International Symposium on Testate Amoebae

ISTA 9 ¾

18-20 October 2021

Online meeting organised by:

The Laboratory of Soil Biodiversity,

University of Neuchâtel, Switzerland

Sponsors:

University of Neuchâtel &

International Society of Protistologists

Program & Book of Abstracts

ISOP International Society of Protistologists

unine UNIVERSITÉ DE NEUCHÂTEL

Organising committee

This meeting was organised by the team of the Laboratory of Soil Biodiveristy at the University of Neuchâtel, especially Dr. Matthieu Mulot for registration and abstract submission and Clément Duckert for handling the online presentations and Prof Edward A. D. Mitchell for overall organisation) with additional help from Prof Micah Dunthorn and Prof David M. Wilkinson.

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Foreword

The International Symposium on Testate Amoebae is a biennial meeting organised by the International Society of Testate Amoeba Researchers (ISTAR). ISTA venues alternate between Europe and the rest of the world in line with the fact that at present a large proportion of testate amoeba scientists are based in Europe (but this may of course change in the future as our community expands in numbers and (bio)geographic range!

The previous meeting was ISTA 9, held in Belfast, UK in 2018. The next planned meeting was ISTA 10, initially planned for 2020 in Niagara, Canada, in line with our habit of holding these meetings every 2 years and alternating between Europe and the rest of the world. However, due to the COVID pandemic, ISTA 10 had to be postponed first to 2021 and then to 2022. Thus, instead of having to wait 2 year between ISTA 9 and 10 we will have a 4-year gap. This would mean that many PhD students would not have an opportunity to meet the community during the time of their thesis. This can't be!!! Therefore, the Soil Biodiversity Lab at the University of Neuchâtel offered to organise the first ever online ISTA meeting. Hence if we don't change the name ISTA 10 for the one planned in Niagara in 2022, and considering that 2021 is 3 years after ISTA 9 and one year before ISTA 10, it logically follows that this 2021 online meeting will be ISTA 9 ¾! For sure this will be a magical meeting! We hope it will be enjoyable and thought provoking and the each and every one of the participants will find answers to some questions and inspiration for his/her own research.

The community of testate amoeba researchers is thriving and growing. It is a pleasure to see several young and promising colleagues obtain permanent academic positions and at each meeting new people, MSc and PhD students especially from different parts of the world join the community. Yet, as time goes by, we sadly have to live with the fact that some colleagues reach the end of their road. We would like to dedicate this meeting to the memory of three colleagues who have passed since the previous meeting: Richard J. Payne, O. W. (Bill) Hill, and Louis Bonnet.

Richard Payne died in a mountaineering accident on Nada Devi, in the Indian Himalayas in May 2019. Richard was among a group of eight experienced mountaineers caught in an avalanche, Mountaineering was a strong passion of his as was of course the study of testate amoebae. Richard's contribution to the ecology and palaeoecology of testate amoebae is major and he especially was keen to explore habitats and questions that had not been studied much such as Mediterranean peatlands or the impact of volcanic eruptions on testate amoebae. He was a brilliant scientist, and a very friendly and collaborative colleague. Working with him on several papers on testate amoeba ecology and addressing some methodological questions such as taxonomic resolution, how many amoebae should be counted and to what extent taxonomic confusion was a source of error in (palaeao)ecology was both fun and very useful. His untimely death left us in shock and feeling very much alone. We miss you terribly Richard!

O. W. Heal (known as Bill Heal) also died this year at the age of 86. Heal is best known to testate workers for a series of papers published in the early 1960's which mainly came from his PhD work, and are still cited today. Heal did his PhD at the University of Durham under the supervision of Prof Jim Cragg, and was one of a series of student that Cragg supervised

working on small invertebrates at Moor House National Nature Reserve in the uplands of northern England (Heal was unusual in working on protozoa, most of these students worked on very small metazoan). He mainly studied testates associated with *Sphagnum fallax*, and his work was unusually ecological at a time when the small amount of testate amoebae work being done in Britain seldom extended beyond compiling species lists. Later Heal became head of soil science – and later director of the northern division – at the British Institute of Terrestrial Ecology. He went on to play important roles in the setting up of long-term ecological monitoring studies (such as the Environmental Change Network in 1992).

Louis Bonnet died at the age of 91 years shortly before the ISTA 9 ¾ started and we were informed about his death on the first day of the meeting. Louis Bonnet contributed like no other researcher to the study of soil testate amoebae. He described many taxa (3 families, 16 genera and 116 species – quite likely more than anyone else since Eugène Penard) and explored the diversity of soil testate amoebae first in southern France and later throughout the world. He was fascinated by statistical analyses and taught biostatistics for many years at the University Paul Sabatier in Toulouse, France. He used statistics extensively on testate amoeba data for calculation of species optima, classification of communities including the development of a hierarchical classification similar to the one used for plant communities by phytosociologists. He also applied his statistical expertise to other topics such as pharmaceutical research, palaeontology, music and chaos theory. This work started in the 1960' at the time of the first computers and Louis Bonnet personally wrote the codes for the computer software he needed. He also contributed significantly to the study of testate amoeba general biology and biogeography and, in the days before molecular phylogeny, hypothesised on the evolutionary relationships among taxa based on morphological characters and especially shell shape… a topic that is discussed in this meeting! I had the privilege of meeting him in 1995 a few years after he retired, as I was starting my PhD. He gave me a precious pile of his publications and we discussed about academia, testate amoeba diversity, ecology and biogeography and the most interesting research avenues on testate amoebae. He told me that in his opinion the most interesting land to explore was New Guinea. In one of life's extraordinary coincidences, we happen to have received samples from Papua New Guinea just a few days ago. As this long dream finally comes true it is sad and ironic that I won't have a chance to share my excitement and discoveries with him. Louis Bonnet deposited his collection of permanent slide, images and much precious scientific material at the Natural History Museum of Geneva. It is a great relief to know that this invaluable scientific material is in good hands.

We thank ISOP for supporting the ISTA 9 ¾ meeting by allowing us to use the ISOP Zoom license and the University of Neuchâtel for logistical support.

Hoping ISTA 10 will take place as planned in Canada in 2022!

Neuchâtel, Switzerland, October 18th, 2021

Edward Mitchell, on behalf of the organising committee

Program

Monday Oct 18th: The Hog's Head Session - Fossils, taxonomy & phylogeny

1:00 PM 1:15 PM Edward Mitchell / Micah Dunthorn: Welcome / general info

1:15 PM 1:45 PM Keynote 1: Luana Morais, Uni. Sao Paulo, Brazil
Biomineralization in testate amoebae in the context of extreme environmental changes during the Neoproterozoic

1:45 PM 2:00 PM Kelly E. Tingle et al. - Organic Preservation of ~740-Million-Year-Old Fossil Arcellinids from the Grand Canyon, Arizona, USA

2:00 PM 2:15 PM Alfredo Porfirio-Sousa et al. - Rab GTPase gene family in Amoebozoa and molecular aspects of the shell formation process in Arcella

2:15 PM 2:30 PM Valentyna Krashevska et al. - Standardization and unification of testate amoeba shell morphological traits: A call for collaboration

2:30 PM 2:45 PM Poster flash presentations

- Maria Beatriz Gomes e Souza: Testate amoebae (Amoebozoa and Cercozoa) from Brazil: A contribution to taxonomy
- Jiahui Su: Diversity partitioning in the testate amoeba communities in the temperate climate zone
- Elena Malysheva et al.: Species composition and structure of testate amoeba communities in different ecoregions of Caucasus

2:45 PM 3:15 PM Break & poster breakout rooms

3:15 PM 3:44 PM Keynote 2: Anush Kosakyan, Czech Academy of Sciences, Czech Republic
The need for basic taxonomy and lessons learned from the monograph saga

3:44 PM 4:00 PM Aleksandr Ivanovskii - Using of taxa-based analysis for classification of microbe communities

4:00 PM 4:15 PM Julia Katalin Török - Assemblage of filose testate amoebae in the sandy river sediments of the River Danube

4:15 PM 4:30 PM Emanuela Samaritani - Introducing "The hidden world of microorganisms" children's book series

4:30 PM 5:00 PM Forum discussion

Tuesday Oct 19th: Gringotts Wizarding Bank Session - Ecology & palaeoecology

1:00 PM 1:15 PM Edward Mitchell / Micah Dunthorn: Welcome / general info ;
Tim Patterson and Françine MCCarthy: Introducing ISTA 10 !

1:15 PM 1:45 PM Keynote 3: Katarzyna Marcisz: Adam Mickiewicz University, Poland
The future of testate amoebae in palaeoecology

1:45 PM 2:00 PM Jean Claude Ndayishimiye et al. - Multi-habitat testate amoeba in temperate and subtropical urban parks

2:00 PM 2:15 PM Angela L. Creevy et al. - A Bit Shady: Response of Mixotrophic Testate Amoeba to Peatland Afforestation and Restoration with implications for the C Cycle

2:15 PM 2:30 PM Mariusz Lamentowicz et al. - Knights Hospitaller affected testate amoeba communities - the paleoecological reconstruction from a peatland archive in W Poland

2:30 PM 2:45 PM Poster flash presentations

- Azálea Pérez-Hernández et al.: Testate amoebae in a ~500-year record of Lake Nahá, Lacandon Forest, Mexico.
- Joanna Moreno et al.: Paleolimnological study of testate amoebae from two tropical high-mountain lakes in central Mexico during the last ~60 years.
- Anne V. Nguyen et al.: Testate amoebae as a proxy for reconstructing paleohydrological changes in the Mackenzie River Basin, Northwest Territories"
- Valentyna Krashevska, David Singer et al.: A community-wide effort to combine testate amoeba datasets

2:45 PM 3:15 PM Break & poster breakout rooms

3:15 PM 3:45 PM Keynote 4: Guillaume Lentendu, Laboratory of Soil Biodiversity, University of Neuchâtel, Switzerland
Testate amoebae in eDNA surveys: general overview and new hints for a successful use of metabarcoding

3:45 PM 4:00 PM Maïwenn Herlédan et al. - Biodiversity and paleobiodiversity of testate amoebae on Kerguelen islands: a key for climate change monitoring?

4:00 PM 4:15 PM Fernanda Charqueño-Celis et al. - Paleoecology of testate amoebae of the last ~200 yrs in a shallow lake from Patagonia, Argentina

4:15 PM 4:30 PM Andrea E. Rodas-Moran et al. - Testate amoebae as indicators of 20th-century environmental management at Laguna de Chichoj, Alta Verapaz Guatemala

4:30 PM 5:00 PM Forum discussion

Wednesday Oct 20th: Weasleys' Wizard Wheezes Session - Anything else dealing with testate amoebae!

1:00 PM 1:15 PM Edward Mitchell / Micah Dunthorn: Welcome / general info

1:15 PM 1:45 PM Keynote 5: Vincent Jassey: CNRS, Université Paul Sabatier Toulouse, F - Contribution of mixotrophic testate amoebae and photoautotrophic protists to peatland carbon cycle

1:45 PM 2:00 PM Elizaveta Ermolaeva et al. - Application of testate amoeba functional traits to infer paleohydrological changes in peatlands in the forest zone of the East-European plain

2:00 PM 2:15 PM Itzel Sigala et al. - Reconstruction of the trophic state of a warm monomictic Mexican lake using testate amoebae

2:15 PM 2:30 PM Michelle M. McKeown et al. - Assessing Testate Amoebae as Biological Indicator s for New Zealand Wetlands

2:30 PM 2:45 PM Poster flash presentations

- Abir Ghaffouli et al. - Modelling the microbial food webs in Sphagnum-dominated peatlands
- Anton Esaulov et al.: Spatial distribution of testate amoeba of the order Arcellinida from aapa mires in different scales
- Pamela García-Plata et al.: Diversity of testate amoebae in karst waterbodies of southern Mexico
- Giulia Ribeiro et al.: Experiments of arsenic resistance in Arcella intermedia

2:45 PM 3:15 PM Break & poster breakout rooms

3:15 PM 3:45 PM Keynote 6: Fatma Gomaa: Harvard University, USA
Protist symbiosis and metabolic adaptation to challenging environments

3:45 PM 4:00 PM Anaïs Bonetti et al. - Can the climatic and micro-environmental conditions of peat bogs be inferred from the morphometry of a single testate amoeba species?

4:00 PM 4:15 PM Kirill Babeshko et al. - Reconstruction of subarctic peatland development in NE Fennoscandia using testate amoebae and other proxies

4:15 PM 4:30 PM Wang W et al. Population and molecular responses to warming in Netzelia tuberspinifera – an endemic and sensitive protist from East Asia

4:30 PM 5:00 PM Award ceremony for prizes for the best talks and posters & conclusions of the meeting

Biographies and abstracts of Keynote speakers

Luana Morais

Institute of Geosciences, University of São Paulo, Brasil

Autobiography

My first academic appointment was at the Federal University of Mato Grosso do Sul, Brazil (2004 - 2008), when I graduated in Biology, studying bioarchaeology of Guarani's funeral urns. During my MSc thesis (2011 - 2013) under Thomas Fairchild supervision (University of São Paulo), I studied the paleobiology of precambrian rocks from Brazil, describing phosphatic and dolomitic microbialites. I obtained my PhD (2013 - 2017) from the same university, under Thomas Rich Fairchild and Daniel Lahr supervision, including an internship at UCSB and Harvard universities, under Susannah Porter and Andrew Knoll supervision, when I started to investigate the diversity of microfossils from Brazilian Precambrian deposits, including Vase-shaped microfossils, attributed to testate amoebae.

My PhD was followed by a postdoc (2017 - present) at the University of São Paulo with Ricardo Trindade and Juliana Leme, including an internship at University of Grenoble-Alpes, France, planned to start in late November (2021) under Alexandre Simionovici supervision. I have been working with the origin and evolution of biomineralization in unicellular and multicellular eukaryotic organisms in the context of environmental changes during the Precambrian (e.g., phosphogenetic events, global glaciations, variations in the magnetic field).

Keynote abstract

Biomineralization in testate amoebae in the context of extreme environmental changes during the Neoproterozoic

Luana Morais

Biomineralization in testate amoebae in the context of extreme environmental changes during the Neoproterozoic The Neoproterozoic was marked by profound changes in Earth's environment and biosphere, including global glaciations, their oceanographic and atmospheric consequences, appearance and spreading of macroscopic life and the acquisition of hard carapaces in unicellular and multicellular organisms. Detailed understanding of these processes and their interconnections is hindered by the limited paleontological record of Cryogenian systems.

In this talk we will integrate new information on morphology and composition of vase-shaped microfossils (VSMs) found throughout Cryogenian and Ediacaran successions associated with major iron formations as well as phosphorite deposits in central South America (Mato Grosso do Sul, Brazil). Our results shed light on the evolution of biomineralization and transition of VSMs and ultimately of testate amoebae to continental environments.

Anush Kosakyan

Institute of Parasitology, Biology Centre, Czech Academy of Sciences (CZ

Autobiography

I obtained my PhD from the University of Neuchâtel, Switzerland in 2014, under the co-supervision of Edward Mitchell and Enrique Lara, followed by a postdoc at the University of Sao Paulo, Brazil, with Dan Lahr. The microbial world has been a passion since my undergraduate days, but I really fell in love with testate amoebae during my PhD studies in Neuchâtel. I was impressed by the ability of a tiny cell to carefully select micro-particles from the environment and build such a variable and beautiful shell, and dying, preserving information about life on Earth.

The objective of my PhD project was to study the diversity, phylogeny and biogeography of free-living protists, using testate amoebae as a model group. We initiated the first studies in single cell barcoding of testate amoebae and extended or proposed new taxonomic concepts of many species, genera and families. At that time, it was obvious that many species groups needed an in-depth taxonomic analysis, and this was the reason for starting a taxonomic monograph on the family Hyalospheniidae, which will be available to the community soon.

With the advancement of next generation molecular techniques, we were eager to explore phylogeny and evolution of the testate amoebae using transcriptomic and genomic approaches. I continued my postdoctoral training in the evolution of testate amoebae in the Department of Biosciences, University of Sao Paulo, Brazil. There I studied the evolutionary history of the arcellinid testate amoebae using detailed morphological and molecular data. This was a pioneering research where we used a single-cell transcriptomic approach to generate the first multigene phylogeny (based on 250 genes) of the group. We presented a different perspective on the evolution of microorganisms on our planet: while the Precambrian period was thought to have had low biotic diversity, we have shown that the major lineages of testate amoebae were diversified before the Sturtian glaciation (720 Mya).

Being fascinated by next generation molecular tools and their potential, I joined (2016) the Institute of Parasitology, Biology Centre, Czech Academy of Sciences (CZ) to study myxozoan

parasites and host-parasite interactions using transcriptomic and genomic techniques. However, this has not stopped me from continuing to work on testate amoebae in parallel in various side projects. I believe that studying testate amoebae will always remain a passion of mine and I hope to explore them further soon using new transcriptomics and comparative genomic approaches.

Keynote abstract

The need for basic taxonomy and lessons learned from the monograph saga

Anush Kosakyan

The application range of testate amoebae is rapidly expanding, from traditional research areas such as environmental monitoring and paleoecology to ecotoxicology, evolutionary studies, transcriptomics, and genomics. All of these developments are very promising, but greatly depend on sound taxonomy. However, taxonomic data on these organisms suffers from number of limitations, and a common, standardized taxonomic data pool accessible to members of the research community is currently lacking.

Undoubtedly, novel molecular tools combined with high performance light and scanning electron microscopy offer the possibility of producing high quality species descriptions. However, the lack of a thorough taxonomic analysis of the species group can often lead to confusion and even question the validity of newly described taxa. While preparing a monograph on a single family of testate amoebae (Hyalospheniidae), we realized how superficial our knowledge of many taxa is and how much this can be an obstacle in recognizing and describing a species, or in leading to precise ecological conclusions. Today, as new molecular tools continue to upend the old taxonomic concepts of species (or higher hierarchical groups), it is more necessary than ever to understand and thoroughly analyze the taxonomic history, ecology and biogeography of each species.

In this talk, I will discuss what the current state of taxonomic research in testate amoebae is and what the most obvious obstacles to progress in this field are. I will also summarize and propose a number of possible tools that can help improve and build a modern taxonomic framework that can provide a solid background for more straightforward and accurate research in the various testate amoebae disciplines.

Katarzyna Marcisz

Climate Change Ecology Research Unit, Institute of Geoecology and Geoinformation,
Adam Mickiewicz University, Poznań, Poland

Autobiography

I obtained my PhD from Adam Mickiewicz University, Poznań, Poland in 2015, under Mariusz Lamentowicz, and I continue to work at AMU. In 2013, during my PhD I got a SCIEX scholarship and worked at the University of Bern, Switzerland in Willy Tinner's lab, where I came back for a postdoc in 2016-2017. I am currently pursuing a habilitation degree in Poland.

My PhD was dedicated to ecology and paleoecology of testate amoebae. I first worked on a global change field experiment with Edward Mitchell and Bertrand Fournier (University of Neuchâtel, Switzerland) which was a great introduction into the microworld of testate amoebae. This was followed by observational seasonal studies conducted on a small peatland in northern Poland with Sandra Słowińska and Michał Słowiński (Polish Academy of Sciences). However, it is palaeoecology that is the most exciting for me and I have been focusing on this area of research while working at the AMU with Mariusz Lamentowicz and colleagues. I worked on different types of peatlands in Europe and Siberia using multi-proxy palaeoecology, incorporating trait-based paleoecology to my research.

Next to testate amoebae, I am interested in past fire reconstructions from peatlands and vegetation history in the Holocene, and was lucky to work on this subject in one of the top fire paleoecology lab with Willy Tinner and Daniele Colombaroli (University of Bern, Switzerland). Since 2019 I am also Secretary General of the International Paleofire Network.

Keynote abstract

The future of testate amoebae in palaeoecology

Katarzyna Marcisz

Testate amoebae are commonly used as proxy in palaeoecological studies of peatlands and lakes. They are especially valuable because they provide quantitative reconstructions of past water table depth, greatly supporting multi-proxy palaeoecological studies. Palaeoecology is constantly changing, even though sometimes it may seem that the novelty is not that high – especially when compared to e.g., quickly developing molecular approaches.

In recent years palaeoecological studies have done a big progress, both when it comes to proxy development and increasing resolution of studies. But what will the future bring?

In this talk I will highlight my predictions on the future development of palaeoecological research, including the role and position of testate amoebae. I will elaborate on multi-proxy studies, integration of paleoecological records, and exploration of new study areas. I will also highlight the need of incorporation of high-resolution sampling and sediment dating that can greatly enhance our understanding of past environmental changes, giving us much better look into the past relationships between palaeoecological proxies and the influence of different environmental components on testate amoeba communities.

Guillaume Lentendu

Laboratory of Soil Biodiversity, Institute of Biology,
University of Neuchâtel, Switzerland

Autobiography

I obtained my PhD from the University of Leipzig, Germany, in 2015, under the supervision of F. Buscot, C. Wilhelm and M. Schlegel followed by a Post-Doc at the Helmoltz Centre for Environmental Research in Halle, Germany, under F. Buscot and T. Wubet.

My PhD was dedicated to the development of new metabarcoding methods to characterize all eukaryotic microbes in terrestrial ecosystem and to investigate the long-term effect of soil fertilization on their diversity, while my first post-doc allows me to expand my metabarcoding analytical skills over the full microbial spectrum.

In a second Post-Doc at the University of Kaiserlautern, Germany, under M. Dunthorn and T. Stoeck, I focus my research on the biogeography and assemby of protist communities in terrestrial and marine biomes.

I am currently a scientific collaborator at the University of Neuchâtel, Switzerland, under Edward Mitchell. I focus my research on protist distribution along elevation gradients and on how island biogeography theories may apply to these organisms. I specialized into the development and use of next-generation sequencing molecular and bioinformatic methods to characterize microbial terrestrial biodiversity, but also in the analyses of their phylogenetic, functional and assembly patterns. I recently start to broaden my interest on soil micro-fauna for which I leverage my metabarcoding skills to allow for their systematic inventory in Switzerland.

Keynote abstract

Testate amoebae in eDNA surveys: general overview and new hints for a successful use of metabarcoding

Guillaume Lentendu

Multiple protist groups are represented in low abundance in soils which make them difficult to detect in environmental DNA surveys. This phenomenon is amplified by the large amount of non-target co-amplification of plant, animal and fungi when using general eukaryotes PCR primers. Different strategies have been adopted to track these low abundant taxa, from which testate amoebae: deep sequencing, target sequencing or enrichment.

In my presentation, I will present the different methods at hands to perform a metabarcoding survey of testate amoebae, the good practices for PCR and sequencing library preparation and the pitfalls to avoid (e.g., co-amplification of sphagnum DNA in peat bog samples). I will also present novel results from physical enrichment of testate amoebae prior to DNA extraction for metabarcoding survey. In this study, the efficiency of the enrichment method on the recovery of the full protist community as well as the specific testate amoebae community were compared to bulk soil samples by mean of V4 18S HTS. Forest and alpine grassland soils from the Swiss Alps, Sierra Nevada, La Réunion and Hokkaido were used to test for patterns of alpha and beta diversity in relation to habitat, country and method.

Differential abundance analyses showed that Euglyphida, Arcellinida, the two main groups of testate amoebae as well as Chrysophyceae were significantly enriched in the filtered samples compared to bulk soil, while, plant, fungi and animal except for tardigrades and rotifers were significantly depleted. Overall protist alpha diversity and community composition were not affected by the enrichment but community structure varied among habitat and region. Both bulk soil DNA and enriched soil DNA provided comparable diversity estimates and led to the same ecological conclusion, while enrichment increased the representativity of shelled unicellular clades or high biomass micro-metazoan clades.

The systematic application of this protocol would improve the description of low abundant soil unicellular eukaryotic clades like testate amoebae, while significantly reducing the signal of plant, animal and fungi, and without compromising the ecological conclusion drawn from the whole protist communities.

Vincent E. J. Jassey

Laboratoire Ecologie Fonctionnelle et Environnement,
Université de Toulouse, UPS, CNRS, Toulouse, France

Autobiography

I obtained my PhD from the University of Franche Comté, France, in 2011, under Geneviève Chiapusio, Philippe Binet and Daniel Gilbert, followed by two postdocs at the Swiss Federal Institute for Forest, Snow and Landscape Research (WSL), Switzerland, with Alexandre Buttler. Following these two post-docs, I got a research position at the French National Centre for Scientific Research (CNRS) in 2017.

I started studying testate amoebae, by chance, during my MSc thesis under Daniel Gilbert (University of Franche Comté). From a simple microbial group among others, testate amoebae quickly became of great interest for me because of their role in microbial food webs and ecosystem processes. Although I am more and more interested by microbial diversity on its own, I still love observing testate amoebae at the microscope.

Starting with community ecology of peatland testate amoebae and their use as indicators of climate warming, my research expanded to microbial ecology, climate change ecology, ecosystem ecology and machine learning approaches to study the diversity and spatio-temporal patterns of soil microbes in terrestrial ecosystems, from local to global scales. I like using combination of field observations and experiments, lab experiments, and mathematical models to figure out how organisms and their specific functions change the dynamics of living communities, and related ecosystem processes. I am particularly interested at understanding and predicting how the response to climate changes of species and their traits affect ecological networks, and how these changes play out in ecosystem functioning. I am an exclusive peatland lover but I not against a little infidelity in tropical rainforests on occasion!

Keynote abstract

Contribution of mixotrophic testate amoebae and photoautotrophic protists to peatland carbon cycle

Vincent E.J. Jassey

Mixotrophic testate amoeba and photoautotrophic protists, also known as microalgae, are omnipresent in peatland's surface. Despite their high abundance, their rate of carbon (C) fixation through photosynthesis remains largely overlooked while it could significantly contribute to peatland C balance.

Here, I will present an overview of the contribution of photoautotrophic microbes to peatland C uptake across local and regional environmental gradients, and how their response to climate change could influence peatland C balance.

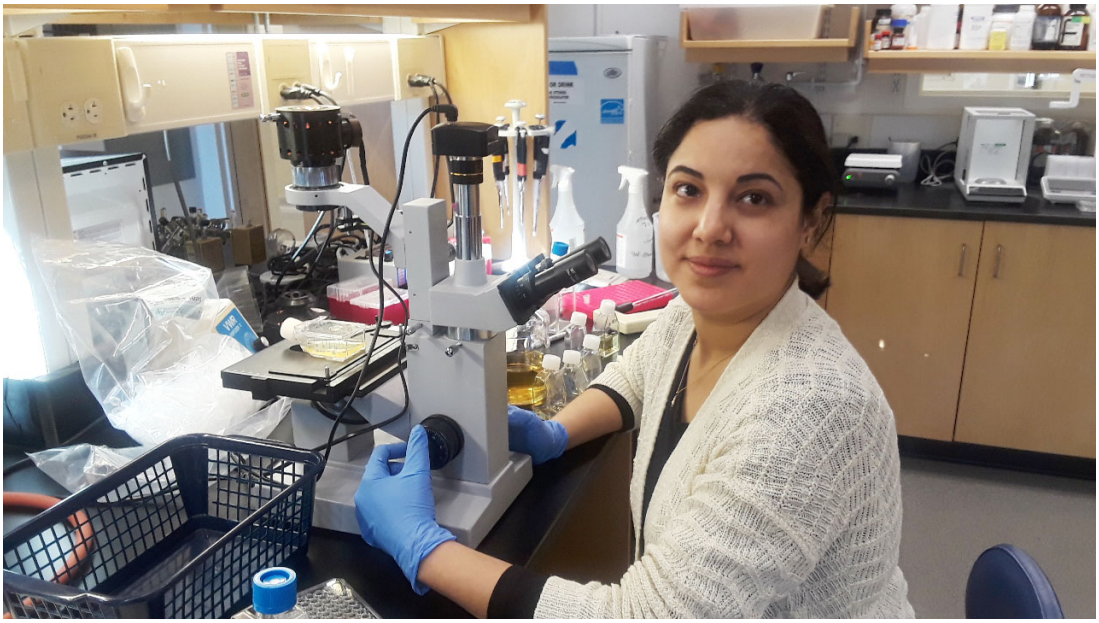
First, I will explore photoautotrophic communities among peatland microhabitats, from pond to forested peatland, and show that the structure of photoautotrophic microbial communities strongly varies across microhabitats. Along with these structural changes, I will further show that photoautotrophic C uptake is higher in the relatively driest and shadiest peatland microhabitats.

Second, I will explore mixotrophic testate amoebae and photoautotrophic protists in five peatlands distributed along a latitudinal gradient in Europe. Despite community turnover from photoautotrophic dominance towards mixotrophic dominance, I will show that microbial photosynthetic rates remain similar along the latitudinal gradient, and represent ca. 10% of peatland C uptake.

Third, I will show that the response of photoautotrophic microbes to climate change, and especially mixotrophic testate amoebae, could strongly impact peatland C uptake. In conclusion, these findings will show that mixotrophic testate amoebae and photoautotrophic microbes significantly contribute to peatland C cycle and should be included in peatland C models.

Fatma Gomaa

Department Geology and Geophysics in Wood Hole Oceanographic Institution &
Department of Organismic and Evolutionary Biology, Harvard University.



Dr. Fatma Gomaa is a Research Associate in the Department Geology and Geophysics in WHOI and a Visiting Research Associate in the Department of Organismic and Evolutionary Biology, Harvard University. She obtained her PhD in 2013 from University of Neuchatel, Switzerland with Prof. Edward Mitchell (Soil Biology Laboratory), where she studied the phylogeny, taxonomy and symbiosis of testate amoebae, a group of amoeboid protists (single cell eukaryotes).

After receiving her PhD, Dr. Gomaa moved to the USA and joined Prof. Cavanaugh lab at Harvard University to study bacterial symbiosis in protists. She used the testate amoeba *Arcella* spp. as model organisms to investigate the specificity and diversity of *Arcella*-associated microbial communities and to explore whether *Arcella* species could be distinguished based on its bacterial composition. Her current research with Dr. Bernhard (WHOI) and Edgcomb (WHOI) focuses on understanding the physiology and the adaptive metabolic pathways in protists that inhabit hostile environments, including oxygen-depleted marine sediments and freshwater environments polluted with heavy metals such as arsenic.

Dr. Gomaa addresses these questions in a wide range of systems with diverse approaches, ranging from measuring gene expression data from benthic foraminifera thriving in the deep-sea to the effects of arsenic pollution on the model laboratory ciliate *Tetrahymena thermophila* to developing CRISPR/Cas9 genome editing systems in marine protists. As protists form myriad lineages in the tree of life and represent the evolutionary ancestors of multicellular animals, plants and fungi, better understanding the roles of the diversity of protists is critical to understanding biogeochemical cycling and the evolution and ecology of the microbial Eukarya.

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Research Gate: https://www.researchgate.net/profile/Fatma_Gomaa

Keynote abstract

Protist symbiosis and metabolic adaptation to challenging environments

Fatma Gomaa

Research on protist-bacteria interactions and symbiosis is increasingly relevant as these associations are now known to play important roles in ecosystem and human health. Free-living amoebae are abundant in all environments and are frequent hosts for bacterial endosymbionts including pathogenic bacteria. Here, we use the testate amoeba Arcella spp. as model organisms to investigate the diversity and specificity of Arcella-associated microbial communities using the 16S rRNA amplicon gene sequence. Our results revealed that Arcella host diverse bacterial communities and that the Arcella-bacteria associations appear to be species-specific and distinct from that of the surrounding media.

The benthic foraminifer Nonionella stella dominates the abundant foraminiferal community inhabiting laminated, oxygen depleted and sometimes sulfidic sediments of the Santa Barbara Basin, comprising up to ~80% of the living assemblage, with densities sometimes exceeding 200 specimens per cubic cm. Gene expression from field-collected and laboratory-incubated samples, showed that N. stella expressed denitrification genes regardless of oxygen regime, and anerobic energy metabolism genes. Our results also revealed, a near-complete expression of a diatom's plastid genome, suggests kleptoplasty, sequestration of functional plastids, conferring a metabolic advantage despite the host living far below the euphotic zone. Benthic foraminifera, through a unique integration of functions largely unrecognized among "typical" eukaryotes, represent winning micro-eukaryotes in the face of ongoing oceanic deoxygenation.

There are many groups of protists known as excellent bioindicators for monitoring ecosystem health. I studied the effect of Arsenic pollution on eukaryotic cell using Ciliate Tetrahymena thermophila as a model organism in laboratory cultures. Transcriptomic data from cells exposed to different concentration of ASIII showed that Arsenic induced changes in gene expression and identified genes and pathways that play roles in AS III metabolism, transportation and detoxification. Our results leverage the use of protists as ecological monitoring and bioremediation.

Abstract of contributed talks and posters

Monday Oct 18th: The Hog's Head Session - Fossils, taxonomy & phylogeny

Contributed talks

Kelly E. Tingle 1, Susannah M. Porter 1, Morgan R. Raven 1, Andrew D. Czaja 2

Department of Earth Science, University of California, Santa Barbara 1, Department of Geology, University of Cincinnati 2, e-mail: kelly.e.tingle@vanderbilt.edu

Organic Preservation of ~740-Million-Year-Old Fossil Arcellinids from the Grand Canyon, Arizona, USA

Vase-shaped microfossils (VSMs) are found globally in 800–730-million-year-old marine rocks and are interpreted as the tests of arcellinids. VSMs are sometimes reported preserved as carbonaceous tests, thought to reflect the original test wall material, but most reports are unconfirmed. Carbonaceous VSMs were described from the Grand Canyon, AZ, USA, but a later study speculated that the fossils were organic-coated siliceous casts. This study re-examined the Grand Canyon VSMs to re-evaluate preservation mode(s). Of the VSMs sampled, 29 are carbonaceous tests and 37 are either partial or complete mineralized casts. We conclude that some of these ancient microfossils are preserved with original organic walls and speculate about what could have promoted this exceptional preservation."

Alfredo Porfirio-Sousa 1 & Alexander Tice 2,3 & Matthew Brown 2,3 & Daniel Lahr 1

1- Dept. of Zoology, University of Sao Paulo 2- Dept. of Biological Sciences, Mississippi State University 3- Institute for Genomics, Biocomputing and Biotechnology, Mississippi State University, e-mail: alfredo.sousa@usp.br

Rab GTPase gene family in Amoebozoa and molecular aspects of the shell formation process in Arcella

The shell represents an evolutionary novelty in Arcellinida (Amoebozoa). Cytomorphological descriptions, especially for the genus *Arcella*, demonstrate that the shell formation process involves polarized exocytosis. Currently, we lack the understanding of the molecular apparatus underlying the shell formation process in these organisms, impairing the inference of the evolutionary events involved in the shell origin. Here, we report a comprehensive phylogenetic reconstruction of the Rab GTPase gene family in Amoebozoa. Rab GTPases comprise the central controller of vesicle traffic and exocytosis in diverse eukaryotes. Our study identified that Arcellinida have expasion of Rab members involved with exocytosis, representing candidate genes that may participate in the shell formation process.

Valentyna Krashevska 1, Andrey N. Tsyganov 2,3, Ferry Siemensma 4, Yuri A. Mazei 2,3

1 J.F. Blumenbach Institute of Zoology and Anthropology, University of Goettingen, Germany, 2 Lomonosov Moscow State University, Moscow, Russia , 3 Severtsov Institute of Ecology and Evolution RAS, Moscow, Russia , 4 Julianaweg 10, 1241VW Kortenhoef, the Netherlands, e-mail: andrey.tsyganov@bk.ru

Standardization and unification of testate amoeba shell morphological traits: A call for collaboration

The morphological description of testate amoebae begun more than 200 years ago, resulting in a wide variety of information published in various languages and inconsistent terminology. Precise descriptions of morphological characteristics are necessary for taxonomic descriptions and for ecological application of these organisms. Unification, standardization and visualization of morphological traits are necessary to facilitate and improve the basis for development in this field of protistology. In this work, we have revised, structured and visualized the most important morphological traits of testate amoeba shells. For new generations of researchers, this provides a chance to take an easy step in this field, whereas advanced researchers will get an easier possibility to spread the knowledge.

Aleksandr Ivanovskii

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Using of taxa-based analysis for classification of microbe communities

The only way for us to cope with variety of communities is a classification of them. Using methods of clustering and ordination, we mostly deal with localities, biotopes. In some methods of clustering and ordination we can involve as well data based on all species via using different similarity indices. But also, we can use less popular (having the less number of R's libraries) methods based on analysis of non-random species associations. It allows us to deal with every certain species in its interrelations with each other species. Using analysis of non-random species associations based on species co-occurrence matrix can help to reveal clusters of interrelated species which can, in turn, mark certain types of biotopes as well as certain repetitive variants of communities.

Julia Katalin Török

Department of Systematic Zoology and Ecology, Eotvos Lorand University, Budapest, e-mail: torokjul@elte.hu

Assemblage of filose testate amoebae in the sandy river sediments of the River Danube

The non-silting, sandy sediments of the Danube River host freshwater, psammobiont and psammophilic testate amoebae. Psammobiont species include freshwater members of the genera *Corythionella* and *Psammonobiotus*. Additional rare species in the same habitat are considered to be psammophilic, based on their previously known habitats: *Cyphoderia calceolus, C. myosurus* and *Paramphitrema lemanense*. This TA assemblage is highly dependent on the water regime of the Danube and has so far not been observed elsewhere together. To our present knowledge, all the mentioned species are restricted to Europe and partly, North America, thus, exhibiting a distinct geographic distribution. Further investigation of nutrient-poor sediments could reveal more about this delicate assemblage.

Emanuela Samaritani

Route de la Gruyère 3, Fribourg, Switzerland e-mail: emanuela.samaritani@gmail.com

The hidden world of microorganisms

Protists have been shown to be crucial in driving and maintaining ecosystems' functioning. Studying and understanding their diversity and dynamics is especially important in the climate crisis we are and will be facing in the years to come. Studies and projects aiming at conservation and protection of biodiversity and ecosystems needs to be supported by policy makers and ideally the population to be swiftly implemented. Despite their importance for the environment, they are far from being a main subject in mainstream education. Thehiddenworld.co.uk is a project aiming at introducing children to the wonders of microorganisms, through a website and the publication of a series of illustrated books. Introducing “The hidden world of diatoms” and “The hidden world of testate amoebae”.

Posters

Maria Beatriz Gomes e Souza,

e-mail: mbiags@gmail.com

Testate amoebae (Amoebozoa and Cercozoa) from Brazil: A contribution to taxonomy.

Since 1985 I have been studying and recording testate amoebae in various regions of different environments in Brazil in preferentially preserved locations: Aquatic, Mosses and Litter Forest. The determination of the taxa followed the original descriptions of the species. So far, 245 samples have been analyzed and 384 taxa were identified, including 71 morphotypes. A single sample collected in the rhizosphere from an aquatic environment, in the Amazon region, presented more of 100 taxa, indicating the high biodiversity of this biome/ecotone for the testate amoebae. The genera *Lesquereusia* and *Euglypha* stand out, very common in shallow and hot lakes in Brazil, which have many taxa to be described, probably endemic to the Continent. All identified taxa in my website: www.tecamebas.com.br.

Jiahui Su

Shenzhen MSU-BIT University, e-mail: 1304518917@qq.com

Diversity partitioning in the testate amoeba communities in the temperate climate zone

In order to better understand the distribution patterns of testate amoeba and the factors governing distribution, we adopted the hierarchical nesting of sampling design, and performed the hierarchical analysis of the alpha and beta-diversity of testate amoebae in western Siberian ecosystems. We analyzed the variation in species richness and community structure of testate amoeba assemblages using an additive partitioning method and two approaches to beta-diversity decomposition. There is a prominent latitudinal diversity gradient which is determined by within-sample α-diversity and among-ecosystem β-diversity. This highlights the role of both small-scale heterogeneity at the micro-habitat level and large-scale heterogeneity determined mostly by vegetation structure.

Elena Malysheva 1, Andrey Tsyganov 3, Boris Levin 2, Yuri Mazey 3

1 Penza State University, Penza, Russia, 2 I.D. Papanin Institute of Biology of Inland Waters of the Russian Academy of Sciences, Yaroslavl Region, Borok, Russia, 3 Lomonosov Moscow State University, Moscow, Russia, e-mail: elenamalysheva@list.ru

Species composition and structure of testate amoeba communities in different ecoregions of Caucasus

The biodiversity, abundance and structure of testate amoeba communities from 72 different biotopes covering all the ecoregions of the Caucasus (Western Caspian Drainages, Kuban, West Transcaucasian, Kura-South Caspian) were studied. 107 species and infraspecific taxa belonging to 27 genera were identified from aquatic sediments and moss biotopes located at different altitudes (20 – 2269 m a.s.l.). The main types of communities are distinguished on the basis of species composition. There is no clear effect of altitude and ecoregion on testate amoeba community structure. Type of the biotope is the main factor of the assembly of testate amoeba assemblages.

Tuesday Oct 19th: Gringotts Wizarding Bank Session - Ecology & palaeoecology

Contributed talks

Jean Claude Ndayishimiye 1, Yuri Mazei 1,2,3, Kirill Babeshko 1,2, Andrey Tsyganov 2,3, Anatoly Bobrov 2, Natalia Mazei 2, Damir Saldaev 1,2, Aleksandr Ivanovskii 1,2, Pascaline Nyirabuhoro 1, Kexin Ren 4, Mamun Abdullah Al 4, Huihuang Chen 4, Wenping Wang 4, Jun Yang 4

1Faculty of Biology, Shenzhen MSU-BIT University, International University, Shenzhen, China, 2 Lomonosov Moscow State University, Moscow, Russia, 3 A.N. Severtsov Institute of Ecology and Evolution, Russsian Academy of Sciences, , Moscow, Russia, 4 Aquatic EcoHealth Group, Fujian Key Laboratory of Watershed Ecology, Key Laboratory of Urban Environment and Health, Institute of Urban Environment, Chinese Academy of Sciences, Xiamen, China, e-mail: ndayiclaude2006@yahoo.fr

Multi-habitat testate amoeba in temperate and subtropical urban parks

Urbanization results in local habitat fragmentation, influencing ecological processes and biodiversity. Testate amoebae from temperate (Moscow) and subtropical (Xiamen) urban parks across four habitats (tree hole, moss, soil and sediment) have been studied. A total of 119 morphospecies were identified. The species richness per habitat was higher in the tree hole and moss microhabitats comparing with soils or sediments. The impact of stochastic processes (random changes in demographic processes) on the community was more important than deterministic (non-random patterns in the biotic neighbourhoods of species) in both temperate and subtropical parks. We acknowledge RFBR (20-54-53017), NNSF of China (31672312, 32011530074) and Shenzhen NSF (20200828181231001) for the financial support."

Angela L. Creevy a*, David M. Wilkinson b, Roxane Andersen c, James G. Rowson a and Richard J. Payne de (deceased)

a Edge Hill University, Geography Department, , Ormskirk, Lancashire, UK, b School of Life Sciences, University of Lincoln, Lincoln, UK, c Environmental Research Institute, University of the Highlands and Islands, Thurso, UK, d University of York, Environment Department, Heslington, York, UK, e Department of Zoology and Ecology, Penza State University, Penza, Russia, e-mail: a.l.creevy@gmail.com

A bit shady: Response of mixotrophic testate amoeba to peatland afforestation and restoration with implications for the C cycle

Afforestation of open peatland compromises their ability to function as a net sink of atmospheric carbon dioxide (CO2) and may become sources of CO2 and other greenhouse gases (GHGs) including methane (CH4). Mixotrophic testate amoebae (MTA) are increasingly recognised for their dual role in peatland carbon (C) cycling. To better understand the role of MTA in peatland C cycling, more work is needed to examine community structure and relate with in situ fluxes of energy in peatland ecosystems. This talk presents studies which investigated the structure of testate amoeba communities at forest-to-bog restoration sites and explores microbial controls on C fluxes. This work highlighted how little we know about the relative role of different microbial groups in driving peatland GHG fluxes."

Mariusz Lamentowicz1, Katarzyna Marcisz1, Piotr Guzowski2, Mariusz Gałka3, Andrei-Cosmin Diaconu4, Piotr Kołaczek1

1 Laboratory of Climate Change Ecology, Faculty of Geographical and Geological Sciences, Adam Mickiewicz University, Poznan, Poland, 2 Institute of History and Political Sciences, University of Bialystok, 15-420 Bialystok, Poland, 3 Department of Geobotany and Plant Ecology, Faculty of Biology and Environmental Protection, University of Lodz, 12/16 Banacha Str., Lodz, Poland, 4 Department of Geology, Babes-Bolyai University, 400084 Cluj-Napoca, Romania, e-mail: mariuszl@amu.edu.pl

Knights Hospitaller affected testate amoeba communities - the paleoecological reconstruction from a peatland archive in W Poland

Knights Hospitaller and testate amoebae (TA) past relationships were rarely explored in palaeoecology. We studied a peat core in W Poland and used an opportunity to study the economic activity of medieval societies that was highly modified by new rulers— the Joannites (Knights Hospitaller). Knights lived in a castle and testate amoebae in a peatland, but their histories appeared be connected. The fen with open water and submerged vegetation switched into the acid Sphagnum dominated by mixotrophic TA. Water table reconstruction showed ca. 0 cm water level before the Joannites arrival which started to decrease since ca. 1350 CE, then stabilized at the level of ca. 11 cm from ca. 1450 CE until 1930 CE. Joannites created a shift into a novel habitat of the peatlands' protists."

Maïwenn Herlédan 1, Marina Hennion 1, Marion Delattre 1, Viviane Bout-Roumazeilles 1, Eric Armynot du Châtelet 1

1-Univ. Lille, CNRS, Univ. Littoral Côte d'Opale, IRD, UMR 8187, LOG, Laboratoire d'Océanologie et de Géosciences, F - 59 000 Lille, France, e-mail: maiwenn.herledan.etu@univ-lille.fr

Biodiversity and paleobiodiversity of testate amoebae on Kerguelen Islands : a key for climate change monitoring?

The Kerguelen Archipelago, located at the level of the polar front, is subject to recent climate changes. Records in the ice cap show a decline in precipitation linked to the oscillations of this front. The amoebae tested were used to monitor these changes. Surface and modern core samples were collected from the archipelago in 2019. The modern samples supplemented the database of tested amoebae made by L. Bonnet with samples from 1972-73. The modern tested amoebae are used in this database for past reconstruction. Results from an *Azorella selago* cushion core with 150 years of accumulation will be presented. An increase in concentration and diversity is observed with a peak when water content is at its maximum. In parallel, we observed an increase in C, N, H and S% along the sediment core."

Fernanda Charqueño-Celis 1; Itzel Sigala 2; Liseth Pérez 3; Julieta Massaferro 1

1. CONICET, CENAC-PNNH, Fagnano 244, 8400 Bariloche, Rio Negro, Argentina. fcharquenocelis@comahue-conicet.gob.ar , 2. Instituto de Geofísica, Universidad Nacional Autónoma de México, Ciudad Universitaria, 04510, Ciudad de México, 3. Institut für Geosysteme und Bioindikation, Technische Universität Braunschweig, Langer Kamp 19c, 38106, Germany. e-mail: feri2000c@hotmail.com

Paleoecology of testate amoebae of the last ~200 yrs in a shallow lake from Patagonia, Argentina

In a 37cm sediment record from Gemelas lake, in southern Patagonian Ice Field (Argentina) we identify 10 taxa divide in 3 groups according to their abundance during the last 200yrs. 1) *Lagenodifflugia vas* assemblage, 2) *Difflugia glans* assemblage, and 3) *D. urens* assemblage. Multivariate analysis identified Ca (5.6%) as the geochemical element with the highest variance explaining the ordination that is related to ash deposition. As a preliminary conclusion, we identify that ash depositions were the most important events causing changes of testate amoebae during the last ~200 yrs in L. Gemelas. However, this signal could mask climate events that have a strong influence on testate amoebae assemblages."

Andrea Rodas-Moran 1, Carlos E. Avendaño1 & Gilles Brocard2

1Universidad de San Carlos de Guatemala 2Université de Lyon 2, e-mail: ducuchu@gmail.com

Testate amoebae as indicators of 20th-century environmental management at Laguna de Chichoj, Alta Verapaz Guatemala

Lake Chichoj, located in the Guatemalan province of Alta Verapaz, has been exposed to rapid environmental deterioration due to improper management during the last 50 years, losing 40% of its surface. To reconstruct the lake's ecological and pollution changes during the 20th century, we reviewed the fossil testate amoebae assemblages collected from a sediment core. Based on conglomerate and similarity analysis, we identified three fossil testate amoebae assemblages: Early 20th-century phase (before 1926), middle 20th-century phase (approximately in the 1940s), and post-1950 (since 1958). The middle 20th-century phase and post-1950 testate amoebae assemblages coincided with the increase of migration and expansion of industrial activities.

Posters

Azálea Pérez-Hernández 1, Itzel Sigala2, Julieta Massaferro3, Alexander Correa-Metrio2, Karla Rubio4, Felipe Franco-Gaviria5 & Liseth Pérez6.

1Facultad de Ciencias, Universidad Nacional Autónoma de México, CDMX, Mexico., 2Instituto de Geología, Universidad Nacional Autónoma de México, CDMX, Mexico., 3CENAC-PNNH-CONICET, Bariloche, Argentina., 4MARUM, Bremen Universität, Bremen, Germany., 5Department of Geography, University of Exeter, Exeter, United Kingdom., 6Institut für Geosysteme und Bioindikation, Technische Universität Braunschweig, Braunschweig, Germany., e-mail: azalea_ph@ciencias.unam.m

Testate amoebae in a ~500-year record of Lake Nahá, Lacandon Forest, Mexico

In Mexico there is little information on the past changes of testate amoebae in lakes. Here, we studied the testate amoebae in a 500-year record of karst Lake Nahá, located in a Protected Natural Area inside Lacandon Forest, southern Mexico. We retrieved a 60-cm long sediment core corresponds to ~ 472 cal years BP. Subsampling was done every 5 cm, sediment samples were sieved and analyzed under a stereomicroscope to extract and count all tests. Preliminary results show us a total of 17 taxa distributed in five genera were identified, being Centropyxis aculeata var. aculeata, *C. aculeata var. discoides, C. constricta var. constricta* and *C. constricta var. spinosa* are always present, while other taxa are randomly distributed. With a Q-mode cluster analysis, four assemblages were identified."

Joanna Moreno 1,2, Margarita Caballero 1, Itzel Sigala 2, Mireya Vega-Flores 1,2, Luis Oseguera A.3, Javier Alcocer 3 and Ana Carolina Ruiz-Fernández 4

1: Laboratorio de Paleolimnología, Instituto de Geofísica, Universidad Nacional Autónoma de México, Ciudad Universitaria, 04510, México City, México, 2: Facultad de Ciencias, Universidad Nacional Autónoma de México, Ciudad Universitaria, 04510, México City, México, 3: Grupo de Investigación en Limnología Tropical, Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México, Av. de los Barrios No.1, Los Reyes Iztacala, 54090 Tlalnepantla, Estado de México, México, 3: Instituto de Ciencias del Mar y Limnología, Universidad Nacional Autónoma de México, Unidad Académica Mazatlán, Joel Montes Camarena s/n, Col. Playa Sur, 82040, Mazatlán, Sinaloa, México., e-mail: joanna_moreno@ciencias.unam.m

Paleolimnological study of testate amoebae from two tropical high-mountain lakes in central Mexico during the last ~60 years.

The tropical high-mountain lakes La Luna and El Sol, inside the crater of the Nevado de Toluca Volcano. To carry out a high-resolution paleolimnological study, two short sediment cores were taken in Lakes La Luna and El Sol. We established a chronological framework with a 210Pb analysis, corresponding to the last ~60 years. Testate amoebae preserved in the first ten centimeters of each core were analyzed, of which, *Difflugia glans* strain “glans” y *Difflugia globulosa*, were the most abundant taxa. On the other hand, changes were observed in the testate amoeba assemblages’ composition (El Sol) and dominance (La Luna) during the last 20 to 25 years, together with an increase in Fe content, mass accumulation rates, and organic carbon. These changes are signs of anthropogenic impact to the lakes."

Anne V. Nguyen, Jennifer M. Galloway, Sarah Lord, Leon Clarke, Mariusz Gałka, R. Timothy Patterson

1 Carleton University, 1125 Colonel By Dr, Ottawa, ON K1S 5B6, 2 Geological Survey of Canada, 3303 33 St NW, Calgary, AB T2L 2A7, 3 Gwich'in Renewable Resources Board, 105 Veteran's Way, Inuvik, NT X0E 0T0, 4 Manchester Metropolitan University, All Saints, Birley Fields, 5 University of Łódź, ul. Prez. Gabriela Narutowicza 68, 90-136 Łódź, Poland. e-mail: annenguyen4@cmail.carleton.ca

Testate amoebae as a proxy for reconstructing paleohydrological changes in the Mackenzie River Basin, Northwest Territories

The Mackenzie River Basin (MRB) is one of the largest drainage basins in Canada. Northern basins such as the MRB are subject to “Arctic amplification”, where average temperatures in the Arctic are increasing twice as fast as the global average. Paleoecological transfer functions calibrated to modern testate amoebae (TA) distributional data will be used to reconstruct hydrological variation in the MRB. This data will be compared to known ocean-atmosphere interactions that have influenced the paleoclimate of North America through the Neoglacial phase of the late Holocene. A multidisciplinary framework will also be produced to provide further insight into drivers of long-term hydrological changes and form the basis for improved predictions using ecohydrological modelling.”

Valentyna Krashevska 1, Testate amoeba community, David Singer 2

1 J.F. Blumenbach Institute of Zoology and Anthropology, University of Göttingen, Germany, 2 UMR CNRS 6112 LPG-BIAF, Université d’Angers, France.

A community-wide effort to combine testate amoeba datasets

To understand ecology at a global scale, requires global data sets. Databases of different organisms/biotic communities and environmental factors form the foundations for global analyses and thereby better understanding interlinkages between different organisms and environment not only at local but also regional and global scale. Constructing a global data base, with data compiled in a standard format, allows analyses that address species and system-specific questions based on micro- to macro scale comparison.

Testate amoebae are a common group of amoeboid protists that build shells. They occur in soils, freshwater habitats and to a lesser extent marine environment. They play a key role in microbial foodwebs and are useful bioindicators due to their responses to major ecological gradients (e.g., water availability, pH and nutrients). Their shells allow species-level identification and are preserved in sediments, peat and dried or frozen soil or moss samples - they are commonly used in palaeoecology for quantitative inference and as model organisms for microbial biogeography. The literature on testate amoebae is composed of well over 100 years of publications, in different languages and is often hard to find and stored in different private archives. Especially at a time of rapid climate change, it has become increasingly important to obtain and cover large temporal and spatial data to be able to predict potential future changes in many ecosystems and to improve our understanding of these changes. Our goal is to compile the existing data in a user-friendly, open database which will facilitate the study of testate amoebae. This will have positive

implications for their use in the study of testate amoeba biodiversity, biogeography, their functional roles, and interactions with other organisms.

Here, in this global effort project, we present for open use and extension a tremendous amount of data collection has been done by the research community. We collected over 10659 samples, covering every continent and many different ecosystems. We also show the geographic gaps that need more attention, as well as the limitations of collected data and perspectives in optimization usability of the data and recommendations for collection of the new. Such a large data base based on morphospecies will also allow a comparison of emerging molecular data on testate amoebae, with over a century of microscope-based work. We recommend for each future work to include the data of their lists of species in our database in order to constantly record all new results in one place to facilitate any future syntheses.

Wednesday Oct 20th: Weasleys' Wizard Wheezes Session - Anything else dealing with testate amoebae!

Contributed talks

Elizaveta Ermolaeva 1,2, Yuri A. Mazei 1,2 & Andrey N. Tsyganov 1,2

1 Lomonosov Moscow State University, Leninskie gory, 1, 119234 Moscow, Russia, 2 Severtsov Institute of Ecology and Evolution RAS, Leninsky Av., 33, 119271 Moscow, Russia ; e-mail: elizaveta.ermolaeva@unine.ch

Application of testate amoeba functional traits to infer paleohydrological changes in peatlands in the forest zone of the East-European plain

Testate amoeba is frequently used for WTD reconstructions due to their high sensitivity to surface moisture. The past responses of testate amoeba community structure to WTD (also known as the species-based approach) were explored in the previous study. In this paper, we investigated the past responses of testate amoeba functional traits (also known as the functional-traits approach) to WTD for the same sites, and further comparing the reconstructions built with these two conceptually different approaches. The reconstruction built with the trait-based transfer function proved to be highly comparable with the previously developed traditional taxonomy-based one, which provides a strong support to the value of trait-based transfer functions.

Itzel Sigala 1, Socorro Lozano2, Margarita Caballero1, Alfonso Lugo3, Alexander Correa2, Liseth Pérez4, Leslie Alberto5

1. Instituto de Geofísica, UNAM, 2. Instituto de Geología, UNAM, 3. Facultad de Estudios Superiores Iztacala, UNAM, 4. Institut für Geosysteme und Bioindikation (IGeo), Technische Universität Braunschweig, 5. Facultad de Ciencias, UNAM ; e-mail: itzelsr@yahoo.com.m

Reconstruction of the trophic state of a warm monomictic Mexican lake using testate amoebae

The warm monomictic Lake Atezca is located in east-central Mexico. Previous studies report a rapid acceleration of its eutrophication, and therefore, the aim of this study is to analyze changes in the testate amoeba species assemblages in a sediment sequence covering the last ~100 years. Our goal is to infer changes in the trophic state and detect when eutrophication started. A short sediment sequence (75 cm long) was recovered with a gravity corer in 2015. Subsampling was done every 4-cm, and all the tests found in 1 cm3 were identified and counted. In total, were found 39 taxa, including *Cucurbitella tricuspis*, a typical indicator of eutrophic environments. Changes in species assemblages suggest cyclic oscillation between hypereutrophic to mesotrophic conditions."

Michelle M. McKeown 1,2, Olivia R. Burge 1, Sarah J. Richardson 1, Jamie R. Wood 1, Edward A. D. Mitchell 3, Alex Fergus 1, Janet M. Wilmshurst 1,4

1 Manaaki Whenua - Landcare Research, Lincoln, New Zealand, 2 School of Biological, Earth and Environmental Sciences, University College Cork, Ireland. 3 Laboratory of Soil Biodiversity, University of Neuchâtel, Switzerland, 4 School of Environment, The University of Auckland, New Zealand; e-mail: mmckeown@ucc.ie

Assessing Testate Amoebae as Biological Indicator s for New Zealand Wetlands

There is increasing demand to develop rapid and reliable assessment tools for early warning of wetland degradation. Our goal is to compare the sensitivity of vegetation and testate amoebae to anthropogenic disturbance in New Zealand wetlands. Here, we analysed vegetation structure, and testate amoeba assemblages and traits across a gradient of anthropogenic disturbance in two regions on New Zealand's South Island. Our findings show that the patterns of vegetation and testate amoebae community structure follow similar trends across the ecological integrity gradient; however, the two peatland complexes are diverging further away from each other in terms of ecological structure as a result of degradation."

Anaïs Bonetti 1, Matthieu Mulot 1, Andrey Tsyganov 2,3, Yuri Mazei 2,3, Anatoly Bobrov 2, Laure Gandois 4, Lara Grandgirard 1, Mark Hines †, Isabelle Köenig 1, Natalie Lemonis 1, Elisa Männistö 5, Johannes Niemi 6, Richard Payne †, Björn Robroek 7, Eeva-Stiina Tuittila 5, Emmi Tuokko 6, Edward A. D. Mitchell 1

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

Testate amoebae (TA) communities are often used as a proxy for environmental conditions. Past conditions could also be inferred using the morphological traits of a single TA. In this study, we investigated the relationship between the biometry of *Hyalosphenia papilio* and environmental and climatic variables such as water table depth (WTD) and annual temperature. We analysed its morphological variability in samples covering a latitudinal gradient in Europe and North America and an elevation gradient in Switzerland, including micro-topography variations. *H. papilio* size was correlated to WTD and to a lesser extent to mean annual temperature, with the largest specimens in wet and warm sites. Following these findings, we were able to develop a model based on *H. papilio* length to infer the WTD.

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Reconstruction of subarctic peatland development in NE Fennoscandia using testate amoebae and other proxies

A better understanding of past long-term environmental changes in the subarctic region is crucial for mitigation of the possible negative effects of climate warming in this vulnerable region. This study provides a new multi-proxy reconstruction of regional vegetation changes and peatland development for north-eastern Fennoscandia (Russia) during most of the Holocene. To that purpose, we performed plant macrofossil, pollen, testate amoebae, peat humification, loss on ignition and radiocarbon analyses of the peat deposits from a mire around Vodoprovodnoe Lake (the Kindo Peninsula, the Republic of Karelia). Our data indicate that the peat deposits started accumulating before 9147 ± 182 cal. yr. BP. The vegetation cover in the area was mainly typical for the northern taiga zone, except for the period ~7800–5600 cal. yr. BP, when it generally resembled the middle taiga zone. The vegetation cover and peatland were greatly affected by reoccurring fires, which can be partly related to human activity. These events were associated with an increased proportion of birch in the vegetation cover (as a pioneer species) and/or water level decreases. By 600 cal. yr. BP, the peatland and the surrounding vegetation reached its current state and only minor changes had been recorded since that time. Overall, our results suggest a considerable and unexpected role of fires in the postglacial dynamics of subarctic peatlands"

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Population and molecular responses to warming in *Netzelia tuberspinifera* – an endemic and sensitive protist from East Asia

With the effects of global warming becoming ever more obvious, biodiversity conservation is facing severe challenges. Currently, a deeper understanding the mechanisms of the effects of warming on sensitive species has become an important topic in aquatic biodiversity and ecological management. Our study first overcame the “challenge” for a sensitive indicator species (*Netzelia tuberspinifera*, an endemic testate amoeba species in East Asia) of culturing under laboratory conditions, and then explored its molecular response mechanisms to warming using transcriptomic analysis. Our data indicate that temperature mainly drove the geographical and seasonal variation of *N. tuberspinifera* populations. Transcriptomic results indicate that when the temperature is < 25°C, rising temperature triggers the biosynthesis of ribosomes; while the temperature is > 25°C, it triggers molecular processes related with cell division, test formation and general biomass increase. However, once the temperature exceeds 40°C, *N. tuberspinifera* is unable to survive. Following from these results, the distribution of *N. tuberspinifera* might expand towards higher altitude or latitude regions under global warming. For the first time, our study showed direct evidence for sensitive protozoa species that presents a very narrow adaptation mechanism to local climate. Our work provides fundamental data for regional biodiversity conservation and scientific reference in subtropical and tropical waterbodies."

Posters

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Modelling the microbial food webs in *Sphagnum*-dominated peatlands

Microbial food web is often considered a black box in most studies. To complete the picture of who-eats-who, we should dig into this black box in order to better understand the dynamics of carbon. However, different techniques have been devised to predict species interactions using theoretical models or abundances. In this study I used Machine Learning algorithm to generate food webs. The data used comes from the "Mixopeat" project on interactions of microorganisms associated to Sphagnum mosses in peatland soils. I selected the more flexible Machine Learning (ML) models (Random Forest, Generalized Linear Models, Bayesian Generalized Linear Models, k-Nearest-Neighbor, Deep Neural Networks and sparse distance weighted discrimination) and tested their ability to predict species interactions based on morphological and trophic traits and taxonomy information on the various microorganisms found in peatlands, with several predictive performance indices (Accuracy, Kappa, TSS and AUC). Then, I cross-validated the final model. The results showed that Random Forest is the best ML model and can successfully predict species interactions in microorganism networks. Particularly, ML approach could be used to support the development of a wider theory of ecosystem responses to environmental change.

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Spatial distribution of testate amoeba of the order Arcellinida from aapa mires in different scales

The study was conducted on the aapa-mire, located in the northern subzone of the taiga in the vicinity of the Pertsov White Sea Biological Station, Moscow State University. We studied the horizontal distribution of testate amoebae on a macro- (40×150m), meso- (10x10 cm), microscale (3x3 cm), and vertical distribution in the deep of the sphagnum. In 86 samples revealed 11574 tests belonging to 109 species and subspecies from 33 genera. The testate amoeba community is structured mainly due to the differentiation of ecological niches of species on the scale of the whole aapa-mire, as well as individual groups diverge on a microscale. The role of horizontal distribution at the mesoscale and vertical distribution in the divergence of spatial components of ecological niches is significantly lower"

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Diversity of testate amoebae in karst waterbodies of southern Mexico

Testate amoebae are unicellular protists that inhabit waterbodies including karst lakes. The aim of this work is to determine and compare the diversity and ecology of testate amoebae from nine neotropical lakes in southern Mexico. We collected and analyzed surface sediment samples from karst lakes in Montebello, Selva Lacandona and Quintana Roo. In each lake we measured limnological variables such as pH, oxygen concentration and electrical conductivity. In addition, 1-cm3 of surface sediments was analyzed under a stereomicroscope, and all tests were counted. In total, 23 taxa were identified, and species richness ranged between 5 and 18. Our study highlights the potential of testate amoebae as bioindicators in (paleo) limnological investigations.

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Experiments of arsenic resistance in *Arcella intermedia*

Although Arcellinids have different arsenic tolerance levels, the extension of the resistance and the mechanisms involved are still obscure. In this work, we tested arsenic tolerance in Arcella intermedia. To determine their tolerance extension, we grew Arcella in several culture media with different levels of arsenic (1-1000 parts per million) and estimated their growth curves. We found that despite Arcella survive up to 100 ppm, they can only proliferate in lower levels (1 ppm). Based on literature, we expected Arcella to be highly tolerant (360-760 ppm). Our results indicate that Arcella has different resistance capacities, and the lineage used in this study is less resistant. One additional possibility is that Arcella strategy is related to temporary survival without population growth.

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