphological, ecological, biogeographical and phylogenetic information. In Arcellinida (lobose testate amoebae), and especially within suborder Hyalospheniformes, this integrative approach is currently revealing high levels of unknown diversity. Here, we focused on genus *Arcella*, a group of Arcellinida distributed in all continents and almost all ecosystems. They have been extensively used as bio-indicators for a wide array of applications that range from palaeoecology to the functioning of wastewater-treatment plants. However, species delimitation in *Arcella* is still based mostly on gross test morphology. To solve this issue, we examined individuals belong to 28 taxa using an integrative approach based on cytochrome oxidase subunit I (COI) barcoding, morphometric of the test analysis and ecology information to infer the evolutionary history of lineages and delimit species. We show that the evolutionary history of genus *Arcella* is characterized by pseudocryptic speciation, thus implying a revision of the group and the description of 8 new species.

Effects of different simulated upwelling intensities on protistan plankton structures in the Peruvian Humboldt current system

Megan Gross (Ecology Group, Technische Universität Kaiserslautern, Kaiserslautern, Germany), **Sven Katzenmeier** (Ecology Group, Technische Universität Kaiserslautern, Kaiserslautern, Germany), the CUSCO consortium (coordinated by Ulf Riebesell, Geomar, Kiel, Germany), **Thorsten Stoeck** (Ecology Group, Technische Universität Kaiserslautern, Kaiserslautern, Germany)

Eastern Boundary Upwelling Systems (EBUS) are among the most productive ocean ecosystems. As such, they are of fundamental importance to secure global food supply. Climate change stressors are affecting EBUS in multiple ways, and models are predicting dramatic changes in upwelling intensities resulting from changes in wind-patterns and thermal ocean stratification. Among the global EBUS, the Humboldt Upwelling System (HUS) is the largest and, in terms of fish harvest, the most productive and economically most important one. This suggests an extraordinarily high trophic transfer efficiency in the HUS. Protistan plankton play a crucial role as a major component in the trophic transfer of carbon to higher trophic levels, including fish larvae. Thereby, the nutritional value and transfer efficiency strongly depends on the taxonomic composition of protistan plankton communities. In ocean-exposed mesocosm experiments off the Peruvian coasts, we simulated an increase in upwelling intensities (15% and 45% increase compared to the current upwelling intensity). We then took time-series samples to monitor changes in protistan plankton communities. The time-series mimicked a successive offshore transport of the upwelled nutrients and the evolution of protistan plankton communities during this offshore transport. In our presentation we will discuss the obtained results and possible consequences for the trophic transfer efficiency in the climate change-stressed HUS and how our results may contribute to a better understanding of the mechanistic links between upwelling intensity and ecosystem productivity and their sensitivity to climate change eastern boundary upwelling systems.

Comparing total RNA sequencing and metagenomics pipelines for multi-domain taxonomic profiling: implications for ecological assessments

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Ecological assessments are necessary to evaluate the status of our deteriorating ecosystems, however, assessment methods traditionally omit most microbes because unicellular organisms are challenging to identify. This omission is not ideal, as microbes might be better indicators for changes in environmental conditions than taxa traditionally used. DNA- and RNA-based techniques are increasingly applied for ecological assessments to overcome this challenge but require more testing and optimization. In this study, we compare metagenomics and total RNA sequencing (total RNA-Seq) for their taxonomic profiling performance for microbial communities. We applied both techniques on two sample sets, 1) a commercially available microbial mock community consisting of eight bacterial and two eukaryotic species, and 2) a display tank water sample. We processed the data using 1,532 bioinformatics pipelines and evaluated each workflow, i.e., the combination of sample type (metagenomics or total RNA-Seq) and pipeline, in terms of their accuracy and precision. This talk will showcase preliminary results and highlight differences in workflow performances. A recommended workflow to maximize taxonomic profiling accuracy of microbial communities will also be presented.

Vertical distribution patterns of benthic protists in the deep sea influenced by sedimented macroalgae

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Due to the absence of light, deep-sea ecosystems strongly depend on the production and sedimentation of organic material from surface waters. As this carbon flux decreases with depth, the deep sea is assumed to be an oligotrophic environment. In recent years, this paradigm of a food-poor environment was drawn into question due to relatively high records of sedimented macroalgae (e.g. *Sargassum*) which were found to represent an important source of carbon sequestered to deep-sea ecosystems. However, it is not yet known how this carbon source is utilized by deep-sea communities and how it influences the composition and distribution of protist communities in this uncharted environment. In the present study, we investigated the structure and dispersal of benthic protist communities from areas in the North Atlantic Ocean and the Caribbean Sea with high and low impact of sedimented macroalgae on the deep-sea floor. Using high-throughput sequencing of the V9 SSU rDNA, we focused especially on small (1 cm) vertical distribution patterns by analyzing four different sediment depth layers. Protist community structure was found to vary along the vertical sediment depth gradient and showed different patterns at stations with and without the presence of sedimented macroalgae. This points to the presence of vertical distribution patterns of protists, which seem to be influenced by the sedimentation of macroalgae. Only 4-11% of OTUs were shared between all sediment depth layers, whereas the majority of OTUs was unique to a single sediment layer indicating that sediment depth might be a factor shaping protist community composition in the deep

Soil protist beta diversity patterns and their drivers along an elevation gradient on Mt. Taisetsu, Hokkaido, Japan

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Describing biodiversity patterns and understanding their drivers at regional to global scales are major topics in biogeography and evolutionary ecology. Elevation gradients represent ideal natural experiments to address these questions. Biogeographical patterns have been extensively studied mostly for animals and plants, and, thanks to recent development in high throughput sequencing of environmental DNA, increasingly for microorganisms. However, among microbial groups the focus has been primarily on bacteria and fungi and much less on protists despite their ecological and evolutionary importance. Using metabarcoding of the V4 region of the 18S rRNA gene, we investigated the soil protist beta diversity pattern in relation to edaphic variables and plant community composition along an elevation gradient ranging from 500 to 2300m on Mountain Taisetsu, Hokkaido, Japan. Beta diversity partitioning showed that taxonomic and phylogenetic beta diversity were primarily driven by species and lineage replacement. Elevation, edaphic variables and plant community composition together explained the majority of the beta diversity variation with elevation being the major driver. Plant community composition had a greater contribution to beta diversity pattern as compare to edaphic variables suggesting a predominant role of biotic interaction. Our study highlighted the relative importance of elevation, plant composition and soil properties in shaping the beta diversity pattern of soil protists.

Community response of protistan plankton and their mediated carbon flow to eddies

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The effect of oceanic mesoscale cyclonic eddies in an eastern boundary upwelling system on protistan community structures was examined using V9 18S rRNA gene amplicons. Therefore, we collected samples along a distance gradient from the centre of a cyclonic eddy towards the eddy periphery. At each transect station we sampled three depths (deep chlorophyll maximum DCM, end of photic zone EPZ and oxygen minimum zone OMZ). Additional stations outside the eddy were sampled as reference. We also conducted grazing experiments in samples of the DCM to determine the carbon transfer from bacteria to phagotrophic protists. Alpha diversity of protistan communities was lowest in the DCM and increased with depth for all sampling stations. The protist community structure also changed along the horizontal transect and the vertical depth gradients. Dinoflagellates were the most abundant (in terms of sequence amplicons) in all three depths. In the DCM Stramenopiles were the second most abundant taxa which are superseded by Rhizaria in the EPZ and OMZ. Bacterial uptake rates of the protistan communities were six times higher within the eddy compared to the reference site. The top-down control of protists on bacteria accounted for a bacterial turnover rate of ca. 20% of the bacterial standing stock (BSS) within the eddy. Our results suggest a high importance of ocean eddies for protistan community structures and carbon transfer within the microbial loop. In subsequent steps, this carbon is available for higher trophic levels, pinpointing the relevance of eddies for the ocean carbon pump and to sustain higher trophic levels, including fish.

Inheritance of mating types in *Paramecium calkinsi*

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The system of mating types (MT) has appeared multiple times in evolution of eukaryotes. MT form a sexual compatibility system in ciliates which is used to prevent self-fertilization and to increase genetic exchange within a population. Various kinds of MT systems, different numbers of MT, and diverse mating type genes are present in different groups of Ciliophora. Ciliates are a perfect example for MT investigation because they easily proceed through mating under laboratory conditions. However, mechanisms of mating type determination and inheritance are highly diverse even among closely related species. *Paramecium* (Oligohymenophorea) is the best-known model ciliate. MT determination and expression patterns for some species were described recently (Singh et al. 2014; Orias et al. 2017; Sawka-Gadek et al. 2020). For instance, three different types of MT inheritance (mendelian, maternal, and stochastic) are known in 16 sibling species of the *P. aurelia* complex. *Paramecium bursaria* and *P. putrinum* have a system of multiple MT. At the same time, the MT systems of many *Paramecium* species have not been sufficiently studied yet. The less known group - the species of *Cypriostomum* subgenus. *Paramecium polycaryum* was even thought to be incapable of mating, while data on other species remain fragmentary. We manage to figure out the mode of MT inheritance for *Paramecium calkinsi*. We established the synchronization protocol allowing to obtain sexually reactive *P. calkinsi* cultures. The cells become capable of mating after mild starvation at 25°C. Several rounds of conjugation revealed that *P. calkinsi* is characterized by maternally inherited determination of MT. It is the first case of maternal inheritance outside of *Paramecium* subgenus. This type of inheritance was previously described only for some species of the *P. aurelia* complex which are not closely related to *P. calkinsi*. Thus, our finding is important to understand the MT evolution within *Paramecium* genus. Supported by RFBR 19-04-00710a.

Revealing the role of carbohydrate-active enzymes in microbial protoplast feeders by transcriptome-informed cell biology

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Orciraptor agilis (Viridiraptoridae, Cercozoa) is a heterotrophic amoeboflagellate that feeds on dead cells of diverse freshwater algae, thereby acting as a microbial scavenger. It attaches to the prey cell, perforates the cell wall, and subsequently extracts the protoplast. Although its specialized lifestyle has been well described, the molecular basis of its complex behavior remains largely unknown. On the basis of transcriptome data from a differential expression analysis, we conduct transcriptome-informed cell biology to uncover some of the molecular players involved in prey recognition, attachment and cell wall dissolution. The transcriptomic data revealed a large set of lytic carbohydrate-active enzymes (including putative cellulases and chitinases) as well as binding proteins. Some of the found candidates were highly upregulated upon contact with the prey cells and their predicted protein structure suggests an extracellular localization. We studied some of these proteins by heterologous expression and *in vitro* activity assays, and made first attempts to localize them in *Orciraptor* cells with immunofluorescence microscopy. In addition, we will present unexpected findings about amorphous material, which is deposited by *Orciraptor* on the algal cell wall and might act as ‘molecular adaptor’ during attack.

Gastronautidae Deroux, 1994 and *Trithigmostoma* Jankowski, 1967: evolutionary links among cyrtophorian ciliates (Protista, Ciliophora, Phyllopharyngea)

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Studies on cyrtophorian ciliates (Cyrtophorina) have accumulated much knowledge on morphological taxonomy and molecular phylogeny, and the general classification and phylogenetic relationships of most families have thereby been revealed. However, the phylogenetic position of the family Gastronautidae Deroux, 1994 remains uncertain. This is due to the presence of specialized characteristics (in particular, a circumoral kinety in a closed circle), and most importantly, a lack of molecular data of this family. In addition, *Trithigmostoma* Jankowski, 1967 holds a special position among genera in Chilodonellidae Deroux, 1970 due to its divergent characteristics. In the present work, we studied a new gastronautid, *Gastronauta paraloisi* sp. n., and three populations of *Trithigmostoma cucullulus* (Müller, 1786) Jankowski, 1967, using integrative methods. Species identifications were confirmed by morphological research. We also obtained SSU rDNA sequences, which included the first available sequence of Gastronautidae. The following SSU rDNA-inferred phylogenetic analyses showed that the establishment of the family Gastronautidae is necessary, and Gastronautidae and *Trithigmostoma* may represent intermediate evolutionary links in the order Chlamyodontida.

Ciliate SSU-rRNA reference alignments for phylogenetic placement

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Although each global metabarcoding study shows ciliates as one of the most dominant eukaryotic single-cell groups in a given environment, there is a lack of within-ciliate diversity investigation in these studies. One of the possibilities to analyse ciliate diversity is through phylogenetic placement, i.e., placing environmental sequences on reference alignment/tree. We prepared three different SSU-rRNA reference alignments of ciliates. Each alignment contained 478 ciliate and six outgroup taxa and was made using a different strategy of masking ambiguously aligned positions (unmasked, masked and masked except the V4 region). We forced monophyly of each ciliate class based on the Adl et al. (2019) classification and added three recently established classes Odontostomatea, Muranotrichea, and Parablepharismaea. Taxa with uncertain phylogenetic position were kept unconstrained except for *Mesodinium* species that we forced to the class Litostomatea as the close relationship between mesodiniids and litostomateans was recently supported by phylogenomic data.

High diversity and the adaptation of aquatic protists to extreme conditions in the Atacama Desert

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At extreme hypersaline conditions, the species richness is generally assumed to be low. On the other hand, various studies showed a high degree of phylogenetic novelty under these extreme conditions. In addition to salinity, the variable chemical parameters of extreme habitats may significantly influence the eukaryotic community structure. These findings call for a more thorough look into the species richness of hypersaline environments, which seems to be more diverse than previously thought. In this study, various hypersaline lakes, as well as further aquatic ecosystems of northern Chile, were investigated regarding protistan species diversity and richness by cultivation and metabarcoding studies of environmental samples. Moreover, heterotrophic flagellates from various inland water bodies were isolated for detailed molecular, morphological and ecological investigations. The recently discovered class Placididea (Stramenopiles) was used as a model group for the analysis of diversity. Comparing these findings with our metabarcoding studies should enlarge the knowledge on the global distribution of placidids as well as the biodiversity of protists in extreme habitats.

Underestimated species richness of nudiform choanoflagellates?

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Lorica-bearing choanoflagellates (Acanthoecida) are divided into two families mainly based on their way of lorica production. In the tectiform condition, the mother cell provides a bundle of costal strips prior to cell division to the juvenile cell, whereas nudiform reproducing species have to develop the lorica after division independently. This observation could be confirmed by molecular analysis, but the ecological and evolutionary significance is still under debate. Nudiform choanoflagellates are discussed as an evolutionary paradox as the species are indeed consistent in their way of cell division and lorica production but in terms of morphological characterization they lack coherency. Considering species richness, tectiform choanoflagellates contain a multitude of species compared to nudiforms, where until now only six species were described. With our study we draw attention to the prior neglected and with low species number described family of nudiform choanoflagellates. Only recently, we could discover a new sister clade within the nudiforms and described the genus *Enibas*, comprising until now the species *E. tolerabilis* and *E. thessalia*, but with high potential of a greater extent as environmental data suggest. Interestingly, these species resemble morphologically the tectiform genus *Stephanoeca*, but show clearly the nudiform cell division, supporting the phylogenetic classification within the nudiforms. It becomes even more obvious that the genus *Stephanoeca* is in need of revision as we could additionally assign a previous only morphologically described *Stephanoeca* species to the nudiform family based on morphological and molecular data. With our study, we could show that within the family of nudiform choanoflagellates the species richness is broadly underestimated. The combination of molecular and morphological tools together with distinct live observations regarding the condition of reproduction will lead to a revision within the Acanthoecida and will help to understand the evolutionary relationship between both conditions.

Arcellinida testate amoebae as climate miner's canaries in Southern Spain

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Southern Spain is currently under threat of desertification as a consequence of global climate change, threatening many fragile ecosystems such as caves. The organisms living in these extremely stable environments are particularly sensitive and prone to extinction, therefore they can be used as bioindicators for climate change. Cyanobacterial mats form peculiar micro-ecosystems at the entrance of caves, and house a diversity of protists. Amongst them, Arcellinida testate amoebae have been traditionally used as bioindicators for environmental quality, notably because their narrow ecological tolerance. Here, we describe two new and conspicuous species of Arcellinida found in the cyanobacterial mats of cave Huididero, in Sierra de Grazalema, Málaga province: *Diffflugia alhadiqa* and *Heleopera baetica* based on morphometrics and 18S rRNA gene data. We propose using the presence of these species to indicate the good health of the cyanobacterial mats, like miner's canaries for local climate.

Expanding knowledge on the biodiversity, ecological adaptations and distribution of vampire amoebae (Vampyrellida, Rhizaria)

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The order Vampyrellida comprises predatory amoebae forming a large and genetically diverse clade of rhizarian protists. We know that these intricate microbes specifically prey on other eukaryotes, but their actual diversity, ecological roles and geographic distribution are still fragmentarily known. In our new and collaborative project of the ‘Taxon-omics’ Priority Programme (German Research Foundation) we examine the vampyrellid amoebae in a modern taxonomic light, rediscover old described taxa, characterize new taxa, and explore their biodiversity through environmental sequencing. Here, we will present some preliminary findings and report on some rediscovered species (e.g. *Vampyrella closterii* and *Arachnula impatiens*) as well as new taxa. These data highlight how fruitful this field of research will prove to be, and how the new project will further our phenotypic understanding of widespread and ecologically interesting microbes.

Using single-cell transcriptomics to study genome traits, population genetics and symbioses in Arcellinida

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Testate amoebae of the order Arcellinida (Amoebozoa) are highly abundant in freshwater ecosystems. Because of their abundance, their sensitivity to abiotic environmental factors and the preservation of their tests in the fossil record, testate amoebae serve as excellent bioindicators of past and present climate change. Although Arcellinida are well studied from a morphological perspective, our knowledge on their genome structures and population genetic diversity remains limited. This is mostly due to the fact that most lineages cannot be cultured in the lab and that to date no reference genome is available. To address these challenges, we have successfully developed protocols for single-cell transcriptomics. We have by now characterized transcriptomes from multiple (~80) individuals of Arcellinida, which we assemble and analyze using our custom-made pipeline PhyloToL. Bioinformatic approaches then allow us to 1) investigate genome characteristics, such as ploidy, codon usage and signatures of sexual reproduction; 2) study the population genetic variability of populations sampled across time and space in New England bogs; and 3) obtain insights into the symbiotic relationships between Arcellinida, prokaryotes and in some lineages, eukaryotic microalgae. Our results reveal surprisingly low levels of intra-population genetic variability, signs of recombination, yet predominant haploidy in our samples as well as complex associations of Arcellinida with other microbes.

Posters

poster presenter names are in bold

POSTER 1

Molecular insights into the protist communities found in the rhizosphere of *Cristaria* sp. and *Eulychnia* sp. from the Atacama Desert, Chile

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The arid Atacama Desert comprises diverse polyextreme environments in which biodiversity is restricted by the extreme environment. Factors as aridity, high UV-radiation and toxic components in the soil limit in particular the occurrence of plants to regions where water is, although limited, available. Understanding the cooperation of plants species and resident microbial consortia (so-called microbiome) may give a clue of association patterns of life adapted to the driest biotope on Earth. Here we present the results of the molecular survey of the rhizosphere of two endemic plant species from the Atacama, the shrub plant *Cristaria* sp. (family Malvaceae) and the arborescent cacti *Eulychnia* sp. High throughput sequencing of the V9 region of the ribosomal SSU gene indicates the presence of biosignatures from communities of small protists collectively grouped as marine stramenopiles (MAST) and pelagomonadales (Ochrophyta) associated with *Cristaria* sp. Dinoflagellates (Alveolata) are the main group assigned for sequences found associated with *Eulychnia* sp. roots while in soil samples from this cacti, the community is mainly composed by Euplotes (Ciliophora). Although, Shannon alpha-diversity index is higher in the protist community found in *Eulychnia* sp., no significant difference was found between microbiomes of both plants. However, phylogenetic distance metrics measured through Unifrac unweighted values suggest a clustering of the retrieved microbial groups for each plant. Our results include a large proportion of unclassified sequences according to the SILVA 138 (www.silva-arb.de) and the Protist Ribosomal Reference Database (PR2) suggesting the detection of an understudied protist diversity. To investigate the microbiome of the plants, prokaryote diversity will be studied in a followup study.

POSTER 2



Ciliates in the “aaare” (mires) of Bornheim: local diversity of *Spirostomum* spp.

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Eight morphospecies of *Spirostomum* spp. are valid species until present day. Despite morphological differences exist, the *Spirostomum minus* clade is considered as environmental modification because of genetic similarities. This work presents the current state of a privately funded project to monitor ciliate species living in the mires of Bornheim, North Rhine-Westphalia, Germany. About 20 ephemeral mires are spread over an area of approximately 35 square kilometres. A novel fluorescence double staining method is successfully tested to observe ciliate species using a fluorescence microscope. Fluorescent life-cell imaging supports quick determination of species, isolation of individuals for further cultivation, and replaces well the classical methyl green-pyronin staining. Samples taken from several mires yielded new insights about the local diversity of *Spirostomum* spp. Along with *Spirostomum ambiguum* and *Spirostomum teres* multiple morphologically different types of *Spirostomum minus* are found abundant in the samples. A new green *Spirostomum* strain with no symbiotic algae is reported here for the first time. White hyaline strains of similar size and shape are also abundant. Present observations confirm existence of at least two hyaline and slender morphospecies, similar to Sp. minus depicted by Kahl (1932). They mainly differ in the length of the AZM, with $1/3$ and $1/2$ of the total length of individuals, respectively. A small morphospecies of about 200 μm in length with a moniliform macronucleus of 6-10 nodules and multiple micronuclei is found similar to a short *Spirostomum* sp. Multiple *Spirostomum minus* strains often are found in dense clumps within the samples. The different morphotypes do not change their shape when isolated in culture. Current observations support well the idea of Kahl (1932) to split the *Spirostomum minus* clade into distinct species, of which he described *Spirostomum intermedium* and *Spirostomum minus*. Three suggested new morphospecies are described here.

POSTER 3

Can the climate and micro-environmental conditions of peat bogs be inferred from the morphometry of a single testate amoeba species?

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Testate amoebae are free-living shelled protists which are useful bioindicators of environmental conditions such as soil moisture or pH. As their shell is preserved in peat and sediments, they are commonly used to infer past environmental changes, based on changes in community structure. However, this method is somewhat limited by taxonomical uncertainty. Here we address the question: could environmental conditions be inferred from morphological traits of a single common species? *Hyalosphenia papilio* is one of the most common testate amoeba species in Holarctic *Sphagnum*-dominated peatlands. Its morphological variation, such as the number of pores has been shown to vary in relation to micro-environmental conditions. We hypothesised that significant relationships could be found between the morphology of *H. papilio* and environmental conditions (water table depth and site climatic characteristics). We measured morphological traits from 136 populations of *H. papilio* (15 individuals in each population). The samples were taken from past and ongoing observational and experimental studies, with fine to broad scale environmental gradients in Switzerland and Europe. The aim was to determine whether a new proxy could be developed based on the morphology of this single species. We found a strong linear correlation between the size of *H. papilio* and water table depth. We also found significant correlation with climatic variables. Both single and mixed predictive model could theoretically be developed. It thus appears that *H. papilio* is a promising candidate species to easily infer past ecological conditions from peat archives. The next step is now to explore how these relationships can be used to build new tools for bioindication and paleoecology.

POSTER 4

In silico comparisons of microsporidian-specific primers

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Microsporidia are intracellular parasites of animals and some protists. They comprise three groups, which are the classical, “long-branch” microsporidians, the chytridiopsids and the metchnikovellids. More recently, “short-branch” microsporidians were recognized. Several metabarcoding primer pairs have been developed to detect long-branch Microsporidia by targeting their small subunit ribosomal RNA gene sequence, with resulting amplicons of different lengths. Few comparisons were made to evaluate the diversity of microsporidians detected by the different primer pairs. And it is unclear whether these primers can detect short-branch microsporidians. To test the two short-read metabarcoding primer pairs V1F/mic-uni3R and CM-V5F/CM-V5R, as well as the long-read primer pair V1F/1342R, in silico PCRs were performed on a data set including publicly available sequence data of long-branch microsporidians, metchnikovellids, Chytridiopsis, short-branch microsporidians, and the close outgroups Rozella, NCLC1 and Aphelidea. All of the analyzed primer pairs were highly specific to the long-branch microsporidians. However, the reverse short-read primer mic-uni3R by itself bound to sequences of all taxa included in the analyses. Designing a suitable forward primer to pair with mic-uni3R could therefore allow for a detection of much more of the microsporidian diversity.

POSTER 5

Identifying potential hosts of short-branch Microsporidia

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Microsporidia are obligate parasites that are closely related to Fungi. While the widely known “long-branch” Microsporidia infect mostly metazoans, the hosts of “short-branch” Microsporidia are only partially characterized or not known at all. Here, we used network analyses from Neotropical rainforest soil metabarcoding data, to infer co-occurrences between environmental lineages of short-branch microsporidians and their potential hosts. We found significant co-occurrences with several taxa, especially with Apicomplexa, Cercozoa, and Fungi, as well as some Metazoa. Our results are the first step to identify potential hosts of the environmental lineages of short-branch microsporidians, which can be targeted in future molecular and microscopic studies.

POSTER 6

Relationships between northern peatland testate amoeba communities and methane emissions – building a transfer function for inferring past methane emissions

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Peatlands are characterized by water-logged organic soils, causing oxygen depletion favouring organic matter accumulation as peat. Although peatlands are efficient carbon sinks, they also emit methane (CH₄), which is a powerful greenhouse gas. CH₄ production is a microbiological process. Soil temperature, moisture and chemistry are the main factors controlling CH₄ production and emission, as well as the composition of soil microbial communities. Among soil microbes, testate amoebae (TA), a polyphyletic group of protists living in a shell they produce, are well-established bioindicators of water table depth and pH in peatlands. In this study, we therefore hypothesised that CH₄ emissions rates could be inferred from TA community composition. As TA produce species-specific, decay-resistant shells, past environmental conditions, like water table levels, can be inferred from subfossil TA communities preserved in the accumulated peat. This is commonly done using predictive mathematical models called “transfer functions”. Measuring CH₄ fluxes is tedious, costly and the high temporal variability of fluxes on daily and seasonal scales makes it difficult to estimate annual fluxes. So far, no transfer function exists to infer past or present methane emission from TA communities. We aimed to build a proof of concept for such a model. To reach this goal, we combined in-situ CH₄ emissions and TA community data from several geographical regions in Europe and Canada and across different peatland types (following a fen to bog gradient). We found a significant correlation between CH₄ fluxes and TA communities, suggesting that past peatland CH₄ emissions could be inferred from TA shells preserved in peat cores.

POSTER 7

DeSignate: detecting signature characters in gene sequence alignments for taxon diagnoses

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Taxon diagnoses primarily comprise morphological characters, whereas molecular characters are only infrequently added in integrative taxonomic approaches. Currently, the inclusion of molecular characters into taxon diagnoses is hampered by both problems in standardisation as well as the lack of efficient and user-friendly tools. DeSignate is a novel tool that detects diagnostic nucleotides (signature characters) in the monophyletic group of interest by analysing a gene sequence alignment. The intuitive web application guides the user through the analysis process in three simple steps comprising (1) the upload of input data (alignment and optionally tree), (2) the specification of search parameters, and (3) the selection of query and reference group. The underlying algorithm calculates metrics for each alignment position based on nucleotide vectors. These metrics subsequently determine the rank of each alignment position in the results according to its diagnostic relevance (signature characters are listed first). Furthermore, the alignment positions can conveniently be assigned to conserved or variable sequence regions based on their entropy values. DeSignate aims to facilitate the regular integration of molecular characters for complementing taxon diagnoses and thus to enable taxon delimitation and identification in various applications. This work was financially supported by the Austrian Science Fund projects P 29859 and I 3268.

POSTER 8

Investigation of the diatom communities in renatured rivers in the Ruhr area (Germany)

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Diatoms are unicellular algae that are common indicators of the ecological status and water quality of freshwater ecosystems. The purpose of this investigation was the characterization of the diatom communities in the Boye river system in order to assess the ecological water quality status of these bodies of water in regard to possible effects of previously applied renaturation measures. The Boye system has undergone several renaturation efforts ranging from 1993 to 2013, but the effect on diatom communities had not yet been studied. We collected diatom samples in November 2019 and April 2020 at different locations within the Boye river system and analyzed them according to the standardized CEN-norms (EN 13946:2014 und EN 14407:2014). The identified diatoms were used to establish a taxa list. A total of 222 species of diatoms with 48 genera were identified in the twelve different stream locations. The distance analysis showed that the species composition varied in different locations within one stream. According to the diatom biomonitoring index, most locations were in an at least good ecological status while a few were moderate. However, regression analyses showed that neither the ecological status of water, nor the diversity according to Shannon correlated with the time since renaturation measures concluded. The results obtained show that even after such recent renaturation efforts as in 2013, diatom communities in the Boye river system had a vast array of diatom species resulting in good ecological status as determined by the diatom biomonitoring index. The establishment of the Boye river system diatom taxa list will be crucial for further research.

POSTER 9

Unraveling the diversity of cercozoa and oomycota in palaeotropical tree canopies

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Tropical rainforests are the undisputed champions of biodiversity among the world's ecosystems, containing far higher numbers of species on a per-area basis relative to sub-tropical, temperate, and boreal ecosystems. Tropical rainforests harbour a vast diversity of multicellular organisms, but it is still little explored if microorganisms, especially protists, reflect similar diversity patterns compared to temperate zones. In this study we sampled protists from three autochthonous tree species (*Pometia pinnata*, *Pterocarpus indicus*, *Pterocymbium beccarii*) in a tropical rainforest in the northeast of Papua New Guinea. We applied high-throughput sequencing using newly designed specific primers for an extensive assessment of the diversity of Cercozoa (Rhizaria) and Oomycota (Stramenopiles) across various microhabitats from forest soils to the canopy region. We hypothesized that tree canopies in the tropical zone would show a large proportion of unknown diversity. The trees harboured 652 and 283 OTUs for Cercozoa and Oomycota, respectively. In Cercozoa most taxa found in Papua New Guinea corresponded to taxa known from temperate zones, only 7% of OTUs could not be assigned to any known order. The dominant orders are Glissomonadida, Euglyphida, Cercomonadida and Cryomonadida. However, in Oomycetes, approximately 50% of all OTUs showed a sequence similarity of less than 70% to any known reference sequence, demonstrating a vast unknown diversity. Oomycete OTUs with more than 70% sequence similarity were mainly assigned to Pythiales and Peronosporales. Overall, our study shows that palaeotropical forests indeed still contain a substantial unknown diversity of microbial eukaryotes. The taxonomy of Protists in the tropics deserves far more attention in future studies. We acknowledge funding from the DFG within the Priority Program: TaxonOmics - New Approaches for Discovering and Naming Biodiversity (SPP 1991).

POSTER 10

Let the weapons speak: extrusome features contribute to a revision of genus *Strombidium* (Alveolata, Ciliophora, Spirotricha)

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Strombidium Claparède & Lachmann, 1859 is a speciose genus of oligotrichid ciliates inhabiting mainly the marine pelagial. In molecular phylogenies, the genus is not monophyletic, and cladistic analyses reveal that it is exclusively characterised by plesiomorphies. Accordingly, new, apomorphic morphological and/or ultrastructural features are required for a reliable split of the genus, such as the extrusome arrangement and ultrastructure. Besides the oligotrichid-typical stripe of extrusome attachment sites just anteriorly to the girdle kinety, *Strombidium biarmatum* Agatha, Strüder-Kypke, Beran & Lynn, 2005 has extrusomes inserting between the collar membranelles. For the first time, transmission electron microscopy was applied for the documentation and description of its extrusomes based on chemically fixed and ultrathin-sectioned material collected in the Baltic Sea. The findings partially support previous data from live observations, but also provide new insights into the taxonomically significant feature complex of extrusomes. Two types of extrusomes differing in placement, arrangement, size, and shape were detected in *S. biarmatum*. A similar pattern of extrusomes was described in two congeners. Small subunit ribosomal DNA sequence trees demonstrate a clustering of the three species with full statistical support. Hence, both morphologic and genetic data corroborate the establishment of a distinct genus within the family Strombidiidae Fauré-Fremiet, 1970. This study was financially supported by the FWF Projects P 28790-B29 and I3268-B29.

POSTER 11

Effect of swarm's *fastidious* option on eDNA clustering results

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Clustering is an essential step in environmental sequencing studies. All clustering methods can suffer from over- or under-clustering: i.e., grouping sequences that should not be grouped, or failing to group sequences that should be grouped together. Swarm is an iterative, single-linkage clustering method that is designed to solve over-clustering, and offers an optional algorithm to solve the under-clustering issue: the "fastidious" option. The fastidious option limits under-clustering by grafting lower abundant clusters onto higher abundant clusters, compensating for missing intermediate sequences between the two clusters. The limit between lower and higher abundant clusters is controlled by the boundary parameter and is set to three by default. Here we evaluate how changes to the boundary value in swarm's fastidious option affects clustering results for two 18S rRNA markers (V4 and V9) and for a wide range of dataset sizes. We observed a reduction of the number of clusters by up to 49% for V4 and 43% for V9 when using the fastidious option. This reduction remains above 40% for V9 and above 45% for V4 for boundary values ranging from 2 to 200. Optimal boundary values were remarkably stable in regards to data set size changes, with optimal values comprised between 2 and 8 for dataset sizes ranging from 100 reads to 100 million reads.

POSTER 12

Concatenated alignment of cytochrome c oxidase gene subunit 1 (Cox1) and SSU rRNA genes as a tool for phylogeny reconstruction and DNA metabarcoding of Amoebozoa

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The most representative taxonomic database for Amoebozoa has been assembled for the small-subunit ribosomal RNA gene that still remains the “backbone” for phylogeny. At the same time, this marker remains technically problematic in amplification and analysis. Many amoebae species demonstrate intragenomic microheterogeneity in their sequences of SSU rRNA. Sometimes it even obscures the interspecific variation and poses difficulties for the resolution of relationships between close species. The sequence database for the cytochrome c oxidase gene subunit 1 (Cox1), a traditional animal DNA barcode, started to accumulate for Amoebozoa 10 years ago. Cox1 seems to be a valuable DNA barcode in Amoebozoa, combining easy amplification, little or no intragenomic variability, and easy analysis due to simplicity of alignment and protein-coding capacities. However, the resolving power of the Cox1 gene remains good only at very low taxonomic levels, i.e., not higher than traditional families or even genera. This is the one of the obstacles in its application as a DNA metabarcode for Amoebozoa: placement of eDNA sequences in the tree may be misleading when only Cox1 reference database is used. We present an improved way to analyze the Cox1 data for phylogeny reconstruction of Amoebozoa and an application of this marker as a metabarcode. The robust phylogenetic tree of Amoebozoa, well resolved in most levels, can be obtained using a partitioned analysis of a concatenated dataset of the SSU rRNA and nucleotide sequences of the Cox1. We assembled a dataset of about 150 species that represent most of the phylogenetic clades of Amoebozoa and reconstructed a well-resolved backbone tree using this approach. For further analysis of environmental sequencing data, the short sequences of any of the markers can be placed on this tree using the reference 2-gene alignment with pplacer or similar algorithm. Partially supported by the RSF grant 20-14-00181 to AK.

POSTER 13

Enrichment of soil testate amoebae by mean of filtration-sedimentation for HTS

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Multiple protist groups are represented in low abundance in soils which make them difficult to detect in environmental DNA surveys. In particular, testate amoebae are usually concentrated from soil samples for direct observation by creating a soil suspension and using a filtration-sedimentation method. In this study, we aimed at testing the effect of this soil suspension filtration-sedimentation on the recovery of the full protist community as well as the specific testate amoebae community compared to bulk soil samples by mean of V4 18S HTS. Forest and alpine grassland soils in four different countries were used to test for enrichment of the main protist clades and changes in alpha and beta diversity due to the habitat, country and method. Six to ten times increase in relative abundance of Euglyphida reads were observed in filtered alpine and forest soils compared to bulk soil, and their OTU richness was significantly increased four times in the filtered alpine samples. Overall, testate amoeba clades were enriched 3.7x in filtered samples, as well as Ciliophora (1.3x), Dinoflagellata (3.4x), Mesozocozoa (2x) and Ochrophyta (2.3x), while Conosoa were depleted 2.5x. The alpha diversity of the whole protist community did not significantly change due to filtration alone, neither in combination with the habitat and country of origin. Changes in the whole protist community composition were significantly explained by the habitat and country of origin, but not by the filtration effect. Both bulk soil DNA and filtered soil DNA provided comparable diversity estimates and led to the same ecological conclusion, while filtering increased the representativity of certain protist groups like testate amoebae. The use of such an enrichment protocol may be of interest to improve the description of low abundant soil clades like testate amoebae without compromising the ecological conclusion drawn from the whole protist communities.

POSTER 14

A taxonomic conundrum: characterizing a morphological polymorphism of two testate amoebae from East Herzegovina

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Species delimitation of testate amoebae possesses great difficulties because of the limited number of good morphological characters in some species groups. The problem is further complicated because some species are polymorphic. Morphological polymorphism is simultaneous presence of two or more phenotypes in a population or interrupted diversity of forms on the common genetic base. Both molecular and morphological taxonomists often overlook or minimize polymorphism by sampling only a single or few specimens per species. In the cases of continuous polymorphism, it is not possible to distinguish two or more clearly defined morphs within a population. This type of polymorphism was observed during a size frequency distribution analysis of shell length and shell width of *Longinebela tubulosa* based on 2630 specimens from a *Sphagnum*-dwelling population from East Herzegovina. In the cases of discontinuous polymorphism, it is possible to distinguish clearly defined morphs within population. *Trinema penardi* was recently morphometrically analyzed based on the population from the Island of Rab (Adriatic Sea), within which three morphometric classes were registered: small, medium and large. In East Herzegovina, this species is registered at several localities and is mainly represented by dimorphic populations. A total of three morphometric classes were registered: very small form (shell length 39–53 μm), small form (shell length 50–64 μm) and medium form (shell length 64–86 μm). In this study, a very small form was described for the first time, while a large form was not registered in East Herzegovina. Environmental and biological causes that may lead to polymorphism have been discussed and the need for further study of the molecular diversity, ecology and life cycle of this population has been outlined.

POSTER 15

Pseudocryptic species diversity in the genus *Nebela* (Arcellinida: Hyalospheniidae): more search, more find

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The genus *Nebela* includes about 15 species of small to medium size that show a tendency to colonize relatively dry habitats such as green mosses, forest humus and *Sphagnum* hummocks. In the past few years, a high number of populations belonging to different species of this genus have been collected, primarily from Eastern Herzegovina, but also from Bosnia, Serbia, France, Switzerland and Northern Ireland. Thanks to a detailed morphometric analysis of the populations from Switzerland, a clear picture was obtained of the morphological variability of the species redefined from this area in a molecular study published in 2013. In that study, *N. minor* has been synonymous with *N. tincta*, but morphometric analyzes of the populations from East Herzegovina and Switzerland has clearly shown that they are separate species. *Nebela aliciae* was described in 2013 based on seven specimens from Costa Rica, but the morphological variability of this species has not been assessed yet. Taxon *N. tincta* var. *major* is a clearly defined morphotype that should be considered as a separate species clearly different from *N. collaris* with which it was synonymous eight years ago. The morphotypes *N. aff. tincta* and *N. aff. tincta* f. *galeata* cannot be identified with certainty because even if they clearly deviate morphometrically from typical populations, their distinction is not enough to take a clear stand on their status as independent species. The most significant finds from East Herzegovina are the morphotypes *N. cf. collaris* and *N. cf. tincta* var. *major* that represent new species for science. All of this suggests that population taxonomy based on morphometrics is a good approach to understanding the diversity of this widespread and common genus.

POSTER 16

Taxonomy of moss-dwelling *Centropyxis* species (Arcellinida: Centropyxidae) from East Herzegovina: achievements based on morphometric information

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The genus *Centropyxis* includes about 150 species and infraspecific taxa. This abundance of species is, at least in part, due to a combination of inadequate descriptions and the lack of good diagnostic features. The taxonomy of this genus is based mainly on shell shape and size, but there is considerable uncertainty as to what characters may be used to circumscribe species. It has often been the case that even slight deviations in shell shape or size have resulted in the establishment of new species or infraspecific taxa, regardless of the range of variability that individual species may exhibit. In East Herzegovina, the genus *Centropyxis* is represented with seven moss-dwelling species. Populations of four species (*C. aerophila*, *C. elongata*, *C. platystoma* and *C. sylvatica*) from East Herzegovina have morphological and morphometric characteristics that fully correspond to the typical populations of these widespread species. The morphotype designated as *C. cf. aerophila* differs from *C. aerophila* in that there is no pair of large quartz particles at the end of the shell, and the shell is slightly longer (46–81 μm in *C. aerophila* compared to 67–88 μm in *C. cf. aerophila*). The morphotype designated as *C. cf. platystoma* differs significantly morphologically from the species *C. platystoma*, and it was concluded that it is an undescribed species. Recently, *C. cavitastoma* has been described from Alaska, which differs from *C. plagiostoma* in the absence of aperture xenosomes, more indented aperture and larger dimensions. Based on the analysis of the population of *C. plagiostoma* from East Herzegovina and the analysis of data from the literature, it can be concluded that the differences between the two species are relative and that detailed taxonomic studies of this complex of morphotypes are needed to determine whether the cause of variability is phenotypic plasticity or speciation.

POSTER 17

Two-family concept of the infraorder Hyalospheniformes (Amoebozoa: Arcellinida) with reference to evolutionary history and diversification

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Majority of testate amoebae with lobopodia are included into order Arcellinida which comprising about 700 nominal species, but the major part of these species needs comprehensive taxonomic revision. A recently published study based on a well-resolved phylogenomic reconstruction defined the infraorder Hyalospheniformes. With more than 200 described taxa distributed over all continents, this group is both highly variable and one of the largest testate amoebae groups. It is possible to distinguish two families within this infraorder: Padaungiellidae and Hyalospheniidae. Since these families are not generally accepted in the literature, the arguments that indicate that they are two clearly separated groups are discussed in detail. Within the family Padaungiellidae there are three well-defined genera: *Alocodera*, *Apodera* and *Padaungiella*. The first two genera are distributed in the southern part of the planet, while the genus *Padaungiella* is a common and widespread genus in both hemispheres. The family Hyalospheniidae comprises twelve genera that can be included into five morphological groups: (1) genera that possess proteinaceous or areolate shells (*Hyalosphenia*, *Pseudohyalosphaenia*), (2) genera that possess agglutinate shells with round and/or oval building units, but without lateral keel and large pores (*Alabasta*, *Longinebela*, *Nebela*), (3) genera that possess agglutinate shells with round and/or oval building units and lateral keel, but without large pores (*Cornutheca*, *Gibbocarina*, *Planocarina*), (4) genera that possess agglutinate shells with round and/or oval building units and two large pores (*Certesella*, *Porosia*), and (5) genera that possess agglutinate shells with square building units (*Mrabella*, *Quadrullella*). These groups are polyphyletic according to molecular cladogram published recently. The relations between genera are primarily interpreted from the aspect of morphological similarities, with reference to evolutionary relationships and diversification within taxa. This approach has practical importance because it facilitates understanding the value of certain taxonomic characters and can help in constructing identification keys.

POSTER 18

Superficially described and ignored for 92 years, rediscovered and emended: *Apodera angatakere* (Amoebozoa: Arcellinida: Hyalospheniiformes) is a new flagship testate amoeba species from Aotearoa (New Zealand)

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Eukaryotic microbial diversity is known to be extensive but remains largely undescribed and uncharted. While much of this unknown diversity is composed of tiny flagellates and inconspicuous parasites, larger and morphologically distinct protists are regularly discovered, most notably from poorly studied regions. Here we report a new flagship species of hyalospheniid (Amoebozoa; Arcellinida; Hyalospheniiformes) testate amoeba from New Zealand and an unusual story of overlooked description under a pre-occupied name and subsequent oversight for nearly one century. Through a process involving Te Taura Whiri I te Reo Māori (The Māori Language Commission), we named the species *Apodera angatakere*, meaning “a shell with a keel” in te reo Māori. This species resembles *Apodera* *vas* but differs by the presence of a distinctive hollow keel, as in genus *Gibbocarina*. Cytochrome Oxidase Subunit 1 (COI) sequence data shows that this species forms a distinct clade nested within genus *Apodera*. This highly conspicuous species is so far known only from New Zealand and is restricted to peatlands. We believe it is the first instance of an endemic microorganism from this biodiversity hotspot and biogeographer’s paradise. As over 90% of New Zealand’s peatlands have been lost since European colonisation and much of the remaining surfaces are threatened by drainage, area loss, fragmentation along with other impacts *Apodera angatakere* could be a flagship species not only for microbial biogeography but also for island biodiversity conservation.

POSTER 19

Separating the inside from the outside: a closer look at Cid1 as the potential cellular component to distinguish between endogenous and exogenous long and small RNAs

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Being in a constant exchange with the environment, a cell has to react to many different external triggers and adapt its gene expression in response to both, external and internal factors. While some triggers are sensed using specific receptors and are processed via signal cascades, some other triggers, e.g. double-stranded RNA (dsRNA) is taken up by the cell, is processed and directly directed into specific cellular mechanisms, which are hardly understood. Interestingly external and internal RNA triggers share a subset of different enzymatic components, but differ in a variety of others. One example of such a mechanism is the gene regulation of *Paramecium tetraurelia* by siRNA. In this mechanism, some key components of siRNAs biogenesis and mode of action, such as Dcr1 and Ptiwi13 are shared by the endogenous gene regulation and in addition by gene regulatory mechanisms induced by exogenous dsRNA., while the exogenous-dsRNA-related siRNAs are also processed by the Piwis Ptiwi12 and 15, which act exclusively for exogenous ones. From this observation, the question arises, how the cell tracks the origin of a produced siRNA and how the cell decides, to which pathway the siRNA has to be assigned. While the interaction of Dcr1 during the production of the siRNA with different pathway-specific proteins might be an answer, the involvement of pathway-specific terminal nucleotide transferases, such as Cid1 for the exogenous dsRNA-pathway, suggests a specific tailing of siRNAs or of their precursors to assign them to their respective pathway. Therefore, goal of this study is to characterize the role of Cid1 within the dsRNA-pathway of *Paramecium* and answering the question, which RNA molecules are tagged by Cid1 in which manner.

POSTER 20

Baltic Sea project: Four potentially new species - resisting anoxic conditions in sediment?

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The Baltic sea is one of the largest brackishwater environments, but regarding benthic protist communities it is rather less investigated. Within a study program on the effects of bottom fishing we focus on the impact on benthic microbial communities in the western Baltic Sea. The project aims to globally investigate a) the development of marine protected areas (MPA) after the exclusion of mobile bottom fishing and b) short and long-term influences of bottom fishing considering sediments, biochemical cycles, substance flow and the benthic biocoenosis - ranging from prokaryotes up to benthic fish. So far, the influence of bottom trawling on the benthic protist community - especially through sediment disturbance - is still unknown. Yet, especially considering carbon flow, protists play an important role as a link to higher trophic levels. During a cruise in June 2020 we visited two sampling areas in the Baltic Sea (one in an MPA and one in a control area) and took sediment samples with the help of a multicorer (MUC). Based on phylogenetic data of 18S rDNA, potentially new species (*Neobodo* sp., *Rhynchomonas* sp., *Pedospumella* sp. and *Cafeteria* sp.) were found in layers between 2-15 cm depth. Besides the resolution of the taxonomic position of the potentially new species in comparison to closely related species and their habitat, those results lead to the question whether these organisms are active in the deeper anoxic sediment layers or may have been transferred through bioturbation or bottom trawling.

POSTER 21

Presence of *Arcella* (Amoebozoa, Tubulinea, Arcellinida) in athalassohaline ecosystems of Central Spain

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Arcellinid testate amoebae play important roles as top microbial predators in nutrient cycling and regulation of microbial communities. They are mainly found in terrestrial and freshwater habitats, where they are ubiquitous and abundant, but only a few species have been reported in environments with high salinity, such as coastal ecosystems. However, their presence in natural inland salt lakes and other athalassohaline environments remains largely unknown. These extreme environments are characterized by very high summer temperatures and fluctuating salinity levels that often exceed marine water. We explored different athalassohaline water ecosystems in Central Spain by collecting the top millimeters of sediment and observing them under the microscope. Here, we report the presence of *Arcella* sp. in these ecosystems, which could be assigned morphologically to the clade of *A. conica*. Empty tests were found between 7 to 140g/L, and active cells between 7 and 50g/l. This is, to our knowledge, the highest salinity in which *Arcella* has been reported. Isolation, culturing and differential expression studies might reveal which are the mechanisms followed by these organisms to adapt to hypersaline environments.

POSTER 22

Novel elphidiid foraminifer from the High Arctic: the enigmatic phylotype

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The Elphidiidae represent a large family of benthic foraminifera within the order Rotaliida, class Globothalamea, and are very common across marine shelves worldwide. The type genus *Elphidium* is characterized by calcareous, planispirally coiled, multichambered test, a spiral umbilical canal system, and “bridges” crossing the deeply incised “sutures” (intraseptal interocular spaces). Complex test morphology and high morphological plasticity obscures the boundaries of many elphidiids. This, multiplied by the high number of species, and the taxonomic history dating back to XVIII century, makes this group a “nightmare for taxonomists”. In the Arctic, over fifteen elphidiid morphospecies are distributed from the intertidal zone to the shelf break. Among them is the one designated ‘phylotype S15’ in the molecular phylogeny of Darling et al. (2016), which has not yet been formally described. We report the finding of many live specimens recently isolated on the outer shelf of the East Siberian Sea (expedition TransArctic 2019), aiming at describing this new species with morphological and molecular tools. Interestingly, all specimens were found firmly attached to tests of larger agglutinated foraminifera (e.g. *Hormosina pilulifera*). Specimens with a very similar morphology have also been isolated from the Kara and Barents Sea samples. The unnamed ‘Phylotype S15’ species is closely related and shares morphological similarities with the widespread, circumpolar *Criboelphidium bartletti*, *C. frigidum*, and represents another peculiar, widely distributed high-arctic elphidiid possibly indicative of the seasonally to perennially ice-covered outer shelf environment.

POSTER 23

Retention of microplastics by biofilms and its ingestion by protists

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Plastic introduction into different ecosystems has become a major problem within the last decades. Though there are many studies on larger plastic particles in marine habitats, we still have to investigate the role of rivers transporting plastic particles into seas. Due to different sources, such as tire abrasion, sewage treatment plants and grinding of larger plastic particles, microplastic particles (<5 mm) are introduced into rivers. These smaller particles might have an effect on river organisms such as fish and mussels, but also microzoobenthos living on biofilms. Biofilms are present in all aquatic ecosystems and play an important role in being a habitat for bacteria, flagellates, ciliates and other protists, but also in being a food source for macrozoobenthic organisms. In this study we want to show, that biofilms are a trap for microplastic particles and therefore makes them available for protists, which might accidentally consume the microplastic particles. Further, we want to investigate if ciliates show a differentiation between natural food items and microplastic particles and if there is a saturation point in ingestion of microplastic particles.

POSTER 24

Experiments on the spatial distribution in a single-species system – Experiments with the ciliate *Tetrahymena pyriformis*

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Spatial distributions of populations are known to have a high impact on the establishment of high biodiversity and the coexistence of multiple species. Patterns of the spatial distribution of organisms provide important clues about the underlying mechanisms that structure ecological communities and promote biological diversity. Although studies showed that even single-species systems can exhibit chaotic behaviors, the causes and consequences of chaotic dynamics and their relation to spatial distributions in single-species models are still unknown. A microcosm experiment for measuring spatial distribution, working with a chamber of interconnected habitat patches, was performed using the model organism *Tetrahymena pyriformis*. Preliminary results of the spatial distribution experiments illustrated that dispersion can be highly affected by environmental conditions. *Tetrahymena pyriformis* showed a positive and negative density-dependent distribution strategy. The results demonstrate that dispersal and movement can be highly complex behaviors. Still, there is a lack of knowledge in the spatial distribution of single-species systems. The developed experimental set-up offers the potential for more complex experiments with multiple-species systems to further investigate distribution patterns and their dynamics.

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