



8th International Symposium on Testate Amoebae (ISTA8)

September, 12th to 15th - Ilha Bela, São Paulo, Brazil



Committees

Scientific Committee

Enrique Lara
Daniel Lahr

Organizing Committee

Daniel Lahr
Paulo Hofstatter
Alfredo Porfírio
Giulia Magri Ribeiro

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Funding



Support



MEETING PROGRAMME

Monday Sept. 12, 2016	
8:00-15:30	Arrival, Registration & Hotel Check-In
15:30-16:30	<p style="text-align: center;">KT1 - Bridging the gap between traditional taxonomy and transcriptomics in arcellinids (Amoebozoa)</p> <p style="text-align: center;">Anush Kosakyan (Institute of Biosciences, University of Sao Paulo, Brasil)</p>
	Oral Presentantion - Taxonomy 1 (Chair LF Velho)
16:30-17:00	<p>PT1 - EXPLORING THE MITOCHONDRIAL GENOMES OF AMOEBOZOA IN SEARCH OF NOVEL MOLECULAR MARKERS: THE EMERGENCE OF A NEW BARCODE FOR ARCELLINIDA. (QUENTIN BLANDENIER)</p> <p>PT2 - MORPHOMETRIC AND GENETIC ANALYSIS OF TESTATE AMOEBAE ARCELLA INTERMEDIA LAEVIS AND ARCELLA INTERMEDIA FROM NATURAL ENVIRONMENTS AND CULTURED CLONES REVEAL THAT MORPHOLOGICAL TECHNIQUES ARE NOT ADEQUATE TO DIFFERENTIATE SPECIES IN THE GENUS ARCELLA. (ALFREDO L. PORFIRIO DE SOUSA)</p>
17:00-17:30	Coffee Break
	Oral Presentantion - Taxonomy 2 (Chair LF Velho)
17:30-18:45	<p>PT15 - BARCODING, MORPHOLOGICAL AND MOLECULAR TAXONOMY OF THE GENUS EUGLYPHA - TOWARDS A CALIBRATION OF THE MOLECULAR CLOCK (CLÉMENT DUCKERT)</p> <p>PT25 - A SURVEY ON BRAZILIAN TESTATE AMOEBAE IDENTIFIES THE POSSIBILITY OF 104 NEW SPECIES (MARIA BEATRIZ GOMES SOUZA)</p> <p>PT27 - MORPHOLOGICAL AND MORPHOMETRIC DESCRIPTION OF ARCELLA GANDALFI N. SP. (AMOEBOZOA, ARCELLINIDA) FROM BRAZILIAN CONTINENTAL WATERS (JORDANA DE CARVALHO E FÉRES)</p> <p>PT26 - BORN IN THE USA: A MOLECULAR PHYLOGEOGRAPHY OF HYALOSPHEINIA PAPILIO (DAVID SINGER)</p> <p>PT32 - QUADRULELLA TEXCALENSE SP. NOV. FROM MEXICAN DESERT: NEW UNUSUAL ENVIRONMENT FOR TESTATE AMOEBAE (HORACIO PEREZ JUAREZ)</p>
19:30-21:00	Dinner

Tuesday Sept. 13, 2016	
8:00-9:00	<p>KT2 - THE NEOPROTEROZOIC DIVERSIFICATION OF EUKARYOTES AND THE RISE OF PROTISTAN PREDATORS SUSANNAH M PORTER (UNIVERSITY OF CALIFORNIA, SANTA BARBARA, USA)</p>
9:00-10:00	Oral Presentantion – Paleontology (Chair EAD Mitchell)
	<p>PT35 - TESTATE AMOEBAE: POTENTIAL IN STUDIES IN ECO AND PALEOECOLOGY IN MEXICO (PAMELA PLATA GARCÍA) PT4 - RECONSTRUCTION OF WATER TABLE DEPTH IN THE PEAT DEPOSIT OF FLOODPLAIN TERRACE SWAMP, SOUTH OF WESTERN SIBERIA, USING RHIZOPOD ANALYSIS (IRINA KURINA) PT6 - TAPHONOMIC OBSERVATIONS AND EVOLUTIONARY IMPLICATIONS IN NEOPROTEROZOIC TESTATE AMOEBAE FROM JACADIGO GROUP – BRAZIL (LUANA MORAIS) PT8 - VASE SHAPED MICROFOSSILS OF NEOPROTEROZOIC (~750 MA) TASMANIA AND THEIR GLOBAL FOSSIL RECORD (LEIGH ANNE SMITH RIEDMAN)</p>
10:00-11:00	Coffee Break and Posters
11:00-12:00	Oral Presentantion - Ecology 1 Talks (Chair EAD Mitchell)
	<p>PT18 - INFLUENCE OF ENVIRONMENTAL AND SPATIAL FACTORS ON PLANKTONIC TESTATE AMOEBAE METACOMMUNITY IN FLOODPLAINS (RODRIGO LEITE ARRIEIRA) PT30 - IMPACT OF ATMOSPHERIC POLLUTANTS ON TESTATE AMOEBEA ASSEMBLAGES OF EUROPEAN PEATBOGS (LARA GRANDGIRARD) PT17 - PRODUCTIVITY GRADIENT AFFECTS THE TEMPORAL DYNAMICS OF TESTATE AMOEBAE PLANKTONIC IN A NEOTROPICAL FLOODPLAIN (LEILANE TALITA FATORETO SCHWIND) PT10 - LAND USE AND LITTER CHEMISTRY AFFECT MICROBIAL COMMUNITIES AND LITTER DECOMPOSITION IN TROPICAL LOWLANDS OF SUMATRA, INDONESIA (VALENTYNA KRASHEVSKA)</p>
12:00-14:00	Lunch
14:00-15:00	<p>KT3 - LOOKING THROUGH THE APERTURE: CAN WE USE THE MORPHOLOGICAL TRAITS OF PEATLAND TESTATE AMOEBAE AS A PROXY OF FUNCTION IN MULTI-PROXY PALAEOECOLOGICAL STUDIES - MARIUSZ LAMENTOWICZ (ADAM MICKIEWICZ UNIVERSITY IN POZNAN)</p>
15:00-16:15	Oral Presentantion - Ecology 2 (Chair A Tsyganov)

	<p>PT9 - RESPONSES OF MODERN TESTATE AMOEBAE ASSEMBLAGES AT LAKE CHICHOJ, GUATEMALA, IN RELATIONSHIP TO DIFFERENT LAND USES (ANDREA EUNICE RODAS-MORAN)</p> <p>PT11 - SEASONAL VS. LAND USE EFFECTS ON TESTATE AMOEBAE COMMUNITIES: IMPLICATIONS FOR ECOLOGICAL ASSESSMENT AND MONITORING (EMMANUELA DAZA DAZA SECCO)</p> <p>PT13 - IMPACT OF EXPERIMENTAL WARMING AND WATER TABLE MANIPULATION ON MICROBIAL COMMUNITY STRUCTURE AND FUNCTIONS AT THE SURFACE OF A SPHAGNUM PEATLAND (MONIKA KATARZYNA REZUGA)</p> <p>PT12 - BETWEEN DROUGHT, FIRE AND POLLUTION: STORY ABOUT THE STRUGGLE OF TESTATE AMOEBAE IN WESTERN SUDETES DURING THE LAST 800 YEARS TOLD BY MULTI-PROXY DATA (KATARZYNA KAJUKAŁO)</p> <p>PT20 - RESPONSE OF TESTATE AMOEBEA COMMUNITY TO EXPERIMENTAL WARMING AND PRECIPITATION DECREASE IN RZECIN PEATLAND.</p>
16:15-17:00	Coffee Break and Posters
	Oral Presentantion - General Bio (Chair A Tsyganov)
17:00-18:15	<p>PT3 - EXPERIMENTS ON COMPETITIVE EXLUSION IN PROTISTS (GIULIA MAGRI RIBEIRO)</p> <p>PT34 - TESTATE AMOEBAE COMMUNITY OF SOIL UNDER AGAVE STRICA IN TEHUACAN MEXICAN DESERT (ANGELICA SERRANO)</p> <p>PT23 - SELECTION OF SILICEOUS STRUCTURES FOR TEST BUILDING IN TESTACEANS FROM A SOUTH AMERICAN PEATBOG (LUCIANA BURDMAN)</p> <p>PT22 - THE PATTERNS AND CAUSES OF LATITUDINAL AND ALTITUDINAL DIVERSITY IN FREE-LIVING UNICELLULAR EUKARYOTES: USING SOIL TESTATE AMOEBAE AS MODEL ORGANISMS (LEONARDO DAVID FERNANDEZ)</p> <p>PT16 - CINDERELLA'S HELPING PIGEONS OF THE MICROBIAL WORLD: THE POTENTIAL OF TESTATE AMOEBAE FOR IDENTIFYING CRYPTOTEPHRA (EDWARD AD MITCHELL)</p>
19:30-21:00	Dinner

Wednesday Sept. 14, 2016	
8:30-9:15	Oral Presentantion - Alka-Seltzer (Chair V Krashevskia)
	<p>PT7 - THEY WERE BEFORE THE COMING OF THE INCAS AND REMAINED AFTER THEIR LEAVING (TESTATE AMOEBAE OF MACHUPICCHU) (YURI MAZEI)</p> <p>PT5 - PERFORMANCE OF A TESTATE AMOEBA TRANSFER FUNCTION ALONG LOCAL HYDROLOGICAL GRADIENTS (ANDREY NIKOLAEVICH TSYGANOV)</p> <p>PT21 - SOIL MICROORGANISMS BEHAVE LIKE MACROSCOPIC ORGANISMS: PATTERNS IN THE GLOBAL DISTRIBUTION OF SOIL EUGLYPHID TESTATE AMOEBAE (ENRIQUE LARA)</p>
9:15-9:30	YoTAR/ISOP Award
	<p>Category: Undergrad</p> <p>PT2 - ALFREDO LEONARDO PORFIRIO DE SOUSA</p> <p>PT3 - GIULIA MAGRI RIBEIRO</p> <p>PT35 - PAMELA GARCÍA</p>
	<p>Category: MSc.</p> <p>PT1 – QUENTIN BLANDENIER</p> <p>PT12 - KATARZYNA KAJUKAŁO</p> <p>PT15 - CLÉMENT DUCKERT</p> <p>PT30 - LARA GRANDGIRARD</p>
	<p>Category: PhD</p> <p>PT6 - LUANA MORAIS</p> <p>PT9 - ANDREA EUNICE RODAS-MORAN</p> <p>PT11 - EMMANUELA DAZA DAZA SECCO</p> <p>PT13 - MONIKA KATARZYNA REZUGA</p> <p>PT22 - LEONARDO DAVID FERNANDEZ</p> <p>PT26 – DAVID SINGER</p> <p>PT23 - LUCIANA BURDMAN</p> <p>PT32 - HORACIO PEREZ JUAREZ</p> <p>PT34 - ANGELICA SERRANO</p>
	<p>Category: PostDoc</p> <p>PT8 - LEIGH ANNE SMITH RIEDMAN</p> <p>PT20 - ANNA MARIA BASINSKA</p>
10:00-18:00	<p>Hotel Check-out (until noon); Departure or 4x4 trip (optional) and lunch available for those who stay.</p>

KEYNOTES

KT1 - Bridging the gap between traditional taxonomy and transcriptomics in arcellinids (Amoebozoa)

Anush Kosakyan¹, Matt W. Brown^{2,3}, Enrique Lara⁴, Edward A.D. Mitchell^{4,5} and Daniel J.G. Lahr¹

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Arcellinid testate amoebae are a diverse group of terrestrial and freshwater microbial eukaryotes. Described by naturalists in the eighteenth century, Arcellinids are frequently used in biomonitoring and paleo-ecological reconstruction of past climates. Their phylogenetic position and long fossil record vests them with a particular importance in the approaching of basal nodes of eukaryotic tree. However, difficulties regarding culturing as well as the application of molecular biology protocols to these organisms are an impediment to deeper investigation.

Our aim in this study was to investigate arcellinid (Amoebozoa, Tubulinea) diversity, and to reconstruct solid and precise phylogeny combining comprehensive taxon sampling, multiple genes and well documented morphological characters. Twenty testate amoebae transcriptomes were used to generate the phylogeny of this group when for most of the species no molecular data was available previously. Phylogenetic reconstruction of Arcellinids combining morphological and molecular data based on about 350 genes and 100 000 amino acid positions will be discussed.

KT2 - THE NEOPROTEROZOIC DIVERSIFICATION OF EUKARYOTES AND THE RISE OF PROTISTAN PREDATORS

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Neoproterozoic (1000–541 million years ago, Ma) fossils record the taxonomic and ecological expansion of eukaryotes in a world previously dominated by Bacteria and Archaea. The early phase of this diversification (1000–720 Ma) is characterized by an increase in protistan microfossil diversity, the first appearance of eukaryotic biomineralization, an increase in the relative contribution of eukaryotic algae to primary productivity, and the appearance of multicellularity in several eukaryotic clades; the later phase, following ~85 million years of global glaciations, is characterized by the dramatic radiation of animals, culminating in the “Cambrian explosion”. It has recently been hypothesized that just as animal predation may have driven the Cambrian diversification of animals, the appearance of protistan predation—protists preying on other protists—may have played an important role in the Neoproterozoic diversification of eukaryotes. In this talk I will discuss evidence from my work on microfossils from the ~780–740 Ma Chuar Group, Grand

Canyon, USA, that supports this view. Upper Chuar rocks preserve an incredible abundance of diverse vase-shaped microfossils interpreted to be the remains of arcellinid testate amoebae; lower Chuar shales and siltstones host beautifully preserved organic-walled remains of eukaryotic cells and cysts. About 10% of both vase-shaped and organic-walled microfossils exhibit perfectly circular or half-moon-shaped holes in their walls, which are interpreted to be perforations made by predatory amoebae. Together with hydrocarbon biomarker molecules from upper Chuar rocks that provide evidence for the presence of toxins capable of lysing eukaryotic cells, these fossils indicate that a diversity of predators lived in the Chuar sea. **Key words:** Arcellinida; fossil; proterozoic

KT3 - LOOKING THROUGH THE APERTURE: CAN WE USE THE MORPHOLOGICAL TRAITS OF PEATLAND TESTATE AMOEBAE AS A PROXY OF FUNCTION IN MULTI-PROXY PALAEOECOLOGICAL STUDIES

MARIUSZ LAMENTOWICZ (1,2), KATARZYNA MARCISZ (1,2), ŁUKASZ LAMENTOWICZ, KATARZYNA KAJUKAŁO (1,2), MARIUSZ GAŁKA (2), VINCENT E. J. JASSEY (3,4)

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High-resolution multi-proxy studies on peatlands provide perfect possibility to infer long-term ecology of testate amoebae. Time scales reaching several millennia enable a novel look at the long lasting processes like disturbances of peatland ecosystem. Testate amoebae through their sensitivity respond by population extinction, recovery from remaining individuals or migration. While taxonomic composition is known to play a key role in interpreting changes in ecosystem functioning, past functional diversity could be equally important and need to be deeply explored. Many of the recent studies on peatland protists are using testate amoebae as bioindicators or proxies of the past environmental change. Moreover, they point out the importance of testate amoeba communities for peatland functioning and how can their functional role shifts in response to environmental change.

Understanding the complex interplay between climate, human disturbances and TA communities, including their function, is thus essential to fully anticipate how ecosystems will react to the fast rate of the current warming. Different approaches are applied to explore the role of testate amoebae in peatlands. Experimental studies are usually chosen to improve our understanding of ecological patterns, but such experiments mostly operate in short time scales not exceeding five years. Recent studies showed the need to explore and combine ecological and palaeoecological approaches for testate amoebae, to determine whether shifts in their community structure and function are linked to environmental changes.

We found that morphological traits of testate amoebae might be used as a proxy of the peatland ecosystem functioning. At least two functional traits: metabolism (mixotrophy vs heterotrophy) and pseudostome position, indicate disturbances such as: drought, dust deposition, forest succession or deforestation. However, some disturbances can overlap and testate amoeba traits composition changes as a result of the synergy of stressors. We hypothesize that rich fen species represent neutral-morphology compared to bog species, which are closely related to bog microforms. Therefore, in fens it is more difficult to find one trait closely related to any of the environmental variables, as well as one strong environmental variable related to testate amoeba community. However, external factors, e.g. soil erosion or atmospheric pollution, can modify pristine, purely organic habitats providing novel niches for different shell architectures.

We acknowledge support from grant PSPB-013/2010 from Switzerland through the Swiss Contribution to the enlarged European Union.

ABSTRACTS

PT1 - EXPLORING THE MITOCHONDRIAL GENOMES OF AMOEBOZOA IN SEARCH OF NOVEL MOLECULAR MARKERS: THE EMERGENCE OF A NEW BARCODE FOR ARCELLINIDA.

QUENTIN BLANDENIER¹; ENRIQUE LARA¹; EDWARD A.D. MITCHELL¹;
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The gene coding for the small subunit ribosomal RNA (SSU rRNA gene) is by far the most commonly used phylogenetic marker in protist phylogeny, as its function is conserved in the whole tree of life. However, in certain groups, its fast evolutionary pace compromises its use for phylogenetic purposes. Arcellinid testate amoebae are a typical case where long evolutionary distances among genera are responsible for low support at the nodes of phylogenetic trees. The use of new marker genes is therefore necessary to infer phylogenetic relationship among Arcellinid taxa with more confidence.

Here, we designed and tested new primers to amplify a short fragment (~250 bp) that includes parts of both mitochondrial NAD9 and NAD7 genes. These genes are encoded in the mitochondrion of Amoebozoa as opposed to Opisthokonta which are often contamination sources (e.g. Fungi). We obtained several sequences with our newly designed primers which belong to Arcellinid genera: Hyalosphenia, Diffflugia, Arcella and Netzelia. We additionally tested this primer on environmental DNA to infer its potential use for high throughput sequencing (HTS) approaches, which is a way to construct a large Arcellinida

sequence dataset and allow the survey of environmental diversity and ecological studies, in which Amoebozoa are typically poorly covered.

We recovered a phylogenetic tree that resembled the tree obtained with SSU rRNA, and recovered the Sphaerothecina clade (*Arcella-Netzelia*), and the monophyly of elongated *Diffugia*. Moreover, the NAD9/NAD7 marker could discriminate efficiently closely related forms (i.e. two isolates of *Diffugia nodosa*). All Arcellinid species surveyed seemed to use a TAA stop codon, while the TGA codon is used to code tryptophan. The respective configuration of both genes varied among taxa but stayed consistent within groups, thus adding a supplementary trait for phylogenetic inferences. These two genes either overlap or are separated by a short intergenic region varying from two to six nucleotides composed only of the nucleotides A and T.

The NAD9/NAD7 marker is easily amplified due to its small size yet it provides valuable phylogenetic information both for resolving deep phylogenetic relationships and for distinguishing closely related taxa. It will therefore likely be of considerable use in the construction of the Arcellinida.

PT2 - MORPHOMETRIC AND GENETIC ANALYSIS OF TESTATE AMOEBAE *ARCELLA INTERMEDIA LAEVIS* AND *ARCELLA INTERMEDIA* FROM NATURAL ENVIRONMENTS AND CULTURED CLONES REVEAL THAT MORPHOLOGICAL TECHNIQUES ARE NOT ADEQUATE TO DIFFERENTIATE SPECIES IN THE GENUS *ARCELLA*.

PORFIRIO DE SOUSA, A.L.; RIBEIRO, G.M.; LAHR, D.J.G.

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Testate amoebae are eukaryotic microorganisms characterized by the presence of an external shell (test). They are large, conspicuous organisms, and as such have been the object of a large body of work using classical morphological methodology. In the last decade, a large number of these organisms were sequenced, typically for the genetic markers SSU rDNA and *CoxI*. Discordance between morphological and molecular data has been demonstrated recently in some groups of arcellinids, one of the principal groups of testate amoebae. The canonical prediction of evolutionary biology, i.e., that the phenotype should reflect the genotype, has not been observed in these organisms, particularly compelling is the case of hyalosphenid testate amoebae. Hyalosphenids represent only a fraction of Arcellinida, and if discordance between morphology and molecules are widespread in the group, the consequences to derivative studies are significant: because morphology of the test is used to differentiate genera and species in ecological, monitoring and paleontological studies, if phenotype does not reflect genotype, conclusions in these types of studies become severely impaired.

The objective of this work is to evaluate the morphometrical and morphological variation of the closely related and similar morphospecies *Arcella intermedia laevis* and *Arcella intermedia* in nature and in cultured individuals and see how these are correlated with molecular data. In both cases, monoclonal cultures were established immediately after sampling, to avoid coalescence effects of the artificial environment (i.e., the clonal cultures should be a fair genetic sub-sampling of the environment). From each culture and from each natural sample, we isolated approximately 30 individuals to obtain the morphometric

data after one month of growth in cultures. We obtained DNA from single cells and ran polymerase chain reactions (PCR) to amplify two different regions: SSU rDNA and the recently proposed NAD9/7 mitochondrial marker.

The morphometry of five distinct *A. intermedia laevis* lineages as well as three *A. intermedia* lineages overlap. However, natural samples of *A. intermedia* compared with laboratory grown clonal lineages occupy clearly distinct morphometric spaces. No morphometric character presented clear differences between *Arcella intermedia laevis* clonal lineages and *Arcella intermedia* clonal lineages. The natural population of *Arcella intermedia* did not show distinction between the first and second natural samples. The presence of depressions in the test of *Arcella intermedia* is the diagnostic character to differentiate morphotype *Arcella intermedia* from morphotype *Arcella intermedia laevis*. In natural samples, we can easily isolate individuals from both morphotypes, the same is not true in clonal (culture) individuals. All clonal lineages of *Arcella intermedia* used in this study lost the depressions of their tests in the first laboratory generation, i.e., the first division yields a depression-free individual. The character was never regained in one year of growth in cultures. Clonal samples of one month of growth already present individuals with externalized aperture. Albeit rare, one individual was found in the natural sample that presented the same characteristic. All lineages considered were identical for SSU rDNA. For the mitochondrial intergenic segment between the genes NAD9/NAD7 only lineage I6 showed substitutions, with a GD= 0.014. In other words, lineage I6 presents 13 substitutions in the surveyed fragment.

Analyses of morphological, morphometric and genetic data presented here demonstrate that the depth of discordance between phenotype and genotype in the genus *Arcella* has been thoroughly underestimated. This incongruence between genetic and morphological data has several implications. Firstly, our data solidly demonstrates that the morphospecies classically separated into *Arcella intermedia laevis* and *Arcella intermedia* are in fact the same species. Secondly, the large effective population sizes associated with these taxa may have an impact in how lineages are defined based on genetic distances. Without further understanding of how big the effective population sizes actually are for these organisms, it will be impossible to determine a cutoff divergence level. The implication is that natural surveys relying only on molecular markers may overestimate diversity significantly. Thirdly, morphometry in culture conditions is significantly distinct from morphometry in the environment, indicating phenotypic plasticity at the morphometric and morphological levels. The cultured organisms occupy a distinct morphometric space, presumably because culture conditions drive them to distinct shell morphology than in the natural environment. The implication is that distinct natural environments may contain a single genetic lineage that presents itself morphometrically distinct, which would lead to overestimation of global diversity of these organisms. The loss of depressions in the shell may also be an indication that these organisms present adaptations to different conditions, increasing the possibility that an overestimation of morphospecies have been recorded for a variety of environments.

This scenario affects the definition of lineages in testate amoebae and can generate practical difficulties, since morphology of the shell is historically used for distinguishing among genera and species. More recently morphometric analyses have been introduced as species separation tools, and we

demonstrate here that there are shortcomings with that approach too. We argue that morphological, morphometric and molecular variability has been historically neglected in these organisms, and as thus, is not fully understood. Further studies will need to carefully compare variation in the myriad morphotypes described for testate amoebae, in order to verify the validity of species delimitations. **Key words:** Testate amoebae; phenotypic plasticity; species delineation

PT3 - EXPERIMENTS ON COMPETITIVE EXCLUSION IN PROTISTS
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Organisms compete for resources in the natural environment. In mixed population situations, when the system reaches a saturation point, one species can exclude another. This process is named competitive exclusion. Rates of multiplication are distinct for each organism and should correlate with body size. To test this idea we have explored a two-organism system in the lineage of shelled lobose amoebae, the Arcellinida. Here, we set out to create experimental conditions where competitive exclusion should occur. We isolated and cultured two species of testate amoebae (*Arcella vulgaris* and *Pyxidicula operculata*). We set up growth curves and competition experiments identically, starting with 50 cells of *Arcella* and 50 *Pyxidicula*, both in isolation and in mixed cultures. We adjusted growth curves by the logistical equation and made the simulations based on the Lotka-Volterra competition model. *Pyxidicula* has a larger carrying capacity in the environment, despite having a lower growth rate. *Pyxidicula* was thus expected to outcompete *Arcella*, but was in fact impaired in competitive situation. Applying a biovolume correcting factor to the experiments demonstrates that the most relevant parameter here is size, and not number of individuals. **Key words:** Competition; protists; experimental ecology

PT4 - RECONSTRUCTION OF WATER TABLE DEPTH IN THE PEAT DEPOSIT OF FLOODPLAIN TERRACE SWAMP, SOUTH OF WESTERN SIBERIA, USING RHIZOPOD ANALYSIS

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In this study rhizopod analysis in the peat deposit of floodplain terrace swamp (further "swamp") is carried out. The goal of our research is to reveal the features of testate amoebae complexes in minerotrophic peat and to reconstruct dynamics of surface wetness during the Holocene in the peat deposit of the swamp.

Complete vertical peat deposit was collected from floodplain terrace swamp, located in the left bank of the Bakchar river in southern taiga zone of West Siberia. The area of the open woodless part of the swamp is 120 ha. The peat deposit thickness is 350 cm. According to age-dating the investigated swamp

deposit dated 8500 cal yr BP. The peat deposit is completely formed by minerotrophic peat.

We conducted rhizopod analysis. Peat samples were taken with step 10 cm and prepared by the standard method. The local conditions of swamp surface wetness was reconstructed from the data on water table depth (WTD) calculated on the basis of rhizopod analysis. Species optima of testate amoebae were obtained in modern mesoeutrophic mires of the research area, including the studied swamp (training set consists of 45 samples).

Total 69 testate amoeba taxa were revealed. The dominant species were: *Centropyxis aculeata*, *Corythion pulchellum*, *Cryptodifflugia* sp, *Euglypha rotunda*, *Trinema enchelys*, *T. lineare*.

Dominance of species from genera *Trinema* and *Centropyxis* both in peat and modern samples is an indirect evidence of high degree of tests preservation in the peat. This is also confirmed by the high values of the concentration of tests in the peat core (69 ± 52 thousands of tests per gram of air dry peat), almost the entire depth.

Our results show that testate amoebae can be numerous not only in the sphagnum peat, but also sedge, grass and hypnum types of peat.

It is important to note the unusually high preservation of tests of species from genera *Corythion*, *Euglypha*, *Trinema*, belonging to the group of Euglyphida. They not only turned out to be abundant in the studied peat core of the swamp, but even dominated in testate amoebae paleocomplexes. Apparently Euglyphid tests can be conserved in conditions of reduced acidity, and therefore is better preserved in the minerotrophic peat, unlike oligotrophic.

Trinema lineare dominated in the majority of the studied peat samples. However, despite the sustained dominance of one species, reconstructed WTD values constantly varied due to changes in species composition of testate amoebae paleocomplexes. These changes are associated primarily with not dominant but the other species.

The dynamics of WTD values are characterized by small amplitude of oscillations (8 cm), which is caused by relatively high surface wetness in the swamp during the period of the formation of peat deposits.

Decrease of WTD in the swamp are observed 8100-7200, 6300-5900, 5200-4600, 4200-4100, 3500-3400, 2800-1400 cal yr BP and increase – in 8500-8100, 7200-6300, 5900-5300, 4300-4200, 4000-3950, 3900-3800, 3600-3500, 3400-2800, 1400-900 cal yr BP.

The greatest variation of WTD values are observed in the period 4600-2800 cal yr BP. At this time, the WTD reached the lowest values that reflect the highest level of water content in the swamp. A maximum reduction of surface wetness marked 8100-7200 cal yr BP.

Reconstructed dynamics of WTD in the studied swamp are agree well with the data of paleoecological reconstructions in different peatlands, located in the territory of the southern taiga of West Siberia. These data, obtained in other research, were conducted on the basis of rhizopod analysis and reconstruction of precipitation using palynological records. Synchronous changes in surface wetness in the different mires of the study area, most likely are the reflection of hydroclimatic fluctuations during the Holocene.

The work was supported by RFBR grant (16-34-60057).

Key words: Testate amoebae; minerotrophic; holocene

**PT5 - PERFORMANCE OF A TESTATE AMOEBA TRANSFER FUNCTION
ALONG LOCAL HYDROLOGICAL GRADIENTS**

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Testate amoeba transfer functions are widely used for reconstruction of palaeo-hydrological regime in peatlands. However, the limitations of this approach have become apparent with increasing attention to validation and assessing sources of uncertainty. This paper investigates effects of peatland type and sampling depth on the performance of a transfer function using an independent test-set from four Sphagnum-dominated sites in European Russia (Penza Region). We focus on transfer function performance along localised hydrological gradients, which is a useful analogue for predictive ability through time. The performance of the transfer function with the independent test-set was generally weaker than for the leave-one-out or bootstrap cross-validations. However, the transfer function was robust for the reconstruction of relative changes in water-table depth, provided the presence of good modern analogues and overlap in water-table depth ranges. When applied to subsurface samples, the performance of the transfer function was reduced due to selective decomposition, the presence of deep-dwelling taxa or vertical transfer of shells. Our results stress the importance of thorough testing of transfer functions, and highlight the role of taphonomic processes in determining results. Further studies of stratification, taxonomy and taphonomy of testate amoebae will be needed to improve the robustness of transfer function output.

This research was funded by the Russian Scientific Fund (grant 14-14-00891) and grant of the President of Russian Federation (MD-7930.2016.4).

Key words: Peatland; reconstruction; moisture

**PT6 - TAPHONOMIC OBSERVATIONS AND EVOLUTIONARY
IMPLICATIONS IN NEOPROTEROZOIC TESTATE AMOEBAE FROM
JACADIGO GROUP – BRAZIL**

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Vase-like vesicles with an aperture at one are here reported in dolomitic clasts of uncertain provenance near the base of the Neoproterozoic Urucum Formation (Jacadigo Group) of south-central Brazil, having a radiometric age constrained between 889 ± 44 (basement rocks) and 587 ± 7 Ma (metamorphic crystallization age of overlying manganese ore). These structures are attributed to an important paleontological group known as “vase-shaped microfossils” (VSMs) that, on the basis of their morphology, have been generally regarded as ancient tests of Arcellinids, within the Amoebozoa. Many of the Urucum tests are coated by fibrous to bladed dolomite cement, which replaced original aragonite or calcite. This early cement appears to have been responsible for the serendipitous preservation of the original carbonaceous (kerogenous) and siliceous-carbonaceous test compositions, unlike practically all other

occurrences of VSMs. At least five different morphotypes may be distinguished in the assemblage whose affinities and taxonomy are under investigation. Although most of the taxonomically important characteristics of these VSMs occur in extant testate amoebae, the occurrence of organic-walled tests having exceptionally long necks exhibiting a terminal aperture are unusual. Our observations suggest that these VSMs provide both evidence of original test compositions, including possible silica biomineralization, and additional important data on the diversity of Neoproterozoic testate protists. Although the provenance of the Urucum VSM-bearing clasts is not firmly established, the possibility exists that the VSMs may rival in age the testate amoebae of the Chuar Group (742 ± 6 Ma) currently regarded as the oldest record of protozoans in the geological record.

Key words: Vase-shaped microfossils; arcellinids; biomineralization

PT7 - THEY WERE BEFORE THE COMING OF THE INCAS AND REMAINED AFTER THEIR LEAVING (TESTATE AMOEBAE OF MACHUPICCHU)

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We analysed the diversity of testate amoebae from 29 soil samples (depth 0-3 cm) collected in the vicinity of the Cusco city in Peru (6 samples of mixed grass, grasses, cacti communities), the city of ancient America Machupicchu, Aguas-Calientes (18 samples from mountain forest, 5 samples of grass, lichen and agave communities) in March 2016. The samples contained 145 testate amoebae species, intra-specific taxa and indefinite taxonomic status belonging to 27 genera. Ten taxa from the genera Cyclopyxis, Plagiopyxis, Nebela, Awerintzewia and Trinema could not be identified to species level and likely represent new taxa. Species richness varied from 1 to 54 taxa per sample. Number of species (including testate amoebae of unclear taxonomic status) in Machupicchu was highest in the mountain forests (134 taxa) followed by those from the meadows (47), lichens (11 taxa) and agave cactus (8 taxa) habitats. Several rare species with limited geographical distribution were observed, namely *Centropyxis castaneus*, *C. compressa*, *C. deflandriana*, *C. latideflandriana*, *C. cf. ohridensis*, *C. cf. ovoides*, *C. cf. pannosus*, *C. stenodeflandriana*, *Cyclopyxis plana*, *C. profundistoma*, *Apodera vas*, *Argygnia retorta*, *A. spicata*, *Diffugia cf. sandbergi*, *Trachelcorythion pulchellum*.

Key words: Testate amoeba; diversity; peru

PT8 - VASE SHAPED MICROFOSSILS OF NEOPROTEROZOIC (~750 MA) TASMANIA AND THEIR GLOBAL FOSSIL RECORD

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A group of fossils known as the 'vase-shaped microfossils' (VSM) are considered almost certainly to be early representatives of the testate amoebae. Their fossil record begins around 750 million years ago when diverse VSM species appear in tremendous abundance in geographically widespread

locations. For a brief and glorious few million years they dominated the fossil record. And then they were gone—absent from the fossil record for ≥ 400 million years.

During this talk I will present new results of a systematic paleontological analysis of a vase-shaped microfossil assemblage from the Neoproterozoic (~750 Ma) Togari Group, northwestern Tasmania and discuss the timing of VSM occurrences (including their apparent hiatus from the fossil record), the global distribution of fossil species, the observed variety of preservational modes and the seeming incongruity of vase-shaped microfossil marine habitats as compared with the dominantly freshwater and terrestrial habitats of most modern testate amoebae. **Key words:**Fossil; vase shaped microfossil; neoproterozoic

PT9 - RESPONSES OF MODERN TESTATE AMOEBAE ASSEMBLAGES AT LAKE CHICHOJ, GUATEMALA, IN RELATIONSHIP TO DIFFERENT LAND USES

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Testate amoebae have been used as in lake environments as indicators of pollution levels and land-use change, which has been applied extensively worldwide for paleolimnological reconstructions. Lake Chichoj is the only deep permanent lake in the central highlands of Guatemala (1,300 m), and has been negatively impacted by pollution in the last 100 years through urbanization and tannery operations of footwear industry. This study aimed to carry out a testate amoebae assemblage's identification to answer several questions: (i) Does land use have an influence on testate amoeba? (ii) Are particular amoebae species common among lake and land use sampling sites? Our research hypothesis predicts a relationship of testate amoebae assemblages and land use. Sampling in the lake was performed on February 2016 on three sites related to different land uses: (1) Urban, (2) cattle pastures, (3) forest. The faunas were dominated by *Centropyxis* and *Diffugia*. Testate amoeba assemblages were compared with measured limnologic parameters: pH, dissolved oxygen, salinity and total dissolved solids. Multivariate analysis methods are being used to explore relationship between testate amoebae assemblages, land use, and limnologic parameters. This study will improve the understanding of how geographic and environmental parameters at the landscape scale influences testate amoeba distribution, which will be useful for lake conservation and restoration planning. This research is the first study of testate amoebas in Guatemala, and will therefore enrich the scant database of Thecamoebian fauna in Mesoamerica. **Key words:**Thecamoebians; pollution; mesoamerican

PT10 - LAND USE AND LITTER CHEMISTRY AFFECT MICROBIAL COMMUNITIES AND LITTER DECOMPOSITION IN TROPICAL LOWLANDS OF SUMATRA, INDONESIA

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We investigated how the conversion of rainforest into jungle rubber, intensive rubber and oil palm plantations affects the decomposer community and decomposition processes in Sumatra, Indonesia. Further, we investigated the role of litter chemistry in structuring the decomposer system. In total 192 litterbags were placed in the field: 3 litter types (forest, rubber, oil palm) in 4 land use systems, with 2 harvest times and 8 replicates, each. After 6 and 12 months litterbags were collected and litter mass loss was measured, testate amoebae and microbial communities were studied, and litter element concentrations were measured.

The decomposition in converted systems was slower as compared to rainforests. After 6 months litter of oil palms and rubber decomposed faster than that of forests, but after 12 months forest litter decomposed faster than that of oil palms and rubber. Microbial biomass increased from the first to the second sampling time in rainforest, but decreased in jungle rubber, rubber and oil palm. Further, in forest litter microbial biomass increased (ca. 12 %) from the first to the second sampling time, while in oil palm and rubber litter microbial biomass decreased (on average by 34 %). A total of 58 species of testate amoebae colonized the litter. Species number and density of testate amoebae were high in rainforest and jungle rubber and decreased significantly in rubber and oil palm plantations. Further, testate amoebae density was highest in rubber litter and was lowest in oil palm and forest litter, whereas testate amoebae species number was at a similar level in rubber and forest litter and was lower in oil palm litter. Overall, our data indicate negative effects of rainforest conversion on the structure and functioning of decomposer community and, thereby litter decomposition. Further, testate amoebae and microorganisms were interactively affected by litter element concentrations. The data suggest that element ratios of litter material as basal resource for the decomposer food web exhibit strong bottom-up control on the structure of decomposer communities and decomposition processes.

Financial support was provided by the German Research Foundation (DFG) in the framework of the collaborative German-Indonesian research project CRC990 (EFForTS). **Key words:** Rainforest conversion; litterbags; decomposition

PT11 - SEASONAL VS. LAND USE EFFECTS ON TESTATE AMOEBAE COMMUNITIES: IMPLICATIONS FOR ECOLOGICAL ASSESSMENT AND MONITORING

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As many other ecosystems, peatlands have been heavily exploited for a variety of purposes. In Finland, peatland use has focused mainly on forestry with a 50% of the total peatland area, followed by 2.6% for agriculture, and 0.6% for peat mining. Peatlands of the boreal and subarctic regions cover only 3% of the global land but due to the accumulation of organic matter as peat they store ca. one third of the terrestrial carbon. Additionally, they play an important balancing role in the water cycle, are a unique habitat for many rare species, and store past information through the remains of flora, fauna, and atmospheric particles accumulated in the peat layers. Such properties have drawn attention to the environmental importance of peatlands and highlighted the need for their restoration. To accurately monitor and determine the success of peatland restoration (i.e. the ecosystem function and structure move towards near pristine conditions) sensitive indicators are needed, however which indicators are the best suited for this purpose still remains an open question.

Testate amoebae (TA) are shell-building protozoans found in soils, lakes, rivers, mostly associated with peatland plants and especially abundant in Sphagnum mosses where they account for almost half of the microorganism community. Through their feeding, TA contribute to nutrient mineralization, nutrition of soil fauna and plant growth, and the regulation of bacterial biomass. As TA can be a more accurate tool to obtain ecological information on microenvironmental conditions than plants, they have been proposed as a potential tool in the assessment of peatland condition. However their usefulness as biological indicators still needs more study. In this sense, only after determining that the magnitude of TA communities' response to ecological fluctuations is higher than their random spatial and temporal fluctuations, TA can be considered as good indicators. In this study, we followed living testate assemblages in i) natural peatlands, ii) forestry peatlands and iii) restored peatlands to assess the temporal and spatial variation of TA communities over the annual cycle in each land use type.

We found that on average, natural sites harboured the highest number of taxa and highest tests concentration, while the lowest numbers were found at forestry sites. The species dominance was relatively constant among years and seasons except at restored sites. Despite the small changes in species dominance, seasonality did not seem to affect TA community structure and composition but instead, changes were related to land use. The environmental variables generally considered among the main drivers of TA communities, pH, temperature and water table depth (WTD), did not have either a major effect on TA communities. This suggests that either: i) seasonal changes in pH, WTD, and temperature are not big enough to affect TA, or ii) land use effects on TA are not necessarily related to changes in these variables but instead, to nutrient concentrations or biotic interactions, and/or iii) microenvironmental gradients could not be avoided when sampling environmental parameters.

Finally, our results suggest that changes in TA communities in response to environmental variation, override their random spatial and temporal fluctuations making them a good indicator for evaluating ecosystem condition of Finnish boreal peatlands. **Key words:** Bioindicators; boreal peatlands; peatland restoration

PT12 - BETWEEN DROUGHT, FIRE AND POLLUTION: STORY ABOUT THE STRUGGLE OF TESTATE AMOEBAE IN WESTERN SUDETES DURING THE LAST 800 YEARS TOLD BY MULTI-PROXY DATA

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We present the first high-resolution study from mountainous peatlands of Western Sudetes. The region is considered a unique habitat in Central Europe, as it contains one of the largest raised bog complexes in temperate Europe and is thus of great importance for biodiversity conservation. The study used long-term ecological data to assess how these mountain wetland ecosystems responded to anthropogenic impacts and climate change. We used testate amoebae (with morphological traits approach), micro- and macroscopic charcoal, pollen and plant macrofossils to reconstruct the history of peatland over 800 years, illustrating shifts in its development and fire dynamics. Five hydrological stages of peatland development were recognized as a result, showing a transition from moderately wet, acidic conditions toward the dryer, more neutral phase and then return to wet, acidic stage. Fire reconstruction revealed increasing burning together with intensifying human activity, including the expansion of a nearby settlement. This study confirms the potential of testate amoeba communities as indicators of ecological effects of land-use change over long-temporal scales.

Research is funded by the National Science Centre, grant no. 2011/01/D/ST10/02579.

Key words: Palaeoecology; fire history; peatland

PT13 - IMPACT OF EXPERIMENTAL WARMING AND WATER TABLE MANIPULATION ON MICROBIAL COMMUNITY STRUCTURE AND FUNCTIONS AT THE SURFACE OF A SPHAGNUM PEATLAND

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Global warming and other impacts of human activities have an increasing influence on living organisms and the functioning of ecosystems. Soil microorganisms play crucial roles in biogeochemical cycles and changes in the microbial community structure may alter the carbon dynamics of terrestrial ecosystems. This is especially important for carbon-rich ecosystems such as

peatlands, which store ca. one third of total soil carbon in an area accounting for only 3–5% of the global terrestrial area. Global warming is likely to cause shifts in the microbial communities of *Sphagnum* dominated peatlands, with potential feedback effects on the carbon storage function of peatlands. Yet the direction and magnitude of these changes is still unclear. Our aim was to assess the response of *Sphagnum* peatland micro-eukaryotic communities (with a strong focus on testate amoebae) to climate change. We conducted a warming experiment in a *Sphagnum* peatland in northern Poland using open top chambers (OTC) which caused a temperature increase of 0.4°C on average over the growing season (maximum : 1.2°C). Furthermore we manipulated the peatland hydrology by excavating the top 30 cm and adding or removing 10 cm of peat. We hypothesized that the response in terms of biomass and biodiversity would vary among key- functional groups of microorganisms. More specifically that warming would cause: (1) an increase in total microbial biomass, (2) an increase in the bacteria/fungi ratio, and (3) a decrease in testate amoeba biomass while drought would decrease the bacteria/fungi ratio as well as testate amoebae and overall microbial biomass. We expect the average size of testate amoebae to increase in wet plots (i.e. increase of top microbial predators), and to decrease in dry and/or warmed plots (i.e. shift to small, bacterial-feeders).

This research was supported by a grant from Switzerland through the Swiss Contribution to the enlarged European Union (Project CLIMPEAT: PSPB-013/2010). **Key words:**Wetlands; climate change; moisture

PT14 - UNVEILING ECOLOGICAL LINKS BETWEEN TESTATE AMOEBAE AND NON-POLLEN PALYNOMORPHS IN SPHAGNUM BOGS (N POLAND)

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The study aims to explore the relations between testate amoebae and the environment, with the focus on non-pollen palynomorphs (NPPs). NPPs are microfossils of various taxonomic origin which are numerous in standard palynological samples. The study is based on 90 surface samples from three *Sphagnum* peatlands (Mechacz Wielki, Gązwa and Kusowskie Bagno) located in northern Poland, along the continentality gradient. Within each sample we analyzed the presence of testate amoebae, non-pollen palynomorphs (NPPs), vegetation, pollen content, water level and pH. Samples were collected from various bog microforms – hummocks, hollows, pools, lawns, forests with *Sphagnum* patches, drainage ditches and animal paths. Few were also taken close to the dung of animals to see if greater diversity of any of the biotic proxies will be recorded. Species richness of testate amoebae varied between peatland microhabitats, especially samples from past drainage ditch overgrown

by *Sphagnum fallax* showed an extraordinary abundance of testate amoebae. We want to check if testate amoebae communities and NPPs are interdependent or somehow related. We assume that NPPs represent a part of the food web therefore we can expect strong relationships between them and TA that are top microbial predators in *Sphagnum*. The preliminary findings show big differences between samples collected in various microtopographic forms, both in the testate amoebae community composition as in the NPP spectra.

Key words: Peatland; non-pollen palynomorphs; testate amoebae ecology

PT15 - BARCODING, MORPHOLOGICAL AND MOLECULAR TAXONOMY OF THE GENUS EUGLYPHA - TOWARDS A CALIBRATION OF THE MOLECULAR CLOCK

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Euglyphidae are small cercozoan testate amoebae that can be found in a broad variety of soil and freshwater environments. They strengthen their tests with ornamented self-secreted silica scales whose shape, dimensions and arrangement are taxonomically informative. However, because of their small size, species identification can be reliably achieved only based on good quality light and/or scanning electron microscopy. For this reason, the taxonomy of these organisms is still incomplete or even controversial. As a consequence, many forms with diverging taxonomic positions (and, most probably, ecologies) are pooled together in ecological studies. We built here a taxonomic revision of the whole family based on both morphological documentation and an SSU rRNA gene based phylogeny.

Our tree showed a basal dichotomy between species with pointed apertural scales (most often aquatic) and species where these structures are rounded (terrestrial). The shape of test body scales and the possible presence of a vesicular nucleus were useful characters to classify species further. Several previously described morphospecies (*Euglypha rotunda*, *E. acanthophora*, *E. compressa* and *E. filifera*) contained a hidden diversity of genetically different forms that differ on subtle ultrastructural traits. Consequently, we propose a new taxonomic framework for family *Euglyphidae*.

Key words: Euglyphidae; taxonomy; diversity

PT16 - CINDERELLA'S HELPING PIGEONS OF THE MICROBIAL WORLD: THE POTENTIAL OF TESTATE AMOEBAE FOR IDENTIFYING CRYPTOTEPHRA

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Cryptotephra (particles <125 µm) is a key record for monitoring past and current volcanic activity. However, its extraction from the host sediment and analysis is often long and difficult because of its small size. Finding a simple method to extract cryptotephra from environmental samples would therefore make its analysis much easier. We hypothesized that arcellinid testate amoebae may hold such a potential. These free-living shelled protists are among the earliest microorganisms to colonize volcanic tephra, and build their shell by agglutinating minerals from their environment. We analyzed by X-ray Spectrometry the mineral signature of tephra from the 2011 Puyehue-Cordon Caulle Volcanic Complex (Chile) eruption ash fallout and compared it to that of the shells of 51 individual testate amoebae (three individuals from each of 17 species) from 13 samples collected at different distances from the active vent. The mineral composition of particles within shells closely matched that of similar size class particles from their environment. The capacity of testate amoebae to randomly use mineral grains from their environment makes it possible to use their shells to assess the mineral composition of cryptotephra from soil, peat or sediment samples. Testate amoebae therefore represent the microbial world's version of Cinderella's helping pigeons.

Key words: Volcanic eruptions; palaeoecology; shell mineral composition

PT17 - PRODUCTIVITY GRADIENT AFFECTS THE TEMPORAL DYNAMICS OF TESTATE AMOEBAE PLANKTONIC IN A NEOTROPICAL FLOODPLAIN

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Testate amoeba communities are influenced by temporal variation in the productivity levels in the environment, and may be used as an indicator group for these changing conditions. Here, we analysed the effect of temporal variation in the levels of productivity variables on testate amoeba community of the upper Paraná River floodplain. We evaluated the hypothesis that the frequency and abundance of the testate amoeba community change along an environmental gradient, with different taxa establishing at different points along the gradient in response to changes in the levels of productivity variables. We predicted that the number of species would increase and decrease at points associated with higher and lower levels of productivity variables, respectively. Testate amoeba species were sampled quarterly between 2000 and 2012 from six lakes in the upper Paraná River floodplain, Brazil. We recorded 110 species belonging to 11 families. Threshold Indicator Taxa Analysis identified positive and negative significant shift points in response to the concentration of chlorophyll-a, total nitrogen, and total phosphorus on the frequency and abundance of the testate amoeba community. Our results indicated that change intervals in the levels of productivity variables were associated with the

establishment of different taxa. The main bioindicator species of productivity were *Diffflugia acuminata*, *D. amphoralis*, *D. helvetica multilobata*, *D. kempny*, *D. lobostoma multilobata*, *D. parva*, *D. schurmanni*, *D. ventricosa*, and *Lesquereusia ovalis*. These species were linked to the increase and decrease in the levels of productivity, confirming the ecological importance of the role of these organisms as bioindicators in aquatic ecosystems. **Key words:** Protozoa; indicator species; threshold productivity

PT18 - INFLUENCE OF ENVIRONMENTAL AND SPATIAL FACTORS ON PLANKTONIC TESTATE AMOEBAE METACOMMUNITY IN FLOODPLAINS

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Metacommunity has been assessed to highlight the relative importance of environmental and spatial processes in assembling ecological communities. Here, we tested the hypothesis that the hydrological regime influences the dispersal of planktonic testate amoebae metacommunity during two hydrological periods. We predicted that environmental factors would exert the most the predominant effects on species dispersal under drought, and would be less significant during of flooding. Testate amoeba species were sampled during two hydrological periods (drought and flooding), in seventy-two lakes of four Brazilian floodplains (Amazonian, Araguaia, Pantanal, and Paraná). Partial redundancy analysis indicated that only environmental factors were significant, which were significant in all floodplain lakes during drought. Only the Paraná floodplain indicated significant results for environmental factors during both hydrological periods. Furthermore, the hydrometric level, pH, and variables related to environmental productivity were selected via the analysis as major predictors in the assembly of testate amoebae community. Our results highlight that hydrological periods play varied relative importance roles in environmental and spatial processes. The species-sorting metacommunity model was predominant during drought, while the neutral model prevailed during flooding in all but the Paraná floodplain. In the Paraná floodplain, the construction of dams could potentially alter the effects of environmental and spatial factors on the dispersal of planktonic testate amoebae metacommunity. The pH and the productivity of the environment were largely responsible for species selection and the structuring of the planktonic testate amoebae metacommunity in Brazilian floodplains. Thus, the elucidation of dispersal models may provide a broader view of the determinant processes in structuring ecological communities and, therefore, how these processes can influence the structure of testate amoebae community. **Key words:** Variance partitioning; dispersal; diversity

PT19 - TESTATE AMOEBAE COMMUNITY ASSOCIATED TO MOSSES OF A SEMIARID AREA OF MEXICO

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Testate amoebae are organisms that have an ecological importance and that have been studied in aquatic environments and in areas with high humidity such as Sphagnum moss mainly as well as others. However, this group of protist is slightly studied in mosses of desert systems and even less in Mexico. That is why; the purpose of this study was to know the wealth of the communities of testate amoebae in mosses of the genera Wessia, Aloina, Didymodon and Pseudocrossidium, taking as a sampling site Chacateca Hill, located in the desert of Tehuacan, Mexico. This study was conducted using a stratified sampling (three altitudinal levels). Samples were also taken in each altitudinal soil to describe the microenvironmental characteristics of temperature, humidity, pH, organic matter, maximum water holding capacity and texture. The organic matter content showed differences ($P < 0.05$) between level one (1700-1900 m) and level three (2300-2600) which were greater at higher altitudes as well as the maximum water holding capacity. The percentage of sand was higher in the second altitudinal soil whereas silts were found in lower percentage compared to the other two altitudinal soils ($P < 0.05$). The mosses Didymodon and Pseudocrossidium showed more wealth of testate amoebae, principally in the range of 2000 to 2300 meters above sea level, altitude located at the southern part of the hill (2nd soil).The most common genera of amoebae were Euglypha, Trinema and Cyclopyxis. A similarity analysis showed that the composition of genera of amoebas in mosses Didymodon taken from soils 2 and 3 was similar to each other (66.67 %) and different from the other communities (49.36 %). This study provides important data about the ecology of testate amoebae in arid areas demonstrating that their communities vary in response to the moss which are associated with as well as altitude. **Key words:** Chacateca hill; pseudocrossidium; didymodon

PT20 - RESPONSE OF TESTATE AMOEBEA COMMUNITY TO EXPERIMENTAL WARMING AND PRECIPITATION DECREASE IN RZECIN PEATLAND.

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In the last years peatlands became the model ecosystems for testing the consequences of different climate change scenarios for plant and microbial communities. Studying the response of living organisms to warming and drought will allow to better understand the future environmental changes. A special attention is dedicated to testate amoeba (TA) species, which are hydrological indicators and play a key role in microbial food webs. Recent research revealed that mixotrophic species of testate amoeba were related to light conditions in peatlands and they contribute to the carbon fixing processes. The experimental site was designed (Polish - Norway "WETMAN" project) to answer the question how biotic and abiotic components of peatland ecosystem will respond to active warming and decrease of precipitation. The aim of this work is to assess the response of TA communities to different treatments: warming, warming and decreased precipitation and only decreased precipitation, in relation to control plots. We analysed separately the taxa living in the upper and lower Sphagnum segments. TA community was characterised by high abundance of mixotrophic species (*Hyalosphenia papilio*, *Archerella flavum*) in all plots. Redundancy analysis (RDA) showed that during the summer period TA species distribution was significantly affected by the treatment type and Sphagnum segment. The combination of warming and decreased precipitation during the experiment lead to significant testate amoeba biomass decrease, especially in the case of *Hyalosphenia papilio*. For less abundant species like *Euglypha strigosa* and *Nebela tinctoria* we found an increase of biomass in all treatments, compared to control plots. **Key words:** Testate amoeba; climate change; experiment

PT21 - SOIL MICROORGANISMS BEHAVE LIKE MACROSCOPIC ORGANISMS: PATTERNS IN THE GLOBAL DISTRIBUTION OF SOIL EUGLYPHID TESTATE AMOEBAE

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Patterns of alpha and beta diversity of soil protist communities and the factors that shape them remain largely unknown. We undertook a world-wide survey of forest litter to investigate the patterns of diversity in a group of testate amoebae. We aimed to assess: (1) whether there is a latitudinal gradient in alpha diversity, and (2) whether beta diversity was correlated solely with environmental factors commonly used in soil biology research or if it was also independently explained by geographical barriers.

We studied the diversity of Euglyphida in 35 samples of forest litter and moss samples from a global survey, using small subunit rRNA gene sequences. We assessed the relationship between sample alpha diversity and latitude using generalized additive models (GAM). Furthermore, we determined the relationships between community composition and geographical models (distance-based Moran's Eigenvector Maps – db-MEM) using Generalized

UniFrac distances (GUniFrac). We also investigated the relationship between individual measured soil parameters, WorldClim data and diversity (alpha plus beta) using both raw data and synthetic variables obtained through principal components analysis.

We recorded 245 phylotypes belonging to 6 out of 7 known Euglyphida families, plus four novel deep clades. Euglyphid alpha diversity was positively correlated with temperature and negatively with latitude and litter C/N ratio. Euglyphida community structure was correlated with the spatial eigenvector Db-MEM31, independently of all measured environmental variables. Db-MEM31 corresponds to a natural barrier constituted by the Northern Hemisphere desert belt. Beta diversity was correlated with other environmental variables, such as pH, isothermality and temperature in the coldest month of the year.

Soil euglyphid alpha diversity displays a latitudinal gradient, and beta diversity is not only correlated with climatic and physicochemical parameters but also with geographical barriers. Such patterns of diversity were until recently believed to be characteristic only for macroscopic organisms. **Key words:** Euglyphida; diversity; biogeography

**PT22 - THE PATTERNS AND CAUSES OF LATITUDINAL AND
ALTITUDINAL DIVERSITY IN FREE-LIVING UNICELLULAR EUKARYOTES:
USING SOIL TESTATE AMOEBAE AS MODEL ORGANISMS**

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The search for causal explanations and general patterns of species distribution along geographical and environmental gradients is a long-standing goal of biogeographers and ecologists. While the patterns and causes of latitudinal and elevational diversity gradients have been well documented for plants and animals; these have been comparatively less studied in microorganisms. This represents a serious gap in our general understanding of biodiversity and prevents the construction of ecological generalisations for all living entities. In recent years there has been growing interest in reverting this situation, which ultimately has resulted in the publication of several papers that have contributed to improve our understanding on the patterns and mechanisms that drive the spatial patterns in microbial diversity. Herein, we will show the findings that we have obtained from the assessment of the patterns and causes of latitudinal and altitudinal diversity gradients in free-living soil eukaryotic unicellular microorganisms with a particular emphasis in those lineages composing testate amoebae, a polyphyletic group of protists. To meet these objectives we have used both incidence data retrieved from historical records and new data obtained either from classical microscopy surveys or molecular studies (environmental DNA analysed by high-throughput sequencing) to assess the latitudinal and altitudinal patterns in microbial diversity and then, the potential ecological and evolutionary deterministic and stochastic forces that determine the assembly of communities at local and broad spatial scales. We estimated the relative importance of these forces by assessing the patterns of latitudinal and altitudinal variation in (1) habitat and biotic filters (e.g. phylogenetic overdispersion/clustering), (2) mass effect (or source-sink dynamics), (3) dispersal limitation (e.g. taxa-range size distributions: the Rapoport effect), (4)

taxonomic and phylogenetic beta diversity (i.e. variation in taxa or lineage composition), and (5) null (stochastic) model predictions (e.g. mid-domain effect). Overall, our findings show that the patterns of soil eukaryotic unicellular microorganisms stem from a combination of historical, evolutionary and current processes. **Key words:** Biogeography; macroecology; soil protists

PT23 - SELECTION OF SILICEOUS STRUCTURES FOR TEST BUILDING IN TESTACEANS FROM A SOUTH AMERICAN PEATBOG

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Testate amoebae are key members of the microbial communities in peatbogs worldwide. They are frequent inhabitants of the interstitial water among Sphagnum mosses and of the periphyton and benthos of peat bog ponds. They also contribute to the silica cycle by accumulating siliceous structures (SS) built by other organisms in their tests. Some species from genera *Diffflugia* and *Phryganella* (Arcellinida) and *Amphitrema* (Labyrinthulomycetes) reinforce their tests with SS, presumably taken from their preys and consisting of diatom valves and chrysophycean cysts.

In this work, we investigated whether these species actively selected the SS forming their tests in two ponds from a peat bog located in Tierra del Fuego. *Phryganella* sp1 and *Phryganella* sp2 from Pond 1 (P1); *Phryganella* sp1, *Diffflugia oblonga* and *Amphitrema* sp1 from Pond 2 (P2). The taxonomic composition and size structure of the SS composing five tests from each species as well as those in the fitobenthic communities, were analysed by means of a new technique of test digestion. Occurrence of length-based selection of SS was evaluated through a nested Variance Analysis. Also, as *Phryganella* sp. 1 was the only species present in both ponds, we tested whether selective behavior, if any, was a constant character. For this purpose Pearre Index (IP) of selectivity was calculated. Relative abundances of SS in the tests and the benthos were analyzed through a Principal Components Analysis and tested by a variance general linear model through a varident function.

For P1, the first two axes of the PCA explained 75.9% of total variability. First axis clearly separated the phytobenthic community from both *Phryganella* species. While P. sp1 and the phytobenthos had higher *Pinnularia* frequencies, P. sp2 presented the highest Chrysophyta frequencies.

For P2, the first two axis of the PCA explained 73.1% of total variability. Nevertheless, no selectivity pattern was observed, as no significant differences were found among the three testaceans studied or with benthic SS.

In the case of *Phryganella* sp1, the first two axis of the PCA explained 75,8% of the variance. Composition of benthic SS in both ponds was significantly different ($p < 0,001^{**}$), with the presence of *Pinnularia* spp. accounting for the higher diversity in P2. Notably, the tests of both populations differed even more

from each other than to their respective benthic samples. In P1, where Pinnularia was present, the testacean population differed significantly ($p < 0,001^{**}$) from the benthic SS due to the absence of Frustulia in all tests and a negative selection of Chamaepinnularia (IP: $-0,113 \pm 0,069$). On the other hand, in P2 where Pinnularia was absent, Phryganella sp1 incorporated a higher proportion of Frustulia and Chamaepinnularia valves.

Our results show a distinct and common selective behavior for both Phryganella species in P1 on one hand, and no selectivity in any of the three species in P2 on the other. Moreover, the different behavior shown by Phryganella sp1 in the two ponds strongly suggests that neither is this a species-specific trait, but rather environmentally driven. While causes for SS selection are not clear at this point, particle size is definitely not a key one, since no size selection of the material was recorded for any of the testacean species in this study. While the presence of Pinnularia seems to relate to selective behavior, such relationship is not due to a positive selection for this species. Whether Pinnularia could be indicative of other environmental conditions driving the selective behavior of Phryganella sp1 remains open to future research. We thus contribute to the scarce knowledge about testaceans ecology by posing new questions on the interaction of these organisms with their environment. New advances can be expected by using the new digestion technique in analyzing trophic relationships between testaceans and diatoms, both of them key environmental and palaeoenvironmental indicators in peatbogs. **Key words:** Silice; diatoms; selection

PT24 - DOCUMENTATION OF AMOEBIA DIVERSITY FROM UNIVERSITY OF SAO PAULO

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Amoebae form a non-natural diverse group. They are found in a diversity of environments. However, relatively little research and documentation has been made for many geographical areas. This documentation is important for several reasons: the elucidation of morphological diversity; deeper functional and ecological understanding; comparison and detection of convergent evolutionary strategies; and advancement in the medical area. This project involves not only the documentation of the group, but also scientific dissemination. This will be done by creating an online database, using an open source Content Management System, and will have every documented organism, which will be later published at the University's website. This database will serve not only the purpose of facilitating access for the general public, but also increase and highlight the importance of scientific dissemination and its vital paper of social transformation, generation of knowledge and support for the scientific community. **ey words:** Amoeba; online database; photographic documentation

PT25 - A SURVEY ON BRAZILIAN TESTATE AMOEBIAE IDENTIFIES THE POSSIBILITY OF 104 NEW SPECIES

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This work presents an inventory of testate amoebae occurring in continental aquatic environments in Brazil. Specimens were collected in the period of 1988-2016, in 114 distinct locations. Many of these are preserved national areas. Samples were made in natural and artificial environments of open water, such as aquatic plants and mosses, swamps, rivers and streams. Shells were photographed and measured, and compared to specific taxonomic publications for identification. At the moment, a total of 336 taxons were identified, however, a significant additinoal 104 specimens cannot be specifically identified. These taxa will require deeper studies for the confirmation of new species status. Lakes and marginal humid zones with high presence of plants have presented the largest numbers of species. Both images and morphometric measurements will be presented to at the talk with the purpose to increase discussion among taxonomists.. **Key words:**Aquatic environments; taxonomy; protect areas

**PT26 - BORN IN THE USA: A MOLECULAR PHYLOGEOGRAPHY OF
HYALOSPHENIA PAPILIO**

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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 have 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. The dataset included 55 sites in the Holarctic and a total of 450 sequences, resulting on 13 different lineages. Nine lineages showed often narrowly restricted geographical distributions and four lineages were well distributed all across the Holarctic realm; only members from these four lineages were found in European peatlands. This evidence, in addition to our phylogenetic tree, suggests a North American origin for *Hyalosphenia papilio*, and four colonisation events of the Palaeartic realm.

Key words:Phylogeography; holarctic realm; narrow endemism

**PT27 - MORPHOLOGICAL AND MORPHOMETRIC DESCRIPTION OF
ARCELLA GANDALFI N. SP. (AMOEBOZOA, ARCELLINIDA) FROM**

BRAZILIAN CONTINENTAL WATERS

FÉRES

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Arcellinids are one of the main groups of testate amoeba, with about 2,000 described species. The taxonomy in this group is based on morphology and morphometry of the test. Arcella is one of the largest genera, with more than 130 taxa described. They inhabit diverse fresh water environments, commonly associated with macrophytes, composing the planktonic and benthic communities. Arcella is characterized by a hemisphaeric shell in side view and circular in apertural view and with a ventral aperture. Due to lack of morphological and morphometric data and phenotypic plasticity, some Arcella species are difficult to distinguish. In this work we describe a new Arcella morphotype (Arcella gandalfi), clearly defined by morphological features. The specimens were collected in Brazilian continental waters, using meshes of 50 µm, in the states of Minas Gerais (1991), Tocantins (2009), Amapá (2015) and Rio de Janeiro (2015). This new species is morphologically similar to Arcella brasiliensis (Cunha, 1913). Both present a distinct marginal ring and an abapertural surface provided with depressions that differentiates them from the other species. The “wizard hat” shape of A. gandalfi shell is the main feature that undoubtedly differentiates this new morphotype from the A. brasiliensis and any other Arcella characterized by an umbrella-shaped shell.

Key words: Testate amoeba ; arcella ; new species

PT28 - HOW MANY CENTIMETRES MAKE A DIFFERENCE?

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The distribution of testate amoeba species in wetland ecosystems depends on water table depth and light diffusion in Sphagnum, especially for mixotrophic species. It was also found that TA community structure differs between types of peatland habitats e.g. hummocks and lawns and the upper and lower Sphagnum segment. Furthermore, the availability of nutrients and physical conditions of microhabitat can be crucial for particular species of testate amoeba and its community structure. In our study we analysed micro-vertical distribution of testate amoeba species biomass and frequency in Sphagnum fallax and Sphagnum magellanicum. We sampled both species in triplicate and precisely cut in five intervals along 12 centimetres (0-1, 1-3, 3-6, 6-9, 9-12). To describe the microhabitat conditions we performed the physiochemical analyses for each layers.

S. magellanicum was characterised by lower pH ((2.98-3.13) than S. fallax (3.43-3.95). In the same way, total carbon and nitrogen concentration were

lower *S. magellanicum*. Nutrient concentrations and conductivity increase from bottom to the top for both species. Total biomass of testate amoeba (TTA) was higher in *S. fallax*, then in *S. magellanicum*. TTA and diversity reach a maximum in the 1-3cm layer and decrease with depth. *Hyalosphenia papilio*, *Archerella flavum*, *Assulina muscorum* were found in the top layers (capitulum, 1-3cm), while *Nebela collaris* and *Nebela militaris* were the most abundant in 6-9cm layer.

The project was financed by the National Service "Peatlands" ("Tourbières", CNRS). Anna M. Basinska acknowledges support from Franche-Comté regional council and Université Bourgogne Franche-Comté.

Key words: Testate amoebae; amoeba species; d

PT29 - ENVIRONMENTAL DIVERSITY OF CRYPTIC SPECIES FROM THE NEBELA COLLARIS COMPLEX IS STRONGLY CORRELATED WITH ENVIRONMENTAL FILTERS

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The phylogenetic niche conservatism theory predicts that closely related species should occupy similar niches and therefore colonize similar environments. Closely related species are therefore not expected to co-exist as they should compete for the same resources. In protists, however, strong top-down regulation has been shown to mitigate competition, at least in plankton and there is also evidence of low competition in the soil environment. Here, we studied the distribution of members of the *Nebela collaris* species complex, a group of at least eight morphologically resembling species of arcellinid testate amoebae in the different micro-habitats of peatlands. We studied community composition in Sphagnum mosses collected from hummocks, lawns, pine forests, poor fens and peatland margin in two peatlands in the Swiss Jura Mountains by environmental DNA sequencing. We applied a protocol for specific amplification of the COI gene of *N. collaris* s.l. to Sphagnum DNA extractions and cloned the PCR products. Sequence analysis revealed six of the eight previously barcoded species, plus three new genetically defined lineages whose morphology is still unknown. The distribution patterns among the studied habitats show that, in agreement with our hypothesis, species do not coexist randomly. Instead, we observed a strong correlation between community composition and both nitrogen content and water table depth. Members of the *Nebela collaris* s.l. exhibit a reduced niche overlap, as suggested by calculating overall, and between pairs Pianka indices. We found no evidence for competitive exclusion, based on C-score and NTI/NRI calculations. Furthermore, plotting NTI values versus nitrogen content suggested strong adaptive pressure for low N values on a specific clade. Our study demonstrates that cryptic species play different roles in the environment, and for this reason should be studied in detail. Furthermore, we confirm that extreme lack of nitrogen in peatlands is a major driver of diversity. **Key words:** *Nebela collaris*; ; .

PT30 - IMPACT OF ATMOSPHERIC POLLUTANTS ON TESTATE AMOEBAS ASSEMBLAGES OF EUROPEAN PEATBOGS

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Climate change and anthropogenic pollution are affecting most natural ecosystems. Peatlands are globally significant carbon sinks and pools but these functions are threatened by environmental change. Thus, it is of major importance to find and assess effective tools to monitor their health. Testate amoebae (TA) are key players in soil biogeochemical cycles (especially N and C cycling) and are widely recognized as being efficient bioindicators as they respond quickly and specifically to the environmental factors that control organic matter decomposition, especially soil moisture and chemistry. Changes in micro-environmental conditions can lead to shifts in density, biodiversity (species diversity metrics), and community composition depending on the sensitivity of each species to a given environmental stress or gradient as well as indirect effects through trophic or other biotic linkages. In this study we analysed the testate amoeba communities from 54 Sphagnum peatlands across Europe. The site covered a broad range of climatic (oceanic-continental, temperate-boreal), and pollution gradients in Europe. At each site we analysed one sample from Sphagnum hummock and one from hollow. We then assessed to what extent the patterns of TA community structure and species distribution varied in relation to 1) broad geographical (three variables) and climatic (six variables) gradients, 2) microtopography (hummock-hollow) and 3) pollution loads (17 variables) with special focus on nitrogen and heavy metals.

We recorded 69 testate amoeba morpho-species in 108 samples. Constrained ordinations (MFA, partial RDA), transfer functions (WA) and indicator species (IndVal) analyses based on relative abundance data revealed that TA community structure was most strongly correlated to longitude, micro-habitat, nitrogen deposition (as NH_x) and Pb. When geographic or climatic effects were partialled out (used as covariables in the analyses), nitrogen deposition and lead contamination still explained a significant fraction of the TA community data. Based on this we calculated the optimum and tolerance of each species for these two variables.

The results confirm that TA are sensitive to atmospheric pollution. Although the measured pollution variables were not the strongest drivers of TA community composition, this study suggests that they could be useful microbial indicators of pollution levels in ombrotrophic bogs. Further experimental studies would be needed to determine the applicability of such a pollution biomonitoring tool.

Key words: Pollution deposition; environmental gradients; bioindication

PT31 - TESTATE AMOEBAS COMMUNITIES AND THE HUMIC GRADIENT IN AQUATIC ECOSYSTEMS

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Coastal freshwater environments show high variability in their organic matter input and content. The incomplete decomposition of organic matter produces humic substances which may influence the composition, abundance and distribution of various organisms, such as testate amoebae. We aim to analyze the direct response of testate amoebae to humic substance gradients and also its indirect response to other features. In order to achieve this, we will sample testate amoebae and measure limnological parameters in approximately 50 lakes and temporary ponds in the Restinga de Jurubatiba National Park. Aquatic environments at Restinga de Jurubatiba show a high variation of dissolved organic carbon (from 5 mg C L⁻¹ to 240 mg C L⁻¹). Samples will be filtered through a 20 µm plankton net and organisms retained will be stained and preserved for lab analysis. We expect to obtain a relationship between the testate amoebae community structure (composition, richness and density) and the sampled DOC environmental gradient. We also believe that it will be possible to identify a group of species suitable to be used as indicator of humic substances gradients. **Key words:** Testate amoebae; ecology; humic substances

PT32 - *QUADRULELLA TEXCALENSE SP. NOV.* FROM MEXICAN DESERT: NEW UNUSUAL ENVIRONMENT FOR TESTATE AMOEBAE

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Quadrullella (Amoebozoa, Arcellinida, Hyalospheniidae) is a genus of testate amoebae with unmistakable morphology which secretes plates in a characteristic square form to reinforce their test. They are mainly found in stable environments characterized by high levels of humidity and organic material. Their presence has never been documented in areas where temperatures are extreme and humidity and nutrients scarce, as in a desert. This study describes a new species of testate amoebae denominated *Quadrullella texcalense*, found in biological soil crusts in the intertropical desert of Tehuacán (state of Puebla, Mexico) dominated by mosses of Pottiaceae family. It occurred systematically at altitudes between 2140-2221 m.a.s.l, in association with the bryophytes *Pseudocrossidium*, *Weissia*, *Bryum*, *Didymodon*, *Neohyphyla* and *Aloina* genera. The soil was extremely dry (moisture of 1.97 to 2.6%), had a basic reaction (pH 7.7-8.0) and was very rich in organic matter content (12.92 to 22.42 %), which contrasts sharply with previous reports for the *Quadrullella* genus. Single cell cytochrome oxidase I (COI) barcoding of twelve isolated cells showed an important morphological variability despite a remarkable genetic homogeneity. Phylogenetic analysis identified *Q. texcalense* as a basal form

compared to other species of the *Quadrullella* genus. **Key words:** *Quadrullella*; amoebae

PT33 - TESTATE AMOEBAE PRESENT IN MOSSES OF GENUS *HYPNUM* (CHRISTMAS MOSSES)

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Mexico is considered a mega-diverse country, located at the meeting point between the Neotropis and Holarctis biogeographical kingdoms, with high rates of endemism. However, there is little knowledge about the diversity of organisms such as testate amoebae. In terrestrial habitats, these protists reach high densities and species richness in the leaves of mosses (Bryophyta). The indiscriminate collection of mosses of the *Hypnum* genus during December for use in Christmas decorations, turns out to be a very aggressive practice, causing significant damage to testate amoebae communities that inhabit these microhabitats. So, the aim of this study was to determine the testate amoebae community of genus *Hypnum* mosses discarded after the holiday season. Our results show high diversity of testate amoebae, mainly of the *Nebela*, *Bullinularia*, *Centropyxis*, *Trigonopyxis*, *Diffugia*, *Euglypha*, *Trinema* and *Arcella* genera. It is known that these organisms have a high local ecological value in nutrient cycling, but also many of these species may be endemic and high evolutionary interest, for their adaptation to adverse environments. However, the anthropogenic impact on the distribution, dispersion and conservation of these organisms is large, so you should consider establishing adequate management to preserve the great diversity of species testate amoebae that are being lost by this cause.

PT34 - TESTATE AMOEBAE COMMUNITY OF SOIL UNDER AGAVE STRICA IN TEHUACAN MEXICAN DESERT

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In arid and semi-arid systems it has been considered that abiotic factors are what mostly control the establishment of different species of microorganisms. However, interactions of nursing are established in these areas offering microhabitats where organisms inhabit, So it is important to know the effect of both biotic and abiotic factors on communities of testate amoebae of soil, since, these studies help to understand the factors that govern and maintain the diversity of these microorganisms on the planet. In this case, it was used as a model an endemic species of the Tehuacán desert, *Agave stricta*, to determine if it worked as nurse of the community of testate amoebae at Chacateca hill in the valley of Tehuacan, Mexico. Samples were taken from soil under plant to it to a depth of 10 cm. The testate amoebae were obtained with a modification of the method of Baerman. In addition, some physicochemical parameters were determined (pH, water holding capacity, organics matter and texture) and the altitude was taken into account. The results showed 17 genera of testate amoebae of which *Euglypha*, *Trinema*, *Centropyxis* and *Phryganella* are the most abundant and frequently found. It is observed a strong positive effect of the plant on the richness and abundance of thecate amoebae in contrast to the soil without plant (only 4 genera and abundance 1:20 ratio), which can be attributed to an important effect of nursing, however, the results indicated that there is a very weak relationship between physicochemical parameters and generic richness ($P > 0.05$). But there was correlation of the percentage of sand and organic matter with the genus *Phryganella*. Likewise, the community was also influenced by the altitude change finding that at higher altitudes it increased the numbers of genera present (16 genera) as well as abundance (78%). In addition, some genera present a possible relationship of coexistence, such as *Heleopera*, *Arcella*, *Diffugia* and *Corythion*. **Key words:** Microhabitat; chacateca hill; tehuacán valley

**PT35 - TESTATE AMOEBAE: POTENTIAL IN STUDIES IN ECO AND
PALEOECOLOGY IN MEXICO**

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Testate amoebae are a polyphyletic group of unicellular protozoa and eukaryotes. They are sensitive to changes in the environmental conditions. They have become a group increasingly used as bio and palaeoindicators. However, there are no detailed studies of testate amoebae in tropical lakes and peats. The purpose is to expand the knowledge about the abundance and diversity of testate amoebae in lakes and peats from Mexico. Surface sediment samples from lakes in the south of Mexico (Bacalar, Muyil, Chancanbacab, Metzabok, Nahá, Ocotlito, Balam, Vuelta del Agua and Peñasquito) were sampled in 2013 in collaboration with Technische Universität Braunschweig. A litter further to the north of the country, was drilled a 4m core in a peat at Cofre de Perote, Veracruz, by the Institute of Geology, UNAM and sub-sampled every 20 cm. Sediment sub-samples of 1 cm³ of both environments (lakes and peat)

were prepared for testate amoebae counting. To remove coarse particles were sieved through a 53 µm mesh to retain testate amoebae. Samples were examined under a stereomicroscope and all tests found were identified. In lakes were registered 10 strains and 27 species belonging to the genera: *Centropyxis*, *Arcella*, *Diffflugia*, *Cyclopyxis*, *Lesquereusia* and *Cucurbitella*. Lake Chancanbacab was the most diverse and with the most abundance of specimens, whereas in lake Metzabok were recorded the lower abundance and diversity. The genera occurring in most samples of the peat include *Nebela*, *Certesella*, *Centropyxis*, *Arcella* and *Diffflugia* with a lower abundance per sample (maximum abundance was of 30 individuals). Based on the results Mexico is a potentially diverse area so it should consider expanding studies in ecology and paleoecology of testate amoebae. **Palavras-chave:** Tropical; lakes; peat

PT36 – Can we predict the response of ecosystems to environmental change based on the traits of species in a long-time scales? A high-resolution palaeoecological study from two Sphagnum-dominated peatlands from Poland

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Although testate amoebae are frequently used as palaeohydrological indicators in peatlands, their traits are not commonly used in palaeoecology. As species' traits reflect species response to environmental changes they could serve as an early signal of ecosystem disturbance and help determining the thresholds of ecosystem resilience to stress. In our study we used the diversity indices of testate amoeba functional groups and testate amoeba functional traits to assess their potential use as disturbance indicators in the Sphagnum-dominated peatlands. We analyzed data from two mires in Poland which experienced human induced disturbances – fire and peat extraction – in the last 2000 years.

We aimed to examine whether the past response of testate amoeba communities to various environmental disturbances is reflected in their traits' composition and we tested the effect of disturbances on the linkages within TA community structure, functional trait composition and functional diversity. Analyzes revealed that testate amoebae morphology and their functional traits were linked to the environmental conditions, and we demonstrate that some of the traits were strongly connected with local disturbances. Therefore we call that testate amoeba traits could be effectively used in palaeoecological studies in the future as indicators of peatland disturbances.

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