

Protists diversity and ecology in aquatic and terrestrial ecosystems

2-3 December 2019

In collaboration with the CUSO doctoral program in Ecology and Evolution

BOOK OF ABSTRACTS

ORAL CONTRIBUTION

Environmental DNA to monitor protist diversity

Singer D.^{1,2}

¹Department of Zoology, Institute of Biosciences, University of São Paulo, São Paulo, Brazil,

*²Ottawa-Carleton Geoscience Centre and Department of Earth Sciences and Carleton
University Ottawa Canada*

Microbial eukaryotes play key roles in ecosystem functioning. The recent development of methods and technology to analyse microeukaryote gene sequences potentially permits for the cost-effective exploration of every component of Earth biosphere. Moreover, the application of molecular techniques to enhance classical microbial ecological research has greatly increased our general knowledge of the ongoing processes, and to track the impact of environmental stressors (e.g. pH, nutrient, pollution...). In this presentation, I will first present a quick overview of the evolution of the molecular tools. I will present the advantages but also the limitations of these methods. Then I will provide a few examples of the use of next generation sequencing to monitor the environment. Metabarcoding allow the evaluation of parasitic diversity and the relation with their hosts. Finally, I will present how we can apply environmental DNA approaches in forensic science and how it can be useful to get potential key information during criminal investigations. In summary, molecular technics are a powerful tool to explore the diversity, ecology and biogeography of microeukaryotes.

ORAL CONTRIBUTION

With nutrients through the trophic levels - From biogeochemistry to the pelagic food web of Lake Tanganyika

Junker J.^{1,2}, Seehausen O.^{1,2}

¹Department of Fish Ecology & Evolution, EAWAG, Kastanienbaum, ²Institute of Ecology and Evolution, Department of Aquatic Ecology & Evolution, University of Bern

Lake Tanganyika is situated in the east African rift valley. With an estimated age of 9 – 12mio years, it hosts a long evolutionary history. Lake Tanganyika is the second largest lake by volume in the world with a rather shallow epilimnion and a deep hypolimnion. The mixing of the upper layers of the water column are regulated by a complex differential cooling and trade winds. These dynamics lead to a nutrient poor northern basin, with a shallow oxycline and a nutrient rich southern basin with a deep oxycline. In our project we investigated the distribution of nitrogen, carbon, the abundance of phytoplankton, zooplankton and its influence on the pelagic fish community in the northern and southern basin of Lake Tanganyika, using abundance data and stable isotopes.

ORAL CONTRIBUTION

Drivers of structure and dynamics of communities in natural microcosms

Korn R.¹, Thallinger G. G.², Bersier L.-F.¹ and Gray S. M.¹

¹University of Fribourg, Department of Biology–Ecology and Evolution, Switzerland. ²Graz University of Technology, Institute of Computational Biotechnology, Austria.

The aim is to unravel extant community structure and its drivers for the *Sarracenia purpurea* pitcher phytotelmata and adjacent *Sphagnum* mosses via 16S- and 18S rRNA metabarcoding. Hereby, step-wise constraints on the extant communities were accounted for with a structural equation modeling approach: (i) colonization of the pitchers is hypothesized to be driven by biogeographical factors reflecting spatial organization on a landscape level, (ii) environmental filters act on a macro- and microhabitat level and (iii) multilevel trophic interactions drive the structure within each realized community at an early and late successional stage. First results showed that microbial diversity was distinctly higher and different in the mosses than in the pitchers, suggesting a stringent filtering in the pitchers. Further, community composition was partitioned on the macrohabitat level; thus, indicating that factors as temperature and geographic position are important drivers of community composition.

ORAL CONTRIBUTION

Understanding and predicting plankton dynamics using in situ automated monitoring

Pomati F.¹

¹Department of Aquatic Ecology, EAWAG: Swiss Federal Institute of Aquatic Science and Technology Überlandstrasse 133, 8600 Dübendorf, Switzerland

Phytoplankton are perhaps the most fundamental indicators of changes in lake ecology and lake ecosystem services. However a naturally fluctuating environment and complex internal interactions among individuals and species make plankton communities difficult to understand and fundamentally hard to predict. To afford understanding and prediction of phytoplankton dynamics in nature we need to acquire environmental data at the appropriate scale of space and time and use advanced data-analysis approaches to turn large and high dimensional datasets into information and knowledge. During this seminar, I will briefly review the above issues hindering the predictability of plankton communities, and show advantages and limitations of approaches based on environmental monitoring data (biological, physical and chemical) sampled at different scales, coupled with machine learning, to forecast phytoplankton dynamics. I will particularly focus on how high-resolution monitoring, particularly by recently developed technology such as underwater imaging, can inform machine-learning tools and deliver targets ecological and data-driven models, helping elucidate the mechanisms underlying plankton dynamics and forecasting of algal blooms.

ORAL CONTRIBUTION

Ecosystem responses to increasing disturbance frequency and intensity: testing the theory with protist microcosms

Jacquet C.^{1,2}, Gounand I.^{1,2}, Altermatt F.^{1,2}.

¹Department of Aquatic Ecology, Swiss Federal Institute of Aquatic Science and Technology, Eawag, Dübendorf, Switzerland, ²Department of Evolutionary Biology and Environmental Studies, University of Zurich, Zürich, Switzerland

Current climate change is expected to increase the frequency and intensity of disturbances such as storms, fires, drought or coral bleaching events. Despite this context, we still lack of theoretical baselines to predict the response of ecological communities to growing disturbance regimes. Here, we experimentally investigate the response of community size-structure to varying disturbance regimes using protist communities that cover a wide range of body sizes and densities. We disentangle the links between disturbance regime, organism growth rates and community resilience to build a size-based theory that predicts the level of disturbances a community can recover from.

ORAL CONTRIBUTION

Phenotypic ability to persist in a changing environment

Govaert L.^{1,2}, Gilarranz L. J.², Altermatt F.^{1,2}.

*¹Department of Evolutionary Biology and Environmental Studies, University of Zurich
Winterthurerstrasse 190. 8057 Zürich, Switzerland, ²Department of Aquatic Ecology,
EAWAG: Swiss Federal Institute of Aquatic Science and Technology Überlandstrasse 133.
8600 Dübendorf, Switzerland*

Environmental change is ubiquitous and acts on entire communities simultaneously. Species can respond to such environmental changes by shifting their geographic range or by shifting their phenotypic distribution. A shift in phenotypic distribution can occur due to an environmental (plastic) response, a genetic response, or a combination of both. Here, we use microcosm experiments to determine a phenotypic shift in the trait distribution of microbe communities along an environmental gradient. We measured key traits (such as size and shape of the cell, and swimming behavior), covering ecological, physiological and behavioral processes. We found strong shifts in the phenotypic distribution, which also depended on the ecological history of the microbe populations.

ORAL CONTRIBUTION

Protist introduction to support plant growth

Amacker N.¹, Gao Z.¹, Karlsson I.², Geisen S.³, Kowalchuk G.¹, Jousset A.¹

¹Utrecht University (NL), ²Swedish University of Agricultural Sciences (SE), ³Netherlands Institute of Ecology, Wageningen (NL)

The microbiome is recognized as a major driver of plant growth, but harnessing its beneficial functions remains a challenge. Introduction of beneficial microorganisms is constrained by the low survival and efficiency of the introduced species. We therefore propose an alternative approach: instead of introducing plant-beneficial organisms, bacterivorous protists are applied as microbiome modulators promoting at once the several native bacteria carrying plant-beneficial traits.

Free-living, heterotrophic protists are major consumers of bacteria in the rhizosphere and provide a competitive edge to species harboring a range of plant-beneficial traits. We therefore expected that introducing bacterivorous protists into the rhizosphere may be a powerful leverage to promote microbiome ability to stimulate plant growth.

We added six different protists species independently to soil containing a predator-free semi-natural bacterial community. After ten days of incubation, lettuce seedlings were transplanted to the resulting soils and plant performance tracked over time. Protist application increased the root to shoot ratio in a species-specific manner. While the shoot content of N and C was similar in all treatments, the introduction of protists, especially *Cercomonas* sp., increased the shoot content of some trace elements including Cu, Mn, Fe and Zn.

We propose that specific protists may be used as an inoculant to promote sustainable plant growth while minimizing fertilizer input.

ORAL CONTRIBUTION

A journey into the world of testate amoebae

Lara E.¹

¹Royal Botanical Garden, Madrid, Spain

Testate amoebae are ubiquitous in most continental systems on Earth, and pre-date the evolution of animals in the fossil record. They are exceptionally diverse, and early estimations of 2000 species are most likely to be multiplied by several orders of magnitude, as assessed with morphometry and DNA barcoding. In contrast with the traditional cliché of “simple organisms”, these highly specialized protists develop a whole array of morphological, physiological and behavioral responses to cope with selective pressures from their environment. They have typically narrow restricted ecological tolerance –a useful feature that can be used in bioindication. As a consequence of their specialized lifestyle and sometimes poor dispersal capacity, many species have geographically restricted distribution areas, often including narrow endemism. Altogether, our journey into the world of testate amoebae is revealing an extremely diverse and fascinating world, a new playground for naturalists.

POSTER

Biodiversity and biogeography of Euglyphida (Rhizaria) in continental and oceanic islands

Bruni E. P.¹, Lentendu G.¹, Mitchell E. A. D.^{1,2}

¹Laboratory of Soil Biodiversity, Institute of Biology, Faculty of Science, University of Neuchâtel, Rue Emile-Argand 11, CH-2000 Neuchâtel, Switzerland, ²Botanical Garden of Neuchâtel, Chemin du Pertuis-du-Sault 58, CH-2000 Neuchâtel, Switzerland

Over the last decades, the rise of new molecular methods (e.g. high throughput sequencing; HTS) have made it possible to shed new light on the biodiversity and the distribution of protists worldwide. However, the true diversity of protists remains unknown and insufficiently studied. Thus, their biogeographical patterns and dispersal mechanisms are still open research fields in microbial ecology.

My PhD thesis focuses on soil testate amoebae and especially on Euglyphida (Rhizaria: Cercozoa), a model group in the study of terrestrial microbial biogeography. The overarching goal of this project is to test how far basic biogeographical rules developed for animals and plants apply to testate amoebae. In this respect, more than 500 fresh soil samples will be collected along elevation gradients in four islands/archipelagos with increasing distance to continents (Canary < Réunion < Azores < Hawaii), two large archipelagos with contrasted distance to the nearest continent (Japan < New-Zealand), and two distant continents of different paleogeographic origin (Laurasia: Western Europe, Gondwana: Chile).

A unique dataset of unprecedented taxonomic and geographic coverage will be obtained for testate amoebae. Combination of HTS data (Illumina, PacBio, Sanger sequencing) and DNA barcoding will give new insights into their diversity, their taxonomy and their phylogeny. Additionally, the community composition and the distribution patterns among elevation gradients will be characterized together with the variables influencing them. Finally, the description of global patterns of diversity and distribution will allow testing the moderate endemism hypothesis and assessing whether paradigms developed for large organisms are equivalently valid for testate amoebae.

POSTER

Mycamoeba gemmipara nov. gen., nov. sp., the First Cultured Member of the Environmental Dermamoebidae Clade LKM74 and its Unusual Life Cycle

Blandenier Q¹, Seppey C. V. W.¹, Singer D.¹, Vlimant M.², Simon A.³, Duckert C.¹ & Lara E.¹

¹Laboratory of Soil Biodiversity, Institute of Biology, University of Neuchâtel, Emile Argand 11, Neuchâtel 2000, Switzerland, ²Laboratory of Ecology and Evolution of Parasites, Institute of Biology, University of Neuchâtel, Emile Argand 11, Neuchâtel 2000, Switzerland, ³Laboratory of Microbiology, Institute of Biology, University of Neuchâtel, Emile Argand 11, Neuchâtel 2000, Switzerland

Since the first environmental DNA surveys, entire groups of sequences called “environmental clades” did not have any cultured representative. LKM74 is an amoebozoan clade affiliated to Dermamoebidae, whose presence is pervasively reported in soil and freshwater. We obtained an isolate from soil that we assigned to LKM74 by molecular phylogeny, close related to freshwater clones. We described *Mycamoeba gemmipara* based on observations made with light- and transmission electron microscopy. It is an extremely small amoeba with typical lingulate shape. Unlike other Dermamoebidae, it lacked ornamentation on its cell membrane, and condensed chromatin formed characteristic patterns in the nucleus. *M. gemmipara* displayed a unique life cycle: trophozoites formed walled coccoid stages which grew through successive buddings and developed into branched structures holding cysts. These structures, measuring hundreds of micrometres, are built as the exclusive product of osmotrophic feeding. To demonstrate that *M. gemmipara* is a genuine soil inhabitant, we screened its presence in an environmental soil DNA diversity survey performed on an experimental setup where pig cadavers were left to decompose in soils to follow changes in eukaryotic communities. *Mycamoeba gemmipara* was present in all samples, although related reads were uncommon underneath the cadaver.

POSTER

Dispersal limitations and historical factors determine the biogeography of terrestrial protists

Singer D.¹, Payne R.², Mitchell E.¹, Blandenier Q.¹, **Duckert C.**¹, Fernández L.³, Hernández C.⁴, Granath G.⁵, Rydin H.⁶, Bragazza L.⁷, Koronatova N.⁸, Goia I.⁹, Harris L.¹⁰, Kajukalo K.¹¹, Lamentowicz M.¹², Kosykh N.⁸, Vellak K.¹¹, Lara E.¹³

¹Laboratory of Soil Biodiversity, University of Neuchâtel, Neuchâtel, Switzerland, ²Environment, University of York, Heslington, York, YO10 5DD, United Kingdom, ³Centro de Investigación en Recursos Naturales y Sustentabilidad (CIRENYS), Universidad Bernardo, O'Higgins, Santiago, Chile, ⁴Universidad de Concepción, Concepción, Chile, ⁵Department of Ecology and Genetics, Evolutionary Biology Centre, Uppsala University, Sweden, ⁶Department of Ecology and Genetics, Evolutionary Biology Centre, Uppsala University, ⁷WSL Swiss Federal Institute for Forest, Snow and Landscape Research, Italy, ⁸Laboratory of Biogeocenology, Institute of Soil Science and Agrochemistry, Siberian Branch of Russian Academy of Sciences, ⁹Babes-Bolyai University, Faculty of Biology and Geology, Department of Taxonomy and Ecology, Romania, ¹⁰School of Geography and Earth Sciences, McMaster University, ¹¹Laboratory of Wetland Ecology and Monitoring, Faculty of Geographical and Geological Sciences and Department of Biogeography and Paleocology, Adam Mickiewicz University, ¹²Laboratory of Wetland Ecology and Monitoring, Faculty of Geographical and Geological Sciences and Department of Biogeography and Paleocology, Adam Mickiewicz University, Poznań, Poland, ¹³Institute of Ecology and Earth Sciences, Natural History Museum, University of Tartu Real Jardín Botánico, CSIC, Madrid, Spain

Assessment of the spatial distribution and diversity of free-living protists remains an open and unresolved question among the scientific community. Recent studies show that some groups of microbial eukaryotes present limited dispersion, sometimes even narrow endemism and contradict the paradigm of cosmopolitan distribution illustrated by the tenet "everything is everywhere, but, the environment selects". However, most studies aimed at demonstrating or contradicting this paradigm, and very few have evidenced phylogeographic processes driven by allopatric speciation. In this study, we investigated the spatial distribution of mitochondrial lineages (based on COI, i.e. partial cytochrome oxidase subunit 1 sequences) within the *Hyalosphenia papilio* complex of cryptic species. This testate amoeba morphotype is supposed to be distributed all over the Northern Hemisphere complex and has been shown previously to host a wide diversity of cryptic species whose distribution is geographically limited. We determined the distribution of these mitochondrial haplotypes on the Northern Hemisphere, based on sequences obtained through data mining in GenBank plus our own data. Our data support the

hypothesis that patterns of phylogenetic diversity and distribution are congruent with the history of Holarctic Sphagnum peatland range expansions/contractions in response to Quaternary glaciations. This suggests that historical processes may contribute in the diversification of terrestrial protists and are partly responsible for their very high overall diversity.

POSTER

NAD9/NAD7 (mitochondrial nicotinamide adenine dinucleotide dehydrogenase gene) — A new “Holy Grail” phylogenetic and DNA-barcoding marker for Arcellinida (Amoebozoa)?

Blandenier Q.^{1,2}, Lara E.¹, Mitchell E. A. D.^{1,3}, Alcantara D. M. C.², Siemensma F. J.⁴, Todorov M.⁵, Lahr D. J. G.²

¹Laboratory of Soil Biodiversity, University of Neuchâtel, Emile-Argand 11, 2000 Neuchâtel, Switzerland, ²Department of Zoology, University of Sao Paulo, 05508-090 Sao Paulo, Brazil, ³Botanical Garden of Neuchâtel, Chemin du Perthuis-du-Sault 58, 2000 Neuchâtel, Switzerland, ⁴Julianaweg 10, 1241VW Kortenhoef, Netherlands, ⁵Institute of Biodiversity and Ecosystem Research, Bulgarian Academy of Sciences, 2 Gagarin St., 1113 Sofia, Bulgaria

Molecular phylogeny is an indispensable tool for assessing evolutionary relationships among protists. The most commonly used marker is the small subunit ribosomal RNA gene, a conserved gene present in many copies in the nuclear genomes. However, this marker is not variable enough at a fine-level taxonomic scale, and intra-genomic polymorphism has already been reported. Finding a marker that could be useful at both deep and fine taxonomic resolution levels seemed like a utopic dream. We designed Amoebozoa-specific primers to amplify a region including partial sequences of two subunits of the mitochondrial nicotinamide adenine dinucleotide dehydrogenase gene (NAD9/NAD7). We applied them to arcellinids belonging to distantly related genera (Arcella, Diffugia, Netzelia and Hyalosphenia) and to Arcellinid-rich environmental samples to obtain additional Amoebozoa sequences. Tree topology was congruent with previous phylogenies, all nodes being highly supported, suggesting that this marker is well-suited for deep phylogenies in Arcellinida and perhaps Amoebozoa. Furthermore, it enabled discrimination of close-related taxa. This short genetic marker (ca. 250 bp) can therefore be used at different taxonomic levels, due to a fast-varying intergenic region presenting either a small intergenic sequence or an overlap, depending on the species.