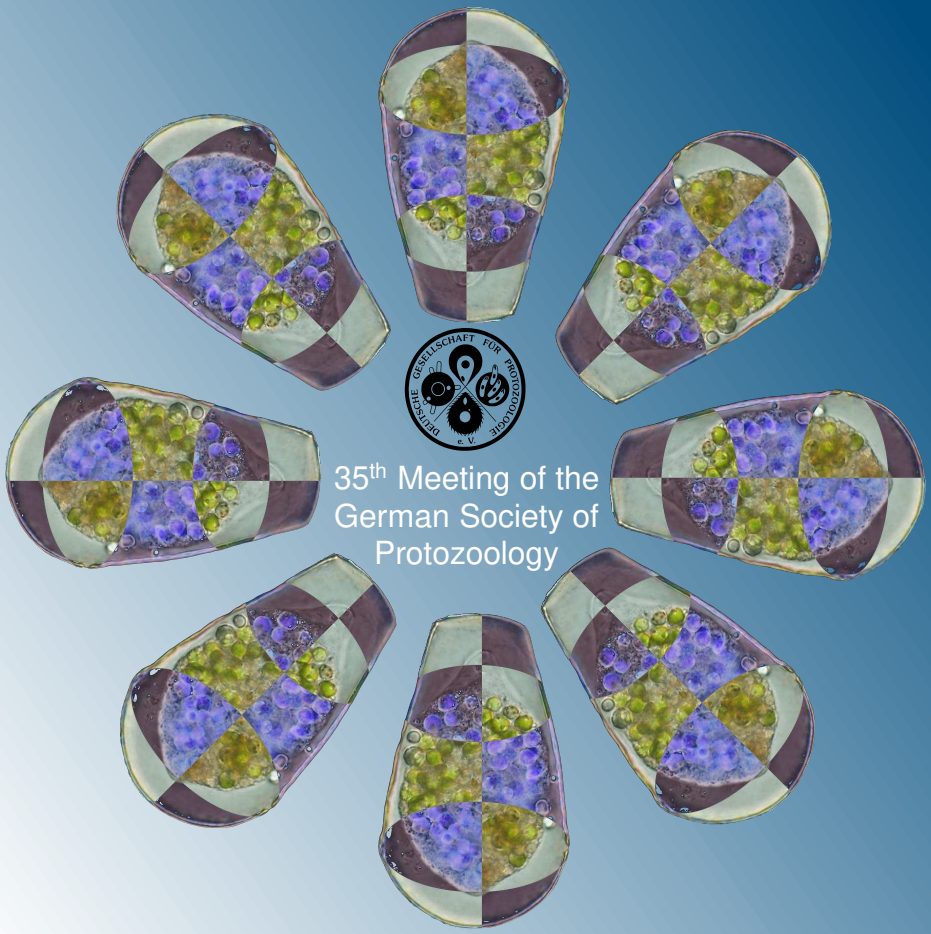
Program, Abstracts & List of Participants



35th Meeting of the German Society of Protozoology

UNIVERSITÉ DE NEUCHÂTEL

Saignelégier
Switzerland
February 23th to 26th, 2016

Organizers:
University of Neuchâtel
Institute of Biology
Laboratory of Soil Biology
Rue Emile-Argand 11
CH-2000 Neuchâtel

Halle du Marché-Concours

Hydrobiologie Stiftung

Deutsche Gesellschaft für Protozoologie e. V.

Ville de Neuchâtel

International Society of Protistology

Brasserie des Franches-Montagnes

hôtel CristaL
wellness - centre de loisirs

Promega

JURA CH
RÉPUBLIQUE ET CANTON DU JURA

MIGROS

Commune de Saignelégier

MERCK

N. Grandjean, gestion de projets et communication, Neuchâtel

Ragusa

LA SEMEUSE
LE CAFÉ QUE L'ON SAVOURE

Limnological Station of the University of Zürich

Special thanks

Mr Ugo Valli for the logistics of the Halle du Marché-Concours.
Mr Laurent Gonzalez for printing this booklet.

Contents

1 Useful information

Meeting locations

Centre de Loisirs (main hosting: Hôtel Cristal)
Chemin des Sports 10, 2350 Saignelégier
tel +41 32 951 24 74, fax +41 32 951 19 04, info@hotelcristal.ch

Breakfasts, pool and WiFi Internet are included in the price for persons who book a room in the Hôtel Cristal. The registration fees include all meals and water. Other beverages are at the expense of participants, except for the icebreaker (Tuesday evening) and the social evening (Thursday evening). A wellness area is open from 10:00 to 21:00. Entry cost is 17 CHF for people who rent a room at the Hotel Cristal.

Halle du Marché-Concours
Rue Chasseral 1, 2350 Saignelégier
tel +41 32 951 22 23,
http://www.saignelegier.ch/CMS/default.asp?ID=37

Registration

Registrations will be located in the:
Centre de Loisirs: Tuesday 23 Feb; 8:00-9:00 and 17:00-18:00
On Tuesday afternoon registration will also be possible before 17:00.
Halle du Marché-Concours: Wednesday 24 Feb; 8:00-9:00

Other accommodations in Saignelégier

Hôtel de Bellevue
Rue de la Gruère 13, 2350 Saignelégier
tel +41 32 951 16 20, info@hotel-le-bellevue.ch

Hôtel de la Gare
Rue de la Gruère 4, 2350 Saignelégier
tel +41 32 951 11 21, info@hotel-la-gare.ch

Gite Chez Toinette
Combe La Noire 7, 2350 Saignelégier
tel +41 32 951 24 11, fax +41 79 778 91 53, info@cheztoinette.ch

Café du Soleil
Rue du Marché-Concours 14, 2350 Saignelégier
tel +41 32 951 16 88, http://www.cafe-du-soleil.ch

In case of emergency

Hôpital du Jura Site de Saignelégier
Rue de l'Hôpital 11, 2350 Saignelégier
tel +41 32 952 12 12

Pharmacieplus des Franches-Montagnes SA
Place du 23 Juin 2, 2350 Saignelégier
tel +41 32 951 12 03, http://www.pharmacieplusfm.ch/

Taxi

Boss taxi et mini-bus Sàrl
La petite Theurre 14, 2350 Saignelégier
tel +41 32 951 21 18

Ice breaking party

Where: Restaurant du Centre de Loisirs

When: Tuesday 23 February; 18:15-22:00

Visit of the Cheese factory or Brewery

Where:
Fromagerie de Saignelégier
Chemin du Finage 19, 2350 Saignelégier
tel +41 32 952 42 20,
http://www.tetedemoine.ch/fr/visites/visite-a-saignelegier

or:
Brasserie des Franches-Montagnes SA (BFM)
Chemin des Buissons 8, 2350 Saignelégier
tel +41 32 951 26 26, http://www.brasseriebfm.ch/

When: Thursday 25 February; 18:00

Social Evening

Where: Brasserie des Franches-Montagnes SA (BFM)

When: Thursday 25 February; 19:30

What: Cheese fondue (with the full selection of BFM beers)

Internet access

Wifi internet is available in the Hôtel Cristal. The access code will be given at the reception during the check-in.

2 Organising committees

Scientific committee

Edward Mitchell (Laboratory of Soil Biology)
University of Neuchâtel (Switzerland)

Enrique Lara (Laboratory of Soil Biology)
University of Neuchâtel (Switzerland)

Ralf Meisterfeld (Institute of Biology II)
University of Aachen (Germany)

Julia Walochnik (Institute of Specific Prophylaxis and Tropical Medicine)
Medical University of Vienna (Austria)

Colomban de Vargas (Station Biologique de Roscoff)
CNRS (France)

Purificación López-García (Ecologie-Systématique-Evolution)
CNRS & Université Paris-Sud (France)

Alastair Simpson (Department of Biology)
Dalhousie University: Halifax (Canada)

Local organisation

Laboratory of Soil Biology
`http://www2.unine.ch/biolsol/`
University of Neuchâtel (Switzerland)

President:
Edward A.D. Mitchell

Organisational leader:
Isabelle Koenig

Registration Desk:
Amandine Pillonel

Registration Desk:
Marie-Jeanne Tschudi

Taxonomic Workshop:
Enrique Lara

Secretary:
Quentin Blandenier

Internet site:
Matthieu Mulot

Abstract booklet:
Christophe Seppey

Accounting & music:
David Singer

Registration:
Mirko D'Inverno

Coffee/tea breaks
Ildikò Szelecz

3 Overview of the meeting

Time	Tuesday 23 Feb	Wednesday 24 Feb	Thursday 25 Feb	Friday 26 Feb
8:00-8:45	Taxonomy workshop & Registration	Breakfast & Registration	Breakfast	Breakfast
8:45-9:00		Welcome Speeches		
9:00-9:15	Introduction & Welcome		Keynote talk 3: **Colomban de Vargas**	Keynote talk 4: **Julia Walochnik**
9:15-9:30	General introduction to protist identification			
9:30-9:45		Keynote talk 1: **Purificación López-García**		
9:45-10:00			Contributed talks (4)	Contributed talks (4)
10:00-10:15	Coffee/tea break			
10:15-10:30		Contributed talks (2)		
10:30-10:45	Practical part I			
10:45-11:15		Coffee/tea break	Coffee/tea break	Coffee/tea break
11:15-12:00		Contributed talks (4)	Contributed talks (3)	Contributed talks (4)
12:00-12:15			Lunch break	
12:15-13:00	Lunch break	Lunch break		Lunch break
13:00-13:30			Eduard-Reichenow medal award & presentation	
13:30-14:15	Introduction to testate amoeba taxonomy	Keynote talk 2: **Alastair Simpson**		End of the meeting
14:15-14:30		Contributed talks (4)	Grell awards ceremony & presentation	
14:30-15:15	Practical part II			
15:15-15:45		Coffee/tea break		
15:45-16:00		Contributed talks (5)	Coffee/tea break	
16:00-16:15			Best posters & talks awards	
16:15-16:30			Break (move to other building)	
16:30-17:00			General meeting of the DGP	
17:00-17:30	Registration	Poster presentations		
17:30-17:45			Break	
17:45-18:00		Members-meeting of the "Förderverein"		
18:00-18:15	18:00-22:00 Ice Breaker Party		Brewery OR Cheese Factory	
18:15-18:45				
18:45-19:30		Beer & posters		
evening		19:30-21:00 Dinner	19:30-2:00 Social evening	

4 Presentations program

Tuesday, 23 February 2015 (Centre de Loisirs)	
8:00-9:00	Pre-congress taxonomy workshop & Registration to the DGP meeting
9:00-9:15	Introduction & Welcome
9:15-10:00	General introduction to protist identification
10:00-10:15	Coffee/tea break
10:30-11:45	Practical part I
11:45-12:15	**Cédric Berney** UniEuk: a universal taxonomic framework and integrated reference gene databases for eukaryotic biology, ecology, and evolution
12:15-13:30	Lunch break
13:30-14:30	Introduction to testate amoeba taxonomy
14:30-17:00	Practical part II
17:00-18:00	Registration to the DGP meeting
18:00-22:00	Ice Breaker Party

Asterisks before names indicate student presentations/posters.

Wednesday, 24 February 2015 (Halle du Marché-Concours)

8:00-9:00	Breakfast & Registration
9:00-9:30	Welcome Speeches

S1: Ecology and biodiversity in the light of new molecular tools,
Chair: **Julia Walochnik**

9:30-10:15	**Purificación López-García (Plenary Lecture 1)** Temporal scales in the study of protist ecology and evolution
10:15-10:30	* **Matthieu Mulot** Detecting ecological changepoints using interaction networks along an environmental gradient
10:30-10:45	* **Julia K. Nuy** Potentials of functional monitoring: Gene expression patterns indicate nutrient limitations
10:45-11:15	Coffee/tea break
11:15-11:30	* **Christophe V.W. Seppey** Contrasting patterns of soil micro-eukaryotic taxonomic and functional diversity among forest, grassland and croplands in Switzerland
11:30-11:45	* **Paul Christiaan Venter** The large protistan microbiome of grassland soil: distribution in the mesoscale
11:45-12:00	* **David Singer** Environmental diversity of cryptic species from the *Nebela collaris* complex is strongly correlated with environmental filters
12:00-12:15	**Stefan Geisen** Functional diversity of soil protists
12:15-13:30	Lunch break

S2: Phylogeny, evolution and cell biology,
Chair: **Colomban de Vargas**

13:30-14:15	**Alastair G.B. Simpson (Plenary Lecture 2)** Protist biodiversity and the evolutionary history of eukaryotes
14:15-14:30	*** Kenneth Dumack** A bowl with marbles; the fungal and algal-eating amoeba genus *Lecythium* (Chlamydophryidae, Tectofilosida, Cercozoa, Rhizaria) revisited; phylogeny and the description of four new species
14:30-14:45	*** Quentin Blandenier** Exploring the mitochondrial genomes of Amoebozoa in search of novel molecular markers: the emergence of a new barcode for Arcellinida.
14:45-15:00	**Matthew W. Brown** A step into the future of protistology, a single cell transcriptome revolution
15:00-15:15	**Thomas Weisse** Sensitivity of aquatic protists to starvation
15:15-15:45	Coffee/tea break
15:45-16:00	**Daniel J.G. Lahr** The evolution of eukaryovory: perspectives from phylogeny and the fossil record
16:00-16:15	*** Lisa Siegmund** The influence of surface modifications of *Escherichia coli* on ingestion and digestion of *Tetrahymena pyriformis*
16:15-16:30	*** Lea Weinisch** Haloadaptation of the ciliate *Schmidingerothrix salinarum*
16:30-16:45	*** Miriam Cheaib** Stable Serotype Expression is regulated by epigenetic mechanisms and uncoupled from transcriptome dynamics in *Paramecium tetraurelia*
16:45-17:00	**Frederick W. Spiegel** Parsimony of morphology in the age of molecular phylogenies

17:00-18:00	Poster presentations

P1	**Sabine Agatha** Do fixatives influence histochemical tests in tintinnid loricae (Alveolata, Ciliophora, Spirotricha, Tintinnina)?
P2	**Sabine Agatha** The Rapunzel tintinnid - Redescription of *Tintinnopsis subacuta* Jörgensen, 1899 (Alveolata, Ciliophora, Spirotricha)
P3	**Anna M. Basińska** Testate amoeba community structure at the beginning of warming experiment *Sphagnum* peatland (Rzecin Mire, W Poland)
P4	**Hartmut Arndt** Deep-sea benthic microeukaryotes: A plea for morphological and ecological studies as a necessary addition to metagenomics
P5	**Cédric Berney** UniEuk: a universal taxonomic framework and integrated reference gene databases for eukaryotic biology, ecology, and evolution
P6	**Enrique Lara** Taxonomic, functional and beta diversities of freshwater planktonic ciliate communities are higher in the Antarctic than in neighbouring Patagonia
P7	*** Josie Antonucci Di Carvalho** Pulsed vs. continuous nutrient addition in a fragmented habitat: modeling anthropogenic stressors in a microbial metacommunity
P8	**Sabine Filker** Protistan plankton communities of high-mountain lakes from three continents exhibit strong biogeographic patterns
P9	*** Nadine Nerat** Chrysophyte community re-assembly and functional differentiation in the wake of flooding events
P10	**Hans-Werner Breiner** When a lake stops mixing - massive sequencing of plankton communities still mirrors the traditional Plankton Ecology Group (PEG) model

*** Gianna Pitsch**

P11 When a lake stops mixing - the fatal effects of warming on the protistan community

Bettina Sonntag

P12 Species-specific parasitism in lake plankton between *Podophrya* nov. sp. (Suctoria) and *Uroleptus willii* (Hypotricha).

*** Katrin Grosser**

P13 Getting closer: interaction analysis between *Paramecium* and *Caedibacter* at functional, molecular and transcriptomic level

*** Patrick Heidbüchel**

P14 Investigations on root-associated microbial communities: An approach to reduce pathogenic planktonic bacteria within rivers

*** Ruibao Li**

P15 Transfection in protists with cell-penetrating peptide

*** Lars Koehler**

P16 Shedding light on the killer trait: new approaches to identify the killer toxin and interspecific sensitivity

Alexandre Jousset

P17 Protozoa induce soil suppressiveness against *Fusarium* wilt

*** Tobias Romankiewicz**

P18 Comparison of thermal tolerance of different strains of heterotrophic flagellates and ciliates

*** Suzana Živaljić**

P19 Survival of marine heterotrophic flagellates isolated from surface and abyssal depths at high hydrostatic pressure

*** Chiara Pasqualetti**

P20 Salinity stress influences the transmission of bacterial *Paramecium* endosymbionts

P21 **Christian F. Bardele**
Trichospira dextrorsa, a very shy ciliate with fancy underwear

P22 *** Clément Duckert**
Barcoding, morphological and molecular taxonomy of the genus *Euglypha* - Towards a calibration of the molecular clock

P23 *** Kenneth Dumack**
The base of cercomonad radiation is still in for a surprise, *Kraken* gen. nov.

P24 **Maria Holzmann**
A new freshwater monothalamid foraminifera from China and its possible relationship to *Allogromia saxicola* (Penard, 1905)

P25 **Carmen Zinßmeister**
Morphological diversity of Dinophysales (Dinophyceae), with emphasis on the delimitation of *Dinophysis* and *Phalacroma*.

P26 **Anna Maria Fiore-Donno**
Diversity of Cercozoa (Protozoa) in soil revealed by Illumina sequencing

P27 *** Maximilian Ganser**
Difficulties in assessing the global distribution of a model organism - the biogeography of *Favella panamensis* (Alveolata, Ciliophora)

P28 **Alexandra Jeuck**
A comparison of some methods to quantify heterotrophic flagellates of different taxonomic groups

P29 **Michael Bonkowski**
Carbon flux from maize roots to key microbes in the rhizosphere and in bulk soil of an arable field

P30 *** Kjetill Christinat**
Impact of a summer draught on the testate amoebae of an artificial peatland in the botanic garden of Neuchâtel

	* **Monika K. Reczuga**
P31	Vertical distribution of microbial communities in two *Sphagnum* peatlands along natural and experimental water table gradients
	* **Ildikó Szelecz**
P32	The lament of scattered bones- a multiproxy approach in a real case investigation in forensic science
	Valentyna Krashevska
P33	Changes in structure and functioning of testate amoeba communities due to conversion of lowland rainforest to rubber and oil palm plantations
	* **Nathalie Amacker**
P34	Impact of pesticides on soil protists - Elaboration of an ecotoxicological protocol for *Euglypha rotunda* (Rhizaria)

17:45-18:45	Meeting of the "Förderverein"
18:45-19:30	Beer & Posters

19:30-21:00	Dinner

Thursday, 25 February 2015 (Halle du Marché-Concours)

8:00-9:00	Breakfast

S3: Taxonomic and functional diversity of terrestrial and aquatic protists,
Chair: **Purification Lopez-Garcia**

9:00-9:45	**Colomban de Vargas (Plenary Lecture 3)** Assessing global plankton biodiversity patterns with high-throughput sequencing and imaging technologies
9:45-10:00	* **Alexandra Schoenle** Unveiling the deep ocean - Methodological approaches and comparative studies on protist communities
10:00-10:15	**Thorsten Stoeck** The TARA Oceans Voyage reveals global diversity and distribution patterns of marine planktonic ciliates
10:15-10:30	**Thomas Posch** Cascade of symbioses - A new *Tetrahymena* (Ciliophora) with zoochlorellae living in feeding traps of the carnivorous aquatic plant *Utricularia reflexa*
10:30-10:45	**Frank Nitsche** Transcriptome studies on the choanoflagellate species *Salpingoeca euryoecia*: Adaptations to differing salinity concentrations
10:45-11:15	Coffee/tea break
11:15-11:30	* **Sarah Carduck** First record of gregarine parasites of the Atacama desert associated to *Scotobius brevipes*
11:30-11:45	* **Elodie Denet** Soil free-living amoeba: reservoir of multi-drug resistant bacterial pathogen species?
11:45-12:00	**Renate Radek** Morphologic and phylogenetic characteristics of Nephridiophagidae
12:00-13:00	Lunch break

13:00-14:15	Eduard-Reichenow-medal

Wilhelm Foissner
This and that; yesterday, today, tomorrow; here and there: a medley.

14:15-15:45	Grell awards

Lars Großmann
Diversity of Protists with Special Emphasis on Chrysomonads: Morphological and molecular diversity, distribution patterns and functional differentiation

Alexandra Jeuck
New insights into the phylogeny of craspedid choanoflagellates

15:45-16:00	Coffee/tea break
16:00-16:15	Best posters and talks award
16:15-16:30	Move to other building
16:30-17:30	General meeting of the DGP meeting

18:00-19:30	Visit of the cheese factory or brewery
19:30-2:00	Social evening

Friday, 26 February 2015 (Centre des Loisirs)

8:00-9:00	Breakfast

S4: Alka-Seltzer pot-pourri,
Chair: **Alastair Simpson**

9:00-9:45	**Julia Walochnik (Plenary Lecture 4)** Protozoan pathogens
9:45-10:00	**Manfred Wanner** Testate amoebae and diatoms in forensic science
10:00-10:15	**Martina Schrallhammer** *Paramecium* growth phase is essential for the outcome of its interaction with *Holospora caryophila*
10:15-10:30	**Mariusz Lamentowicz** Exploring ecology of protists in long and short time scales on the basis of the recent testate amoeba research
10:30-10:45	**Denis H. Lynn** *Askenasia volvox*, once a haptorid, now a homeless ciliate with surprising ultrastructure
10:45-11:15	Coffee/tea break
11:15-11:30	**Ute Risse-Buhl** The effect of hydrodynamics on protozoans within stream biofilms
11:30-11:45	**Katarzyna Marcisz** Here comes the sun: exploring light intensity as important variable driving testate amoeba communities in *Sphagnum*
11:45-12:00	**Sebastian Flues** Grazing of Cercomonads (Protists: Rhizaria: Cercozoa) structures bacterial phyllosphere communities
12:00-12:15	**Anja Scherwass** Comparison of grazing effects of protozoans on biofilm formation of bacteria
12:15-13:30	Lunch break

5 Abstracts: Plenary lectures, Eduard Reichenow Medal and Grell awards

Temporal scales in the study of protist ecology and evolution

Purificación López-García

Evolution et Systématique Laboratoire ESE, CNRS & Université Paris-Sud, Orsay, France

Comparing microbial community composition based on deep 16S/18S rRNA gene amplicon sequencing makes it possible to study microbial biogeography and its underlying ecological and evolutionary determinants. However, most studies only focus on spatial scales. Studying how communities vary through time within and across sites is essential to understand microbial biogeography, especially because of the impact of dormancy and its influence on community dynamics. To illustrate this, I will present a comparative study of protist diversity based on massive 18S RNA gene sequencing of samples collected monthly for 2 years in several shallow freshwater systems located at the Natural Regional Park of the Chevreuse Valley, France. Integrating temporal scales showed that marine-freshwater transitions are easier for some groups than previously thought. Despite the large diversity and apparent hectic dynamics of many lineages, the relative proportion of primary producers, free-living heterotrophs and parasites remains constant in similar biotopes. In addition, the occurrence of severe drought events leading to the desiccation of two of the studied systems allowed us to show a remarkable resilience of protist communities face to such extreme disturbances. This ability will be crucial for the adaptation of aquatic protist communities to the increasingly frequent drought episodes promoted by climate change in temperate areas.

Protist biodiversity and the evolutionary history of eukaryotes

Alastair G.B. Simpson

Department of Biology, Dalhousie University, Halifax, Canada

Understanding the evolutionary history of eukaryotic lifeforms depends on our knowledge of the major-lineage-level biodiversity of protists, and on an accurately inferred eukaryote 'tree of life'. These requirements are strongly intertwined: The information that can be derived from phylogenies depends on the taxa they include; furthermore, taxon sampling is known to have an important influence the accuracy of phylogenetic inference. Over the last $\sim$15 years, novel (or effectively novel) major lineages of protists have been reported with surprising frequency; In hindsight this has been a "golden age" of biodiversity discovery, that is likely still ongoing. Interestingly, a high proportion of such discoveries so far have been due simply to increased interest and effort with traditional isolation and/or cultivation, rather than technological advances. Examples from the 'excavate' lineages, and taxa related to the Amorphea supergroup will be discussed. Despite this availability of new major lineages, and the advent of taxonomically broad phylogenomic datasets for eukaryotes, important regions of the eukaryote tree-of-life remain uncertainly resolved. This will probably remain the case until taxon sampling improves markedly within certain groups. Consequently, achieving a modest density of taxon sampling within new major lineages is as critical as their initial discovery (at least from a phylogenetic perspective). This may be impossible in some groups due to their particular histories of speciation and extinction; however, recent cultivation and/or environmental sequences studies suggest (directly or indirectly) that novel major lineages will usually include a broad diversity of extant, accessible organisms.

Assessing global plankton biodiversity patterns with high-throughput sequencing and imaging technologies

Colomban de Vargas[1,2], Stéphane Audic[1,2], Sébastien Colin[1,2], the EPEP team[1,2] & Tara-Oceans consortium

[1]CNRS UMR 7144, Station Biologique de Roscoff, Roscoff, France, [2]Sorbonne Universités, Station Biologique de Roscoff, Roscoff, France

Automated, high-throughput DNA sequencing and imaging technologies are revolutionizing ecology, allowing to dramatically increase spatio-temporal sampling granularity while erasing the boundaries between organismal size fractions and taxonomic divisions. In Tara Oceans, we used massive DNA metabarcoding to assess the entire diversity of eukaryotic organisms from the smallest unicell (or protist) to small animals across a planetary biome. The sequencing of ∼800 million metabarcodes from >300 size-fractionated plankton communities allowed biodiversity assessment close to saturation, both locally and globally. We estimated that sunlit marine plankton contain ∼150 000 genetic types of eukaryotes, which is much greater than the ∼11 000 described species of eukaryotic plankton. The large majority of this biodiversity belongs to protists, and most of it comes from unknown and uncultured organisms. This eukaryotic biodiversity is significantly greater than the bacterial one, and ∼2/3 of it belongs to poorly known groups of heterotrophic protists, including a huge variety of parasites and species known to live in symbiosis. We assigned broad ecological functions to the metabarcodes and used OTUs abundance profiles to better understand the ecological behavior of this unveiled majority of plankton life, and reconstruct a global photic plankton interactome including viruses, prokaryotes, eukaryotes, and environmental parameters. Eukaryotes appear to play a fundamental role in structuring the plankton network, and, overall, biotic and positive interactions -in particular through parasites- are significantly more prevalent than abiotic and/or negative interactions. We finally developed a new automated confocal fluorescent imaging process (eHCFM) to validate network-generated hypotheses, unveil and quantify the complexity of novel plankton symbioses, and provide the needed tool to link genetic and morpho-functional diversity for future holistic studies of plankton systems.

Protozoan pathogens

Julia Walochnik

Institute for Specific Prophylaxis and Tropical Medicine, Medical University of Vienna, Vienna, Austria

Around 100 protozoan species can be assumed as parasites of humans, but not even half of them are significantly harmful to their hosts. Nevertheless, some protozoa can cause severe diseases, including malaria, leishmaniasis, Chagas disease, sleeping sickness and amoebiasis. Moreover, quite a number of protozoa have gained medical relevance with the appearance of acquired immunodeficiencies. Altogether, approximately 2 billion people are infected with protozoan parasites, the most common ones being *Toxoplasma gondii* and *Giardia duodenalis* but not every infection results in disease. The progression of an infection mainly depends on the infectious dose, the virulence of the respective strain and the immune state of the patient. Protozoan pathogens account for 1-3 million deaths per year worldwide, the majority of these cases occurring in poor countries and in large part being attributed to *Plasmodium falciparum*, the causative agent of malaria tropica. To date there are still no protective vaccines against any disease caused by protozoan parasites available, but almost all protozoan infections can be treated adequately if diagnosed in time.

Protozoan pathogens can be found in the Amoebozoa (e.g. *Entamoeba*, *Acanthamoeba*), the Alveolata (e.g. *Plasmodium*, *Babesia*, *Toxoplasma*, *Cryptosporidium*, *Sarcocystis*, *Cyclospora*, *Isospora*, *Balantidium*) and the Excavata (e.g. *Trichomonas*, *Giardia*, *Naegleria*, *Leishmania*, *Trypanosoma*), their sizes vary from <5 µm (amastigote *Leishmania* spp.: 2-4 µm) up to 150 µm (*Balantidium coli*). and they often show complicated life cycles with several different developmental stages. While many protozoan pathogens have extremely resistant cysts/ oocysts that can persist in the environment for long periods of time (e.g. *G. duodenalis*, *T. gondii*, *Cryptosporidium* spp.), those parasites, that are directly transmitted from humans to humans (e.g. *Trichomonas vaginalis*) or via a vector (e.g. *Plasmodium* spp., *Leishmania* spp., *Trypanosoma* spp.) do not develop permanent stages and cannot survive without a host.

This and that; yesterday, today, tomorrow; here and there: a medley.

Wilhelm Foissner

Department of Ecology and Evolution, University of Salzburg, Salzburg, Austria

I thank the Reichenow medal committee for choosing me as an appropriate recipient. I also thank many other people, especially co-workers, former students and reviewers of our grant proposals, who made it possible to do a lot of work during the past 55 years. In my lecture, I shall very briefly inform you on my scientific activities and how I became interested in protists.

When I was thirteen, a teacher showed us some algae and insect pieces in the microscope. This fascinated me so much that I wished a microscope as a Christmas gift. This microscope was very simple but sufficient to keep my interest alive. When I was 17, I bought a better microscope and began to concentrate on protists, especially ciliates because I found a protocol for silverline preparations. Suddenly, these small creatures, which looked rather pale and unstructured, became full of details and beautiful. However, Klein's silver method rarely gave good preparations. Thus, I tried to improve it and was successful resulting in my first publication in 1967. Fortunately, Dr. Bruno Klein, who discovered silver impregnation of ciliates, was still alive and became my teacher. Thus, I studied the nature of the silverlines and was the first who investigated silvered ciliates with the electron microscope. This showed that they were associated with fibres or the epiplasm. These studies showed that the silverlines are more than simple precipitations between the cortical alveoli. Still, the chemical nature and function of the silverlines are unknown.

During this time, I became fascinated by the diversity and beautiness of the ciliates and recognized that there were many poorly described and undescribed species. Thus, my doctoral dissertation was on diversity and ecology of ciliates in alpine ponds. As a post-doc, I became engaged in soil protists which were poorly known, most being the same as in polluted rivers and activated sludge. However, soon I recognized that this is incorrect and soil is full of undescribed protists.

Compared to the traditional way of studying protists by live observation, silver impregnation and, later, molecular characterization became a prerequisite for publication in international journals. But applying all these methods is time consuming and the descriptions become much more detailed and longer. These studies showed that soil protists are not cosmopolitan, as supposed by ecologists, but one third of them have a restricted distribution.

Now, I am 68 and have described about 700 new ciliates and authored or co-authored 12 books and monographs. However, I still have about 150 undescribed species in my folders sufficient for further 10 years.

Diversity of Protists with Special Emphasis on Chrysomonads: Morphological and molecular diversity, distribution patterns and functional differentiation

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Protistan diversity is tremendous. And it is largely understudied. Although the microbial sphere is the basis of all life and the driver of ecosystem functions, most attention is given to the organisms that one can observe with the bare eye. Therefore, the biology, the diversity and the functional differentiation of microbial eukaryotes is dramatically understudied. Many ecological hypotheses have not yet been tested for protists. The extent of protistan diversity and its relevance to ecosystems are largely unknown. Addressing protistan diversity can profitably make use of a comprehensive approach including alpha-taxonomy, phylogenetics, phylogeography and molecular diversity as well as functional and physiological diversity. My thesis aims at this broad interdisciplinary approach to protist biodiversity. Small colourless flagellates are among the most problematic protists as the scarceness of characters makes species identification questionable. Such small flagellates, specifically chrysomonads, are, therefore, a consequent starting point for investigating protistan diversity. As a detailed study of the cryptic diversity within small heterotrophic colourless chrysophytes, I reveal polyphyly within this group of organisms and, thereby, set the ground for assessing their true diversity in the field based on molecular signatures. Addressing protistan distribution patterns again is usually restricted by a limited and scattered set of sampling sites. Based on an unequalled sample set focusing on European protist communities, I demonstrate differential occurrence patterns in different protistan metagroups among habitat types. Last but not least, the vast diversity of protists raises the question for their coexistence and potential functional differentiation. I address this last aspect with a metatranscriptomic approach, investigating the degree of functional redundancy within protistan communities. Thus, in my thesis I reveal protistan diversity starting from species delimitation to large scale patterns of protistan diversity and distribution and further to the functional role and functional differentiation of protists.

New insights into the phylogeny of craspedid choanoflagellates

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Choanoflagellates are small heterotrophic protists ubiquitously distributed in marine and freshwater habitats. They possess a single apical flagellum surrounded by a collar of microvilli. As being the closest non-animal relatives to Metazoa (within the group of Opisthokonta), the interest in the evolutionary biology of choanoflagellates has recently increased. Phylogenetic and morphologic studies of choanoflagellates might help reconstructing the origin of multicellularity and the cell biology and genome composition of the first animals. Choanoflagellates are currently classified into two orders according to the presence or absence of a lorica - Acanthoecida (loricates) and Craspedida (non-loricates). Molecular data, mainly based on 18S ribosomal DNA, show that on the one hand the phylogeny of loricate species is well defined and monophyletic families exist. On the other hand the two craspedid families of Salpingoecidae and Codosigidae, based on morphologic characters only, were abandoned as they were clearly not monophyletic. Different morphological and life cycle forms exist within the order of Craspedida, inter alia, the presence or absence of a theca (organic cell covering) and the ability to form colonies.

The present studies aimed at revealing new insights into this controversially discussed taxonomy and systematics of the craspedid choanoflagellates by adding 18S and 28S rDNA sequences and morphological descriptions of twelve world-wide sampled isolates (marine, brackish, and freshwater). Among these, a complete new group of undescribed sequences from suboxic/anoxic environments, closely related to the order Acanthoecida, could be characterized. This group could be described by one isolate which was assigned to a new genus with a surprising morphological similarity to the order Craspedida. Taken together, this combination of both morphological and molecular data extended the existing choanoflagellate sequence database by about one third. To sum up, the diversity and systematic view of choanoflagellates, especially the clustering of the different genera of Craspedida is far from being resolved. Thus, this updated systematic view of choanoflagellates might hopefully serve as an additional step in the direction towards the highly demanded complete revision of choanoflagellates and hence, in the direction towards further evolutionary studies regarding the origin of multicellularity.

6 Abstracts: Presentations

Detecting ecological changepoints using interaction networks along an environmental gradient

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Understanding the communities dynamics in relation to biotic and abiotic perturbations is key to forecast ecosystems evolution in the actual context of global environmental changes. Such studies are routinely conducted using classical diversity indices and species distribution, but seldom take into account the dynamics of species interactions along a perturbation. Co-occurrence networks are becoming a pivotal tool to model species interactions. Co-occurrence, on the basis of correlation, represents the whole range of biotic and ecologic (direct and indirect) interactions driving community structure. One of the main strengths of co-occurrence networks is their ability to describe the state of a system regardless of the trophic position of the involved taxa.

The development of high throughput sequencing (HTS) now allows investigating distribution patterns of microbial communities, which drive soil biogeochemical cycles. However, the Operational Taxonomic Units (OTUs) unveiled by HTS have so far rarely been adequately documented in term of taxonomy and thus interpreted in any depth with respect to ecology. Co-occurrence networks allow inferring the implication of poorly known taxa without prior knowledge about their ecology. Several metrics exists to describe network topology, at different scale of the network: global (e.g. network connectivity, number of edges, etc.) or local (e.g. node centrality - the relative contribution of a node in the network). Centrality measures are often used to infer keystone species, i.e. species whose removal would have a major impact on the network topology and thus likely also on ecosystem functioning.

We hypothesized that network topology indices could be used to infer ecological changepoints along an environmental gradient. The rationale was that network topology, representing community dynamic structure, is a proxy for the functioning of the system. We set up a mesocosm experiment to study the effect of water table changes on Sphagnum peatlands. Forty-five mesocosms (peat cores with a Sphagnum fallax layer) were exposed to three water levels treatments (range: -237 mm to +124 mm relative to the top of the Sphagnum layer). We sequenced the 18S SSU V9 region of micro eukaryotes inhabiting the Sphagnum mosses along a water level gradient using HTS. We computed interaction networks along the water level gradient on the basis of the resulting OTU matrix. We then calculated network topology and centrality indices and inferred changepoints based on piecewise regression, either from raw community matrices or matrices aggregated by trophic groups. We then compared the inferred changepoints with results obtained from beta diversity threshold detection algorithm. Overall, changepoints inferred from network topology are consistent with beta diversity based changepoints. Strikingly our results revealed a tipping point at 10cm DWT for both the microbial networks as well as the functioning of the ecosystems (soil respiration).

Potentials of functional monitoring: Gene expression patterns indicate nutrient limitations

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Environmental monitoring aims at assessing the occurring processes and functions in ecosystems and at detecting environmental changes. With the upcoming challenges of environmental changes, the efforts to establish a representative monitoring system are high. So far, environmental monitoring focusses on the occurrence of indicator organisms whose diversity can now be captured by high throughput sequencing technologies. However, the presence of distinct species and organismic groups does not necessarily reflect its effective functional participation in the respective ecosystem. To date, approaches for functional monitoring are sparse. Here, we analysed metatranscriptomes from 21 European freshwater lakes for indicator genes reflecting limiting nutrient conditions. We demonstrate that metatranscriptomes have the potential to picture metabolic pathways. Further, we could show that limiting nitrogen conditions are associated with increased expression of nitrate and ammonia transporter genes. Here, only transporter genes expressed by distinct taxonomic groups show this indicator function for nitrogen limitation. We hypothesize that gene expression levels could potentially indicate limiting nutrient conditions. In future, we aim at detecting limiting nutrient conditions on the basis of gene expression profiles of bacterial taxonomic groups as well as eukaryotic taxonomic groups.

Contrasting patterns of soil micro-eukaryotic taxonomic and functional diversity among forest, grassland and croplands in Switzerland

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Micro-eukaryotes play a broad range of functional roles in soils as decomposers, plant parasites, microbe predators and primary producers. However, our understanding of the functional ecology of soil microbial eukaryotes is still poor. New high throughput sequencing methods allow an unprecedented sequencing depth, and open the way for molecular surveys of eukaryotic diversity in soils where the dominance of animal and fungal DNA previously masked the full diversity of protists. Furthermore, the increasingly complete reference databases allow inferring the functional role for most OTUs.

We used Illumina sequencing of the V9 region of the SSUrRNA gene to assess the diversity of micro-eukaryotes from soil samples collected in permanent plots of the Swiss Biodiversity Monitoring (BDM) program. We targeted three categories of land use: forests (16 samples), meadows (16 samples) and croplands (12 samples). We grouped most (75%) OTUs into 41 high ranked taxa that we assigned to three functional categories: osmotrophs (including plant parasites and mycorrhizae), phototrophs or phagotrophs.

Taxonomic and functional micro-Eukaryotes community composition differed significantly among land use types. Within osmotrophs, Basidiomycota related to wood decomposition and ectomycorrhizal species were dominant in forests. In contrast, parasites and/or grass mycorrhiza (Chytridiomycota, Glomeromycota, Phytomyxea, Oomycota) were more represented in open habitats (meadows and croplands). These results illustrate the fact that osmotrophic micro-Eukaryotes are directly linked to plant communities. Phototrophic organisms i.e. subaerial microalgae (Chlorophyceae, Trebouxiophyceae, Bacillariophyta and Xanthophyceae) were significantly more abundant in open habitats, probably due higher light availability. Phagotrophic taxa were overall more abundant in open habitats than in forests, in agreement with the higher bacterial to fungal ratio in open habitats that should favour bacterivores.

This study illustrates the pivotal role of above/below ground relationships in shaping soil micro-eukaryotic communities. It also shows that although existing databases only cover a very small proportion of overall protistan diversity they already allow meaningful ecological interpretations, which will only get better if major efforts are undertaken to feed and curate taxonomic databases.

The large protistan microbiome of grassland soil: distribution in the mesoscale

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Genomic data for ±22% (±411,000) species on earth occur in GenBank of which 164,027 are protist reference sequences. Very little information exists on the small size class (1-100µm) heterotrophic nanoflagellates and ciliates and their taxa-area relationship. This study is a first attempt to get a comprehensive comparative data set on grassland soil protist species richness, community structure, taxa-area relationship and what effects land use intensity/intensification (LUI) has on them. To achieve this, environmental DNA (eDNA) from 150 geo-referenced grassland plots representing topographical and land-use ranges typical for central Europe was analyzed. Using high through-put 454 sequencing for the small subunit (SSU) ribosomal RNA (rRNA) gene and assuming that single base differences could indicate evolutionary distance, original raw sequences was investigated at various levels of sequence certainty cut-offs. BLASTn alignment of operational taxonomic units (OTUs) to the well curated protist ribosomal reference (PR2) database identified 56 deep eukaryotic class taxa and a species richness in the region of 102 OTUs per one gram of soil in the mesoscale (1 - 1000km) at 97% sequence identity. OTUs comprised mostly rare and uncertain taxonomic lineages as well as lower pairwise identity annotations illuminated gaps in databases. Phylogenetically unresolved taxa disappeared with increased sequence identity cut-offs . Parasitic SAR supergroup members, e.g. oomycotan plant parasites (*Pythium attrantheridium*) occurring at 141 sites, dominated, but no single OTU occurred ubiquitous across all sites. Moderate land use disturbance increased OTU diversity. Local taxa-area relationships were steeper than provincial mesoscale z-scores and low LUI indicated the highest taxa-area separation.

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.

Functional diversity of soil protists

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Soil protists are the most diverse and abundant soil eukaryotes. Nevertheless, knowledge remains scarce especially on protist functioning as they are predominantly considered to represent the major controllers of bacteria in the soil food web. This potential bias likely emerged at least partially from the fact that many protists were isolated and kept using bacterial enrichment medium and from those, most ecological studies used just a single model protist.

Using a combination of classical cultivation-based techniques, functional essays and state-of-the-are sequencing approaches we show that protists others than bacterivores, such as mycophages, nematophages, parasites and pathogens are diverse and common soil protists and most likely of substantial importance for functioning of soil food webs. Furthermore, the respective groups showed species-specific differences on their prey items, e.g. not all mycophages fed on all fungi equally.

Therefore, soil protists cannot be grouped into the single functional group “bacterivores”; evidence for multiple functional roles of distinct protist taxa strongly suggests that the enormous protist diversity is meaningful for soil functioning. This, however, implies that a species specific resolution is essential to assign functions with consequences for community analyses: high taxonomic resolution needed for functional evaluations of protists and other soil organisms necessitates careful data interpretation, especially with the now commonly applied high-throughput sequencing approaches. Furthermore, functional studies need to supplement HTS data in order to fill the massive knowledge gaps on functioning of individual protist taxa to enable most meaningful data interpretation in future efforts.

A bowl with marbles; the fungal and algal-eating amoeba genus *Lecythium* (Chlamydophryidae, Tectofilosida, Cercozoa, Rhizaria) revisited; phylogeny and the description of four new species

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Although testate amoebae have attracted interest of protistologists for more than 150 years, some groups especially those with a hyaline test are still poorly known. One of those is the genus *Lecythium* (Chlamydophryidae, Tectofilosida, Cercozoa, Rhizaria), first described by Hertwig & Lesser in 1874. Only old, sometimes obscure, species descriptions were available until only recently a new species of *Lecythium* was described and a small ribosomal subunit RNA gene (SSU) sequence was provided. To shed light on the phylogeny and taxonomy of *Lecythium*, we cultured 6 isolates of 5 *Lecythium* species and provide morphological as well as ecological observations and obtained six new SSU sequences and conducted phylogenetic analyses of the Tectofilosida, showing that *Lecythium* splits into a terrestrial and freshwater clade. Our results suggest that there could still be many undescribed *Lecythium* species.

Exploring the mitochondrial genomes of Amoebozoa in search of novel molecular markers: the emergence of a new barcode for Arcellinida.

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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 ($\sim$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 sequences from the following Arcellinid genera: *Hyalosphenia* (1 isolate), *Difflugia* (4 isolates), *Arcella* (2 isolates) and *Netzelia* (2 isolates), plus a clone sequence obtained by amplifying environmental DNA with our newly designed primers, and which appeared to branch close to *Hyalosphenia*.

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 *Difflugia*. Moreover, the NAD9/NAD7 marker could discriminate efficiently closely related forms (i.e. both isolates of *Difflugia nodosa*). All Arcellinid species surveyed seemed to use a TAA stop codon, while the TGA codon is use 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 (*Arcella* spp., *Difflugia nodosa* and *Hyalosphenia papilio* + environmental clone) or are separated by a short intergenic region varying from two to six nucleotides composed only of the nucleotides A and T (all other taxa).

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.

A step into the future of protistology, a single cell transcriptome revolution

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Recent advances of both sequencing technologies and sequence library production have revolutionized the field of transcriptomics. With these new technologies we are now able to examine the expression profiles of cell types at developmental stages. We are also able to use single cell RNAseq to robustly examine the evolutionary positions of organisms that are rare and or difficult to culture. Here we detail the methodologies, pitfalls, costs, and benefits associated with the production of such data. We also provide several case studies of the use of this technology for both types of experiments. We apply these single cell RNAseq methods to phylogenomically examine the position of the rarely observed and poorly examined "leatherback" testate amoebozoans (*Amphizonella*, *Diplochlamys*, and *Microchamys*). These data represent the first molecular data from these organisms. While *Microchlamys* branches with other testate amoebae, *Amphizonella* and *Diplochlamys* robustly occupy a novel basal position on the tree of Amoebozoa, branching distantly from the other testate amoebae. Additionally, with these methods we examine the developmental pathways using expression profiling of discrete developmental stages of life cycle of protosteloid amoebozoans. Protosteloid amoebae are solitary amoebae that all have a life cycle that includes the production of spore-bearing aerial structures (sporocarps). Protosteloids are unique to Amoebozoa, but occur in at least seven distinct lineages of Amoebozoa. Here we begin to unravel the developmental program of these dispersant taxa to examine if these organisms use underlying homologous mechanisms.

Sensitivity of aquatic protists to starvation

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Aquatic protists are generally subjected to large fluctuations in their food supply and, accordingly, are adapted to leading a 'feast and famine existence'. The response to moderate and high food levels has been studied in great detail with many protist species. However, their sensitivity to starvation received comparatively little attention in spite of the fact that most free-living species typically live under conditions of temporarily or permanently scarce food supply. There are three general adaptive responses to survive food deplete conditions: 1) to resist starvation by decreasing metabolic rates and/or formation of dormant stages (cysts) ; 2) to store resources under food replete conditions for use when supply declines; and 3) to increase motility and dispersal to find a new food patch with higher prey levels. Only the first of these responses has been studied experimentally across different protist taxa, namely with ciliates and dinoflagellates. Protist survival under starvation can be inferred indirectly from numerical response curves or studied directly in the absence of food. Results from the literature and own experimental work revealed large taxonomic differences in the sensitivity to starvation; for example, dinoflagellates tend to sustain starvation better (i.e., for weeks) than ciliates that typically survive for a few days only at food levels below the critical threshold concentration needed to sustain a population. Motile cells of cyst-forming species seem to be more sensitive than species unable to encyst. Temperature affects survival under food deplete conditions strongly and non-linearly. With respect to storage, not only food quantity but also food quality may affect survival rates during starvation.

The evolution of eukaryovory: perspectives from phylogeny and the fossil record

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Modern phylogenetic reconstructions of eukaryotic clades provide a novel perspective to explore the interplay between feeding types and diversification of eukaryotes. Here, we combine the phylogenetic insights of five previously published large-scale phylogenetic reconstructions with natural history observations of carbon uptake strategies for hundreds of taxa in order to reconstruct potential ancestral feeding modes, as well as dates when novel feeding modes first evolved. We conclude that the last common eukaryotic ancestor was a bacterivore and that feeding innovations began early in eukaryotic divergence, strongly influencing the subsequent evolutionary history of individual clades. Molecular clock estimates suggest that the major eukaryovorous clades diversified in Neoproterozoic oceans, providing a functional and ecological perspective on the Neoproterozoic diversification of eukaryotes observed in the fossil record.

The influence of surface modifications of *Escherichia coli* on ingestion and digestion of *Tetrahymena pyriformis*

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Endosymbiosis is an abundant phenomenon in nature and occurs in diverse groups of organisms, also in protists in a certain variety (Görtz 2010). It appears to be a logical prerequisite for establishment of endosymbiotic relationships that ingested bacteria evade digestion and escape from food vacuoles of the potential host. The details of the mechanistic and physiological processes necessary for escaping food vacuoles remain unknown, and investigating established endosymbiotic relationships seem to reveal no clues for these initial processes. For understanding the initialisation of endosymbiosis a laboratory model is required. Recently we have shown that a non-pathogenic strain of *Escherichia coli* K12 is able to evade digestion and to escape from food vacuoles of *Tetrahymena pyriformis*, resulting in persistence of the bacteria in the ciliate's cytoplasm (Siegmund et al. 2013). Based on this and further studies, revealing an influence of defined biochemical and physical surface properties of microparticles on ingestion and digestion (Dürichen et al. 2016), we designed a different experimental setup to investigate effects of different bacterial surface traits on feeding behaviour and digestion on *T. pyriformis*.

Therefore, different substances were covalently coupled to the surface of *E. coli* by means of a carbodiimide. After feeding a starved culture of *T. pyriformis* with variously labelled bacteria, the fate of the latter was followed by fluorescence microscopy, since our *E. coli* transformant strains express either red (DsRed) or green fluorescence (GFP).

Depending on the coupled substance different ingestion rates of bacteria were observed, resulting in either decreased (e. g. amino acids) or increased uptake (e. g. endoporter, an artificial oligopeptide). These findings taken together with results obtained by feeding modified microparticles clearly indicate a recognition site acting prior to phagocytosis. Further, decreasing of fluorescence intensity was used as an indicator for digestion, since both marker proteins are digested concomitantly with the bacteria. Bacteria with enhanced surface hydrophobicity were not always digested completely. Even surviving *E. coli* cells were observed within fecal pellets.

By binding further substances, combined with double feeding and appropriate staining, bacterial surface traits may be revealed that enable food bacteria to evade digestion and presumably also to escape food vacuoles of *T. pyriformis* and, thus, will shed light on the initial prerequisites for establishing endosymbiosis.

References:

Dürichen, H., Siegmund, L., Burmester, A., Fischer, M.S., Wöstemeyer, J., 2016. Eur. J. of Protistol. 52, 45-57.

Görtz, H.-D., 2010. Crit. Rev. Immunol. 30, 95-106.

Siegmund, L., Burmester, A., Fischer, M. S., Wöstemeyer, J., 2013. Eur. J. Protistol. 49, 552-563.

Haloadaptation of the ciliate *Schmidingerothrix salinarum*

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High salt environments pose a major challenge to their residents. Thus far, studies on haloadaptations have focused primarily on prokaryotes while eukaryotes were largely ignored in this respect. This is mainly due to (i) methodological shortcomings and (ii) the erroneous assumption that eukaryotes play only a minor role in high-salt environments. A series of recent protistan molecular diversity studies, however, disproved this assumption. Thus, possible strategies of protists to combat high-salt conditions come more and more to the fore. Therefore, we have investigated haloadaptation in the heterotrophic ciliate *Schmidingerothrix salinarum* (Foissner, Filker, Stoeck 2014), a true halophile with a wide geographic distribution. To this aim, we established two approaches: (I) Ion imaging with ion-specific fluorescent dyes as a tool to analyze the intracellular ion concentrations in living cells and (II) 1H-NMR as a fast and simple technique for the detection, identification and quantification of intracellular compatible solutes. Despite an increase of salinity in the exterior medium up to 22% salt, Ion imaging did not show an accumulation of Na+ ions in *S. salinarum*. Instead, 1H-NMR spectroscopy identified glycine betaine (GB) as a compatible solute in *S. salinarum* to counterbalance high salt concentrations. Intracellular GB increase correlated significantly with an increase of salinity in the exterior medium. Addition of exogenous GB and choline as a precursor of GB stimulated the growth of *S. salinarum* notably, indicating that the organism is both able to accumulate GB out of the culture medium and to synthesize GB by the oxidation of choline. This first data reveal that *S. salinarum* uses GB as a main haloprotectant and identifies the organism as an interesting model organism to further study haloadaptation in heterotrophic protists.

Stable Serotype Expression is regulated by epigenetic mechanisms and uncoupled from transcriptome dynamics in *Paramecium tetraurelia*

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High phenotypic plasticity defines the ability to rapid adaptation to environmental changes. The expression of specific serotypes is known to depend on climatic conditions in *P.tetraurelia* and serves as an indication for adaptation. Here, we investigated the difference on transcriptome-level by RNA-Seq analysis between serotype pure cultures which were cultivated under long-term and stable conditions while exposing them to extreme conditions (heatshock, cold, starvation). Through the differential expression analysis we were able to show that the regulation of the surface antigen genes (SAg) relies on epigenetic mechanisms which is unaffected by environmental short-time changes: One the one hand they are epigenetically maintained and stable heritable to the next generation, on the other hand serotype-shift can occur spontaneously. We were able to show that serotypes cannot be restricted to the activation of a single gene, moreover a group of co-regulated genes built a complex, which pre-determine the phenotype of a culture. In combination with the transcriptome-analysis we investigated the chromatin-dynamics in serotype pure cultures by chromatin immunoprecipitation (ChIP) of specific modifications. We assumed through the results that the long-time multigene family organized surface antigen genes are pre-installed to be in stand-by modus and poised for activation, whereas fast-inducible and short-time regulated genes, like the heatshock-genes (HSPs) show the classical on-/off state on transcriptional level.

Parsimony of morphology in the age of molecular phylogenies

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Morphology based phylogenetic hypotheses that met the prinicple of parsimony when first proposed often run into problems following the development of molecular phylogenies. Most often morphologically different organisms are found to be closer relatives than morphologically similar ones. However, morphology based hypotheses still have lots to offer if one parsimoniously resolves the conflicts between them and molecularly based hypotheses. Some examples will be provided from consideration of groups within Amoebozoa.

Unveiling the deep ocean - Methodological approaches and comparative studies on protist communities

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Extreme environmental conditions in the deep sea hamper access to protist communities. In combination with the potentially highly diverse species composition, it demands a wide range of methods to be applied at the same time to guarantee a high resolution of quantitative and qualitative studies of deep-sea heterotrophic flagellates (HF). We tried to provide a recommendation of culture-dependent and culture-independent methods for investigating abundance and diversity of deep-sea nanoprotists by combining different techniques available at present underlined by preliminary results from the deep sea of the Atlantic Ocean, Pacific Ocean and Mediterranean Sea. Estimates of abundance and diversity can be accomplished by culture-independent methods such as live-counting of untreated samples as well as counting of fixed and stained samples. Abundances in the Atlantic Ocean obtained by fixed counts were significantly larger than live-counts supporting the assumption of underestimating live-count abundances. Cultivation of defined aliquots of the diluted sample (liquid aliquot method, LAM) offers the possibility of morphological characterization and later molecular surveys (PCR, single-cell genomics/transcriptomics) for identifying corresponding genotypes. Phylogenetic analyses of isolated cultivable protists from the Atlantic Ocean were carried out and revealed flagellate species such as *Cafeteria roenbergensis*, *Pseudobodo* sp., *Massisteria* sp., *Keelungia* sp. and *Fabomonas tropica*. Generally, not all species appear in cultures due to selective conditions like enrichment of bacteria or the lack of suitable other food sources (e.g. other protists). However, sometimes even seldom recorded species may appear, showing that a massive cultivation effort is needed to enhance successful cultivation. To partially overcome this problem, molecular investigations such as next generation sequencing (NGS) are applied to detect uncultivable organisms. To get an idea regarding the active genotypes in deep-sea samples, NGS of RNA is necessary. Clone libraries or NGS are helpful tools but the results must be verified regarding the origin of the organisms. Laboratory experiments under deep-sea conditions such as high pressure (>200 bar) and low temperature (<4° C) may confirm the deep-sea origin of sample d HF. The combination of different methods offers a unique possibility to receive detailed information on nanofaunal life in the deep sea. Specific fixation techniques to preserve samples directly at the sampling depth must be applied in further studies to reflect the real biodiversity of the largest habitat on earth.

The TARA Oceans Voyage reveals global diversity and distribution patterns of marine planktonic ciliates

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Ciliates are among the most diverse heterotrophic protists in marine plankton. As trophic links between bacteria, smaller protists and metazoan, they play a major role for energy and carbon transfer in the oceanic ecosystem. Surveys of their biodiversity in the marine realm have hitherto been geographically restricted, with a major focus on coastal environments. We here analysed 6,137,350 Illumina reads of the small subunit ribosomal DNA V9 region obtained from ocean surface waters (SRF) and the deep chlorophyll maximum (DCM) during the circumglobal Tara Oceans voyage. Diversity estimators predicted 1247 operational taxonomic units (OTUs) for the seven investigated oceanic regions, corroborating with the total number of observed ciliate OTUs. More than one half of these OTUs shared less than 90% sequence similarity with reference sequences of described ciliate species. The geographic distribution of the observed OTUs is not random, but follows strict patterns. OTU richness observed in the seven oceanic regions under study are notably lower than global ciliate diversity. Regional richness was lowest in the Southern Ocean. Only 1% of all OTUs was cosmopolitan. These OTUs, however, accounted for 33.2% of the total number of sequence reads. These observed patterns corroborate well with diversity distribution patterns of macrobial organisms. Logistic regression models found significant correlations between the occurrence of specific ciliate genera and individual nutrients, the oceanic carbonate system and temperature. Therefore, it is reasonable to assume that future environmental change will alter ciliate community structures in ocean waters.

Cascade of symbioses - A new *Tetrahymena* (Ciliophora) with zoochlorellae living in feeding traps of the carnivorous aquatic plant *Utricularia reflexa*

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Utricularia reflexa is a carnivorous water plant with specific traps to catch living zooplankton and even larvae of insects. Our studied hydrophytes originate from the Okavango Delta and are since then cultivated in the wetland plant collection Trebon (Czech Republic). Newly build traps of plants are sterile but get soon colonized by rich bacterial and unique protistan assemblages, which seem to be not digested by enzymes of the hydrophyte. Anaerobic and nutrient rich trap fluids are colonized by one euglenid species and a yet undescribed green (with 40-50 zoochlorellae) ciliate identified as *Tetrahymena*. Here we present a detailed species description of the ciliate and its algae based on various morphological and molecular techniques. Additionally, we document the full, *T. pyriformis* type like, life cycle of the ciliate. We were successful in cultivating the ciliate and the isolated symbiotic algae. When ciliates are kept outside the traps under aerobic and bacterial rich conditions, they loose their symbionts and get completely colorless. By decreasing bacterial food levels, ciliates can be ‚reinfected' with algae. We present first hypotheses why this harsh environment gets colonized by ciliates and why *Tetrahymena* lives there in symbiosis with algae.

Transcriptome studies on the choanoflagellate species *Salpingoeca euryoecia*: Adaptations to differing salinity concentrations

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Little is known about the genetic mechanisms behind physiological adaptation of flagellates to different environmental conditions. These unicellular eukaryotes are ubiquitous in marine, limnic and soil ecosystems. Many are extremely tolerant, surviving drought, cold, high pressure and high salinity conditions. However, the genetic adaptations, explaining the ability of survival under such conditions are far from understood.

This study aimed to provide a first approach to investigate the intracellular processes involved in the adaptation to differing salinity adaptatis in protists. We examined a euryoecious choanoflagellate, *Salpingoeca euryoecia*, from an estuary, showing the same growthrates in freshwater and marine medium. A de novo transcriptome assembly was constructed using Trinity and the assembled contigs were annotated using the Trinotate and Interpro pipelines. Differential expression analysis revealed 4963 genes to be differentially expressed in freshwater vs. marine water adapted cultures. Along many others we found protein domains, shown to be involved in the High Osmolarity Glycerol (HOG) pathway in *Saccharomyces*, stress-involved domains, as well as antiporters, and response regulatory elements in various organisms, and a BEACH protein with similarity to a protein regulating contractile vacuole formation in *Dictyostelium.*

First record of gregarine parasites of the Atacama desert associated to *Scotobius brevipes*

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Gregarines inhabit the intestines, coeloms and reproductive vesicles of aquatic as well as terrestrial invertebrates. The infection rate with gregarines may vary significantly between individuals and species, though most invertebrate groups which have been investigated intensively possess its own specific gregarine species. Due to their widespread presence in animals, gregarine-host interactions may form a suitable system for evolutionary and co-evolutionary studies. In this respect, the interaction between endemic wingless darkling beetles and its potential hosts should form an interesting model system. However, the molecular diversity of gregarines associated to darkling beetles is not well understood. In previous studies three new gregarine species were reported from tenebrionid Eleodes beetles, with emphasis on molecular techniques. Here, we discovered another novel gregarine species from *Scotobius brevipes* (Coleoptera: Tenebrionidae) inhabiting the mid gut of this beetle living in the Atacama region in Northern Chile. The new species *Atacamagregarina paposa* n. gen., n. sp., (Apicomplexa: Eugregarinorida, Stylocephalidae) clusters within the clade of gregarines from other terrestrial organisms and forms a cluster with gregarines living associated with North American darkling beetles.

Soil free-living amoeba: reservoir of multi-drug resistant bacterial pathogen species?

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The occurrence of bacteria harboring a multi-drug resistance (MDR) phenotype in clinical environment is linked to the intensive use of therapeutic antibiotics. This phenotype is frequent in opportunistic pathogen species. Outside the hospital, the roles played by the micro- or the macro-fauna as reservoir of bacterial pathogen species and their resistance properties remained unknown. Hence, if free-living amoebae (FLA) are known for their predator role[1], some bacteria have evolved mechanisms to escape phagocytosis[2] such as *Legionella pneumophila* which have the ability to resist to the lysis by *Acanthamoeba*[3]. Recently, metagenomic investigations of the amoebal and intra-amoebal diversity from water samples revealed the presence of numerous pathogenic species belonging to *Stenotrophomonas*, *Pseudomonas*, or *Acinetobacter*[4] genus. So far, no data is available concerning the role played by FLA in soils. The aim of this study was to evaluate the prevalence of bacterial pathogens in FLA isolated from anthropogenic soils (mining, agricultural) and sampled in diverse geographical areas (France, Burkina-Faso, Vietnam). After optimization of FLA extraction from soil samples, the diversity was analyzed. This diversity was different according to the area sampled and revealed the presence of genus like *Tetramitus*, *Acanthamoeba*, *Naegleria*, *Willaertia*, or *Micriamoeba* but also some genus not yet identified. Then, the associated cultural microflora has been characterized. The abundance and the taxonomic diversity varied according to the FLA genus and the isolation area. Opportunistic bacterial pathogens such as *S. maltophilia*, or *P. aeruginosa* have been identified and some of them harbored a MDR phenotype. These data were analyzed taking into account the physico-chemical properties of soils and FLA diversity. Co-culture experiments revealed the ability of strains from these bacterial species to multiply in amoeba. The results highlight the potential health hazard linked to the presence of MDR bacterial pathogens reservoirs in anthropogenic areas.

Key-words: free-living amoeba, opportunistic bacterial pathogens, Multi-Drug resistance

References:
1. Rodriguez-Zaragoza, 1994
2. Greub & Raoult, 2004
3. Thomas et al. 2006
4. Delafont et al. 2013

Morphologic and phylogenetic characteristics of Nephridiophagidae

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Nephridiophagids are unicellular spore-formers infecting the Malpighian tubules of insects. Their life cycle includes merogony with multinucleate plasmodia and sporogony which leads to small, uninucleate spores. The morphological features do not allow a clear affiliation with one of the known protist groups. We have now performed a molecular phylogenetic approach with three species of *Nephridiophaga*, including one yet undescribed species from the Madeira cockroach *Leucophaea maderae*. Besides its specific host, the new species slightly differs from known ones by the size of its spores and by the number of spores within the sporogenic plasmodium. The constructed trees on the basis of 18S-rRNA sequences show that nephridiophagids belong to the fungal base. In order to prevent a biased view by long branch attractions we calculated bayesian trees on a conservative species selection and found a polytomy of nephridiophagids with the Chytridiomycota sensu latu (flagellate fungi). The nephridiophagids may represent a novel basal fungal phylum.

Testate amoebae and diatoms in forensic science

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Unicellular protists, e.g. testate amoebae and diatoms, play an important role in terrestrial ecosystems, since their individual densities and biomasses can reach tremendous amounts and at least heterotrophic testate amoebae occur immediately at newly exposed land surfaces facilitating the establishment of plants and animals. Moreover, they are sensitive and well-known bioindicators for all kinds of environmental conditions. In this study, we tested the suitability of these protists in forensic science. We wanted to know if a) testate amoebae and diatoms are usable to detect soil sites where recently or even years ago a corpse had been deposited and b) a non-specialist, neither used to work with a microscope, nor used to any protist taxonomy, is able to work successfully in this field of science.

We exposed on the surface of predominantly open and dry sandy sites three corpes of the red deer (*Cervus elaphus*): in summer 2011, 2013, and on September 22, 2014. On October 10, 2014, six soil samples were taken directly at the corpse site and, as a control, about 20 metres away at a comparable but undisturbed site.

Our results demonstrated a) on the 2011 site, slightly more testate amoebae and diatoms occurred on the control site (compared to the carcass site), while on the 2013 site these conditions were more pronounced. In contrast, we found considerably more testate amoebae (but less diatoms) directly at the 18 days old cadaver compared to the control. This may be attributed to the fact that these sandy sites were extremely dry. We assume that the putatively detrimental effect of body fluids of the still fresh but open cadaver on soil organisms had been outweighted by the positive effect of water. Thus, environmental conditions have to be taken into account, as well as the pronounced variance between replicates. Furthermore, b) it was shown that a non-biologist (in the context of a bachelor thesis) was able to get used to light microscopy and protist enumeration within a few weeks. Here, a successful quantitative estimation of “idiosomic” and “xenosomic” testate amoebae and ”pennate diatoms” was possible.

This preliminary study (we exposed considerably more carcasses of red deer and wild boar between 2008 and 2014) demonstrated that soil protists could be potentially useful in forensic science. They are sensitive bioindicators and even open to scientists not specialized on these protists but working in forensics. To our knowledge, diatoms were used for the first time for the forensic examination of soil evidence.

Paramecium growth phase is essential for the outcome of its interaction with *Holospora caryophila*

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Despite an unambiguous definition, in many biological systems we do not find a neat delineation between mutualism and parasitism. Biotic and abiotic factors influence symbiotic interactions, thus under certain circumstances parasites can provide benefits and mutualists can harm their host. Here we addressed the question which intrinsic biotic factors are pivotal for the outcome of an intimate host-symbiont interaction.

As model system we used the obligate intranuclear symbiont *Holospora caryophila* and its unicellular eukaryotic host *Paramecium biaurelia*. The impact on host fitness of the supposed energy parasite was determined in presence and absence of *H. caryophila* via growth assays with several genetically identical *P. biaurelia* lines. Maintenance of the intranuclear bacteria was confirmed at the beginning and end of the experiment using fluorescence in situ hybridisation and microscopy. Following factors were considered as potentially involved in shaping the outcome of the interaction: (1) the host genotype, (2) the parasite genotype, and (3) the growth phase of the host.

All three factors revealed a strong influence on the outcome of the host-symbiont interaction. In presence of *H. caryophila*, the *Paramecium* density in the stationary growth phase decreased. Conversely, a positive effect of the bacteria during the exponential phase was observed for several host x parasite combinations resulting in an increased growth rate of infected *P. biaurelia*.

The fitness impact of the tested endosymbionts on different *P. biaurelia* lines were not only dependent on either genotype but were specific for the genotype x genotype combination. Interestingly, a typical parasite such as *H. caryophila* has not only negative effects on host fitness. Depending on the actual host growth phase, the presence of these obligate endosymbionts can even be advantageous for *P. biaurelia*.

Thus, under the here tested experimental conditions, the harmful parasite can be a beneficial mutualist changing from one kind of interaction to the next within the same host and a time-span of less than six days.

Exploring ecology of protists in long and short time scales on the basis of the recent testate amoeba research

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Many of the recent studies on peatland protists are using testate amoebae as bioindicators or proxies of the past environmental change. Recent studies also pointed out the importance of testate amoebae in peatland functioning and how their functional role can shift with environmental change. Understanding the complex interplay between climate and populations, including function, is thus essential for fully anticipating how ecosystems will respond to the fast rates of current warming. Different approaches are applied to explore the ecology of testate amoebae. 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. Despite a high complexity of the data covering all possible biotic and abiotic components, experimental and descriptive approaches can only catch the recent high-frequency change in peatland ecosystem, far different from the past environmental changes ranging from years to millenia. Therefore, long-term ecology is needed to look closely on testate amoeba communities in time. Recent research proved that there is a need to explore and combine ecological and palaeoecological approaches on testate amoebae and determine whether a shift in their community structure and function are linked to environmental changes. In this talk we will present several recent published and not published studies that reveal new patterns in testate amoeba ecology. Finally, several important questions in testate amoeba ecology will be underlined e.g. what is the functional value of morphological traits of TA for palaeoecology? We call for the need of integration of different disciplines to study testate amoebae ecology in various spatial and temporal scales.

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Askenasia volvox, once a haptorid, now a homeless ciliate with surprising ultrastructure

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Thanks to its spectacular locomotion life specimen of *Askenasia volvox* are well known.

This planktonic ciliate has been studied by numerous light microscopists, but to our knowledge there is no single EM study yet. The most recent paper on Askenasia volvox and its close relatives is by Krainer and Foissner (J.Protozool. 37, 414, 1990), showing Protargol-stained specimen and several impressive drawings. There is no agreement on the terminology, but the plates will show what is meant.

Askenasia volvox was collected from Schlöhsee near Plön. Laboratory cultures were grown in Eau Volvic and fed with *Rhodomonas* spec. Mildly centrifuged cells were fixed with Parducz and processed for SEM. Parallel samples were treated with 4 % ethanol in Eau Volvic to rip off the cilia for better documentation of the cell surface. Thin sections were prepared in the conventional way.

Our stock culture was a small form with about 40-50 µm in length and diameter and with 32-34 somatic kineties. The ciliate shows two types of pectinelles, anterior ones made of 8 -9 monokinetids and posterior ones made of 9-11 dikinetids. Immediately behind the posterior pectinelles at the height of the cell's equator there are 3 long and perhaps stiff cilia called bristles. The entire posterior of the cell shows no cilia, only pellicular alveoli with a barren kinetosome in each alveolus. The apical dome or apical disc shows numerous toxicyst accompanied by 32-34 kinetosomes (KS), with ciliary stubs. These stubs, arranged in a flour-like pattern, and 0,25 µm in height, have no axoneme but a granular content. There is no rhabdos in *A. volvox* as already noted by Krainer and Foissner (1990). Moreover, there are no cytopharyngeal mt. The tripartite telescopic toxicysts, surrounded by 14-18 mt, are probably involved in food capture. The toxicyst tip looks like the tip of a pointed pencil. After discharge of the toxicysts the surrounding mt stay in the apical dome. One might speculate that they serve as guiding structures during food intake, but details of food ingestion are completely unknown.

The ciliated mono- and dikinetids of the pectinelles have thin, flat, staggered kinetodesmal fibers, which reach into the apical dome. In addition to 3 pcmt, 1-3 trmt, 2 longitudinal mt and 4-5 basal mt there are genus-specific lateral fibers with periodic striations. The latter are most elaborate between the KS of the bristles. Mitochondria with tubular cristae, a single C-shaped macronucleus and the micronucleus show no specialities. SEM of resting cysts of *A. volvox* will also be shown.

Contrary to *Mesodinium* and/or *Myrionecta*, for which there are several EM studies available, this report is the first EM investigation of *A. volvox*. It should help to decide whether these 3 genera, which clearly are no haptorids, might deserve a new class.

The effect of hydrodynamics on protozoans within stream biofilms

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Stream biofilms are surface-associated microbial communities typically composed of bacteria, cyanobacteria, algae and protozoans embedded in a matrix of extracellular polymeric substances. They constitute an integral part of lotic aquatic ecosystems and are controlled primarily by light, resource availability, grazing and hydrodynamics. Mountainous streams are characterized by a spatial and temporal variable stream bed and corresponding flow field. As a consequence, hydrodynamics become a dominant factor affecting biofilm community structure through drag forces and control the supply of carbon and nutrients through mass transfer processes. Previous studies have been restricted to laboratory experiments, where the highly complex flow field of streams cannot be reconstructed to the full extent. In a novel approach we are aiming at linking detailed measurements on stream bed heterogeneity and associated development of flow fields to the community structure of protozoans in stream biofilms. Two mountainous streams (Harz region, Germany) were studied that are comparable in stream bed morphology but distinctly differing in water chemistry. The mean N : P ratio of the stream water of the Selke was always lower than that of the Kalte Bode. Biofilms in both streams were highly variable regarding the abundance and community structure of protozoans. Abundance of ciliates and flagellates was highest and highly variable at an intermediate turbulent kinetic energy range both in spring and summer, whereas this pattern was not found for flagellates in summer. Correlations between turbulent kinetic energy and protozoan abundance were stronger for Selke biofilms (adjusted R sqr > 0.4) than for Kalte Bode biofilms (adjusted R sqr < 0.3). We observed differential effects of turbulent kinetic energy on protozoans at contrasting trophic conditions and seasons due to the interplay of nutrient supply and hydrodynamics.

Here comes the sun: exploring light intensity as important variable driving testate amoeba communities in *Sphagnum*

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Testate amoebae (TA), a group of free-living protists, are abundant in soils and mosses and especially in *Sphagnum*-dominated peatlands. As they are very sensitive to water table changes they are commonly used as indicators of present and past water table depth in *Sphagnum* peatlands. Within TA communities, mixotrophic testate amoebae (MTA) have recently been shown to play a major role in the carbon cycling of *Sphagnum* peatlands. MTA are known to depend on light but their response to seasonal changes in light intensity has not been studied. We hypothesized that the abundance of MTA matches the seasonally changing photosynthetically active radiation (PAR) and that these changes considerably affect the overall structure of TA communities. We monitored the seasonal changes in *Sphagnum*-inhabiting TA communities in contrasted micro-topographical settings in a *Sphagnum*-dominated peatland in N Poland (Linje mire) over two vegetation seasons (May 2012-October 2013). Twenty-five sampling plots were established, located around five piezometers and five micro-meteorological stations measuring air temperature and humidity, precipitation, and PAR, and from which vapour pressure deficit (VPD) was calculated. Depth to the water table (DWT), pH, conductivity, and dissolved oxygen were also measured. TA community composition and density varied among seasons. Communities were strongly dominated by MTA in spring and early summer (up to 74% in May 2012). Mean testate amoeba densities were highest in late summer (Sept., average: 1296 ind.g-1) and lowest in autumn (Nov., 573 ind.g-1). Shannon diversity was highest in late autumn (Oct. & Nov., 1.33) and lowest in spring (May, 0.97). Plots with highest water tables (i.e. wetter) were dominated by two MTA species (*Hyalosphenia papilio*-35.3% average and *Archerella flavum*-16.4%), and by *Assulina muscorum* (14.8%) and *Hyalosphenia elegans* (10.6%), but had lower species richness and Shannon diversity values. Testate amoeba communities were most strongly correlated to PAR, VPD and conductivity (all significant at P=0.001 in redundancy analyses) and to water table depth (P=0.002). In *Sphagnum* peatlands, MTA are a significant group of protists in terms of carbon cycling and organic matter decomposition, and it seems that their abundance in testate amoeba communities is mostly dependent on light intensity and water table changes. As on-going climate change may affect the former moderately by changes cloud cover, more significantly by changes in the duration of the snow cover and mostly by changes in hydrology (e.g. increasing drought periods in summer) it is important to better understand the factors controlling the abundance and thus functional role of *Sphagnum* peatland MTA.

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Grazing of Cercomonads (Protists: Rhizaria: Cercozoa) structures bacterial phyllosphere communities

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Protists are important predators of bacteria on plant surfaces (Bonkowski, 2004; Rosenberg et al, 2009), and known to substantially change both, the structure and function of bacterial communities (Matz and Kjelleberg, 2005; Pernthaler, 2005). This is important, because many of the plant-associated bacteria evolved mechanisms to increase their access to plant metabolites and to improve their competitiveness against other microorganisms (Spaepen et al, 2007). Several of these bacterial traits have been proven to enhance plant performance (Lugtenberg et al, 2013) and there is growing evidence that the grazer-induced shifts in bacterial community composition and function are responsible for indirect effects of bacterivores on plant performance (Bonkowski and Clarholm, 2012). In contrast to interactions in the rhizosphere, virtually nothing is known on interactions of protozoa and bacteria on leaf surfaces. Although the occurrence of phyllosphere protists has long been recognized (Bamforth, 1973), they were until now mostly considered as potential vectors of pathogenic bacteria or as potential human pathogens on vegetables (Vaerewijck et al, 2011; Vaerewijck and Houf, 2014).

Experiments on interactions of protists with selected bacterial prey species have highlighted the complexity of these predator-prey interactions (Pernthaler, 2005). It has also been shown that morphologically similar protists differ in their feeding preferences (Weisse et al, 2001; Glucksman et al, 2010) and that they exert strain specific grazing even on closely related bacteria (Boenigk et al, 2004). Due to this mixture of direct and indirect grazing effects, the outcome of protist predation at the bacterial community levels seems inherently complex and hard to predict. Furthermore it is not well understood how competitive relationships between bacteria increase or decrease under grazing pressure.

Using modern high throughput sequencing techniques now enable us to answer these questions by explaining variation in bacterial community composition on high taxonomic resolution. We explored the grazing effects of closely related and morphological similar cercomonads on a diverse, standardized, phyllosphere bacterial community under controlled conditions using an experimental microcosm approach and shotgun metagenomic sequencing. The three protist species used in this study were isolated from the phyllosphere. Thus include two *Cercomonas* and one *Paracercomonas* species.

Comparison of grazing effects of protozoans on biofilm formation of bacteria

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Biofilms are thought to serve as grazing protection against predators. From aquatic pelagic systems it is known that feeding of bacterivorous protists may strongly influence the morphology, taxonomic composition and physiological status of bacterial communities and thus may be an important driving force for a change in bacterial growth and shift in morphology towards filaments and flocs.

Studies on grazing of bacterial biofilms have shown, that grazing of bacterivorous organisms like protozoa can effectively reduce the biovolume and morphology of bacterial biofilms and that their feeding mode plays an important role as especially amoebae may reduce biofilms clearly. However, formation of microcolonies may protect bacteria in biofilms from grazing as studies have shown. Up to now, these studies showed mainly that grazing protection due to microcolony formation in bacterial biofilms was dependent on the protozoans' feeding mode and the phase of succession of the biofilm.

In the talk, we will focus on a study where the influence of the browsing ciliate *Tetrahymena pyriformis* on a mono-species biofilm built by the microcolony-forming /textitAcinetobacter sp. strain C6 variant by using a continuous flow channel system was investigated. The strain C6 of /textitAcinetobacter used for these experiments forms round-shaped microcolonies from start of biofilm growth on. In natural biofilms, microcolonies are usually built as response to (protozoan) grazing. In our analysis we therefore hypothesized that bacteria that generally build microcolonies (like the /textitAcinetobacter strain C6 in our study) are per se protected against protozoan grazing. The influence of the browsing ciliate /textitTetrahymena pyriformis on a mono-species biofilm built by the microcolony-forming /textitAcinetobacter sp. strain C6 variant was investigated using a continuous flow channel system. We used two different medium supply rates and two different carbon sources to investigate bacterial microcolony formation under different growth conditions with and without grazing of /textitTetrahymena. The structure of the biofilms was changed in the presence of /textitTetrahymena in all treatments.

Depending on the carbon source the structure of the biofilm developed completely different shapes of microcolonies in presence of the grazer, compared to non-grazed biofilms. The grazer could stimulate (at high medium supply) as well as reduce (at low medium supply and with citrate as carbon source) the biovolume of the bacterial biofilm. Experiments revealed that microcolony formation of /textitAcinetobacter did not generally act as grazing defence against protozoan grazing. Under certain growth conditions (low medium supply, citrate as carbon source) bacteria were faced with an increased vulnerability to grazing.

7 Abstracts: Posters

P1: Do fixatives influence histochemical tests in tintinnid loricae (Alveolata, Ciliophora, Spirotricha, Tintinnina)?

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Tintinnids are extraordinary marine planktonic ciliates as they form vase-shaped loricae (houses). Additionally, they are intermittently highly abundant (∼104 cells litre-1) and have a considerable grazing impact on the nano- and microplankton (up to 62% of the primary production). For assessing their precise role in ecological and geochemical processes, also knowledge about the chemical lorica composition is indispensable. After cell death, the lorica sediments; both during its sedimentation and in the benthic deposition, bacteria might decompose the hyaline loricae or the lorica matrix in agglutinated loricae, contributing to the recycling of the nutrients. The chemical lorica composition does not only determine which bacteria might be involved in the decomposition, but also influences the degradation rate; hence, it has an impact on the fossilization probability. Additionally, the chemical composition might be of taxonomical significance. Actually, it has been investigated since the 1880s in about 24 out of the 75 genera. Owing to its impressive resistance against strong alkaline solutions, the studies suggested a chitinous or keratinaceous nature of the lorica forming material. The most comprehensive recent study clearly indicated proteins in the lorica material (Agatha & Simon 2012); yet the usage of exclusively preserved material could have prevented the detection of further substances as well as the staining and enzymatic digestion in some species.

Therefore, common fixatives (formaldehyde, Bouin's and Lugol's solution, mercuric chloride plus osmium tetroxide) were tested for their effects on four histochemical reactions detecting polysaccharides, proteins, and lipids. For the first time, loricae of the tintinnid *Schmidingerella meunieri* were analysed. The preservatives did not influence the staining properties of the species' loricae which contain proteins with the amino acid tyrosine and possibly some lipids; polysaccharides could again not be detected. An identification of the extraordinarily resistant proteins is now needed. Deviations in the lorica wall structure of *S. meunieri* found in the present study were ascribed to different growth phases of the cultures used, although an influence of extrinsic factors could not be excluded.

P2: The Rapunzel tintinnid - Redescription of *Tintinnopsis subacuta* Jörgensen, 1899 (Alveolata, Ciliophora, Spirotricha)

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Tintinnids contribute distinctly to the microbial biomass in the marine plankton. Since the species have specific requirements concerning physico-chemical conditions and food items, reliable identification is indispensable for assessing their role in the food web. About one thousand extant tintinnid species are known, whose descriptions are exclusively based on the features of their loricae (houses); merely in about 30 species, cell characteristics have been studied. Since lorica shape and size are affected by environmental conditions and might show a polymorphism in the cell cycle, the tintinnid classification is artificial. Investigations of the cell, especially of the ciliary pattern and nuclear apparatus (generative micronuclei and somatic macronucleus nodules) are, however, supposed to provide features for a natural classification; these characters are revealed by protargol (silver proteinate) staining.

Tintinnopsis subacuta was collected from surface waters of the Indiana River at the Atlantic coast of Florida (United States of America) and stained with protargol. Cell and lorica morphology were investigated under a compound microscope at up to 1250x magnification. The lorica is 55-119 µm, on average 79 µm long and consists of a cylindroidal collar about 34 µm across and a subspherical bowl about 45 µm wide. The lorica wall has agglutinated mainly mineral particles. The contracted cell measures 30 x 28 µm and is attached to the bottom of the lorica by a contractile peduncle. The somatic ciliary pattern is of the most complex type, i.e., it comprises a ventral, dorsal, and posterior kinety as well as a right, left, and lateral ciliary field. The ventral kinety has associated an extraordinary ciliary tuft of cell length that extends outside the lorica posteriorly, resembling the golden hair let down from the tower by Rapunzel; *T. subacuta* is unique in this respect. The right and left ciliary fields are composed of about 11 ciliary rows each, the lateral field consists of invariably 15 rows. While the majority of tintinnids have only two macronucleus nodules, *T. subacuta* has 4-34, on average 14 nodules.

P3: Testate amoeba community structure at the beginning of warming experiment *Sphagnum* peatland (Rzecin Mire, W Poland)

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Due to plants structure and huge among of stored water and carbon peatlands are precious and specific habitats for microorganisms and microscopic animals. Wetland ecosystems are also one of the most endangers by climate change and anthropogenic activities. For that reason, scientists are interested in recognition of the past and present response of peatland organisms to environment changes. Testate amoebae (TA) are sensitive to environmental factors like water table level and mineral content. The recent studies show a high abundance of mixotrophic protists related to the temperature and their role in peatland carbon fixing. For this reasons knowledge about particular testate amoeba species contribution in *Sphagnum* communities' biomass as well as factors shaping TA structure may be crucial for the estimation of carbon accumulation.

The Polish - Norway "WETMAN" project is an experimental manipulation of temperature and precipitation and the aim of study is to test an effect of the manipulation on biotic and abiotic components of the peatland ecosystem. Considering microbial groups living in *Sphagnum* we focused on testate amoebae biomass and species richness. To examine the response TA to different treatment: warming, warming and decreased precipitation and only decreased precipitation, it is obligatory to recognise the TA community structure at the beginning of the experiment. The Rzecin peatland TA community was characterised by high abundance of mixotropic species (*Hyalosphenia papilio*, *Archerella flavum*, *Heleopera sphagni*). During sampling cut *Sphagnum* stems to analyse separately the taxa living in the upper and lower segment of mosses. TA species biomass revealed the significant differences between upper and lower *Sphagnum* segment. The contribution of *Hyalosphenia papilio* in total TA biomass was higher in the upper *Sphagnum* segment, while the *Hyalosphenia elegans*, *Physochila griseola*, *Nebela tincta* and *N. collaris* reviled higher biomass in *Sphagnum* stem. The *Archerella flavum* contribution in total TA biomass did not show variation between *Sphagnum* segments. Multivariate analyses showed that in the beginning of experiment the TA species distribution was affected mostly by *Sphagnum* segment factor, water table level and oxygen content in the water.

Due to natural heterogeneity, which is difficult to avoid in field experiments, it is crucial to analyse the community data of every plot before starting the manipulation. This knowledge allows us to recognize the natural changes in control plot and an response of testate amoeba community to different manipulation types.

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P4: Deep-sea benthic microeukaryotes: A plea for morphological and ecological studies as a necessary addition to metagenomics

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Microeukaryotes form a substantial part of deep-sea ecosystems. However, their real diversity is still obscure. Surveys of their biodiversity based on metagenomics have up to now been restricted to a few selected sites of the deep ocean which have indicated a large pool of genotypes completely separated from that of surface waters. Extensive metagenomic investigations of oceanic surface waters by the Tara Ocean Expedition showed that microeukaryote ribosomal diversity saturated at a very high number of operational taxonomic units, one-third of which could not be assigned to any known eukaryotic group. We have to expect an even more diverse and probably very different community in the deep ocean and metabarcoding of the abyssal communities is of great need. There is an obvious great gap between the knowledge of the diversity of genotypes and that of morphotypes. We request to fill this gap by applying a combination of methods comprising metabarcoding, microscopic live-observations, aliquot cultivation, single cell PCR, pressure experiments and morphological studies. We will present new or not well resolved deep-branching lineages of protists (opisthokonts, placidids, etc.) and will discuss speciation mechanisms of marine microeukaryotes.

P5: UniEuk: a universal taxonomic framework and integrated reference gene databases for eukaryotic biology, ecology, and evolution

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Universal taxonomic frameworks have been critical tools to structure the fields of Botany, Zoology, and Microbiology as well as their large research communities. Plants and animals have solid, stable morpho-taxonomies built over the last 3 centuries, while bacteria and viruses have been classified for the last 3 decades under coherent molecular taxonomic frameworks. By contrast, no such common language exists yet for protists, even though environmental -omics surveys are showing that microbial eukaryotes make up most of the organismal and genetic complexity of our planet's ecosystems! In fact, the extreme morpho-functional complexity of protists has historically divided the relatively small research community into sub-communities (protozoology vs. phycology, marine vs. terrestrial protistology, etc.) speaking different languages. With the current deluge of meta-omics data clearly pushing us into the century of protistology, we urgently need to build a universal taxonomy bridging the Protist New Age to the centuries-old body of classical knowledge that has effectively linked protist taxa to morphological, physiological, and ecological information.

UniEuk is a community-based project to address this fundamental challenge and achieve a morpho-genetic reference system for eukaryotic biology, ecology and evolution, including 2 components. First, a standardized curation process based on the EukRef initiative and realized predominantly by PhD students and post-docs will generate phylogenetically-informed reference databases of genetic markers with reference alignments and trees. Second, the generated knowledge will be structured into a universal taxonomic framework, integrating information from relevant genetic markers and classical morphology-based data, and validated by an extensive network of taxonomy experts. The system's broad use and long-term preservation will be ensured by a direct implementation into the INSDC genetic data repositories via their EMBL-EBI node.

P6: Taxonomic, functional and beta diversities of freshwater planktonic ciliate communities are higher in the Antarctic than in neighbouring Patagonia

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We compared the diversity of planktonic ciliate communities from eight lakes located in Patagonia and six in the Antarctic Peninsula by environmental DNA survey. We inferred then taxonomic composition and functional diversity from the obtained ciliate phylotypes. Surprisingly, diversity was higher in Antarctic lakes than in Patagonia. Small algivorous taxa dominated Patagonian communities but were underrepresented in Antarctic lakes, probably because oflight limitation during the winter. In contrast, Antarctic lakes hosted diverse bacterivores and omnivorescommunities, practically absent from South America. We suggest that the latter replaced algivores in the Antarctic foodwebs due to their higher versatility towards a food source that changes over time. Furthermore, variation in ciliate community composition (β-diversity) between Patagonian and Antarctic lakes was determined by phylotype turnover. This was unexpected as β-diversity is often driven by nestedness along environmental gradients that move from benign (Patagonia) to harsh (Antarctic) conditions. Turnover drove also β-diversity among Patagonian and Antarctic lakes, suggesting highly specialized communities. This shows that extreme biomes (Antarctic) can harbour diverse communities composed of taxa that do not necessarily come from communities situated in benign biomes. These findings highlight Antarctic lakes as ecosystems with a high biological value which deserve to be further explored.

P7: Pulsed vs. continuous nutrient addition in a fragmented habitat: modeling anthropogenic stressors in a microbial metacommunity

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Maintenance of biodiversity is essential to preserve many ecosystem functions, but is increasingly under threat. This experiment deals with the temporal and spatial aspects of two of these threats: habitat fragmentation and eutrophication. Eutrophication can reduce diversity in natural aquatic systems, but it has also been shown that pulsed nutrient addition raises the biodiversity. It is also known that a fragmented but connected landscape (metacommunity) can hold higher biodiversity than a single large patch. What is still unclear is how the temporal scale of nutrient additions (continuous or pulsed) will interact with the spatial scale (fragmented or isolated habitat). The main goal of the experiment was to understand how the anthropogenic stressors of eutrophication impacts on biodiversity. To achieve the objectives, we worked with three hypotheses:(1)When nutrient addition is pulsed rather than continuous, diversity will be higher, and this effects will be even greater in a metacommunity;(2)the biodiversity will be higher in fragmented habitat when compared with isolated communities;(3)the effects of habitat fragmentation and pulsed nutrient addition will be additive: the highest biodiversity will be seen in fragmented habitats with pulsed nutrient addition. The model community was composed of three species of autotrophs and a total of six species of ciliates and rotifers as their consumers; the design of the experiment was formed by two different topologies: the metacommunities (four connectioned patches) and the isolated communities. One metacommunity consisted of four 125ml polycarbonate bottles, each connected to two neighboring bottles by plastic tubes, while the isolated communities were a single 640ml bottle filled to the same total volume as the metacommunitites. The nutrients added were Phosphrus, Nitrogen and Silia; the number of replicates was three per treatment combination; the experiment was run for 6 weeks. As a measure of biodiversity, the Shannon index was calculated for each treatment, with local and regional biodiversity calculated separately for zooplankton and phytoplankton. In addition, the biomass ratio between prey and predator was calculated to determine the prey capacity to support a system. Comparing the different treatments of nutrient addition, the pulsed form promoted higher biodiversity in local scale in both phytoplankton and zooplankton. In contrast, the regional biodiversity was different for phytoplankton and zooplankton. The first had higher diversity in a pulsed treatment, but analyzing the second, was not possible to see difference between treatments. In relation with resource use efficiency, the biomass ratio between prey and predator was higher in a pulsed nutrient addition in metacommunities. In conclusion, the different treatments had higher impact on phytoplankton rather than in zooplankton, and higher biodiversity was obtained with pulsed treatment in communities with connections.

P8: Protistan plankton communities of high-mountain lakes from three continents exhibit strong biogeographic patterns

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Protists hold a key role in aquatic ecosystem function(ing). Yet, their diversity in freshwater lakes, particularly in remote high-mountain lakes, is relatively unknown compared to the marine realm. As a consequence, the structure and potential geographic differences of protistan lake communities over continental scales remains elusive. We analyzed nearly 2 million hypervariable V4-fragments of the small subunit ribosomal RNA gene to compare genetic protistan diversity in high-mountain lakes located in three distant regions: the European Alps, the Chilean Altiplano, and the Ethiopian Bale Mountains. Protists were not globally distributed corroborating patterns found for bacteria and multicellular animals and plants. Instead, the protistan community composition emerged as a highly specific fingerprint of a geographic region even on higher taxonomic levels. The intra-regional heterogeneity of the investigated lakes was mirrored in shifts in protistan community structure, which, however, was much less pronounced compared to inter-regional beta-diversity. Statistical analyses revealed that on a regional scale, environmental factors are strong predictors for protistan community structures in high-mountain lakes. While on long-distance scales (>10,000 km), isolation-by-distance is the most plausible scenario. On intermediate scales (up to 6000 km), both, contemporary environmental factors and historical contingencies are playing in concerto to shift protistan community structures. The degree of novel diversity in the Altiplano lakes and the Bale Mountain lakes was much higher than in the Alpine lakes supporting our finding that different geographic regions hold different sets of protistan diversity.

P9: Chrysophyte community re-assembly and functional differentiation in the wake of flooding events

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In the last centuries flooding events increased all over the world. Their effects on microbial communities and thereby on ecosystem services are hardly understood. Flooding events may lead to an organismic exchange and local extinctions. Therefore flooding events play potentially a key role in invasion and repopulation processes. By means of metatransciptomics we aim at new insights in the effects of floodings on the functional diversity of Chrysophytes. Experiments were conducted in six experimental stream systems. Each of the systems was composed of a series of tanks and channels simulating the riffle and pool sequence of streams. Water from the upper river Emscher and the A-horizon of soils from the vicinity of the Emscher was used in the experiments. We simulated flooding followed by a drying period. We investigated the organismic exchange as well as the diversity and regulation of metabolic pathways. We show that flooding events causes shifts in local community structure and that floodings have a differential effect on metabolic pathway of Chrysophytes depending on habitat type.

P10: When a lake stops mixing - massive sequencing of plankton communities still mirrors the traditional Plankton Ecology Group (PEG) model

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The PEG (Plankton Ecology Group) model is a standard template in aquatic ecology, which describes seasonal succession of phyto- and zooplankton in lakes. Thereby, the annually repeated process of community assembly is build upon seasonally unfolding biotic interactions (such as competition, herbivory and predation) constrained by a framework of abiotic control mechanisms. One basic element of the abiotic control mechanisms is seasonal stratification and water column mixing. However, what happens with the PEG model if mixing holds off and stratification prevails throughout all seasons? Since 2012 temperature anomalies in Lake Zürich due to warm winters resulted in an attenuation of lake mixing until mixing of the lake failed completely in 2014. Due to these anomalies, abundance patterns of planktonic protistan morphospecies, which were traditionally following the PEG model, became disrupted (see also Poster of Pitsch et al.). Strikingly, community statistical analyses of taxonomic marker genes (V4 region of the SSU rDNA), obtained from 33 sampling events of Lake Zürich surface waters over a 14 months period, identified protistan plankton community patterns, which corroborate well with the traditional PEG model. Therefore, despite a permanent (annual) stratification, community dynamics is still resilient and follows the proposed steps of the PEG model. Because the abundance of most protists is largely reduced during permanent stratification, seasonal plankton succession patterns may escape microscopy surveys, which largely rely on very abundant taxa. Further research will reveal whether resilient community structure dynamics during long-term stratification also shows in functional ecosystem stability. This is a crucial question for Lake Zürich, which is of fundamental importance for a variety of ecosystem services.

P11: When a lake stops mixing - the fatal effects of warming on the protistan community

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Here we present the striking consequences of lake warming on the composition of algal and ciliate assemblages in Lake Zürich (136m deep), Switzerland. The exceptional warm winter in 2014 caused an incomplete water turnover, only reaching down to 60m. In consequence, there was no measurable mixis of phosphorus rich deep water with surface layers during winter. Due to this nutrient limitation, the annually reoccurring phytoplankton spring bloom (mainly cryptophytes and centric diatoms) did not develop at all. Notably, algal mass developments in spring are the major basis for the annual successions of various consumers within the entire food web in deep temperate lakes. Increased primary production usually induced a rise in various bacterial taxa and bacterivorous protistan predators, but also served as resource for algivorous ciliates and metazoans in Lake Zürich. The 'absence' of an algal bloom in 2014 seemed to propagate and even aggravate along all trophic levels, causing drastic quantitative decreases and changed evenness of consumer assemblages. Especially algivorous ciliates (Prostomatea and Spirotrichea) were negatively affected and appeared in quite low numbers. In general, the succession of taxonomic ciliate groups differed strongly from patterns observed during former spring bloom events. We highlight, that a further series of warm winters will indeed cause an additional oligotrophication of the lake and drastic changes in protistan communities.

P12: Species-specific parasitism in lake plankton between *Podophrya* nov. sp. (Suctoria) and *Uroleptus willii* (Hypotricha).

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In lake plankton, a natural population of *Uroleptus willii* suffered from a heavy infection of the parasitoid suctorian *Podophrya* nov. sp. Species-specificity is obvious as more than 30 other ciliate species present at the same time in the same water samples were not infected. Parasitic infections among ciliates have been described earlier from, e.g. *Podophrya grelli* infecting *Stylonychia lemnae*, *Sphaerophrya paruroleptí* parasitizing on *Paruroleptus caudatus* or *Podophrya* sol infecting *Paramecium*. Different life stages of the suctorian are commonly found and they include free-living swarmers and cysts as well as so-called 'adults' that divide and conjugate inside the host. In detail, the infection cycle of *Podophrya* nov. sp. starts by the attachment of a ciliated swarmer with tentacles on the host. Then, the swarmer loses its cilia and provokes the host to induce a pellicular invagination remaining open to the environment (chemical trigger?). While embedded in the host cytoplasm, the suctorian 'adult' divides and conjugates and finally, two new stages are formed for further dispersal: cysts and swarmers. We assume that swarmers were generated when the chance of direct infection of more host individuals was relatively high and that cysts were formed after the *U. willii* population broke down. Interestingly, we found conjugating *U. willii* individuals irrespective of the parasitoid infestation (did *U. willii* conjugate before or after the suctorian invasion?). We show the species description of *Podophrya* nov. sp. and its life cycle and ecological data prevailing during and around the 'parasitoid bloom'. Our findings elucidate a highly complex ciliate-ciliate relationship including a set of open questions remaining.

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P13: Getting closer: interaction analysis between *Paramecium* and *Caedibacter* at functional, molecular and transcriptomic level

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caedibacter are obligate bacterial endosymbionts of *paramecium*. a special feature of this symbiosis is the killer trait which provides the host a competitive advantage against *caedibacter*-free *paramecium* cells. however, several studies demonstrated that *paramecium tetraurelia* harboring *caedibacter taeniospiralis* do not reach the same cell densities as endosymbiont-free *p. tetraurelia*. therefore, *c. taeniospiralis* is considered as obligate parasite which ensures the survival of its host population by eliminating uninfected food competitors. contrary to those studies we discovered through comparative fitness assays that *c. taeniospiralis* can act as a beneficial symbiont, depending on the host growth phase, food organism, and culture medium. this finding adds a new layer to the complex symbiosis between killer bacteria and their *paramecium* host. furthermore, we raise the question how the presence of the endosymbiont is reflected on host's gene expression levels to unravel the underlying molecular mechanisms behind this intimate host-symbiont interaction. for comparative transcriptome analysis we established genetically identical *p. tetraurelia* cell lines, with *c. taeniospiralis* and symbiont-free. after cell cycle synchronization of these lines, total rna was extracted and its purity and integrity was verified. to our best knowledge, our study represents the first comparative transcriptome analysis of an eukaryotic microorganism either infected by a conditional beneficial bacterium or symbiont-free. the obtained results will provide insights into the alteration of gene expression profiles caused by the presence of *c. taeniospiralis* and help to identify genes involved in this special host-symbiont interaction thus revealing the host's responses to symbiosis, parasitism, and mutualism as well.

P14: Investigations on root-associated microbial communities: An approach to reduce pathogenic planktonic bacteria within rivers

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Pathogenic bacteria and viruses in freshwater bodies can cause severe health issues, especially close to mixed wastewater effluents. Many benthic microbes feed on planktonic organisms, such as algae or bacteria, rather than on surface-associated prey, thus linking nutrient cycling between benthic and pelagic habitats. This process may be used to efficiently improve water quality in a natural way. Accordingly, providing more surfaces in the water column at hotspots of wastewater input will likely reduce planktonic bacteria, including pathogenic bacteria, through grazing of biofilm-dwelling microorganisms and/or by attachment to the surface. For this purpose, floating macrophyte islands can be established, whereby the root systems of plants provide a large surface area and serve as substrate for benthic organisms. As part of a larger project, we investigated microbial communities on plant roots concerning their potential reduction of planktonic bacteria in a flow system connected to the River Rhine. Therefore, we designed an experimental setup that was suitable for quantifying grazing effects of near natural root-associated biofilms on the abundance of planktonic bacteria. We further investigated abundances and taxonomic compositions of functional biofilm-dwelling groups with a focus on heterotrophic protists. On the poster, these results will be presented and discussed for potential future studies.

P15: Transfection in protists with cell-penetrating peptide

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Up to now, no reliable and efficient method for transfection of protist in general has been establishes. One of the main reason is that protists compromise highly divergent groups of organisms. In this approach we try to use Cell Penetrating Peptides (CPP) for transfection. We started our experiments with the class of choanoflagellates, the sister group of metazoans, to establish a method for silencing genes of interest by siRNA. First preliminary results indicate that this rather gentle method is applicable for these organisms. Still the reliability has to be improved as little is known about the cell cycle of choanoflagellates. One the one hand we were able to introduce a plasmid into the cell (GFP) which was express and one the other hand siRNA to silence the silicon transporter gene (SIT) in acanthoecid choanoflagellates.

We will extend our experiments to members of all groups to test, whether this is an universal applicable method of transfection for protists in general.

P16: Shedding light on the killer trait: new approaches to identify the killer toxin and interspecific sensitivity

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Caedibacter, a bacterial endosymbiont of *Paramecium*, is responsible for the so-called killer trait: *Caedibacter*-free paramecia get killed by taking up the bacterium which is released from *Caedibacter*-carrying cells into the environment. Large protein structures, the refractile bodies (R-bodies), produced by *Caedibacter* play an important role in this phenomenon. Involvements of additional factors in the killer trait e. g. a lethal toxin which disturbs the osmotic regulation of affected cells are predicted but have not been identified so far. In this study we investigated two potentially toxins: a protein with homologies to a membrane associated ATPase of the Soj /ParA-family encoded on the plasmid of *Caedibacter taeniospiralis* 298, and a protein with homologies to a patatin-like phospholipase encoded by *Caedibacter caryophilus* 224. In a first attempt to shed light upon the molecular mechanisms of the killer trait, the putative toxin genes were cloned and heterologously expressed in *E. coli* cells. *E. coli* clones over-expressing a putative toxin candidate alone or co-expressing it with R-bodies were used to feed sensitive *Paramecium* cells. Survival rates of sensitive paramecia were monitored for eight hours. No pre-lethal effects typical for the killer trait were observed for both recombinant proteins. Thus, the killer effect might depend on a more complex mechanism or other toxic substances are responsible for the lethality. Nevertheless, a suitable approach to express and verify putative toxin candidates was established.

So far, killing activity related to the killer trait was only observed in *Paramecium*. We aimed to assess the interspecific sensitivity of other eukaryotic microorganisms to the killer trait mechanism. Therefore, potential toxic effects of *C. taeniospiralis* for freshwater ciliates other than *Paramecium* were examined by exposing food competitors and predators to a lysate of killer paramecia. In addition, *Climacostomum virens* and *Dileptus* sp. were fed with living *Paramecium* cells carrying *C. taeniospiralis* or *Caedibacter varicaedens*. Neither ciliates mixed with lysate nor with living paramecia showed any typical pre-lethal symptoms or suffered from toxic effects. These results confirm observations from former studies and strengthen the hypothesis that the killer trait is an intraspecific phenomenon among the genus *Paramecium*.

The questions what kills sensitive paramecia and what protects infected ones and other ciliates from the toxin still await their answer. However, with this study we established approaches which shed light on the killer trait and the involved toxin.

P17: Protozoa induce soil suppressiveness against *Fusarium* wilt

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Soil borne diseases are responsible for important harvest losses worldwide and are a threat to global food safety. Some soils are naturally suppressive to pathogens and there is a growing corpus of evidence that microbiota play an essential role in shaping suppressiveness. Most research has focused on bacterial communities. Here we show that protozoa are an essential component of soil suppressiveness. Soil protozoa are major consumers of bacteria and have a strong impact on the structure and function of soil microbial communities. Here we show that addition of low amount of protozoa to a natural soil are sufficient to induce suppressiveness to *Fusarium oxysporum*, a major disease affecting several plant families. We saw faba beans in a natural soil infested with pathogens and inoculated the plants with three different protozoa. Protozoa addition reduced pathogen load to a factor 10'000 in soil and completely suppressed disease symptoms. We conclude that protozoa should be taken into account when investigating pathogen suppression by the soil microbiome.

P18: Comparison of thermal tolerance of different strains of heterotrophic flagellates and ciliates

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Thermal adaption of protists to their environmental temperature is one key issue for understanding the role of protists in microbial food webs. The environmental temperature in most aquatic ecosystems does generally not exceed 30° C. However, surviv al of protists in extreme environments like hot springs, thermal wastewater or soil exposed to solar radiation require an adaption to higher temperatures. Here, we compare experimentally determined lethal temperatures of a high number of different flagellate and ciliate strains of various taxonomic groups. Protist strains were isolated from different habitats ranging from polar regions to temperate regions and thermal wastewater. General patterns regarding temperature adaptations will be demonstrated.

P19: Survival of marine heterotrophic flagellates isolated from surface and abyssal depths at high hydrostatic pressure

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Although the abyssal seafloor represents the most common benthic environment on Earth, eukaryotic microbial life at abyssal depths is still uncharted territory in microbiology. This is in striking contrast to their potential importance regarding the material flux and bacteria consumption. One important problem is the fact that protists are usually exposed to high variations in pressure and temperature during sampling procedures compared to their constant original environment. Flagellates being active in the deep sea might be disrupted and not detectable when samples are investigated at surface atmospheric pressure. On the other hand, flagellates isolated from deep-sea samples might originate from cysts of organisms sedimented from surface waters but never being active under deep-sea conditions. We present studies on the pressure tolerance of different flagellate strains isolated from different marine habitats to check for their ability to survive exposure to high hydrostatic pressure.

Strains belonging to different taxonomic groups of heterotrophic flagellates (bicosoecids, cercomonads, choanotlagellates, chrysomonads, euglenids, kinetoplastids and Protista incertae sedis) were used for survival experiments conducted under high hydrostatic pressure (up to 670 bar). Flagellate strains were isolated from samples collected during deep-sea expeditions with research vessels “Meteor”, “Polarstern” and “Sonne”. Surface isolates of the same species were used for comparative experiments. For conducting the laboratory experiments, a pressure generating system with pressure chambers was constructed. Survival of protists after pressure incubations was checked under an inverted microscope. Experiments were performed at different hydrostatic pressures ranging between 50 and 670 bar and at different temperatures (2 °C, 13 °C, 20 °C). Exposure to pressure varied between 1.5 h and 168 h ours. In some experiments, the effect of additional bacterial food was studied. We summarize and compare our studies regarding the different taxonomic position and origin of strains. Our results demonstrated that many different flagellate species are able to survive even drastic changes in hydrostatic pressure. We concluded that several (not all) isolates from deep-sea samples originate from vital deep-sea populations.

P20: Salinity stress influences the transmission of bacterial *Paramecium* endosymbionts

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Paramecium (Alveolata, Ciliophora) can be found in freshwater and brackish environments. Changes in salinity concentrations present an environmental stress important for the ecology of this microorganism. Thus paramecia need to adapt to changing salinity concentrations to survive in unstable habitats like brackish ponds. Observations from brackish environments indicate that protists including *Paramecium* living there might be more frequently infected with bacterial endosymbionts than those from freshwater conditions. This might indicate an evolutionary advantage for symbiont-carrying microorganisms in habitats with variable salinity concentrations.

In this study we addressed the question if intracellular bacteria can increase the fitness of their host in experiments exposing them to increasing salinity concentrations. Additionally, we investigated the occurrence of horizontal transmission and symbiont maintenance under osmotic stress conditions.

Comparative growth analyses of infected versus uninfected strains at different salinity concentrations were performed to determine if the endosymbionts provide advantages or disadvantages (or none) to their host when exposed to different levels of osmolarity stress for a period of seven days. This experiment was carried out with the bacterial endosymbionts *Candidatus Megaira polyxenophila* and *Holospora caryophila*. No clear effect was observed at weak salinity stress, but infected cells reached higher cell numbers exposed to high salinity conditions compared to the corresponding symbiont-free cell lines.

A higher frequency of infected microorganisms in brackish water habitats might be the result of increased horizontal transmission of advantageous symbionts. Therefore, the horizontal transmission of *Candidatus Megaira polyxenophila* was tested at three different salinity concentrations: no, weak, and strong salinity stress. Therefore, donor (infected with the bacterial symbiont) and receiver strains (symbiont-free) were mixed and exposed to different salinities for three months. The combined *Paramecium* strains were morphologically distinguishable. Population and infection dynamics were observed by microscopy and fluorescence in situ hybridization (FISH) in regular intervals. No symbiont transmission was observed in freshwater conditions, but at weak salinity stress, horizontal transmission of *Can. M. polyxenophila* was observed. Surprisingly, the donor strains lost their endosymbionts at high salinity stress.

We could show that salinity stress influences endosymbiont transmission frequency and maintenance. Our results indicate that certain symbiont-carrying *Paramecium* strains might benefit from their endosymbiont under salinity stress. Additional experiments including more symbiotic systems are planned to confirm our observations and verify our conclusions.

P21: *Trichospira dextrorsa*, a very shy ciliate with fancy underwear

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Trichospira is a rare anaerobic ciliate, studied for the last time 85 years ago by Bruno Klein (Arch. Protistenkd. 69, 235, 1930). Based on silver-stained preparations he published only line drawings, part of which look rather technical. Thanks to Dr. Erna Aescht (OÖLM Linz), I had the chance to photograph a particular cell on which one of the drawings was based. It is fascinating to compare Klein's drawings with the results of our SEM and TEM studies. The cortex of *T. dextrorsa* eludes from written description, it has to be seen by eye. Klein was right for many aspects of the middle and posterior part of the cell, but his description of the oral area needs further studies.

Taken from a polysaprobic pond at the Federsee Station in Bad Buchau, *Trichospira* was kept in completely filled Tomato Juice bottles with no food for a period of two years. Probably it feeds on bacteria. At varying intervals probes were checked and whenever a maximum of 20 cells could be collected various approaches were undertaken to yield reasonable results. *Trichospira* is very sensitive to oxygen. Single cells were immersed into the fixative (Parducz or GA/Os) directly and processed for TEM and SEM. Deciliation was done with 4 % ethanol.

A helicospiral kinety (HSK) starting from the inner wall of the buccal cavity, following a helical course and then switching into spiral turn at the posterior end is the most characteristic feature of *Trichospira*. The kinetosomes (KS) form a double-stranded zigzag array in the closest possible arrangement. Contrary to the ordinary somatic ciliature, which is mostly made of monokinetids (with the usual fiber system: 8 radial postciliary mt, 6 radial transverse mt, kinetodesmal fiber), in the HSK several additional fibers form complex scaffoldings joining the kinetosomes in all dimensions. A broad epiplasmic plate accompanies the HSK on its left side. This plate shows 3 indentations at right angle to the dikinetids of the HSK. Simple needle-like trichocysts may attach to these indentations. The majority of the trichocysts are arranged in twisted serpentine lines corresponding to the silverline pattern.

All somatic kineties reach over the oral rim. For comparison with other ciliates it is interesting to note that the anterior end of Kn, Kn-1 and Kn-2 (to the left of the HSK) show 2-3 dikinetids. The deeper oral ciliature consists of a single-stranded anterior oral polykinetid and a deeper posterior polykinetid. A "cryptic" tetrahymenine configuration is discussed but not yet proven. Instead of mitochondria the cell has hydrogenosomes and methanogenic bacteria. Though no molecular studies exist, *T. dextrorsa* might belong to the riboclass Plagiopylea as suggested by Lynn (2008). Studying morphogenesis and molecular biology of this strange ciliate is highly recommended. (Supported by the DFG).

P22: 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 small 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 are currently building a revision of the whole family based on sound morphological documentation of isolates in combination with molecular phylogeny based on partial SSU rRNA gene sequences obtained from cultured organisms. The species Euglypha rotunda is represented here by six different strains that do not constitute a monophyletic group. Scaling patterns and the presence of a vesicular nucleus confirms the paraphyly of this taxon. Furthermore, the species E. acanthophora and E. filifera are represented also by several sequences corresponding to slightly diverging morphologies. This high diversity, and the presence of several subgroups in the tree of euglyphidae suggest the erection of several new genera within the family. Based on the combination of molecular and morphological data, we plan to date the appearance of different clades based on the fossil data that have been encountered recently.

P23: The base of cercomonad radiation is still in for a surprise, *Kraken* gen. nov.

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The term 'filose amoebae' describes a highly polyphyletic assemblage of protists whose phylogenetic placement can be unpredictable based on gross morphology alone. We isolated 6 filose amoebae from soils of two European countries and describe a new genus of naked filose amoebae, *Kraken* gen. nov. comprising one new species *Kraken carinae* sp. nov. We provide a morphological description based on light microscopy and small subunit 18S rRNA gene sequences (SSU rDNA). In culture, *Kraken carinae* is very slow-moving and prey on bacteria using a network of filopodia. Phylogenetic analyses of SSU sequences reveal that *Kraken* are core Cercozoa, branching weakly at the base of the cercomonad radiation, most closely related to *Paracercomonas*, *Metabolomonas*, and *Brevimastigomonas*. *Kraken* sequences are >99% similar to an environmental sequence obtained from a freshwater lake in Antarctica, indicating that *Kraken carinae* is not exclusively soil dwelling, but also inhabits freshwater habitats.

P24: A new freshwater monothalamid foraminifera from China and its possible relationship to *Allogromia saxicola* (Penard, 1905)

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Monothalamid foraminifera inhabit marine habitats from shallow water to the deep sea and are especially abundant in high latitude regions. Some species have also been described from freshwater environments by scientists in the 19th century. Among them, the Swiss protozoologist Eugène Penard has reported five freshwater foraminiferal species from Lake Geneva.

We found several specimens of monothalamid agglutinated foraminifera in sediment samples from a shallow pond in the city of Yangshuo, China, collected in 2015. The newly discovered species has an agglutinated tubular test with a flexible pseudostome and multiple nuclei. It resembles morphologically *Allogromia saxicola* (Penard, 1905), which is characterized by an elongated agglutinated test and a flexible test wall as well as multiple nuclei.

We extracted DNA from several specimens and amplified and sequenced a fragment of the SSU rDNA typically used as foraminiferal barcode. Nine sequences were obtained from four extractions. Phylogenetic analysis shows that the freshwater foraminifera from China build a strongly supported (100%BV) monophyletic group. The molecular results reveal a close relationship of the new species to an environmental sequence (OTU22) from uncultured foraminifera obtained from sediment samples of the Aire, a river in the Geneva basin. Furthermore, two environmental sequences obtained from lake sediments, in Albany, N.Y. (AF381181-82) branch as a sister to the former group. The whole clade is very well supported (100% BV). Sequence divergence between Chinese foraminifera and environmental sequences suggest that they belong to different species, the mean distance within Chinese foraminifera being 0.011 and within the environmental sequences 0,076 while the between group mean distance is 0.098. Because of morphological similarity between Chinese specimens and *A. saxicola*, it is possible that the OTU from Geneva corresponds to Penard's species and that the clade contains related species.

P25: Morphological diversity of Dinophysales (Dinophyceae), with emphasis on the delimitation of *Dinophysis* and *Phalacroma*.

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Dinophysales are thecate dinoflagellates, which comprise phototrophic as well as heterotrophic and some toxin producing species. The majority of this morphologically diverse group attracts attention by exhibiting extraordinary appendages at the cingular as well as the sulcal lists and the cell body. Nevertheless, all Dinophysales show a particular tabulation with a constant amount of plates, and a laterally flattened cell body. Molecular phylogenetic analyses have shown discordances compared to the common morphology based classification. Especially the most species rich genera, *Dinophysis* Ehrenb. and *Phalacroma* F.Stein, seem both to be polyphyletic. It becomes apparent, that the suitability of the morphological character traits used for taxonomic work so far is not given and a revision is needed.

Planktonic samples have been collected and fixed with Lugol's solution from different marine regions. This includes the Clarion Clipperton Fracture Zone area in the subtropic eastern Pacific and the German Bight belonging to the North Sea. For detailed morphological (re)investigations, Dinophysales cells have been isolated and analyzed with light- and electron microscopy methods. The morphological diversity of the genera *Amphisolenia* F.Stein, *Citharistes* F.Stein, *Dinophysis*, *Histioneis* F.Stein, *Metaphalacroma* L.S.Tai, *Phalacroma*, *Pseudophalacroma* Jørg., *Ornithocercus* F.Stein and *Triposolenia* Kof. from the Clarion Clipperton Fracture Zone area was analyzed. Intraspecific variation, character traits and the recognition of possibly new genera will be pointed out. An additional focus will be on the species *Phalacroma rotundata*, which showed character traits in between *Dinophysis* and *Phalacroma*. The taxonomically doubtful position of this species will be discussed.

P26: Diversity of Cercozoa (Protozoa) in soil revealed by Illumina sequencing

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We investigated the spatial and temporal distribution of the Cercozoa, a very abundant and diverse phylum of protists that includes testate and naked amoebae, amoeboflagellates and flagellates, in an unfertilized grassland soil. The study site is located in the Swabian Alps, a limestone middle mountain range in southwest Germany; it is part of a large interdisciplinary project of the German Biodiversity Exploratories for which results about the spatial variability of soil bacterial community structure, plant diversity, and soil properties have been already published. Our final aim was to conduct network analyses for predator-prey interactions with Acidobacteria (for which Illumina data have been obtained in the frame of the SCALEMIC project). We developed specific primers targeting the V4 variable region of the small subunit of the ribosomal RNA gene for Illumina high-throughput sequencing. From 180 soil samples, collected six times from April to November 2011 in a 10 m2 plot, we obtained $\sim$10 millions good quality reads, of which $\sim$5.5 millions were unique. Only three soil samples did not give positive results. We also included a test community made of 11 cercozoans species, amplified in the same conditions as the soil samples, to fine tune the parameters of our pipeline of filtering and clustering. To identify the sequences the PR2 protistan and the Silva SSU database were used, giving different outputs, but showing that our primers were highly specific: 91-97 % of the reads were assigned to Cercozoa. Sequences from the whole phylum were obtained, spanning from the basal plant parasites Plasmodiophorida (Endomyxa), to the filosean Sarcomonadea, Cryomonadida, the testate amoebae *Euglyphida* and the very abundant - in environmental sampling - Glissomonadida. Analyses are still in progress, preliminary results will be shown and discussed.

P27: Difficulties in assessing the global distribution of a model organism - the biogeography of *Favella panamensis* (Alveolata, Ciliophora)

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Accurate circumscriptions and determinations of species are essential for biodiversity and biogeography assessments; traditionally, the morphospecies concept was employed. Tintinnid ciliates are exceptional as - in contrast to the vast majority of ciliates - the whole taxonomy and classification of the more than one thousand marine planktonic species are almost exclusively based on characteristics of their vase-shaped loricae (houses). Because it is relatively easy to collect, preserve, examine, and classify, the lorica has allowed the accumulation of invaluable diversity and distribution data for more than two centuries. However, lorica-based taxonomy is problematic because of the high intraspecific variability and interspecific similarity of the loricae; so, the species limitations are currently unknown. Besides misidentifications, the diversity and geographic ranges perceived are especially affected by revisionary taxonomic treatises differing in their species circumscriptions from the original descriptions due to synonymisation (range of morphologic features became wider) and splitting (range of features became smaller) of species. Despite these difficulties, Montagnes (2013) suggested the tintinnid genus *Favella* as a model for planktonic ciliates. In the present study on the biogeography of *Favella panamensis*, the species records from about one hundred of taxonomical and ecological studies were classified according to their quality: (i) reliable records from the type and neotype localities mentioned in the original description and authoritative redescription; (ii) more or less reliable records supported by descriptions, measurements, and/or illustrations that fit the original description and redescription; and (iii) unsubstantiated records (mostly simple species lists) based on uncertain identifications. The comparison of the data provided by substantiated records with the original description revealed false positive and negative identifications. Since currently the species circumscriptions are uncertain, the usage of the original descriptions or authoritative redescriptions for the identification of tintinnid ciliates is strongly recommended. Only later, when the cell features and barcodes of the morphotypes are known, we might be able to perform justified synonymisations.

References

Montagnes (2013): Ecophysiology and behavior of tintinnids. In: Dolan J.R., Montagnes D.J.S., Agatha S., Coats W.D. & Stoecker D.K. (2013): The Biology and Ecology of Tintinnid Ciliates: Models for Marine Plank¬ton. Wiley-Blackwell: 85-121.

P28: A comparison of some methods to quantify heterotrophic flagellates of different taxonomic groups

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Heterotrophic flagellates contribute significantly to the matter flux in aquatic and terrestrial ecosystems. Still today their quantification and taxonomic classification bear several problems in field studies, though these methodological problems seem to be increasingly ignored in current ecological studies. Here we describe and test different methods, the live-counting technique, different fixation methods, cultivation methods like the liquid aliquot method (LAM), and a molecular survey called aliquot PCR (aPCR). All these methods have been tested either using field samples or cultures of freshwater and marine taxa. Each of the described methods has its advantages and disadvantages, which have to be considered in every single case. With the live-counting technique a detection of living cells up to morphospecies level is possible. Fixation and staining methods are advantageous due to the possible long-term storage and observation of samples. Cultivation methods (LAM) offer the possibility of subsequent molecular surveys, and aPCR tools might complete the deficiency of LAM in terms of the missing detection of non-cultivable flagellates. In summary, we propose a combination of several investigation techniques reducing the gap between the different methodological problems.

P29: Carbon flux from maize roots to key microbes in the rhizosphere and in bulk soil of an arable field

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The flow of carbon via plant roots into root-associated microorganisms and soil food webs, and thus the coupling of belowground and aboveground systems, is one of the key processes in terrestrial ecosystem functioning. Given the highly dynamic nature of growing roots, and the ease by which root-derived C will spread through root-associated microorganisms, the impression of a plant's rhizosphere microbiome as a static community might be strongly misleading. In particular the roles as C sinks of root-infecting microorganisms, such as arbuscular mycorrhizal fungi, compared to free-living assimilate-utilizing microorganisms and their taxonomic identities will greatly advance our functional understanding of rhizosphere processes. Furthermore, the identity of active microbial predators as well as the organization of rhizosphere food webs is virtually unknown, despite microbial grazers can significantly influence the composition and function of root-associated microorganisms. Only few studies to date were able to picture the microbial food web actively depending on C-input from root exudates, even though great efforts have been spend to describe microbial communities in the plant rhizosphere.

In a plant labeling experiment using a combined rRNA-SIP and pyrosequencing approach with 13C-labeled rhizodeposits we traced the C flow from roots of maize (*Zea mays* L.) through the communities of bacteria, fungi and heterotrophic protists. We found a very diverse microbial community in rhizosphere as well as in bulk soil but only few taxa actively relied on root exudates. Mycorrhizal fungi were the determining factor for the allocation of plant-derived C into bulk soil communities, thereby providing food webs in the rhizosphere and in bulk soil with energy from plant photosynthates.

We revealed the organization of the plant C-associated microbial soil food web, identified specific microbial key players and outlined a succession of plant-derived C through bacterial, fungal and protistan communities. These findings provide crucial insights into the temporal dynamics and functioning of the root-associated microbiome and the identity of associated key predators in soil food webs.

P30: Impact of a summer draught on the testate amoebae of an artificial peatland in the botanic garden of Neuchâtel

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Ongoing climate changes are affecting many ecosystems worldwide. Peatlands depend on a positive balance between water input and output and are especially threatened by draught (decreasing water input) and temperature (increasing evaporation). Additionally many peatlands, especially at the southern limit of distribution of northern Sphagnum peatlands have been strongly damaged by human impacts (drainage, peat harvesting etc.). Conservation efforts now aim to preserve the remaining sites and to restore damaged ones and such efforts are potentially jeopardized by on-going climate warming.

We built a small (ca. 100m^2) peatland in the botanical garden of Neuchâtel in the autumn of 2014 with the aims of 1) showing this ecosystem to the public and using it as a teaching tool, 2) conserving rare and endangered species ex-situ, and 3) studying the challenges of peatland restoration in a climatically challenging situation (the Swiss lowlands). The very hot and dry summer 2015 represented a first real challenge that represented an unintentional experiment to test the resistance of communities to unfavourable conditions.

In this study we assess the effect of draught on testate amoebae communities living in Sphagnum patches introduced on the peatland in autumn 2014. Testate amoebae play a key role in microbial food webs at the surface of Sphagnum peatlands and are used as indicators of current and past (palaeoecology) ecological conditions (water table depth, pH, etc.). We selected patches of contrasted sizes (small = 6-15 cm diameter; intermediate = 15-23 cm diam.; large = 23-44 cm diam.) and shading (no = 0-30% vascular plant cover, intermediate = 40-60% cover, high = 70-100% cover). We hypothesised that the proportion of living individuals would increase with patch size and shading as both factors would contribute to maintaining moisture in the moss carpet.

Our results show that in small and medium size patches, the augmentation of vascular plants cover decrease the proportion of dead testate amoebae, but not in larger patches. This suggests that the resistance of testate amoeba communities is positively influenced by the shade provided by vascular plants in patches smaller than 23 cm. In larger patches, the positive effect of shading decreases and other factors such as the structure of the moss carpet seem to play a larger role in the resistance of microbial communities during climatic stress.

P31: Vertical distribution of microbial communities in two *Sphagnum* peatlands along natural and experimental water table gradients

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Microorganisms living at the surface of peatlands play key roles in biogeochemical processes including carbon and nutrient cycling. Microbial communities and microbe-mediated functions are very sensitive to changes in environmental conditions and especially hydrology. Patterns of precipitation are expected to shift with ongoing climate change. This is thus essential to understand how microbial communities, and related processes, will respond to ongoing climatic changes considering the key role of peatlands as carbon stock.

Here we studied the vertical structure of microbial communities in the living *Sphagnum* mosses of two peatlands under different moisture conditions using an experimental (Linje peatland, northern Poland) and a natural (Forbonnet peatland, French Jura) water table depth and moisture gradients. In Linje the water table was manipulated by raising or lowering the peat surface of 28 plots (1 m2). We cut the peat to a depth of 30 cm and added (dry treatment) or removed (wet treatment) 10 cm of peat. In Forbonnet we studied a natural gradient of soil moisture (lawn and hummock microhabitats). We analysed separately communities living in the upper (first 3 cm - living) and lower (3 - 8 cm - mostly dead) parts of *Sphagnum* stems.

The biomass of bacteria (+74 % and +73 % in Linje and Forbonnet, respectively), fungi (+449 % and +442 %), testate amoebae (+110 % and +62 %), ciliates (+177 %, only in Forbonnet), rotifers (+161 %, only in Linje) and nematodes (+285 % and +160 %) was significantly higher in the lower than in the upper segment. The higher overall microbial biomass in the lower segments may suggest that they play a more important role for nutrient cycling. Microbial communities from the upper *Sphagnum* segments were more sensitive to shifts in moisture conditions than those from the lower segments. The biomass of testate amoebae, which act as top predators, and other consumers (i.e. rotifers, ciliates) in these microbial food webs, decreased under drier conditions. Our results show that the sensitivity of different microbial groups to moisture variations is size dependent - larger microorganisms being more sensitive to drying.

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

P32: The lament of scattered bones- a multiproxy approach in a real case investigation in forensic science

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When a cadaver has been lying in a forest for many weeks, months or even years the estimation of the time since death (post-mortem interval - PMI) becomes increasingly difficult. Entomological evidence provides reliable PMI estimations for up to 4-6 weeks. Additional forensic tools are therefore needed for longer PMIs and promising indicators include soil organisms and soil chemical characteristics and such indicators are being developed in experimental studies. But they also need to be tested on real cases when they occur.

We had the opportunity to study such a real case: Human bones were found by some dog walkers in a forest in Switzerland. The bones were collected as well as seven soil samples, three from beneath the remains (head, upper and lower body) and four control samples from the surrounding area. We conducted a multiproxy study of bones, soil biodiversity (morphological analyses of nematodes and mites and high throughput sequencing of all Eukaryotes) and soil chemical characteristics (pH, NH4+, NO3-, C, N, Mg2+, Ca2+ and P).

Soil samples collected beneath the remains clearly differed with respect to the nematode, mites, and Eukaryote communities as well as soil chemical markers. Furthermore, samples from underneath the head/ upper body differed from the ones from the lower body. The most common forest ectomycorrhizal Basidiomycetes and Ascomycetes were absent from underneath the head/upper body. Furthermore, reticulate (and fragile!) amoebae of genus *Ischnamoeba* (Variosea) were characteristic for the control and lower body parts samples. The basal fungus *Rhopalomyces*, a nematode egg parasite, was representative of the head/upper body samples, corroborating the increased presence of these metazoans observed by morphological analysis.

These results clearly show that the cadaver caused a major disturbance on the soil environment and that this disturbance was strongest beneath the head and upper body, which went through all the decomposition process, while the lower body parts seem to have been partly burned (by the murderer?) and thus did not modify the soil underneath as strongly.

P33: Changes in structure and functioning of testate amoeba communities due to conversion of lowland rainforest to rubber and oil palm plantations

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In the last decades Sumatra lost millions of hectares of tropical lowland rainforest mostly due to conversion into oil palm and rubber plantations. Despite the massive conversion, little is known on the biodiversity and ecological functions of the ecosystems replacing rainforest. We investigated effects of the conversion of rainforests into jungle rubber, intensive rubber and oil palm plantations on highly diverse and functionally important groups of protists in litter and soil, i.e. testate amoebae. Additionally, biotic and abiotic factors (potentially) responsible for these changes were investigated. Rainforest conversion detrimentally affected live testate amoebae species richness, density and biomass. The results indicate that the impact of rainforest conversion is more pronounced in litter as compared to soil due to litter buffering fluctuations in abiotic factors, thus in litter and to a lesser extent in soil, the community of testate amoebae is structured strongly by abiotic factors. Habitat space and number of niches for protists declined with conversion of rainforest into rubber and oil palm plantations. Similar abundance of taxa of high and low trophic level suggests that rainforest is a balanced system with a high number of functionally redundant species. This changed in converted ecosystems, especially in oil palm plantations, where reduced diversity of high trophic level taxa indicate losses in soil functions. Additionally, the relative density of taxa with siliceous shells declined by >50 % in oil palm and rubber litter as compared to rainforest and jungle rubber suggesting that rainforest conversion changes biogenic silicon pools and increases silicon losses. Overall, decreasing species richness, density and biomass, and changes in the functional composition of the testate amoebae community indicate detrimental effects of rainforest conversion on the structure and functioning of the decomposer community.

P34: Impact of pesticides on soil protists - Elaboration of an ecotoxicological protocol for *Euglypha rotunda* (Rhizaria)

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Pesticides have been widely used for decades in our modern society. It hence became crucial to develop tools to assess their impact on ecosystems. Thus, many ecotoxicological tests have been elaborated in order to determine the toxic effects of such substances on living organisms. The choice of a model organism (i.e. an organism representative of a broader group) is not straightforward. Most model organisms used in ecotoxicology are metazoans, while protists that constitute the major part of eukaryotic diversity and drive ecosystems functions (such as biogeochemical cycles) are clearly under-represented. To our knowledge not a single model organism for ecotoxicology exists among the Rhizaria, a highly diverse group or terrestrial and aquatic protists.

We aim to fill this gap by developing an ecotoxicological protocol for the common testate amoeba species *Euglypha rotunda*. We evaluate the growth response of *Euglypha rotunda* cultures incubated with *Escherichia coli* as carbon source to a pesticide (S-Metolachlor). We test both direct and indirect effect of the pesticide on the growth of *Euglypha rotunda*. Direct effect can for instance occur by disturbing a metabolic pathway of the protist, and an indirect effect can be the alteration of the carbon source of the protists (i.e. bottom up control). The investigated pesticide, S-Metolachlor, is an inhibitor of very long chain fatty acids synthesis. If the synthesis is blocked, the right proportion of fatty acids cannot anymore be achieved, and membrane functionalities are affected, thus preventing cell division. The major aim of this study is to determine the conditions allowing good experimental reproducibility, based on which a reliable tool for pesticide impact assessment can be proposed.

Our data show that the optimal setup is to start the culture with a low number of *E. rotunda* (100 to 300 individuals in 10ml of growth medium). Indeed, such numbers allows *E. rotunda* to multiply exponentially, whereas with higher initial numbers the multiplication rate is slower and linear. Bacterial density does not seem to affect the protists growth rate, but the presence of *Euglypha rotunda* promotes the bacterial growth up to a certain density.

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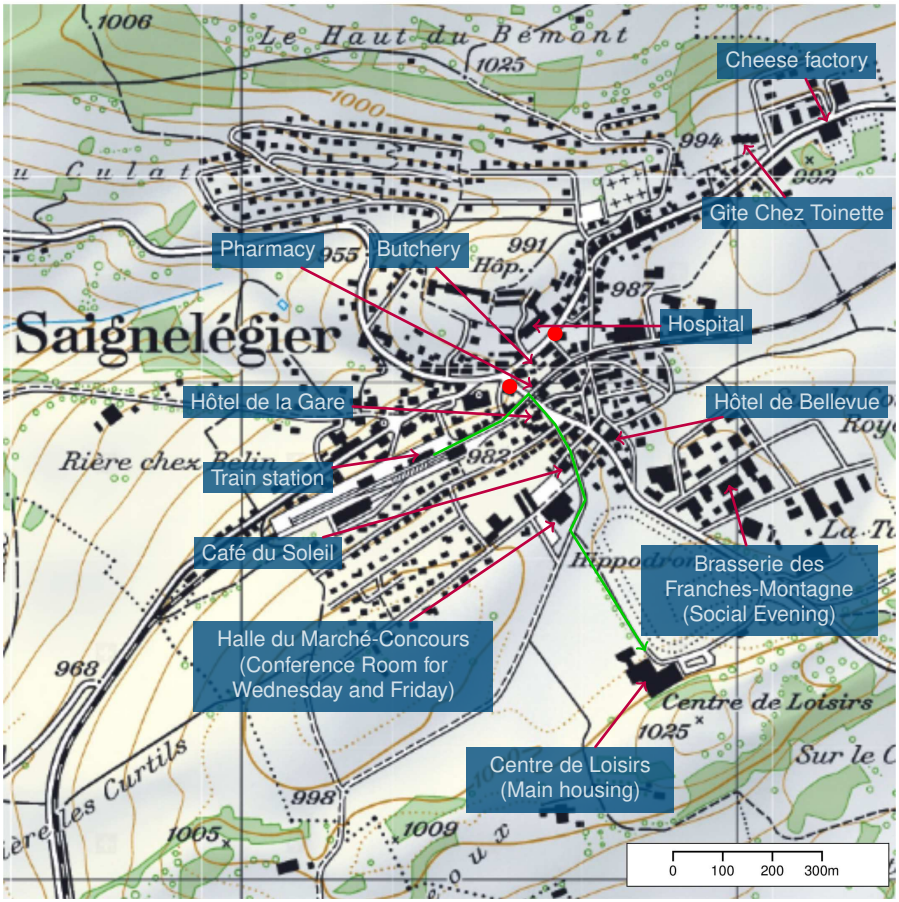

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