TECHNISCHE UNIVERSITÄT KAISERSLAUTERN

ECOLOGY GROUP University of Kaiserslautern

MOLECULAR ECOLOGY University of Kaiserslautern

Meeting of the
GERMAN SOCIETY FOR PROTOZOOLOGY

39

4 - 6 March 2020

Kaiserslautern
Germany

DEUTSCHE GESELLSCHAFT FÜR PROTOZOOLOGIE e. V.

Programme & Abstracts

Dear participants of the DGP2020 meeting,

we are delighted to welcome you at the 39th annual meeting of the German Society for Protozoology. It is being hosted, under the patronage of university president Prof. Dr. Helmut J. Schmidt, by the Departments of Ecology and Molecular Ecology at the Technische Universität Kaiserslautern from March 4th – 6th, 2020.

With 106 participants, 44 lectures and 31 poster contributions, the conference promises to reflect the current state of research in protozoology, including aquatic and terrestrial ecology, cell physiology, species interactions, evolution, diversity, advances in methodological approaches, and much more. We are very pleased that half of the contributions are given by Bachelor, Master and PhD students. Furthermore, we thank four outstanding keynote speakers for presenting novel insights into various fields of protozoology. Due to the high variety of topics, we are very much looking forward to lively, fruitful and inspiring discussions. We have planned various evening activities, which will round off the official conference program and give room for discussions in a relaxed atmosphere.

Preceding the conference, we offer a hands-on workshop focusing on state-of-the-art sequence data analysis to young and young-at-heart scientists at the Regional University Computing Center (RHRK) at the Technische Universität Kaiserslautern on March 3rd, 2020.

We hope that you will enjoy the meeting and your stay in Kaiserslautern and wish you an inspiring conference.

Your DGP2020 Organization Team

DGP2020 Organization Team

Conference Chairs:

Prof. Dr. Thorsten Stoeck
Jun. Prof. Dr. Sabine Filker

Co-Organizers:

Dr. Dominik Forster
Melanie Kissel
Hans-Werner Breiner

Workshop Organizers:

Dr. Dominik Forster
Dr. Guillaume Lentendu

Assistants:

Heinrich Balliet
Elyssa Dubois
Verena Dully
Larissa Frühe
Vanessa Immel
Sarah Mergel
Maren Nothof
Zhishuai „Dex“ Qu
Sören Salvatore
Romy Werst

Content

General Information

Congress Venue

The 39th annual meeting of the German Society for Protozoology takes place at the Technische Universität Kaiserslautern, located at the edge of the Palatinate forest.

Address: Technische Universität Kaiserslautern
Rotunda
Erwin-Schroedinger-Str. 57
67663 Kaiserslautern

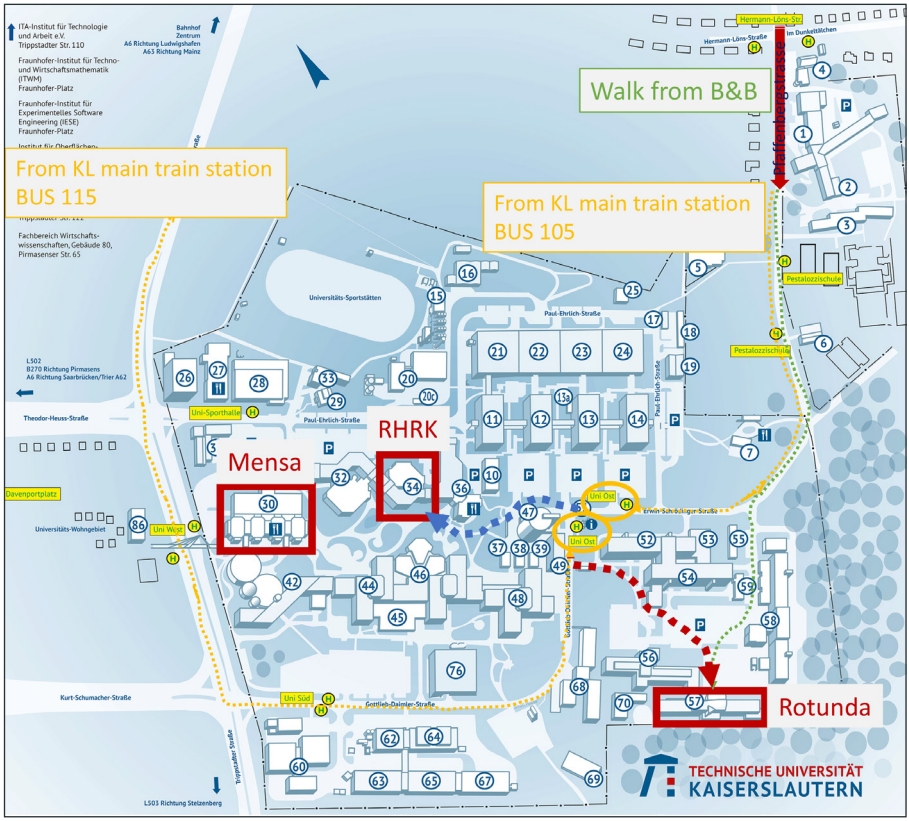
The University of Kaiserslautern (TUK) was founded in 1970 and celebrates its 50th anniversary in 2020. It is the only technical and scientific university in Rhineland-Palatinate.
Being a campus university with around 14,900 students, it offers a wide range of academic courses in twelve faculties. Most courses of study have an interdisciplinary approach and thus combine different subject areas. Fore more information about TUK visit: www.uni-kl.de.

The scientific programme takes place in the Rotunda in building 57, which was established as the university‘s main venue for official and festive events, and adjacent rooms.

How to get there:
By bus from Kaiserslautern main train station:
a) Bus line 105: depart at „Steig A Kaiserslautern, Hauptbahnhof“ (direction: Kaiserslautern, Kurt-Schumacher-Str.), leave bus at station „Kaiserslautern, Uni Ost“ (9 min), and follow the red path on the map
Bus line 105 departs every 30 min.

b) Bus line 115: depart at „Steig B Kaiserslautern, Hauptbahnhof“ (direction: Kaiserslautern, Uni Ost), leave bus at station „Kaiserslautern, Uni Ost“ (8 min) and follow the red path on the map
Bus line 115 departs every 15 min.

For detailed bus schedules or other departure locations please visit: www.vrn.de. Bus tickets can be purchased directly from the bus driver.



Site plan of the Technische Universität Kaiserslautern. Yellow paths indicate bus routes of lines 115 and 105, both starting from Kaiserslautern main train station. Leave busses at the circled stations „Kaiserslautern, Uni Ost“. Follow the blue path to get to the bioinformatics workshop at the Regional University Computing Center and the red path to get to the Rotunda.

Registration

The registration desk is located in the foyer of the Rotunda and is open on Wednesday from 8 – 12 am.
Workshop participants will be able to register in the Regional University Computing Center (RHRK, building 34) on Tuesday from 9.30 – 10 am.
At the registration desk, you will receive your name badge and a congress bag, including a programme booklet, certificate of attendance and payment receipt, city map, poster presentation ballot paper, writing pad and pen. Participants are kindly requested to wear their name badge at all times during the meeting.

Workshop

The bioinformatics workshop takes place in the Regional University Computing Center (RHRK), building 34, room 251 on Tuesday, March 3rd, 2020 from 10 am to 5 pm.
If you arrive by bus, follow the blue path on the map. Please use the entrance between building 32 and 34 to find the registration desk. In building 34, signs will guide you the way to the workshop room.
Computer working stations, access to our server and training data sets will be provided. Workshop costs include coffee breaks and lunch.

Presentations

Time slots for oral presentations are 15 min, i.e. 12 min talk and 3 min for discussions. A computer and laser pointer will be provided. Accepted presentation formats are ppt, pptx and pdf.
Speakers are kindly asked to upload their presentations to the seafile server using the link provided previously in an eMail not later than 6 pm on the day before the scheduled presentation.

Posters can be displayed in the poster exhibition room on Wednesday morning and during the lunch break.
Poster size should be A0 portrait oriented (width: 84.1 cm, length: 118.0 cm). Please do not exceed these dimensions. A freestanding compatible poster board and pins will be provided for your poster. Your poster number will appear on the top right-hand side of the board so you can locate your board easily. Please check your poster number in the programme booklet.
Posters will be on display throughout the conference. Poster sessions will take place on Wednesday and Thursday afternoon. Authors are requested to be available at their posters during the poster sessions. Please also prepare a 1-minute presentation (1 slide!) to introduce your poster during the flash talk session on Wednesday. Slides have to be sent to the organizing committee by Monday, March 2nd, 2020.

All posters and student talks are eligible to participate in the selection of the best presentation/poster during the DGP2020 meeting. Eligible talks are marked in the programme booklet by an asterisk.
The three best presentations will be chosen by a committee, and the three best posters by all conference participants. Corresponding ballot papers are included in the congress bag. Please fill in the ballot paper by Thursday at 5.30 pm and put it in the ballot box provided in the poster exhibition room.
The award ceremony will take place during the Congress Dinner on Thursday.

Social Programme

The *Welcome Reception* takes place on Tuesday, March 3rd, 2020 at 7 pm at the Villa Denis in Frankenstein.

Address: Villa Denis
Diemerstein 9
67468 Frankenstein

Costs are included in the conference fee.

How to get there:
Take the train S1 leaving at 6.26 pm from Kaiserslautern main train station. At the second stop, leave the train at Frankenstein (Pfalz) station. Leave the train station and turn left towards Hauptstrasse/B37. After 160 m, turn right and pass the Landgasthof Schlossberg. Follow the street for 600 m. Villa Denis will be on your right-hand side.

All *guided tours* take place on Wednesday, March 4th, 2020 and start at 5.30 pm. Members of the Organization Team will bring you to the respective meeting points. Please make sure you have a valid bus ticket so as not to delay the departure of the bus. Both tours last about 90 minutes.
Participants of the „Story of beer and ice"-tour should bring a flashlight or a mobile phone with flashlight function.

The *Wednesday Dinner* takes place in Kaiserslautern´s oldest half-timbered house, the Spinnrädl at 7 pm.

Address: Spinnrädl
Schillerstrasse 1
67655 Kaiserslautern

Costs: meal included in the conference fee, drinks have to be paid individually

How to get there:
If you joined one of the guided tours, a member of the Organization Team will bring you to the restaurant.
From the university, take bus line 115 (direction: Kaiserslautern, city center) from station "Kaiserslautern, Uni Ost" and leave the bus at station "Kaiserslautern, Stadtmitte, Steig F" (21 min). After a 3-minute walk you reach the Spinnrädl.

The *Congress Dinner* takes place on Wednesday, March 5th, 2020 at 7 pm at the restaurant "TwentyOne", located at the roof top of Kaiserslautern´s town hall.

Address: TwentyOne
Willy-Brandt-Platz 1
67655 Kaiserslautern

Costs are included in the conference fee.

How to get there:
From the university, take bus line 115 (direction: Kaiserslautern, city center) from station “Kaiserslautern, Uni Ost” and leave the bus at station “Kaiserslautern, Stadtmitte, Steig F” (21 min). After a 4-minute walk you reach the town hall.

Coffee Breaks and Lunch Breaks

Hot and cold beverages will be served to all registered participants during the coffee breaks from Wednesday to Friday. The coffee bar station will be located in the foyer of the Rotunda.
Please note that it is not allowed to bring food and drinks into the Rotunda!

Lunch is served in the Mensa (building 30), which is in walking distance (5 minutes). You will be able to choose between several meals, salads, sandwiches and drinks (vending machines are not covered). Vegetarian dishes are also offered. Please wear your conference badge at all times.

Congress Language

The official language of the 39th meeting of the German Society for Protozoology is English.

Certificate of Attendance & Payment Receipt

A certificate of attendance and payment receipt will be handed out together with the conference bag.

Programme Changes

The organizers cannot assume liability for any changes in the conference programme due to external or unforeseen circumstances.
Possible changes in the programme will be announced during the conference and also on the internet at www.bio.uni-kl.de/DGP2020.

Internet Access

Wifi access is available throughout the buildings of the TUK campus via eduroam.

Programme Overview

Time	Tuesday, March 3rd	Wednesday, March 4th	Thursday, March 5th	Friday, March 6th
08:00 - 08:45		Registration		
08:45 - 09:00		Welcome address		
09:00 - 09:30		Keynote lecture 1: **Bettina Sonntag**	Keynote lecture 3: **Jan Pawlowski**	Keynote lecture 4: **Lucie Bittner**
09:30 - 10:00		Session 1: **Ciliates in the Planktonic Food Web**	Session 5: **Protists & Ecosystem Services**	Session 9: **Functional Traits**
10:00 - 10:30	Bioinformatics workshop	Session 2a: **Diversity & Distribution of Ciliates**		Coffee break
10:30 - 11:00			Coffee break	
11:00 - 11:30		Coffee break	Session 6: **Diversity & Distribution of Protists**	Session 10: **Taxonomy & Phylogeny**
11:30 - 12:00		Session 2b: **Diversity & Distribution of Ciliates**		
12:00 - 12:30		Session 3: **Young Taxonomists**	Session 7: **Ecophysiology & Autecology of Protists**	Farewell
12:30 - 13:00	Lunch	Lunch	Lunch	Lunch
13:00 - 13:30				
13:30 - 14:00	Bioinformatics workshop			
14:00 - 14:30		Keynote lecture 2: **Marcel Deponte**	Session 8: **Parasites & Symbionts**	
14:30 - 15:00		Session 4: **Cell Biology**		
15:00 - 15:30		Coffee break		
15:30 - 16:00		Poster session	Coffee break	
16:00 - 16:30			Poster session	
16:30 - 17:00				
17.00 - 17.30			DGP member meeting	
17.30 - 18.00		Guided tours		
18:00 - 19:00				
19:00	Welcome Reception	Dinner	Congress Dinner	

Meeting Programme

Wednesday, March 4th, 2020

08:45 – 09:00 Welcome Addresses
Prof. Dr. Helmut J. Schmidt
Conference Chairs: Prof. Dr. Thorsten Stoeck & Jun. Prof. Dr. Sabine Filker

Session 1: Ciliates in the planktonic food web
Chair: Dominik Forster

09:00 – 09:30 Keynote lecture by **Sonntag, Bettina** (Leopold-Franzens University, Austria)
Lost world: Return of ciliates into planktonic food web analyses

09:30 – 09:45 **Flöder, Sabine***
Competitive interactions between heterotrophic and mixotrophic ciliates depend on resource fluctuation regime and feeding traits

09:45 – 10:00 **Weisse, Thomas**
Container volume has little effect on growth and grazing rates of ciliates and microcrustaceans in microcosm experiments

Session 2a: Diversity & Distribution of Ciliates
Chair: Micah Dunthorn

10:00 – 10:15 **Sommer, Fabian***
Ciliates and skiers share the same man-made mountain reservoirs

10:15 – 10:30 **Kammerlander, Barbara**
"Meet the ciliates" in the planktonic food web of Lake Mondsee

10:30 – 10:45 **Lu, Xiaoteng***
Species diversity of planktonic ciliates: Does connectivity make a difference?

10:45 – 11:15 **Coffee break**

Session 2b: Diversity & Distribution of Ciliates
Chair: Micah Dunthorn

11:15 – 11:30 **Posch, Thomas**
Sequencing versus morphotype-based monitoring of phytoplankton in Lake Zurich – facts and future challenges

11:30 – 11:45	**Lentendu, Guillaume** *Network analyses enhance sequence grouping algorithms*
11:45 – 12:00	**Ganser, Maximilian*** *Diversity and distribution of marine planktonic ciliates from coastal waters of the South China Sea and Europe*
	Session 3: Young Taxonomists Chair: Jürgen Strassert
12:00 – 12:15	**Frantal, Daniela*** *Catch me if you can – fast, faster,* Urotricha*!*
12:15 – 12:30	**Duckert, Clément*** *Description of* Hyalosphenia paynei*, a local endemic from Wales*
12:30 – 12:45	**Hohlfeld, Manon*** *Extended phylogeny of* Percolomonas*-like flagellates from marine and hypersaline environments*
12:45 – 14:00	**Lunch**
	Session 4: Cell Biology Chair: Martin Simon
14:00 – 14:30	Keynote lecture by **Deponte, Marcel** (Technische Universität Kaiserslautern, Germany) *The oxidative stress hypothesis in malaria research: Facts and fiction*
14:30 – 14:45	**Nitsche, Frank** *Transformation of choanoflagellates, a reliable and efficient method*
14:45 – 15:00	**Drews, Franziska*** *The epigenome of a highly condensed genome: how does* Paramecium *control gene expression without intergenic regions and canonical heterochromatin?*
15:00 – 15:15	**Pirritano, Marcello*** *Dual-Seq reveals genome and transcriptome of* Caedibacter taeniospiralis*, an obligate endosymbiont of* Paramecium
15:15 – 15:45	**Coffee break**
15:45 – 17:00	Flash talks & Poster session
17:30 – 19:00	Guided tours: Count palatinate hall / Story of beer and ice
19:00	**Dinner**

Thursday, March 5th, 2020

	Session 5:	Protists & Ecosystem Services
	Chair:	Jens Boenigk
09:00 – 09:30	Keynote lecture by **Pawlowski, Jan** (University of Geneva, Switzerland) *Protist metabarcoding and next generation biomonitoring*	
09:30 – 09:45	**Werner, Jennifer*** *Annual course of retention effects through protistan dominated biofilms regarding planktonic bacteria in the River Rhine*	
09:45 – 10:00	**Walochnik, Julia** *Prevalence and diversity of the intestinal parasite* Giardia *spp. in urban waters in Vienna, Austria*	
10:00 – 10:15	**Moorthi, Stefanie** *Local and regional factors determine the dominance of the harmful dinoflagellate* Alexandrium catenella *along a nutrient gradient: A meta-ecosystem study*	
10:15 – 10:30	**Auer, Brigitte** *The far side: life for protozoologists beyond research*	
10:30 – 11:00	**Coffee break**	
	Session 6:	Diversity & Distribution of Protists
	Chair:	Hartmut Arndt
11:00 – 11:15	**Plotnikov, Andrey** *The structure and diversity of protist communities in the water column of the meromictic Kislo-Sladkoe Lake (Kandalaksha Bay, White Sea) studied with microsopy and DNA metabarcoding*	
11:15 – 11:30	**Schiwitza, Sabine*** *Can surface water currents act as natural barriers? A survey on several protist groups shows different biogeographical distribution patterns*	
11:30 – 11:45	**Walden, Susanne*** *Temperate versus tropical forest canopies – a comparison of cercozoan diversity across biomes using Illumina high-throughput sequencing*	
11:45 – 12:00	**Duarte Ritter, Camila** *Diversity and co-occurrence patterns in Amazonian protists*	

	Session 7:	Ecophysiology & Autecology of Protists
	Chair:	Sabine Filker

12:00 – 12:15 **Stappert, Hannah-Marie***
Cool and shady – ecophysiological preferences of chrysophytes

12:15 – 12:30 **Busch, Anna***
A UV-inducible sunscreen pigment found in the extracellular mucilage of aerophytic green algae (Zygnematophyceae)

12:30 – 12:45 **Teixeira Pereira Bassiaridis, Justin***
Prey range specificity and feeding modes in leptophryid amoebae (Vampyrellida, Rhizaria) from freshwater and soil ecosystems

12:45 – 14:00 **Lunch**

	Session 8:	Parasites & Symbionts
	Chair:	Julia Walochnik

14:00 – 14:15 **Singer, David**
Evaluation of parasitic diversity using environmental DNA approach

14:15 – 14:30 **Solbach, Marcel Dominik***
The diversity of bacterial endosymbionts in rhizarian amoebae implies a universal infection of rather unrelated free-living amoebae by Legionellales

14:30 – 14:45 **Hess, Sebastian**
Two co-occuring varieties of Pseudoblepharisma *KAHL (Heterotrichea, Ciliophora) represent distinct tripartite symbioses with eubacteria and green algae*

14:45 – 15:00 **Flemming, Felicitas E.***
Paramecium bursaria *and its photobionts - shedding light on the photobionts' influence on host behavior*

15:00 – 15:15 **Jauss, Robin-Tobias***
A parasite's paradise: Biotrophic species prevail oomycete community composition in tree canopies

15:15 – 15:30 **Strassert, Jürgen F. H.**
Insect-infecting nephridiophagids are affiliated to the Chytridiomycota

15:30 – 16:00 **Coffee break**

16:00 – 17:00	Poster session
16:45 – 18:00	DGP member meeting
19:00	**Congress Dinner**

Friday, March 6th, 2020

	Session 9:	Functional Traits
	Chair:	Thomas Posch

09:00 – 09:30 Keynote lecture by **Bittner, Lucie** (Sorbonne University, France)
From omic dark matter to traits: Exploring the (meta)omic bases of traits within microbial eukaryotes

09:30 – 09:45 **Fiore-Donno, Anna Maria**
Functional traits of two important protistan lineages, Cercozoa and Endomyxa, reveal contrasting distribution patterns of plant parasites and phagotrophs in soil of temperate grassland and forest

09:45 – 10:00 **Mulot, Matthieu**
Linking micro-eukaryotic communities to carbon export in peatlands using (statistically) true co-occurrence networks topological properties

10:00 – 10:15 **Boenigk, Jens**
Nutrient-driven genome evolution of chrysomonad flagellates

10:15 – 10:45 **Coffee break**

	Session 10:	Taxonomy & Phylogeny
	Chair:	Thomas Pröschold

10:45 – 11:00 **Rajter, Lubomir**
A 3-step fluorescent staining technique to visualize ciliates

11:00 – 11:15 **Foissner, Wilhelm**
Morphologic and molecular phylogeny of Pseudoblepharisma *Kahl, 1927, a loricate Spirostomidae (Ciliophora, Hetertrichea)*

11:15 – 11:30 **Radek, Renate**
Phylogeny and morphology of a new, deviant flagellate lineage in termites of the family Serritermitidae

11:30 – 11:45 **Dumack, Kenneth**
Morphological investigation of the Trivalvulariida ord. nov. (Cercozoa, Rhizaria) and what we can infer from it about shell evolution in Cercozoa

11:45 – 12:00 **Kudryavtsev, Alexander**
Phylogeny, cryptic diversity, and benefits of investigating marine lobose amoebae (Amoebozoa)

12:00 – 12:15 **Volkova, Ekaterina**
Not all that looks like a Tubulinean is a Tubulinean: expectations and reality for the parasitic amoeba Janickina pigmentifera *(Grassi, 1881)*

12:15 – 12:25 **Farewell**

12:25 – 13:45 **Lunch**

Abstracts

Keynote Lectures

Protist metabarcoding and next generation biomonitoring

Jan Pawlowski

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Biological monitoring is being revolutionized by the application of DNA barcoding and metabarcoding for species identification, biodiversity inventorying, and assessment of environmental impacts. Compared to the traditional biomonitoring that is based on visual observation and morphological identification of a few well-known, easily identifiable taxa, the DNA-based biomonitoring offers the possibility to expand the range of bioindicators and to take advantage of highly sensitive but often inconspicuous and difficult to identify groups of organisms. Some groups of protists have already been successfully tested as potential candidates to become new generation of bioindicators. However, wider application of these groups is often impeded by limited knowledge of their ecology, gaps in reference database for taxonomic assignment and biases related to quantitative interpretation of metabarcoding data. To overcome some of these limitations, taxonomy-free approaches to analyse metabarcoding data have been proposed recently. These approaches are based either on indicator values assigned directly to metabarcodes or on biotic indices predicted using machine learning analysis of training datasets of metabarcodes. The machine-learning has been shown to be as efficient as traditional biomonitoring for environmental impact assessment of some industrial activities. Further development of taxonomy-free approaches opens unlimited opportunities to use protists for fast, sensitive and cost-effective bioindication. However, to fully integrate them into regulatory compliant routine practice more research is needed to better understand the response of protist community to environmental pressures and to better manage the limitations and challenges of the new technology.

The oxidative stress hypothesis in malaria research: Facts and fiction

Marcel Deponte

University of Kaiserslautern, Kaiserslautern, Germany

Mail: deponte@chemie.uni-kl.de

The redox metabolism of the malaria parasite *Plasmodium falciparum* and its human host has been suggested to play a central role for parasite survival and clearance. For example, excessive hemoglobin degradation within the erythrocyte as well as rapid parasite growth and DNA synthesis are thought to cause intrinsic metabolically derived oxidative stress. Oxidative stress in malaria parasites was also suggested to be caused by extrinsic factors, including the immune system as well as genetic traits that are selected in malaria-endemic areas and that result in (partial) protection of the human host. Furthermore, oxidative stress might be involved in the mode of action of several antimalarial drugs. I will present and discuss supporting as well as conflicting data regarding the oxidative stress hypothesis in malaria research and will highlight current conceptual limitations and their general implications for redox research.

Lost world: Return of ciliates into planktonic food web analyses

Bettina Sonntag

Leopold-Franzenz University, Innsbruck, Austria

Mail: Bettina.Sonntag@uibk.ac.at

In an international research project, we follow an interdisciplinary approach studying freshwater planktonic protists with a focus on ciliates. Our goal was to integrate and match morphological, molecular and ecological datasets to elucidate the autecology of ciliate species in aquatic food webs. In detail, we studied natural plankton assemblages in Lake Mondsee (Austria) and Lake Zurich (Switzerland) over a one-year cycle in biweekly intervals along vertical depths gradients. Apart from measuring abiotic parameters, we investigated almost all heterotrophic, autotrophic and mixotrophic protists as well as zooplankton and viruses. All organism-based analyses were carried out in parallel from a morphological quantitative assessment via microscopy, from single-cell sequencing of ciliates and from high throughput sequencing of raw water samples. Based on these morphological and molecular datasets, co-occurrence networks were constructed and key ciliate players in the two lakes identified. The networks in turn provided the basis for species-specific functional and numerical response experiments revealing predator-prey relationships, e.g., between an alga and a ciliate. Moreover, we involve citizens and pupils to understand that aquatic food webs form the basis for lake ecosystem functioning and why basic research is important. Overall, this challenging D-A-CH approach includes many networking scientists, students and co-workers who put their heart and soul into this interesting project finally gaining insight into a ciliates' point of view living in an aquatic microbial food web.

From omic dark matter to traits: Exploring the (meta)omic bases of traits within microbial eukaryotes

Lucie Bittner

Sorbonne University, Paris, France

Mail: lucie.bittner@upmc.fr

The advent of high-throughput sequencing approaches has unveiled the extent of Earth biodiversity and revealed our ignorance with respect to the role of this diversity in ecosystems' functioning. The fundamental molecular mechanisms associated to the ecological traits of organisms are poorly known, and often restricted to model organisms. For instance, symbiotic relationships are widespread and are critically important for the functioning of ecosystems but the genomic bases of the establishment and the maintenance of these associations remain largely unknown, and this especially between unicellular eukaryotes. Besides, the study of omic datasets from holobiont(s) involving non-model lineages represents bioinformatic challenges such as the production of chimeric sequences or deciphering the taxonomic origin of the sequences. Finally, the vast majority of these molecular sequences remain functionally unknown, limiting the analyses to a subpart of the genomic data newly produced. My research focuses on developing strategies to circumvent these pitfalls. I will present approaches developed in my team, that we applied on marine holobionts involving non model unicellular eukaryotic partners. First, using *k-mer* based similarity methods and independent assemblies, I will show how a significant diminution of *de novo* assembled chimeras compared to classical assembly methods can be obtained. Second, using sequence similarity network analyses, I will illustrate how one can investigate the (meta)genomic basis of organismal traits, while including the functionally unknown sequences. Following this strategy, we identified candidate protein domains associated to traits, and notably here to symbiosis. These genomic markers constitute working hypotheses, to be further confirmed by targeted molecular studies. This exercise represents one of the very few studies available to date to expand our knowledge about traits of non-model organisms, while exploring (meta-)omic datasets, and offers perspectives to study the ecology and evolution of microorganisms, this time concretely and truly, at a massive scale.

Talks

The far side: life for protozoologists beyond research

Brigitte Auer (1)

(1) Biomontan Produktions und Handels GmbH, Ennns, Austria

Mail: b.auer@biomontan.at

Taxonomic knowledge is essential for the work of a protozoologist, especially in ecological studies. But is there a benefit of this knowledge outside of scientific research?
In wastewater treatment plants, we find a special type of ecosystem based on bacteria which also includes a high number of protozoans. Taxonomic composition of ciliates and flagellates can be used as indicators for operating conditions such as nutrient concentration, oxygen content or sludge age.
Some examples: *Vorticella infusionum* can tolerate lower oxygen concentration than *Vorticella convallaria*. *Chaetospira muelleri* is observed only in sludges with high salinity. High numbers of *Bodo saltans* is present in plants with a large denitrification zone. *Drepanomonas revoluta* occurs in high loaded plants mainly with wastewater from food industry.
Therefore, the analysis of the protist community provides useful information for conditions and for the operation of the plants. Especially because most operators still consider the activated sludge as a negligible black box. We can change their mind.

Nutrient-driven genome evolution of chrysomonad fagellates

Stephan Majda (1), Daniela Beisser (1), Jens Boenigk (1)

(1) University Duisburg-Essen, Essen, Germany

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Phototrophic eukaryotes have evolved mainly by the primary or secondary uptake of photosynthetic organisms. A return to heterotrophy occurred multiple times in various protistan groups such as the Chrysophyceae. Based on genome sequencing of 16 chrysophyte strains we analysed the genomic shifts accommodating the loss of phototrophy. The comparative analysis of the parallel evolution of heterotrophy revealed general pattern in genome evolution associated with the loss of photosynthesis. Our results substantiate the idea that the evolutionary shift to mixotrophy and further to heterotrophy is triggered by a differential importance of nutrient and carbon shortage leaving distinct signatures in the genome.

A UV-inducible sunscreen pigment found in the extracellular mucilage of aerophytic green algae (Zygnematophyceae)

Anna Busch (1), Sebastian Hess (1)

(1) University of Cologne, Cologne, Germany

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Aeroterrestrial microalgae colonise various natural and anthropogenic surfaces on land. Compared to their aquatic counterparts, they face not only periodic desiccation, but also increased solar radiation. Some aeroterrestrial microalgae synthesize light-absorbing 'sunscreen compounds', which shield the cells from excess radiation, in particular from harmful ultraviolet radiation (UV). Although some algal sunscreens are well studied, our general understanding of the chemical diversity and taxonomic distribution of such compounds is poor. Here, we report a so far uncharacterised non-photosynthetic pigment from a lineage of unicellular conjugating green algae (Zygnematophyceae), the closest relatives of land plants. These algae, formerly lumped in the polyphyletic genus *Mesotaenium*, show a wide geographic distribution and an unexpected genetic diversity. In the natural habitat, all reported species displayed a striking pigmentation of their extracellular mucilage, which is unusual for eukaryotic algae. So far, extracellular pigments with potential sunscreen function have only been known from prokaryotic algae. Under standard laboratory conditions, the extracellular pigmentation of *Serritaenia* cells disappeared, but could be induced by artificial UV-PAR exposure. Analysis of experimentally induced pigment revealed that it is simultaneously secreted with extracellular mucilage, and that its colour is pH-dependent. We further identified UV-B as the main inducing factor, and show that pigmented mucilage of *Serritaenia* absorbs over the entire solar UV-PAR spectrum, with a broad maximum below 350 nm (UV). We conclude that the pigmented mucilage of these Zygnematophyceae may provide effective photoprotection - likely representing a crucial adaptation to their life on land.

The epigenome of a highly condensed genome: how does *Paramecium* control gene expression without intergenic regions and canonical heterochromatin?

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With its high coding density due to tiny introns and short or non-existing intergenic regions, the compressed *Paramecium* genome shows distinct differences to genomes of multicellular species. Facing this, precise transcriptional initiation, elongation and termination must be accomplished with fundamental differences in comparison to mammalian genomes.
Accessibility of the chromatin for the transcription machinery is highly regulated by the positioning of nucleosomes, which function as the main subunit of chromatin and are the basic layer in the complex regulation of gene expression. Still, little is known about the distribution of nucleosomes in correlation to gene expression in *Paramecium*. To address this, we performed micrococcal nuclease (MNase) digestion of fixed chromatin samples isolated from vegetative macronuclei by applying an adapted NEXSON protocol. This procedure allows us to carry out MNase - seq and Chromatin immunoprecipitation (ChIP) - seq from the same sample material.
First insights give a hint for distinct positioning of the +1 nucleosome downstream of the TSS and a clear phasing pattern towards the transcription end site (TES) with a loss of positioned nucleosomes inside the gene body. Simultaneously, ChIP - seq for individual histone marks was carried out, and the signals were combined and attributed to segments of the genome by ChromHMM. This reveals accumulation of activating histone marks at + 1 nucleosomes but also broad signal peaks inside open reading frames with activating and repressive marks appearing in a non-mutually exclusive manner. Strikingly, comparison of MNase - and ChIP - seq data reveals areas without any signal for histone modifications neither than positioned nucleosomes, which seems contradictory the general assumption that DNA never remains unprotected.
Surprisingly, also tiny introns are flanked by nucleosomes. In the absence of any reports of alternative splicing in *Paramecium*, we conclude that they are necessary for efficient splicing rather than the control of alternative splicing. We hypothesize that the linker DNA between nucleosomes therefore determines the minimal intron length in this organism.

Diversity and co-occurrences patterns in Amazonian protists

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Amazonia is composed of different habitats types that can be divided into non-flooded rainforests forests (terra-firme), forests that are seasonally flooded by fertile white waters (várzeas), by unfertile black water (igapós), and open areas associated with white sand soil (campinas). Here we use metabarcoding data to investigate the richness and community composition of protists inhabiting litter and soil in a longitudinal transect across Brazilian Amazonia in the four habitats type. Beyond the alpha (richness) and beta (composition) diversities, we explored the patterns of co-occurrence and co-exclusion between protists and others microbial taxa. Campinas were the richest habitat (mean = 429) followed by várzeas (419), terra-firme (386) and igapós (385). The habitat type was the factor that more explained the OTUs composition ($R2 = 0.18$, $p < 0.001$) and due to this we investigated co-occurrence patterns by habitat type. All habitats networks were dominated by highly-connected bacteria, while the protists had very little co-occurrence in all habitats and usually co-occured with fungi and metazoans. The terra-firme and igapós had a more centralized network with some very sparse co-occurrence not connected, whereas campinas had two main groups of highly connected OTUs, that are also connected between themselves, with also some very sparse co-occurrence not connected. The co-exclusion is relatively strong in várzea, compared with its co-occurrence, and smaller for campinas. The protists are proportionally abundant in the co-exclusion network. These patterns can be explained by the competition between protists and bacteria with similar ecology.

Description of *Hyalosphenia paynei*, a local endemic from Wales

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Hyalosphenia papilio (Arcellinida, Hyalospheniidae) is a morphospecies of testate amoeba restricted to *Sphagnum* peatlands of the Northern Hemisphere. Due to its conspicuous morphology, abundance and Holarctic distribution, it has been actively studied for ecological and phylogeographical studies. Barcoding of its mitochondrial COI gene sequence revealed that *H. papilio* is constituted of at least 13 lineages that could each represent a distinct species despite the absence of consistent morphological differences among these lineages. Until now, the *H. papilio* complex formed a monophyletic complex, and no other species had been placed into this clade. Here based on morphology and DNA barcoding we describe *Hyalosphenia paynei*, a new species that is genetically almost identical to one lineage of *H. papilio* but morphologically distinct. Furthermore, in contrary of the pan-Holarctic lineage to which it was associated, *H. paynei* has currently only been found in the Cors Fochno peatland in Wales and may therefore be a local endemic. We further discuss the event that could have led to its apparition and what it implies for the current species concept in testate amoebae.

Morphological investigation of the Trivalvulariida ord. nov. (Cercozoa, Rhizaria) and what we can infer from it about shell evolution in Cercozoa

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We rediscovered the testate amoeba *Leptogromia operculata* (Valkanov 1970) and describe a closely related novel species *Trivalvularis immunda* sp. nov. Based on SSU rDNA phylogenetic analyses we establish a novel order, the Trivalvulariida (Imbricatea, Cercozoa, Rhizaria), which forms a sister group to the Euglyphida. Although both species differ in the structure of their test, they share a unique oral apparatus with three valves that are used by the amoeba to close the aperture of the test. During morphological analysis of the Trivalvulariida we noticed a pattern of shell colour in Cercozoa that can be used to distinguish Thecofilosea and Imbricatea on morphological basis, even light microscopically. We argue that shells in Thecofilosea and Imbricatea independently evolved and consist of different organic cement. This hypothesis provides valuable information for taxonomists, evolutionary biologists and ecologists that aim to determine the rough evolutionary position of an observed protist with an extracellular structure.

Functional traits of two important protistan lineages, Cercozoa and Endomyxa, reveal contrasting distribution patterns of plant parasites and phagotrophs in soil of temperate grassland and forest

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Functional traits are increasingly used in ecology to link the structure of microbial communities to ecosystem processes. We investigated two important soil protistan lineages, Cercozoa and Endomyxa (Rhizaria) using Illumina sequencing and analyzed their diversity and functional traits along with their interactions with response to environmental factors in temperate grassland and forest soils ecosystems across Germany. From 600 soil samples, we obtained 2,101 Operational Taxonomy Units (OTUs) representing ~18 million Illumina reads (region V4, 18S rRNA gene). All major cercozoan and endomyxan taxonomic and functional groups were present, dominated by small bacterivorous flagellates (Glissomonadida). We found that endomyxan plant parasites were absent from forests and depleted in low-intensity extensively managed grasslands, e.g. being less abundant dominant in pastures than in meadows. Bacterivores and eukaryvores (i.e. fungivores, algivores, etc.) showed opposite distribution patterns and were differentially contrastingly influenced by ecological and edaphic factors, suggesting that food availability resources are a major limiting factor driving factor of community assembly. Communities of grassland and forest sites were strikingly different. The most influential soil edaphic and ecological factors were soil type, land usage and pH in grasslands, and proportion of clay and main the dominant tree species in forests. These patterns potentially allow new insights into onto the functional organization of the soil ecosystem and provide hints for a more sustainable land-use management.

Paramecium bursaria and its photobionts - shedding light on the photobionts' influence on host behaviour

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Symbiotic systems occur all over the tree of life and encompass a huge diversity of organisms. We use the ciliate *Paramecium bursaria* and its endosymbiotic *Chlorella*-like algae as model to address questions regarding molecular, ecological and evolutionary consequences of this mutualistic symbiosis.
Among other advantages, the ciliate profits from this interaction by gaining access to photosynthesis products and the algae benefit by increasing their motility. Symbiotic paramecia (‚green' paramecia) accumulate in the light. Previous studies exploring the photoaccumulative behaviour of green paramecia reveal contradicting results. While some report that aposymbiotic *P. bursaria* (‚white' paramecia) loose this ability indicating a crucial role of the photobionts, others still observe photoaccumulation even after their elimination.
We combined quantitative photoaccumulation assays including green and white paramecia with molecular phylogeny of several *P. bursaria* strains and their algae to shed light on the photobionts' impact on host behavior. This allows us to answer the questions to which extend symbiont abundance or genotypic variation can explain the observed differences in the symbiosis' phenotypes in our system.
We detect statistically significant accumulation of green paramecia in illuminated areas regardless of the photobiont species. Such clear pattern is missing for aposymbiotic paramecia.
White cells show a clearly reduced accumulation compared to their green counterparts, but they still have a significant preference for illuminated over shaded areas. After prolonged aposymbiotic cultivation this preference is lost and white cells show random behavior. Thus, our data extend previous results and reveal: the *Chlorella*-like photobionts influence *P. bursaria*'s photoaccumulative behavior potentially via mechanisms which are epigenetically inherited.

Competitive interactions between heterotrophic and mixotrophic ciliates depend on resource fluctuation regime and feeding traits

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Structure and stability of food webs depend on the feeding interactions between species of adjacent trophic levels that are determined by corresponding resource use, defence and offense traits of the organisms. Such functional traits and associated trade-offs play a key role for ecosystem functioning. In our project we evaluate the importance of consumer trait variation in a freshwater ciliate consumer - microalgal prey system, focusing specifically on the consumer trade-off between starvation resistance and maximum grazing rate. In the present study we investigated the role of mixotrophy (the ability of photosynthetic carbon fixation in addition to phagotrophy) as a mechanism of starvation resistance for trait and biomass dynamics under constant and fluctuating resource supply. We conducted a 48-day chemostat experiment and studied the interactions of two combinations of heterotrophic and mixotrophic ciliates under different regimes of resource (prey and light) supply. Resources were provided either continuously or in pulses, entailing periods of resource depletion. Prey and light regimes interactively affected the proportions of mixotrophs and heterotrophs; however, the effects strongly depended on species composition. While continuous prey supply promoted mixotrophs in one species combination in under both constant and fluctuating light regime, heterotrophs were promoted in the other combination. The contribution of mixotrophs increased with prey pulses in one species combination, but only under continuous light supply when photosynthetic carbon fixation, i.e. the relevant trait to enhance starvation resistance in mixotrophs, was ensured. Fluctuations of both resources tended to promote consumer coexistence. These experimental findings are supported by corresponding simulation results of a mathematical model that was designed to reflect the experimental conditions. In the second half of the experiment, however, when consumer densities increased and per capita algal prey supply decreased, the outcome of competition seemed to be more strongly determined by the ability of the consumers to utilize bacteria in addition to algal prey than by their nutritional mode (mixotrophy versus heterotrophy). This finding emphasizes that the relevance of different traits and trade-offs for food web dynamics and community composition may change over time, even though environmental forcing remains the same.

Morphologic and molecular phylogeny of *Pseudoblepharisma* Kahl, 1927, a loricate Spirostomidae (Ciliophora, Hetertrichea)

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We discovered a probably undescribed species of the heterotrichous genus *Pseudoblepharisma* Kahl, 1927 in the microaerobic mud of the Simmelried moorland near to the town of Constance, Germany. This linear species lives in a mucous lorica, has an average in vivo size of 300 x 32 µm, and is filled with sulphur bacteria and zoochlorellas of the *Chlorella* group. Further, it can contract when touched with a needle or chemically fixed for protargol impregnation or scanning electron microscopy. There are two to four micronuclei attached to an ellipsoid macronucleus, and a contractile vacuole with a long canal extending to the anterior third of the cell. The somatic ciliature is as in many other heterotrichs while the oral apparatus shows a unique structure, i.e., a short cytopharynx (?) in the last third (not at end!) of the adoral zone of membranelles which occupies the anterior quarter of the body.
At first glance, the Simmelried ciliate resembles *P. tenue* (Kahl, 1926) Kahl, 1927. However, it is considerably larger (~300 µm vs. 100-200 µm), contractile (vs. acontractile) and the contractile vacuole has a long collecting canal absent in Kahl's species. The molecular tree assigns our species to the genus *Spirostomum*. Basically, this matches the morphologic data except for the curious cytopharynx (?) in the last third of the adoral zone. This organelle is absent in three *Spirostomum* species re-investigated for this purpose. As this is a unique character, *Pseudoblepharisma* might be considered as a distinct genus.

Catch me if you can – fast, faster, *Urotricha*!

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Species of the genus *Urotricha* (Ciliophora: Prostomatea) are known to be key planktonic ciliates. Especially during the phytoplankton spring bloom in various freshwater systems, they consume a large part of the algal biomass. In lake plankton, around 20 different species of urotrichs occur throughout an annual cycle and some of them turned out to be key species in co-occurrence networks. Astonishingly, these ciliates are often insufficiently identified and assigned to ‚*Urotricha* sp.' and grouped in two size classes in ecological studies. Initially, we studied the ciliates' annual distribution in Lake Mondsee (Austria) and Lake Zurich (Switzerland) and reached the conclusion that a detailed study was essential to elucidate their ecological role among other organisms in aquatic microbial food webs. So far, several issues occurred specifically for the small species <20 µm because (i) no accurate identification key for these species having 1-2 caudal cilia is available, (ii) a precise morphological characterization from living as well as from preserved urotrichs is challenging, (iii) reliable genetic sequences are absent from public molecular databases, (iv) several species are yet undescribed, and, (v) only very few species-specific autecological data exist. Our integrative approach included morphology (*in vivo* observation, protargol impregnation, scanning electron microscopy) and molecular analyses (SSU rRNA, ITS-1, and ITS-2). From this combination, we are confident to cumulate valuable autecological datasets for, especially small *Urotricha* species.

Diversity and distribution of marine planktonic ciliates from coastal waters of the South China Sea and Europe

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The diversity and global distribution patterns of marine planktonic ciliates are still largely unexplored. This hampers inferences of evolutionary history due to missing lineages and of ecosystem functioning because of missing key players in the microbial loop. Most marine planktonic ciliates belong to the Oligotrichea and about two-hundred aloricate species and one-thousand tintinnid species characterized by their loricae are known to date. Diversity estimates from molecular studies suggest the presence of numerous undescribed species and even higher taxa. The frequency of new species descriptions and studies based on morphospecies counts suggest that a considerable portion of oligotrich ciliate species occur exclusively in the China Seas. However, the much higher productivity of Chinese protistologists in ciliate species descriptions compared to European protistologists may bias the assumption of a putative ciliate diversity hotspot in the China Seas.
To shed light on this subject, we collected 80 samples from Chinese and European coastal surface waters throughout the course of one year and obtained Illumina sequence reads of the SSU-rDNA-V4 region from the extracted environmental DNA. Initial statistical and sequence similarity network analyses of the resulting Amplicon Sequence Variants (ASVs) showed that most ciliates from both regions distinctly differed on the community and sequence level. A high number of ASVs occurred exclusively in either European or in Chinese coastal waters supporting indeed the existence of distinct biogeographical patterns for oligotrich ciliates. The network approach effectively generated distinct sequence clusters mostly matching taxonomic groupings and therefore facilitates a detailed diversity assessment. In conclusion, the findings indicate that careful taxonomic work is needed when identifying, re-/describing, and comparing species from both regions based mainly on historic European literature.

Two co-occuring varieties of *Pseudoblepharisma* KAHL (Heterotrichea, Ciliophora) represent distinct tripartite symbioses with eubacteria and green algae

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Intracellular symbionts are not uncommon in free-living protists and especially well-studied in ciliates (Ciliophora). Endosymbionts of ciliates comprise green algae of different phylogenetic lineages (so-called “zoochlorellae”) as well as various eubacteria (e.g. Rickettsiales, Holosporales). Except few well-studied symbiotic systems, the roles and the physiological contributions of the partners are still unclear in most cases, and many symbiotic systems have yet to be characterized. We studied two ciliate taxa, both of which contain endosymbiotic green algae plus bacterial symbionts, thereby forming tripartite symbioses. Both ciliates belong to the heterotrich genus *Pseudoblepharisma* KAHL and were found to coexist in the same habitat, the *Sphagnum* ponds of Simmelried (near Lake Constance). *Pseudoblepharisma tenue* shows a remarkable pink color due to numerous purple bacteria (“rhodobacteria”) and contains few green algal cells as well. The other, morphologically similar taxon, *P. tenue* var. *chlorelligera*, is instead densely packed with algal endosymbionts (thus bright green) and - in addition - contains some colorless, less prominent bacteria. So far, it was unclear whether these two varieties of *Pseudoblepharisma* are indeed distinct biological entities or two ecologically adapted states of the same organism (same host with shifted symbiont ratios). We characterized the two symbiotic systems by light and electron microscopy, single cell PCR targeting marker genes for all partners (ciliate host, green algae, bacteria), and confirmed the identity of the bacterial endosymbionts by fluorescence-*in-situ*-hybridization (FISH). Surprisingly, the two varieties of *Pseudoblepharisma tenue* are genetically distinct and form two sister species in the *Spirostomum* clade (Heterotrichea, Ciliophora). The algal endosymbionts of these two ciliates seem to be identical (*Chlorella* sp.), but the ciliates harbor different bacterial symbionts. The pink *P. tenue* contains a phototrophic bacterium close to the purple sulphur bacterium *Thiodictyon syntrophicum* (Chromatiaceae, Gammaproteobacteria), whereas the green *P. tenue* var. *chlorelligera* is inhabited by a relative of “*Candidatus* Accumulibacter phosphatis”, a colourless, phosphate-accumulating gammaproteobacterium. We therefore expect that the two closely related ciliate species might have a very different physiology and occupy distinct ecological niches.

Extended phylogeny of *Percolomonas*-like flagellates from marine and hypersaline environments

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Percolomonads (Heterolobosea) are aquatic heterotrophic flagellates found in freshwaters up to hypersaline environments throughout the world. Several *P. cosmopolitus*-like strains are morphologically difficult to distinguish while they share only a low genetic identity. Up to now, percolomonads comprise six morphologically described species, but only two are associated with a deposited sequence in available databases, hence more information on *Percolomonas*-like flagellates are needed to resolve and understand their phylogeny, geographical distribution and ecological adaptation. In the present study, we were able to isolate and cultivate seven *Percolomonas*-like strains obtained from marine waters around the Azores and the Chilean coast as well as from a hypersaline inland lake in the Atacama Desert. Phylogenetic analyses revealed several separated clusters illustrating the genetic variability within this morphological complex. One clade solely comprised strains originating from hypersaline waters, whereas other clades exclusively consisted of representatives from marine environments indicating a separation by ecological parameters. To gain more insights into the geographical distribution of percolomonads, we combined our cultivation-based approach with data from environmental sequencing studies. We scanned the metabarcodes of the Tara Ocean surface water dataset, as well as deep-sea data covering 20 stations in bathyal to hadal depths for the V9-sequences of our seven *Percolomonas*-like strains.

A parasite's paradise: Biotrophic species prevail oomycete community composition in tree canopies

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Oomycetes are fungus-like eukaryotic microorganisms, which occupy both saprotrophic and pathogenic lifestyles. The attention of research has been drawn by their severe impact on natural and managed ecosystems. Forest canopies form a huge and heterogeneous ecosystem, providing diverse habitats for microorganisms. Our recent study revealed that oomycete abundances differ significantly across the ecological compartments – from forest soils to canopy microhabitats – and that oomycetes found in soil and leaf litter are not a subset of the communities from the canopy. However, the increase in habitat heterogeneity did not increase oomycete species richness in tree canopies, as the majority of OTUs were present in all sampled microhabitats. Consequently, we wanted to determine the factors driving this compositional heterogeneity of oomycetes in this study. We hypothesized that the homogeneity observed at the incidence level does not imply functional homogenization in ecological compartments. Functional annotation of OTUs revealed that canopy microhabitats are dominated by obligate biotrophic species, while the majority of oomycetes in soils and leaf litter occupy a hemibiotrophic lifestyle. Some detected biotrophs are considered to show a narrow host specificity, though for hosts that were not sampled in this study. Thus, we tested air samples as a possible vector for the distribution of these parasitic species, which revealed an extraordinarily high amount of obligate biotrophs in the air surrounding both strata – ground and canopy. This leads to the conclusion that tree canopies harbor a high proportion of parasitic oomycetes, which reach the crown via air and might not be as host specific as hitherto described.

‚Meet the ciliates' in the planktonic food web of Lake Mondsee

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Despite their role as hubs for carbon and energy transfer across trophic levels, ciliates received little or no consideration in many aquatic food web studies. Therefore, we investigated their seasonal and spatial distribution including biotic (e.g., phyto-, zooplankton, bacteria, heterotrophic flagellates) and abiotic parameters by monthly samplings of Lake Mondsee (sampling depth: 0 - 65 m) throughout one year (June 2016 – May 2017). Half of ciliates' total biovolume and abundance (mean abundance: 6,200 Ind. L-1; ca. 70 morphospecies) were mainly assigned to Spirotrichea (e.g., *Halteria* spp., *Rimostrombidium* spp., *Tintinnidium* spp.), followed by Oligohymenophorea (mainly *Histiobalantium bodamicum*) and Prostomatea such as *Balanion planctonicum* and *Urotricha* spp. Mainly algivorous and omnivorous feeding types (ca. 80% on average) were predominant. The seasonal occurrence of ciliates based on abundance and biovolume data showed that ciliates peaked strongly during summer followed by two smaller peaks in autumn and late spring/early summer. During summer months, mainly haptorid, choreotrich, oligotrich, prostomatid and stichotrich ciliates were abundant, while peritrichs and scuticociliates in the cold season. The seasonal dynamics of phytoplankton, heterotrophic nanoflagellates and bacteria were similar whereas zooplankton showed a divergent course. Our results show that only an in-depth view on species level could detect and explain the coherence of the food web players.

Phylogeny, cryptic diversity, and benefits of investigating marine lobose amoebae (Amoebozoa)

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Marine Amoebozoa are less well-known than the freshwater ones due to their generally smaller size, absence of several charismatic model taxa that have not (yet) been found in the sea, and difficulties of cultivation. Yet, most of the key Amoebozoan taxa comprise representatives that inhabit marine/brackish water or continental saline habitats. The number of the described species of marine amoebae is about 200 and counting. In this talk, we present an update on taxonomy and phylogeny of several naked lobose amoebae taxa from marine and continental saline habitats. Investigations of these organisms from remote and poorly accessible biotopes provide new data on their morphological and ultrastructural diversity demonstrating a number of novel, previously undetected lineages in marine plankton and deep benthos. While some of the species show ubiquitous distribution in the ocean, other taxa seem to be restricted in their distribution. In particular, we report the finding of a previously unknown marine lineage of amoebae that comprises at least two species seemingly restricted to the deep-sea biotopes. This lineage appears to comprise deeply-branching amoebozoans that superficially resemble Variosea, but have only SSU rRNA gene sequences of uncultured amoebozoans among close relatives. A number of novel phylogenetic lineages of amoebae may be isolated from the habitats where one does not really expect to find a lot of amoebae diversity. We will illustrate this by the first results of the investigation of marine amoebae associated with different floating substrates in plankton of the Bay of Villefranche. Here, several new species of Vannellida, Dactylopodida and Himatismenida have been found, as well as new amoebae that clarify morphological diversity of several discosean lineages poorly represented in the phylogenetic tree. Besides morphological and molecular studies, ecological investigations to determine the salinity tolerance ranges in different strains of naked lobose amoebae, may demonstrate a significant cryptic diversity even among morphologically identical strains. We revealed examples of euryhaline and stenohaline species that may prompt for the potential of their distribution in biosphere.

Network analyses enhance sequence grouping algorithms

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Grouping sequences of eDNA based metabarcoding studies remains a challenge for the estimation of microbial diversity. There are currently two main approaches either based on local or global clustering of sequences into OTUs using nucleotide similarities (e.g. Swarm) or based on error correction models (e.g. DADA2) to create amplicon sequence variants (ASV). In the first step of this study, we compared the performance of these two widely used algorithms to assess the diversity in sequence libraries of 29 individual ciliate species isolates. Neither of the algorithms was capable of correctly reflecting the known species richness in the samples. In a second step, we therefore introduced sequence similarity networks (SSN) to group representative sequences of OTUs or ASVs into network sequence clusters (NSC). The first level sequence grouping algorithms produced up to 19 OTUs or up to 11 ASVs in a single species library. This represented an overestimation of the total species richness over all libraries by a factor of 7.9 or 3.5, respectively, though Swarm overestimation could be reduced to a factor of 4.5 using an appropriate abundance filter. At 94% sequence similarity, the SSN approach reduced the original overestimated results of Swarm by 89.96% and the original overestimated results of DADA2 by 74.26%. Using Rand index cluster analyses, the optimal binning threshold for NSCs was predicted to be in the range from 94 to 97 % sequence similarity. At these thresholds, the total number of NSCs almost matched the original species richness over all libraries, with best matches at 94 % similarity for OTUs and 95% similarity for ASVs. The results strongly advocate to enhance the classical first level sequence grouping by the sequence similarity network approach for producing more robust estimates of alpha diversity in protist environmental studies.

Species diversity of planktonic ciliates: Does connectivity make a difference?

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We studied species diversity of planktonic ciliates in five lakes of the Salzkammergut area in central Austria on two occasions during spring and summer, 2019. The Lakes Irrsee, Mondsee, Attersee, and Fuschlsee are all connected by rivers; Wolfgangsee is disconnected. We hypothesized that the tighter a lake is connected to surrounding lakes, the higher are its ciliate species richness and diversity. Life analyses by an imaging flow cytometer (FlowCAM) showed that in terms of species richness, Irrsee is highest, followed by Mondsee, Wolfgangsee, Attersee and Fuschlsee. Surprisingly, the four connected lakes did not have higher species diversity than the disconnected Wolfgangsee, and statistical tests indicated that there are slight differences of species diversity among the five lakes. Contrasting species diversity, ciliate abundance followed the expected trend, i.e. it was highest in Irrsee and lowest in Wolfgangsee. Chlorophyll a level and zooplankton biomass (mainly rotifers) were both highest in Irrsee and lowest in Attersee, reflecting the trophic status of the lakes. Our preliminary results suggest that connectivity plays only a minor a role for species diversity; the latter is more likely related to the trophic status. However, the taxonomic resolution of the FlowCAM method is limited. Therefore, we will perform a more detailed analysis using an improved quantitative protargol stain (QPS) technique to verify the preliminary results.

Local and regional factors determine the dominance of the harmful dinoflagellate *Alexandrium catenella* along a nutrient gradient: A meta-ecosystem study

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Harmful algal blooms (HABs) are globally increasing in number and spatial extent. However, their propagation dynamics along environmental gradients and the associated interplay of abiotic factors and biotic interactions are still poorly understood. In this study, a nutrient gradient was established in a linear meta-ecosystem setup of five interconnected flasks containing a phytoplankton community. The harmful dinoflagellate *Alexandrium catenella* was introduced into different positions along the nutrient gradient to investigate dispersal and spatial community dynamics. Overall, total algal biovolume increased, while community evenness decreased with increasing nutrient concentrations along the gradient. *A. catenella* was able to disperse through all flasks. On the regional scale, diatoms dominated the community, whereas on the local scale the dinoflagellate showed higher contributions at low nutrient concentrations and even dominated the community at the lowest nutrient concentration, but only when initiated into this flask. A control treatment without dispersal revealed an even stronger dominance of *A. catenella* at the lowest nutrient concentration, indicating that dispersal and the associated nutrient exchange may weaken dinoflagellate dominance under low nutrient conditions. This study presents a first approach to experimentally investigate spatial dynamics and ecological interactions of a harmful dinoflagellate along an environmental gradient in a meta-ecosystem set-up, which has the potential to substantially enhance our understanding of the relevance of dispersal for HAB formation and propagation in combination with local environmental factors.

Linking micro-eukaryotic communities to carbon export in peatlands using (statistically) true co-occurrence networks topological properties

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Peatlands are ecosystems whose formation and functioning are driven by high water level. The near soil surface water table induces anoxia leading to low rates of organic matter decomposition. Consequently, peatlands act as carbon sinks, as dead organic material accumulates, forming peat. The underlying mechanisms controlling this carbon sink function rely on the composition and dynamics of surface microbial food webs, including protists, which are strongly impacted by the water table depth. Peatlands hold ca. ⅓ of the world soil C pool; as ecosystems, they are directly threatened by ongoing climate change. Indeed, warming and drought, by acting on peatland hydrology and thus on the microbiomes, threaten the C sink function, turning peatlands into C sources.
Using a mesocosm experiment reproducing peatlands under various water table depth, we sought to decipher the impact of the water regime on microeukaryotic communities and carbon dynamics. We used the v9 region of the 18S SSU rRNA gene to document microeukaryotic diversity and to unveil changes in microeukaryotic community composition. We measured then CO2 fluxes with a Licor IR gas analyzer. We linked microeukaryotic communities with carbon export using a novel method derived from related work on marine plankton. We characterized/documented the structure of the microeukaryotic community by computing statistically true co-occurrence and clustering the obtained network into subnetworks using hierarchical clustering on the Topological Overlap Matrix. It was then possible to identify subnetworks correlated (positively or negatively) to carbon export. Within each subnetwork, it was possible to identify key OTUs, based on the strength of subnetwork membership; this strategy allowed us to highlight the central role of certain organisms in carbon fluxes. Finally, we were able to compute the effect of water table depth on the structure of the subnetworks, thus allowing us to draw a picture linking carbon export, microbial communities, and water table depth.

Transformation of choanoflagellates, a reliable and efficient method

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The lack of tools for a reliable transformation of choanoflagellates has hindered genetic approaches like gene silencing, to understand the underlying molecular mechanisms within these organisms.
Cell penetrating peptides or CPPs are a high efficient carrier for plasmid DNA or siRNA, enabling us to transform choanoflagellates. In an approach to test the reliability and efficiency of this method, we silenced the silicon transporter gene (SIT) by introducing siRNA into the cell. Acanthoecid choanoflagellates, possessing a siliceous lorica, in particular stephanoecids or tectiforms, produce the siliceous costal strips prior to cell division, preparing a complete set for the next generation. We could show, that silencing these genes, we suppress the accumulation of silica within the cell without killing it. The offspring of these cells is lacking a lorica but fully viable. After the siRNA is degraded, these naked cells produce costal strips for the third generation, which is morphologically identical to the first generation while the second generation remains lorica less.

Dual-Seq reveals genome and transcriptome of *Caedibacter taeniospiralis*, an obligate endosymbiont of *Paramecium*

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Interest in host-symbiont interactions is continuously increasing, not only due to the recognized importance of microbiomes, but also due to the rising understanding on how the microbiomes can interact and influence its host. Started with the detection and description of novel symbionts, attention moves to the molecular consequences and innovations of symbioses. However, molecular analysis requires genomic data, which is difficult to obtain from obligate intracellular and uncultivatable bacteria. This leads to the need of appropriate approaches, that can be used to extract pure, uncontaminated DNA and RNA from those symbionts for the generation of genomic and transcriptomic data.
By using a combination of antibiotic-hypersensitive food bacteria and dual-Seq of DNA and RNA from infected paramecia, we were able to obtain the genome and transcriptome from *Caedibacter taeniospiralis*, an endo-symbiont that grants its host the ability to kill uninfected paramecia by an unknown toxin while being immune to this toxin and extending this immunity to its host.
Comparison of codon usage and expression level indicates that genes necessary for a specific trait of this symbiosis, i.e. the delivery of the unknown toxin, result from horizontal gene transfer, hinting to the relevance of DNA transfer for acquiring new characters. Prediction of secreted proteins of *Caedibacter* as major agents of contact and communication with the host reveal a rather uncharacterized secretome, which appears to be highly adapted to this symbiosis.
Our data provides new insight into the molecular establishment and evolution of this obligate symbiosis and lays the ground for further characterization of the mechanisms behind the toxicity and immunity of the granted “killer-trait”.

The structure and diversity of protist communities in the water column of the meromictic Kislo-Sladkoe Lake (Kandalaksha Bay, White Sea) studied with microscopy and DNA metabarcoding

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Meromictic lakes vertically stratified by temperature, salinity, oxygen concentration, pH, Eh are popular objects of microbiological researches. However, protist communities in such water bodies are poorly studied. The aim of this research was the characterization of structure and biodiversity of protist communities in the Kislo-Sladkoe Lake located on the shore of the Kandalaksha Bay of the White Sea with light microscopy and high-throughput sequencing of 18S rDNA amplicons.
Plankton samples were taken from the water column at different depths and filtered through membranes with diameter of pores 2.4-4.5 and 0.45 µm. Total genomic DNA was extracted from the samples by phenol–chloroform method. 18S DNA libraries were prepared according to Illumina workflow with universal primers targeting the V4 region of the SSU rRNA gene of Eukarya (TAReuk454FWD1 and TAReukRev3). The libraries were sequenced in MiSeq (Illumina) using 2 × 300 bp paired-end v3 reagent kit. Bioinformatic analysis was conducted using USEARCH v10.0.240.
The most numerous protists in the lake were represented by taxa from the supergroups Alveolata, Archaeplastida, Excavata, Hacrobia Stramenopiles, Rhizaria and Opisthokonta. Dominant species and genera were specific for different layers of the water column. The diversity and patterns of vertical distribution for different protist taxa were analyzed.

Sequencing versus morphotype-based monitoring of phytoplankton in Lake Zurich – facts and future challenges

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For many European lakes, environmental agencies collected impressive long-term datasets based on algal morphotype counts to document restoration measures in the past and to define the current ecological status. However, in many cases the continuation of these initiatives is endangered by two facts: (i) young experts with a profound taxonomic knowledge are increasingly missing, and (ii) due to the time intensive work, microscopic analyses are considered as too costly and not timely anymore. Sequencing based methods have been proposed as possible fast and cheap alternatives for phytoplankton analyses, however, real empirical tests of the comparability of datasets are still rare.

In cooperation with the Water Supply Zurich, we compared the annual succession of total eukaryotic phytoplankton determined via classical microscopic work with patterns based on high throughput sequencing of the V9 region (18S rDNA). This comparison highlighted fundamental differences in the outcome of the two methods. Sequencing based data did not mirror patterns of morphotype based qualitative and quantitative phytoplankton composition at all. As algae (phototrophic protists) are assigned to various phyla, it is questionable if the use of only one general primer pair for eukaryotes is indeed sufficient to resolve the complex *in situ* community composition. However, by applying several primer pairs, also sequencing approaches will get costlier and more work intensive. Additionally, sequence information is still missing for several well-known morphospecies. However, we could also demonstrate that sequencing can result in a higher taxonomic resolution of some 'problematic species' which cannot be determined by microscopy alone.

In sum, immediate changes from microscopic to sequencing techniques would create real breakpoints in long-term (decadal) datasets. Sequencing data will help to describe precisely algal biodiversity in future monitoring studies, however, applied science also asks for a quantification in terms of abundances and biovolumes. It is still a real challenge to combine these two aspects.

Phylogeny and morphology of a new, deviant flagellate lineage in termites of the family Serritermitidae

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Lower termites harbor host-specific consortia of symbiotic gut flagellates, which are generally more similar in related host termites. While a cospeciation is obvious, there is only few evidence for coevolution, and even horizontal transmissions between unrelated host taxa seem to have occurred. Further, numerous flagellate species are yet undescribed or even undetected. Here, we present a new flagellate genus from serritermitid termites that morphologically resembles the genus *Pseudotrichonympha* (Trichonymphida, Teranymphidae). Analysis of the SSU rRNA of the flagellates supports that is a member of the Trichonymphida but it is in a sister position to the family Teranymphidae. We name the new lineage *Retractinympha glossotermitis*. Its morphology and ultrastructure is compared to a yet undescribed bona fide member of the genus *Pseudotrichonympha* from *Termitogeton planus* (Rhinotermitidae). The new species *Pseudotrichonympha solitaria* is the only flagellate species in the gut of *T. planus*. The two parabasalids resemble each other morphologically in being large, slender, completely flagellated and lignocellulose-consuming cells. Such life forms seem to have been evolved twice in termites. Both flagellate genera have a bilaterally symmetric rostrum with an anterior, flagella-free operculum and an internal rostral tube. The most conspicuous morphological difference is the possession of two series of rostral flagella in *Pseudotrichonympha* (1. series short, 2. series long) while there is only one series of rostral flagella in *Retractinympha*. *Retractinympha* is able to retract its anterior end considerably into a newly formed deep invagination. The presence of deviant flagellate lineages in Serritermitidae can be explained by a combination of two hypotheses. 1. *Retractinympha* and the members of the Teranymphidae, including *Pseudotrichonympha*, may have evolved from a common ancestor within the Neoisoptera. 2. The second big parabasalid in Serritermitidae, *Heliconympha*, has been acquired by horizontal transmission from a stolotermitid ancestor.

A 3-step fluorescent staining technique to visualize ciliates

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Ciliates have a long history of scientific investigation, they occur in many classical microscopy studies and nowadays, play an essential role in ecological and diversity research. It is vital in all of these various analyses to correctly identify the species involved. The visualization of ciliates and their diagnostic features for species identification are usually performed by silver staining techniques. These techniques are widely used, although they are arduous, time-consuming, and not universally applicable for every taxon. We aim to develop an alternative fluorescence staining technique that will be universal, friendly-to-use, and efficient. Our new 3-step protocol consists of: i) deciliation, ii) taxoid probes to visualize the kinetosomes, and iii) DAPI to visualize the nuclei. We used *Paramecium tetraurelia* to optimize these steps. Here we present some of our initial results and discuss how these can be applied to other ciliates in ecological and diversity research.

Can surface water currents act as natural barriers? A survey on several protist groups shows different biogeographical distribution patterns

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The debate about microbial biogeography is an ongoing topic. Despite the fact, that this hypothesis cannot either be proven nor disproven, due to methodological reasons, several studies revealed potential biogeography within the microbial world. With rise of high throughput sequencing, differences in protist community compositions even in small spatial scales could be shown at a molecular level, indicating the high potential of different biogeographical patterns. However, these analyses lack taxonomical and autecological information allowing for an encompassing understanding of the role of protist species in certain habitats and possible dispersal mechanisms. Within our study, we focused on a cultivation-based approach and sampled heterotrophic protists from surface water of a transect across the South and North Atlantic Ocean (35 °S to 23 °N) addressing the question whether the equatorial counter currents could act as a natural barrier for protist dispersal. With a high isolation and cultivation effort, we were able to isolate, cultivate and sequence (SSU rDNA) over 50 protistan strains from several groups. The obtained data revealed on the one hand phylogeographical patterns within craspedid choanoflagellates, but also a very heterogeneous distribution with no clear biogeographical restrictions for other protist species, in particular for kinetoplastids. With this study, we aim to show that biogeographically patterns may be formed even by weak barriers like surface water currents not only for the large Rhizaria but also for nanoflagellates. It also highlights the necessity of an extended, cultivation-based taxonomic approach, allowing for a clearer species definition of protists, based not only on morphology and molecular biology but also autecology.

Evaluation of parasitic diversity using environmental DNA approach

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The diversity of terrestrial and to a lesser extent aquatic protists was tedious to study and thus underestimated until the recent development high throughput sequencing (HTS) of environmental DNA (eDNA). HTS of eDNA is now a common approach and allows documenting local to global patterns of biodiversity estimates more efficiently and understanding the interactions and functional roles of all microorganisms. This is especially welcome for parasitic protists which were hitherto little studied beyond those affecting humans and economically relevant crops and animals.
We conducted eDNA HTS surveys on peatland oomycetes and alpine Apicomplexa using the V9 region of the SSU rRNA gene sequenced by Illumina HiSeq.
We recovered 34 phylotypes from all major clades of Oomycetes in peatlands in the Jura mountains. Phylotypes were affiliated to both well-known species (i.e. the highly damaging invasive pathogens *Aphanomyces astaci* and *Saprolegnia parasitica*) and members of undescribed, basal clades. This shows that natural ecosystems such as peatlands may act as pathogen reservoirs.
The Apicomplexa diversity was assessed in litter and mosses samples from 11 contrasted habitats (meadows, fen and snowbed, glacier forefront) of the Furka pass in Switzerland. We observed an important phylogenetic diversity with known parasite of insect (*Gregarina*) and annelida (*Monocystis*). The number of phylotypes of Apicomplexa was significantly correlated to the number of phylotypes of their potential metazoan hosts, suggesting that even small soil samples can provide relevant information on soil invertebrate diversity.
These two studies illustrate the usefulness of HTS of eDNA to explore unknown biodiversity of parasite protists as well as to assess potential host-parasite interactions. Although the V9 region of the SSU rRNA gene is a short fragment and does not allow very high taxonomic resolution it is useful to document general diversity patterns and potential biotic interactions.

The diversity of bacterial endosymbionts in rhizarian amoebae implies a universal infection of rather unrelated free-living amoebae by Legionellales

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Endosymbiotic bacteria are increasingly shifting into focus of current research, still however, novel clades are described and their specific distribution is poorly understood. Endosymbiotic bacteria have been reported for various groups of protists, but especially Cercozoa are understudied in this regard. To fill this gap of knowledge, strains of Thecofilosea (Cercozoa, Rhizaria) have been isolated, cultivated and investigated for potential endosymbiotic bacteria. Presence of endosymbiotic bacteria has been verified by sequencing of the bacterial 16S rDNA and subsequent fluorescence *in situ* hybridization (FISH) with specific FISH probes. We revealed a surprising richness of endosymbionts belonging to the order Legionellales, including *Legionella* and two so far undescribed lineages, leading to the establishment of two new candidatus genera ("*Ca*. Fiscibacter", "*Ca*. Pokemonas"). Bacteria of the order Legionellales proliferate within eukaryotic cells and have been strikingly often isolated from amoebae. However, sampling has been taxonomically biased with most investigated hosts belonging to the Amorphea or Excavata; Legionellales in rhizarian hosts are to our knowledge new to science. Considering the widespread dispersal of Legionellales bacteria in somewhat unrelated amoebae we conclude that the morphotype and not evolutionary background of amoebae makes them suitable hosts for Legionellales.

Ciliates and skiers share the same man-made mountain reservoirs

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Climate warming has a direct impact not only on the environment but also on the economy of Tyrolian winter-sports tourism. Man-made mountain reservoirs are created in sensitive remote alpine regions, providing the basis for artificial snow production. These reservoirs are yet unexplored habitats on an organismic level. Here, we investigated the species composition and abundance of ciliated protists, which are considered as indicator organisms in aquatic ecosystems. Between July and September 2018, we sampled eleven such high-mountain reservoirs at two different occasions each for water chemistry, chlorophyll a, bacteria, zooplankton, and ciliates. The ciliates were identified morphologically and their abundance determined from quantitatively protargol stained samples. In total, we detected 20 different species including generalists (e.g., *Urotricha* spp.) that were present in almost all reservoirs as well as specialists that we found only in some samples. The assemblage structure differed among most reservoirs and abundances were lower during the autumn sampling. Compared to water bodies at lower elevation, ciliate abundances were generally low, but comparable to natural alpine lakes. Our results show that man-made mountain reservoirs located at high elevation are a challenging habitat for the colonization by ciliates as the artificial basin and fluctuating water levels due to anthropogenic usage influence the primary succession in such aquatic habitats.

Cool and shady - ecophysiological preferences of chrysophytes

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Chrysophytes are widespread and among the dominant flagellates in a wide range of habitats. This protist group includes heterotrophic, mixotrophic and phototrophic taxa which can co-exist in different habitats. Due to their diverse life-styles, they appear as primary producers as well as natural predators for bacteria-sized microorganisms and thus play an important role in the microbial food web. Main drivers for protist growth are temperature and light intensity which influence the physiology of algal cells in various ways. In a series of experiments, we compared the reaction of mixotrophic and phototrophic chrysophytes to different temperatures and light intensities. Our results showed a strain specific response to different temperatures in terms of maximum growth rate. In general, the mixotrophic strains showed highest growth rates at around 19°C. Whereas the phototrophic strains investigated herein reach a “plateau”, i.e. a broad temperature range between 12-23°C where growth rates do not change much. Our experiments showed further the preference of mixo- and phototrophic strains of low light intensities, with maximum growth rates at low light intensities (12-36µE). Some strains such as phototrophic strain *Mallomonas* sp. and mixotrophic strain *Dinobryon sociale* responded only slightly to changes in light intensity, whereas other strains (e.g. *Mallomonas annulata*) showed lower growth rates with increasing light intensity.

Insect-infecting nephridiophagids are affiliated to the Chytridiomycota

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Nephridiophagids are unicellular eukaryotes that have been shown to parasitize the Malpighian tubules of numerous insects. Their life cycle comprises multinucleate merogonial plasmodia that divide into oligonucleate and uninucleate cells, and sporogonial plasmodia that form uninucleate spores. Despite their identification as early-branching fungi about 15 years ago, their closer phylogenetic placement within the fungal tree of live remained enigmatic. Nephridiophagids are poor in morphological characteristics and so far, sequence data is limited to the SSU rRNA gene sequences of only three species. In this study, we increased the phylogenetic signal by long read sequencing of the rDNA operon of ten nephridiophagid species isolated from cockroaches and earwigs. Our analyses of this dataset show an unambiguous affiliation of nephridiophagids to the Chytridiomycota — a group of zoosporic fungi comprising parasites of diverse host taxa (e.g., microphytes, plants, amphibians), among them species causing global amphibian declines.

Prey range specificity and feeding modes in leptophryid amoebae (Vampyrellida, Rhizaria) from freshwater and soil ecosystems

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Vampyrellid amoebae (order Vampyrellida, Rhizaria) are genetically diverse, naked, filose amoebae that occur in marine and freshwater systems, including soil. Although some taxa, especially species of the genus *Vampyrella*, have been known for about 160 years, our knowledge about the phenotypic diversity of the order Vampyrellida with its several family-level clades is still fragmentary. The Leptophryidae HESS et al., 2012 represent one of the better-known vampyrellid families comprising branched and mostly surface-bound amoebae, which have been reported to feed on a range of other eukaryotes. The autecology of the individual species, however, needs still to be explored. Here, we established bacteria-free cultures of two leptophryids, *Theratromyxa weberi* and *Platyreta germanica*, isolated from soil samples. Both species have been studied and described in former times, but – so far – have not been subjected to a more detailed analysis of their feeding habits. While *Theratromyxa* is known to engulf and digest nematodes, *Platyreta* was mainly described as a mycophagous species, able to perforate fungal conidiospores. We conducted a comprehensive feeding experiment involving algae from three major groups (Zygnematophyceae, Euglenophyceae and Volvocales), several fungi and nematodes. The comparison of *Theratromyxa* and *Platyreta* with *Leptophrys vorax*, an omnivorous vampyrellid frequently found in freshwater systems, revealed that all three leptophryids show a broad, yet different prey range. Furthermore, we studied details of food uptake and digestion with time-lapse microscopy and cytochemical staining techniques, and report so-far overlooked details of the leptophryid feeding modes.

Not all that looks like a Tubulinean is a Tubulinean: expectations and reality for the parasitic amoeba *Janickina pigmentifera* (Grassi, 1881)

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A parasitic amoeba living in the testes that occupy the caudal part of chaetognaths was firstly reported by Grassi in 1881. Later, two species *Janickina pigmentifera* and *Janickina chaetognathi* were re-isolated four times from different places in the Mediterranean Sea: from the strait of Messine, Naples, near Algeria, and near Villefranche-sur-mer. *Janickina* has a monopodial, or limax locomotive form similar to *Hartmannella*, *Saccamoeba* or *Glaesseria* (Amoebozoa, Tubulinea). Also, it was reported the presence of an "ocellus" in the cell similar to intracellular symbiont *Perkinsela*-like organism (PLO) of *Paramoeba eilhardi* (Paramoebidae). Only in 1980, Hollande presented the ultrastructural data of *J. pigmentifera* showing the kinetoplastid nature of the "ocellus" later also confirmed in *Paramoeba*. He also showed that the cell coat of *Janickina* was a stratified glycocalyx. It was not similar to the microscales of *Paramoeba* or glycocalyx of *Neoparamoeba*, but usual for *Thecamoeba* instead. These morphological characters were too contradictory, so the genus *Janickina* was placed *incertae sedis*. The studies of these amoebae were always illustrated with drawings and not light microscopic micrographs. Molecular phylogenetic data are not yet available for *Janickina*. Therefore, the genus remains *incertae sedis* today. We re-isolated *Janickina pigmentifera* from planktonic chaetognaths of the Bay of Villefranche. The first microphotographs of locomotive forms for *J. pigmentifera* were obtained. These amoebae showed a monopodial locomotive form typical for Tubulinea. For the first time, we obtained the 18S rRNA gene sequences of *Janickina pigmentifera* and its PLO. Contrary to our expectations based on morphology, the preliminary molecular phylogenetic analysis based on 18S rRNA gene showed that in spite of its morphological characters, *Janickina pigmentifera* grouped within the clade of *Neoparamoeba* as a sister to *Neoparamoeba branchiphila*. A similar result was obtained for molecular phylogenetic analysis of 18S rRNA gene of PLO from *J. pigmentifera*. It grouped as a separate long branch – sister to the PLO of *Neoparamoeba branchiphila*. This result undermines the morphological concept of the Tubulinea.

Temperate versus tropical forest canopies – a comparison of cercozoan diversity across biomes using Illumina high throughput sequencing

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Forest canopies form the largest interface between earth and atmosphere, and provide a huge surface area and various heterogeneous habitats for colonizing organisms. One of the most general patterns in community ecology is the increase in species richness with increasing habitat heterogeneity. Thus, environmental heterogeneity of tree canopies is among the most important factors governing community structure and diversity in high animal and plant richness in forest ecosystems. Tropical rainforests are the undisputed champions of biodiversity among the world's ecosystems, containing far higher numbers of species on a per-area basis relative to sub-tropical, temperate, and boreal ecosystems. The habitat complexity of tropical rainforests is known to have an impact on the vast diversity of multicellular organisms. Nevertheless, it is unknown if similar diversity patterns are reflected at the microbial scale with protists. In this study we sampled autochthonous tree species from a temperate forest in Germany and a tropical rainforest in the northeast of Papua New Guinea. We applied high-throughput sequencing using newly designed specific primers for a complete and comparative assessment of the diversity of Cercozoa (Rhizaria) across ecological compartments, from forest soils (litter layer & mineral soil) to the canopy region (leaves, deadwood, epiphytes, bark, arboreal soil). Our results show highly specific protist cercozoan communities within investigated microhabitat compartments in the temperate forest, suggesting that habitat richness is a main driver of compositional heterogeneity of protist communities on trees. We hypothesize that tree canopies in the tropical zone would show higher protistan diversity, while the rapid mineralization of litter layers on the soil surface reduces habitat complexity, compared to temperate forests. We show first results to which degree diversity of habitat heterogeneity in tree canopies influences diversity and community compositions of Cercozoa across biomes.

Prevalence and diversity of the intestinal parasite *Giardia* spp. in urban waters in Vienna, Austria

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Giardia spp. can infect a wide range of animals including humans, causing a watery diarrhea. Currently, the genus is divided into eight genetic assemblages (A-H) and numerous sub-assemblages, partly with different host specificities. In Austria, giardiosis is not a reportable disease and epidemiological data is largely missing. In a previous study, we performed a first assessment of *Giardia* genotypes involved in clinically manifest cases diagnosed in Austria and found a high level of genetic diversity, which is in accordance with the general assumption that most cases are imported, namely from various regions of the world. However, there have also been cases without travel history and there has been a rise of chronic infections, the sources of infection remaining unresolved.
Urban water bodies are important for recreational use and thus faecal contamination of such water bodies with pathogens poses a risk for public health. Potential sources of faecal pollution are wastewater discharges, combined sewer overflows, deposits of domestic animals and wildlife and also bathers. The aim of the current study was to evaluate the prevalence and diversity of *Giardia* spp. in urban water bodies in Vienna.
A monthly monitoring was performed over the period of 18 months, screening various urban water bodies for *Giardia* spp. and including also bacterial standard fecal indicators (SFIs) and microbial source tracking markers. SFIs were 2-3 logs higher in influent wastewater samples in comparison to effluent wastewater samples and approximately 5 logs higher than in surface water samples. The concentrations of *Giardia* varied from up to 1846 cysts/100mL in influent wastewater samples, to 0-4 cysts/100mL in effluent and 0-2 cysts/100mL in surface water samples. Interestingly, significant increases in *Giardia* concentrations were observed after heavy rainfall events. Genotyping revealed mainly sub-assemblages AII and AI, rarely **BII** and BIII, and only sporadically other genotypes. Microbial source tracking revealed humans, ruminants and pigs as major faecal sources, while birds and dogs only played minor roles.

Container volume has little effect on growth and grazing rates of ciliates and microcrustaceans in microcosm experiments

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Scaling has been largely ignored in the design of experimental aquatic ecosystems. To this end, we studied the volume effect in small containers (microcosms) ranging from 10-200 mL on five planktonic freshwater ciliate and three zooplankton species, namely *Daphnia*, a calanoid (*Eudiaptomus* sp.) and a cyclopoid (*Cyclops* sp.) copepod. The ciliate species used in the experiments were the free-swimming peritrich *Vorticella natans*, the scuticociliate *Histiobalantium bodamicum*, the prostomatid *Urotricha agilis*, and the choreotrich ciliates *Rimostrombidium caudatum* and *R. lacustris*. We measured ciliate specific growth rates and their loss rates due to microcrustacean predation in short-term experiments (1 d). We hypothesized that neither volume nor surface-to-volume ratio of the containers would affect the activity of our prey and predator species. Overall, we found no significant effect of container volume and surface-to-volume ratio on ciliate growth and grazing loss rates, supporting our hypothesis. However, individual ciliate species appeared sensitive to container size. Our results are similar to comparable research with the same or other planktonic predator and prey species. We conclude that the small microcosms that we used yielded valid estimates of *in situ* growth and grazing loss rates of the ciliates. Therefore, our results may be used to grossly calculate top-down control of ciliates by microcrustaceans in other lakes.

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Annual course of retention effects through protistan dominated biofilms regarding planktonic bacteria in the River Rhine

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Biofilm communities, also known as „Aufwuchs“ or periphyton, were often investigated regarding the community structure, ignoring the importance of the biofilm for the surrounding environment. Biofilms can be found on different surfaces such as stones, macrophytes, animals, and different artificial substrates and should be considered as important constituents of river ecosystems. The biofilm community of the River Rhine consists of a variety of organisms from bacteria to macro-invertebrates with a high network of trophic interactions. Heterotrophic flagellates, ciliates and algae were the most important components in terms of biovolume. The biofilms in moist and aquatic environments such as the Rhine play a major role for the entire ecosystem. In a very small area a variety of protozoan, micro- and macrozoan benthos can be found. They can influence and form food sources for each other. In this study the focus on the seasonal changes is mainly on the protozoa and other microzoan benthos and their effects on the reduction of bacteria (incl. potential and pathogens in the surrounding water body. The results of this study show that there is a fluctuating but always detectable retention effect on bacteria throughout the year. The ciliates of the biofilm feed on the passing flagellates and bacteria and the heterotrophic flagellates predominantly feed on of the biofilm consume bacteria. On annual average, the experimental natural biofilm exposed to the River Rhine eliminated about 46.8 per cent of the bacteria passing the biofilm. Since sewage treatment plants along the Rhine introduce mechanically and biologically purified water which also contains a certain number of pathogenic bacteria, but they also introduce bacterially contaminated water and also agriculture contributes to the discharge of contaminated water into the Rhine. As a result of the straightening of the Rhine for inland navigation and the restriction of habitats, the Rhine is no longer able to carry out adequate self-purification and deal with the contaminated water. The promotion and support of biofilms in rivers can have a very positive effect on the water quality of our rivers. Experiments are running at the moment to quantify the retention effect and to evaluate the potential of the surface of the river bed to increase the self-purification potential. Therefore, the renaturation of rivers and the provision of surfaces must be promoted to withstand the pollution. Furthermore, the use of biofilms in sewage treatment plants is a possibility that should be considered.

Posters

P1 **Andean uncovered biosphere: revealing the vertical milliscale bacterial and eukaryotic community structure within a freshwater microbial mat from Salar de Huasco**

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High altitude wetlands in the Altiplano are unique remote aquatic ecosystems considered as part of the cold biosphere. Microbial mats, vertically stratified tridimensional structures, shaped by geochemical gradients and considered as complex microbial ecosystems are present in Altiplano basins. Here we investigated the upper seven mm of what appeared to be a microbial mat formed in the freshwater site of Salar de Huasco, a high-altitude wetland from the Chilean Altiplano. The presence of the microbial mat was determined by the dissolved oxygen microprofile measured throughout each colored layer as a typical microbial mat steep oxygen stratification. Oxygen levels ranked from 166 µM at 0 millimeters to 448 µM dissolved oxygen at 2-3 millimeter depth during midday in the studied structure. Furthermore, we used 454 pyrosequencing of the 16S and 18S rRNA genes and sequences were clustered into Operational Taxonomic Units (OTU) and classified using a 97% similarity to the SILVA 128 database. A total 30.524 bacterial sequences, covering 24 phyla including 15 candidate divisions were detected and analyzed using an OTU co-occurrence network. Classes α and β from Proteobacteria and Cyanobacteria phylum appeared to dominate the bacterial communities. The eukaryotic community detected as 10.217 sequences was mainly associated to phototrophs as chlorophytes and diatoms and in minor proportions to ciliates and fungi. Micro eukaryotes were distributed in total taxa, representing four eukaryotic Super-Groups (Archaeplastida, SAR, Opisthokonta and Amoebozoa). We highlight the presence of these communities as potential part of the energy transfer to higher trophic levels thriving in this wetland.

P2 **Studies on the specific association of gregarines to tenebrionid beetles from the Atacama Desert**

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The apicomplexan gregarines are typical endobionts inhabiting the intestines, coeloms and reproductive vesicles of aquatic as well as terrestrial invertebrates. They form a highly diversified and early branching group of protists which remain, although common and widely distributed, understudied regarding their morphology, phylogeny and effect on their hosts. As gregarines are believed to be host specific, gregarine-host relationships may form a suitable system for evolutionary studies, illuminating hitherto unknown or misunderstood phylogenetic relationships or geographical distributions. The endemic darkling beetles (Tenebrionidae) of the Atacama Desert especially adapted to hyperarid conditions. The coevolution of gregarines and their hosts was studied, especially in the context of intra-host specificity and possible coevolution within separated host populations. Molecular studies posed significant methodological difficulties which prevented conclusive studies on gregarine phylogeny and patterns of co-evolution. With this study, those methods were improved, enabling successful and replicable sequencing of gregarine rDNA, and providing, with nearly complete rDNA sequences, a more accurate marker gene. With those improvements, gregarines isolated from tenebrionid beetles of the Atacama Desert were analyzed. Faster lysation and more often successful amplification allowed sequencing of nearly complete rDNA of two gregarine species isolated from *Psectrascelis* and *Scotobius* beetles, with previously inconclusive data, and added 18S rDNA of one newly discovered gregarine species. Those species were implemented and put in taxonomic context to other gregarines of terrestrial hosts. Closely related gregarine species were found to inhabit closely related beetle species, as they were found to form a clade with other gregarines inhabiting tenebrionid beetles from South America, supporting the hypothesis on host specificity and close coevolution of gregarines and their hosts.

P3 *Salmonella* transcriptional profile during phagocytosis *by Acanthamoeba*

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Salmonella is a facultative intracellular pathogen capable to persist in natural environments often interacting there with protists. Despite a proverbial fact that bacteria are predated by protists, salmonella have developed numerous mechanisms for survival within the eukaryotic cells. Besides, salmonella are able to survive and replicate inside protozoan hosts, and moreover to enhance their virulence and resistance during the interaction with protists. Conditions inside the protozoan cell preadapt bacteria for conditions inside the human phagocytes. Therefore, understanding the mechanisms of interaction between *Salmonella* and protozoa is important for understanding evolution and epidemiology of the *Salmonella* infection. This report presents differential gene expression of *Salmonella typhimurium* inside phagosomes of *Acanthamoeba castellanii* using Cappble-Seq approach. Control salmonella in a medium without amoebae demonstrated significant differential expression of 594 genes compared to trial bacteria located inside the amoebae phagosomes. Within amoebae 309 genes of salmonella were upregulated, 285 genes were downregulated. The upregulated genes were involved in the metabolic pathways of ABC-transport, biosynthesis of amino acids, folate and secondary metabolism, lipopolysaccharide biosynthesis and bacterial secretion. The downregulated genes were involved in the carbon, pyruvate and propanoate metabolism, oxidative phosphorylation and TCA cycle.

Global gene expression of salmonella during phagocytosis by amoebae and macrophages have a lot of common features. Salmonella pathogenicity islands (SPI), iron uptake, lysozyme inhibitors genes are upregulated within both *A. castellanii* and mammalian macrophages. In addition, upregulation of SPI-1 accompanied by a lower activity of SPI-2 highly likes gene expression of salmonella within epithelial cells. At last, upregulation of salmonella flagellar genes during phagocytosis by the amoebae resembles salmonella gene expression inside epithelial cells unlike macrophages.

P4 **Comparative study of the symbiosis between R-body producing bacteria and *Paramecium***

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Endosymbiosis is a widespread phenomenon and hosts of bacterial endosymbionts can be found all over in the eukaryotic tree of life. Many ciliates, the most prominent example is likely *Paramecium*, are known to contain a diversity of bacteria endosymbionts. *Paramecium* is a free-living aerobic ciliate, which can be found in many fresh- and brackish water habitats. Here we focus on *Caedibacter* and *Caedimonas*, which are both obligate endosymbionts of *Paramecium*. A special feature of these bacteria living in symbiosis with *Paramecium* is the killer trait, which provides *Paramecium* with the ability to kill symbiont-free and thus sensitive paramecia. *Paramecia* bearing the symbionts have a resistance to the toxin of the killer trait, so the immunity is provided by the intracellular bacteria. The central structures of the killer trait are refractile bodies (R-bodies), a protein structure build of a long protein ribbon which is rolled up. During the process of killing, the R-body unrolls and releases a toxin. The effect of the killer trait and the R-body structures are very similar for both endosymbionts, nevertheless these bacteria are only distantly related as *Caedibacter* is a member of Gamma-proteobacteria whereas *Caedimonas* belongs the Alpha-proteobacteria. While the killer trait is considered as a competitive advantage for the host of R-body producers, our understanding of its target range and effectiveness against diverse symbiont-bearing paramecia is limited.
Thus, we are testing the effectiveness of the killer trait of *Caedibacter*- and *Caedimonas*-harboring paramecia against a variety of potential targets including aposymbiotic and infected paramecia belonging to different species. Additional to the killer trait different aspects of host biology, like growth parameters, can be influenced by the endosymbionts. For comparative fitness analyzes we established genetically identical cell lines through antibiotic treatment. To see the mentioned advantage and to compare the effect of the killer trait of the two different symbionts we performed killer test with different strains. Comparative fitness assays will be applied to assess the influence of *Caedibacter* and *Caedimonas*.

P5 **Impact of intracellular algae on the swimming behaviour of *Paramecium bursaria***

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Paramecium bursaria (`green *Paramecium*`) lives in a mutualistic symbiosis with unicellular microalgae. In this symbiotic unit, the host is provided with photosynthetic products (mainly maltose and oxygen) by its algal symbionts and hence features a mixotrophic mode of nutrition. Further, the symbiont confers protection to its host against damaging UV-radiation. In return, *P. bursaria* provides carbon dioxide as well as an increased motility to the endosymbiotic photobiont. Within their host, the algae are additionally protected against predators and the lytic *Chlorella* virus. Among *Paramecium* species, only two species are capable of harbouring algae inside the cytoplasm. Besides *P. bursaria*, this includes *P. chlorelligerum*, which occurrence is, however, quite rare. Green paramecia are mixotroph organisms and show a light-induced movement, whereby they accumulate in illuminated areas. This behavioural pattern is speculated to be an adaption to the photosynthetic lifestyle, to increase the yield of the algal photosynthesis. The mechanisms involved in this light-induced mobility, as well as the degree of regulation by the algae and the host cell, are still unclear.
Here we address the question if photoaccumulation is indeed a behavior occurring only in *P. bursaria* and if other *Paramecium* species, which are not able to harbor algal symbionts, also do show photoaccumulation. Therefore, we performed quantitative photoaccumulation assays including green *P. bursaria* and algal-free paramecia belonging to several other *Paramecium* species.

P6 **FISHing for ciliates – fluorescence *in situ* hybridization for the detection of planktonic freshwater ciliates**

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Major topics in aquatic ecology concern complex interactions and seasonal dynamics in aquatic food webs. Progress in molecular analytical tools, such as environmental high throughput sequencing techniques, opened new insight into ciliate assemblage structures and dynamics in aquatic ecosystems. However, for exact determination of abundances, the classical morphology-based method QPS (quantitative protargol staining) is still the most reliable way. QPS enables quite high taxonomical resolution in parallel with a reliable quantification of ciliates. Nonetheless, the whole procedure of QPS, as well as the subsequent evaluation of preparations at the microscope, are very time consuming and analyzed sample volumes are rather small. Therefore, new methodological approaches for further researches on seasonal dynamics and quantitative assemblage analysis of planktonic ciliates, would be highly beneficial.
Fluorescence *in situ* hybridization (FISH) appears to be an optimal method for analyses of planktonic ciliates. Larger sample volumes at high sampling frequencies can be evaluated with species-specific probes for even closely related, similar looking as well as very tiny ciliates.
This study was started with seven ciliate species, that were already cultured and their 18S rDNA sequences were known, namely *Askenasia* sp., *Balanion planctonicum*, *Cinetochilum margaritaceum* and 4 different *Urotricha* spp.. Species-specific oligonucleotide probes for FISH as well as a modified general probe for eukaryotes, were newly designed. At the beginning, many problems arose during FISH performances, which led to a “list of horror” (which will be also presented). But nevertheless, with several amendments and modifications to the protocol, we can now present an applicable and reliable workflow. Fluorescence *in situ* hybridization of ciliates was first tested on single cell cultures, afterwards on mock communities and finally on field samples. Further on, also CARD-FISH was conducted. To test the specificity of probes, all seven cultured species were hybridized with all different species-specific probes. Cell counts of live, DAPI, FISH and CARD-FISH preparations proved the quantitative character of this new method, for the determination of species abundances. Finally, first successful tests on field samples suggest that CARD-FISH could become a promising new methodological approach for the determination and quantification of planktonic ciliates.

P7 **Multiple origin of zoochlorellae in ciliates and invertebrates discovered by an integrative approach**

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For more than hundred years, symbiosis of green algae with protists and invertebrates has been studied and is still of general interest in modern biology. Endosymbiotic green algae are widely distributed in different ciliates (e.g., *Paramecium*, *Stentor*, *Coleps*, *Euplotes*, *Cyrtolophosis*), heliozoa (e.g., *Acanthocystis*) and invertebrates (e.g., *Hydra*, *Spongilla*) and were traditionally classified as members of the genera *Chlorella* or *Zoochlorella*. Considering solely the morphology, these *Chlorella*-like algae are difficult to identify at species, sometimes even at the generic level. We studied zoochlorellae isolated from different hosts and from different geographical regions using polyphasic approaches (SSU and ITS rDNA sequences including their secondary structures, morphology, and virus sensitivity). Phylogenetic analyses have revealed the polyphyletic origin of the endosymbiotic green algae. The strains examined belong to at least eight independent lineages within the Trebouxiophyceae (Chlorophyta). Considering our results, we propose a taxonomic revision of the endosymbiotic „*Chlorella*"-like green algae. We transfer some of them to other genera and propose new species.

P8 **Molecular taxonomy of three Chonotrichia (Ciliophora) from Roscoff (Brittany, France). First results**.

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The chonotrichs (Chonotrichia, Ciliophora) live settled on diverse appendices of several kinds of marine and freshwater crustaceans. On the base of microscopical observations, Jankowski (1973) has described more than 40 genera and 100 species living all around the world. Ultrastructural datas are know for some species, but molecular datas exist for three species only. Here, we present the full 18S rRNA sequences of three species living on marine crustaceans sampled in Roscoff (Brittany, France).

P9 **DeSigNate: Detecting signature nucleotides for taxon diagnoses**

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Taxon diagnoses primarily comprise morphological characters, whereas molecular characters are only infrequently added in integrative taxonomic approaches. Currently, the inclusion of molecular characters into taxon diagnoses is hampered by both problems in standardization as well as the lack of efficient and user-friendly tools.
DeSigNate is a novel tool that detects diagnostic signature nucleotides for the taxon of interest in a sequence alignment. An intuitive web application guides the user through the analysis process in three simple steps comprising (1) the upload of input data, (2) the specification of search parameters, and (3) the taxon selection. The underlying algorithm uses so-called nucleotide vectors to calculate metrics for each position in the alignment. These metrics are subsequently analyzed to detect candidate nucleotides and to rank them according to their diagnostic relevance. The results clearly display the ranking and the classification of the signature nucleotide positions. Furthermore, the positions can be assigned to conserved or variable sequence regions by entropy calculations based on the alignment. The aim is to facilitate the regular integration of signature nucleotides as molecular characters for complementing taxon diagnoses and thus to enable taxon delimitation and identification in various applications.

P10 **New phylogenetic lineages of centrohelids revealed with high-throughput sequencing of 18S rDNA**

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Centrohelid heliozoans (Centroplasthelida Febvre-Chevalier et Febvre 1984) represent a ubiquitous group of unciliated free-living predatory protists inhabiting marine and freshwater ecosystems and forming cysts. The main marker gene for molecular phylogeny of centrohelids is 18S rDNA, which broadly used to test evolutionary assumptions and hypotheses, as well as to improve the taxonomy. Sequencing of 18S rDNA amplicons from the total DNA of environmental samples has revealed a considerable diversity of centrohelids, and it was suggested that over 90% of centrohelid species probably remain undescribed.

The diversity of centrohelids in inland saline waters was studied with metabarcoding for the first time using newly designed taxon-specific primers. The phylogenetic analysis of the obtained OTUs combined with the comparison of specific signatures in the alignment allowed to successfully identify a vast majority of the OTUs. However, the part of obtained OTUs formed novel environmental clades or represent new genotypes, which had no obvious homology to any sequence in the reference dataset.

A large group composed of 23 OTUs from a broad range of salinities (2–78 ppt) formed a novel moderately supported clade NC9, contained four subclades NC9.1 – NC9.4 in the phylogenetic tree. All the subclades included similar or identical genotypes from contrastingly different salinities demonstrating a broad salinity tolerance: NC9.1 (2–78 ppt), NC9.2 (1–54 ppt), NC9.3 (2–78 ppt), and NC9.4 (2–78 ppt).

One OTU from a 2 ppt sample represented a novel genotype with 34-bp insertion, and had no obvious homology to any sequence in the reference dataset. Six OTUs from the samples with salinity 1, 2, 14, and 18 ppt could not be reliably identified based on either utilized phylogenetic analysis or comparing of signatures. Their position in the tree was not supported, and probably they represent first sequenced representatives of understudied lineages.

P11 **Environmental meiotic gene inventories**

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Although meiotic sex is beneficial, sex has not been observed in many protist species and higher clades. To evaluate if putative asexual species are able to have secretive sex, a well-known approach is to sequence genomes or transcriptomes to uncover meiotic genes from cultures and isolates in the laboratory. But even when it has been shown that putative asexual protists have the gene complements to construct meiotic machinery, it has not been shown where and when these meiotic genes are being expressed in the environment. Here we show, using environmental metatranscriptomic data, that meiotic genes are indeed been expressed and likely being used, when the protists are in their natural surroundings. To do this we constructed a database of taxonomically assigned meiosis-specific and meiosis-related genes, which can be used for other putative asexual protists in other environments.

P12 **Phylogenetic comparison of the oral ultrastructure within the *Perilemmaphora* (Alveolata, Ciliophora)**

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The ultrastructure of the oral apparatus is supposed to be significant for elucidating more recent common ancestry and might thus provide support for particular groupings of oligotrichean ciliates. The findings on the oral apparatus of the loricate choreotrichid *Schmidingerella meunieri* (Kofoid and Campbell, 1929) Agatha and Strüder-Kypke, 2012 are the first detailed ones on tintinnid ciliates and Oligotrichea in general. Together with the very limited body of literature, they suggest that substantial changes in the oral ultrastructure correlate only with the formation of a circular adoral zone in choreotrichids. Despite homoplasious morphologic and ontogenetic adaptations to the planktonic lifestyle in halteriids and oligotrichids, parallel developments concerning the ultrastructure of their oral apparatuses are not apparent as both generally retain the plesiomorphic features of the benthic hypotrichs. The highly complex ultrastructure of the adoral zone is thus able to accomplish an extension in the zone's functionality (feeding only in typical hypotrichs to feeding plus locomotion in halteriid hypotrichs and oligotrichids) without obvious changes; only the position of the adoral zone at the apical cell portion together with a globular to obconical cell shape are apparently crucial. Merely, minute apomorphies characterise the Oligotrichea and tintinnids, respectively. Tintinnids with derived somatic ciliary patterns possess distinct microtubular bundles connecting the oral apparatus with the myoneme in the peduncle.

P13 **Ciliates in the Arctic Ocean: Molecular and morphological methods for species delimitation**

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Ciliophora play an important role in many ecological studies. However, the functional significance and evolutionary relationships of this unicellular monophyletic group of eukaryotes remain unclear. The recent advances in high throughput sequencing technologies reform our understanding of the diversity and ecology of marine heterotrophs in particular. Nevertheless, the holistic interpretation of the phylum's diversification, distribution and ecological functions is restricted by species delimitation.

This study aims for a taxonomically representative data set of ciliate transcriptomes to resolve the diverse phylogeny and the morphological as well as functional trait development. The dataset will close important gaps regarding their morphological transitions and the evolution of the functional core genes. In this context, we performed both single-cell Sanger and SC-mRNA sequencing from fresh field samples in the Arctic Ocean and evaluated various de novo assembly approaches for the later. By comparing partial sequences of ribosomal RNA molecules and using distance matrix and maximum parsimony tree construction methods on mRNA-predicted genes, we are able to decipher previously unknown environmental sequences in previous studies. Finally, we will be able to characterize deeply branched ciliate lines to study the origin and evolution of life in marine ecosystems.

Phylogenetic reconstruction is an open-ended process and its correct evolutionary and taxonomic interpretation depends crucially on the tree's rooting and outgroups involved. Thus, we encourage discussion and exchange upon existing data and the mutual identification of missing roots as well as species representatives in phylogenetic assignments.

P14 **Studies on microplastic consumption by ciliates**

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It is well known that the abundance of plastic and microplastic particles in oceans increased enormously over the past few decades. The decomposition of larger plastic items and the pollution by microplastic particles originating from tyre wear or cosmetic products lead to this trend. Only recently, the dispersal and effects of plastic and microplastic in freshwater habitats and their effects on flora and fauna have been studied. Uptake of microplastics can cause malnutrition, decrease in fitness and intoxication by transferring toxins on microplastic particles to various organisms. Up to now, only a very limited number of organisms has been included in studies on the impact of microplastics, and protists have only been investigated regarding their uptake of bacteria-like particles. The present study is about the consumption of microplastics and the involved mechanisms in selected ciliates. We investigated the selectivity of ciliates regarding different microplastic size classes (1µm, 6µm and 10µm) offered at different concentrations. First results showed that several groups of ciliates are able to consume microplastic depending on its size and concentration while others reject microplastic particles. Our studies support the assumption that not only microplastic in marine habitats poses a threat to ecological systems but can also influence freshwater environments.

P15 **Vaginicolidae: an under-researched loricate peritrich family**

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The family Vaginicolidae is a species-rich group of loricate sessilids, with nearly 200 nominal species. Base on modern criteria, this family is severely under-researched in the taxonomy, especially in infraciliature which is absent in over 90% of the species. Furthermore, the insufficient description and the lack of photomicrographs of many old species cause great difficulties in discriminating species. Furthermore, the molecular data still remain extremely scarce for this family, although they can help to elucidate some problems in the taxonomy and systematics of ciliates. In the last three years, we investigated more than 20 species of vaginicolids assigned to five commonly found genera, i.e. *Cothurnia*, *Platycola*, *Pyxicola*, *Thuricola*, and *Vaginicola*. We obtained the photomicrographs, videos, morphological and morphometric information, and sequence data of a few marker gene (e.g. SSU rDNA) for each species. They are almost lacking previously, such as no molecular data available in the genus *Platycola*. In our protargol-stained specimens, species of the *Cothurnia* have a three-isometric-rowed infundibular polykinety 3 (P3). The oral ciliature within the genus *Thuricola* is relatively conservative and distinctive, whose P3 consists of one long and two conspicuously shorter rows of kinetosomes. Species of the *Vaginicola* show two conspicuous different patterns of P3. The oral ciliature of the only two studied species within the genus *Pyxicola* was approximately identical. Phylogenetic analyses based on SSU rDNA sequence indicated that all species of the Vaginicolidae form a monophyly, but the *Vaginicola* is not monophyletic, which does not accord well with current taxonomy. In our opinion, some species (e.g. *Vaginicola angusta*) of this genus very likely belong to a new genus that is closely related to the *Thuricola*; however, some so-called *Vaginicola* have a closer relationship with the *Cothurnia*, which is also not monophyletic. Part of the work has been published.

P16 **NGS based molecular characterization extracellular RNA-species and their function in *Paramecium tetraurelia***

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RNA does not only exist within the cells, it is also known to be exported from cells and can be found in human body fluids like blood, urine, saliva. The discovery of extracellular RNA (exRNA) has emerged an important role of cell-to-cell communication and participates in transmitting information between cells. This extracellular function of RNA holds capacity for both potential disease biomarkers and additionally therapeutic targets. Consequently, advancing exRNA research promises to revolutionize biology and transform clinical practice.
While communication via RNA is practicable in multicellular organisms, the question arises whether unicellular organisms, like *Paramecium tetraurelia*, are capable to interact and communicate with each other in a similar manner.
To address this question, we isolated total RNA from medium supernatants of exponentially growing *P. tetraurelia*. On the one hand, different isolation techniques were tested and several approaches were carried out to identify exRNA. On the other hand, we also screened for secreted proteins capable for RNA interaction such as Piwi proteins (Ptiwis in *Paramecium*). Characterization of secreted RNA species reveal short RNAs at first glance with a typical size distribution comparable to sRNAs isolated from human plasma.
We further characterize the composition of these sRNAs. As it has been shown before, that exRNA is an essential component of axenic media, the question raises whether this is due to metabolism, only, or in addition for regulation of gene expression. We plan to functionally analyze exRNAs by exogenous addition of *Paramecium* RNA to cell cultures, hypothesizing that exRNA could equilibrate gene expression between individual cells of a culture.
This poster represents a first approach to answer the question for the function of exRNAs in ciliate cultures.

P17 **The most abundant protist in wastewater treatment plants and its potential to spread diseases**

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Legionellales-contaminated water regularly leads to local outbreaks of diseases like Legionnaires' disease, Pontiac fever, or Q fever. Recent findings indicate that the rhizarian amoeba genus *Rhogostoma* (a) may function as a vector for Legionellales and (b) dominates microbial communities in water treatment systems like wastewater treatment plants (WWTPs). We isolated *Rhogostoma* strains from 7 WWTPs in Germany. We determined the amoeba species and their associated bacteria by morphological and molecular means. Three of the seven *Rhogostoma minus* isolates accommodated Legionellales as endosymbionts. All found Legionellales belong to the same novel genus here described as '*Ca*. Rhogoubacter'. Although potential pathogenicity of '*Ca*. Rhogoubacter' cannot be inferred from our data, *Rhogostoma* is abundant in WWTPs, also in Germany; in our survey it accommodated frequently Legionellales symbionts and thus may function as a treatment-resistant breeding ground for Legionellales, potentially including bacteria causing Legionnaires' disease, Pontiac fever or Q fever.

P18 **Protist diversity in hypersaline water bodies of Russia studied by NGS method**

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Salinity is one of the most important factors globally selecting and structuring microbial assemblages. However, inland hypersaline water bodies contain an unexpected large genetic diversity of novel protists. A number of new eukaryotic taxa in these environments remains to be elucidated. In the same time, there are only few studies analyzing the genetic diversity of eukaryotic assemblages in hypersaline environments.
In the present work, we have analyzed the genetic diversity of protists in the hypersaline water bodies with mineralization from 158‰ to 360‰ located in the Crimea. Water samples were filtered through membranes with diameter of pores 0.45 and 5.0 µm. The membranes were stored in the DNA/RNA Shield. Total DNA from the filters was extracted by a combined method, including mechanical homogenization and enzymatic lysis. Amplicon-based 18S rDNA libraries were created with the primers TAReuk454FWD1–TAReukRev3 using the Illumina protocol. High-throughput sequencing was performed in MiSeq (Illumina) using v3 reagent kit for 2×300 bp paired-end sequencing. The obtained data were processed with the complex of bioinformatic tools including merging of raw reads, quality filtering, amplicon size selecting, dereplicating and clustering into OTUs.
Richness of the eukaryotes in hypersaline water bodies of Republic of Crimea was significant, from 165 to 382 OTU were identified. Representatives of class Chlorophyta prevailed in the studied lakes. Green algae of genera *Dunaliella* and *Asteromonas* were predominant.

P19 **SSU and ITS secondary structures reveal new insights into the phylogeny and evolution of ciliates**

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Nuclear SSU rDNA sequences have been used for phylogenetic reconstructions of eukaryotes for a long time. The variable regions V4 and V9 of the SSU are often applied as barcode markers in environmental studies. However, the phylogenetic signals are often hidden in analyses of the primary sequences on which most evolutionary models are based. Recent phylogenetic methods include new information about the secondary structures, which provide more robust phylogenies and higher support at higher ranks such as classes of organisms. In addition, the secondary structures of the internal transcribed spacer region 1 and 2 (ITS-1 and ITS-2) provide additional information at the generic and the species level. Compensatory base changes (CBCs) in the conserved region of the ITS-2 correlate with the mating ability of closely related taxa and the biological species concept. The latest phylogenetic study revealed that the Ciliophora were subdivided into 14 classes. However, the Bayesian and bootstrap support of some classes were often weak. Especially, the relationship between classes was not resolved. Analyses using secondary structures provided a higher support at all ranks and delivered molecular signatures for all levels. In addition, the ITS-2/CBC approach revealed a hidden diversity among several ciliate species and provided a molecular tool for taxonomic revision.

P20 **Rippled sediments - Impact of sediment shifting on the metabolism and trophic structure of the microbial community in migrating ripples**

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Sandy sediments of fluvial systems are shifting not only during floods but already at base flow. Migrating ripples are the smallest bed forms of shifting sediments that are characterized by an environment of periodic alteration between dynamic (= shifting of sediment grains) and static (= resting of sediment grains) conditions. We expect sediment shifting by migrating ripples likely to act as a selective factor, negatively affecting some community components, while others may not change or benefit. Despite the wide distribution of migrating ripples, effects on metabolism, community structure and food web interactions have rarely been investigated. The overall objective of the project is to better understand the significance of sediment shifting in migrating sand ripples for the structure of the microbial food web and the metabolism in streams and rivers. The poster will present our conceptual idea considering knowledge gaps, research questions and the design of planned field samplings. We expect larger sized algae to be more sensitive to sediment shifting than bacteria. Hence, changes in the potential food composition will partly be responsible for changes in the grazer community. We propose that microbial communities in migrating ripples are dominated by heterotrophs and food web interactions are based on a bacterivorous diet, while in stable beds autotrophs contribute more to the community and algivorous protozoans are prominent. Preliminary results indicate that epipsammic diatoms were less abundant in migrating ripples and that larger sized diatoms were more sensitive to sediment shifting than smaller sized diatoms. The ciliate grazer community had a lower richness and seemed to be dominated by bacterivorous species in migrating ripples, whereas many algivorous species were present in stable sediments.

P21 **Description of new species and strains of colorless and pigmented chrysophytes**

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The chrysophyte flagellates represent a diverse and dominant group of aquatic protists. The group includes colourless as well as chloroplast carrying species. Further characteristics of genera are the formation of loricas, colonies and cysts.
Among the Chrysophyceae the genus *Ochromonas* was originally a large genus with more than 100 described species. However, recent phylogenetic analysis revealed that the genus is polyphyletic. The type species of the genus, *Ochromonas triangulata* was rediscovered leading to the need of redescription of most other *Ochromonas*-like species. A second polyphyletic group of the Chrysophyceae is the genus *Spumella* which is often described as the colourless counterpart of *Ochromonas.* Due to a similar or even indistinguishable morphology it is hard to identify *Spumella*-like flagellates without molecular tools.
We isolated and cultivated a number of different chrysophycean genotypes from a variety of different habitats including freshwater and desert habitats. We will present a number of new species and strains of colorless and pigmented single-celled chrysophytes belonging to different taxonomic groups including groups which were closely associated to the *Ochromonas*-like and *Spumella*-like flagellates.

P22 **Biodiversity and adaptation of protists to extreme aquatic environments in the Atacama Desert**

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Hypersaline environments tend to decrease the amount of species richness, on the other hand, various studies show a high degree of phylogenetic novelty under these extreme conditions. In addition to salinity, the variable chemical parameters of the environment significantly influence the eukaryotic community structure. These findings call for a more thorough look into the species richness of hypersaline environments, which seems to be more diverse than previously thought. In this study, various hypersaline lakes of northern Chile were investigated regarding protistan species diversity and richness by sequencing and analysing the V9 region of the SSU rDNA of environmental samples. The chemical composition of these lakes was determined by Inductively Coupled Plasma Optical Emission Spectrometry (ICP-OES) at the Institute of Geology and Mineralogy in Cologne to get more information about the abiotic environment. Moreover, heterotrophic flagellates from various inland water bodies were isolated for molecular, morphological and ecological investigations. The recently discovered class Placididea (Stramenopiles) was previously described as halophilic protists. Up to now, only few species from various aquatic environments across the globe were described, leaving the phylogeny broadly unresolved. We were able to isolate and cultivate 28 novel strains of Placididea from various locations in the Atacama Desert, Chile, and, in addition, for deeper phylogenetic analysis, from Germany, Kenya, the Atlantic Ocean and the abyssal zone of the Caribbean Sea. These strains resulted in the description of four new genera and eight new species, giving a more detailed phylogenetic insight into the systematics and distribution of this class. These data enlarge the knowledge on the biodiversity of protists from extreme habitats. Additionally, we compared the results of metabarcoding studies to check for the recovery of isolated strains and to analyse their potential global distribution.

P23 **Unicellular parasites in amphibians and environment in the Cologne Bay, Germany**

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Chytridiomycosis, a disease induced by the chytrid fungi *Batrachochytrium dendrobatidis* (*Bd*) or *B. salamandrivorans* (*Bsal*), has strongly contributed to the ongoing worldwide amphibian conservation crisis. While *Bd* infection has caused amphibian declines for decades on several continents, *Bsal* is a novel threat to Central European salamanders and newts, being responsible for the collapse of Fire Salamander populations in the Netherlands, Belgium, and western Germany. Even though there are other parasites that can cause harm to amphibians they have received much less attention than the chytrid fungi. The goal of the present study was to contribute to the understanding of relatively little studied declines of the Green Toad, *Bufotes viridis*, at its northwestern distribution border, in the area of Cologne, Germany. We combined the data from four years of *Bd* monitoring in the area of Cologne with a metabarcoding approach to detect other, mainly unicellular parasites, from amphibian feces and environmental samples from the same sites. Additionally, we started monitoring *Bsal* infections at the same locations in 2019. To test for chytrid infection, overall, skin swabs of approximately 280 anuran and urodelan individuals were tested for *Bd* and 66 for *Bsal*. Additionally, 150 cloacal swabs and environmental samples from five sites were collected to identify other pathogens and parasites. We found *Bd* in all sampled locations with a high prevalence and partly high individual infection loads, but so far with no clinical signs of infection. None of the samples tested for *Bsal* was positive for this pathogen. We further detected eight additional potential amphibian pathogens from fecal samples: three metamonads (*Tritrichomonas augusta*, *Trichomitus batrachorum* and *Hexamita inflata*), three ciliates (*Balantidium duodeni*, *Nyctotherus cordiformis* and *Nyctotherus hubeiensis*), one stramenopile (*Blastocystis* sp.) and one metazoan, a nematode (*Rhabdias ranae*). In the environmental samples, we detected OTUs of nine organisms potentially harmful for amphibians: *Blastocystis* sp., *Hexamita inflata*, *Tritrichomonas augusta*, *Trichomitus batrachorum*, two oomycetes (*Leptolegnia* sp., *Saprolegnia* sp.), two ichthyosporeans (*Amphibiocystidium ranae*, *Anurofeca* sp.) and the myxozoan *Myxobolus* sp.

P24 **Comparison of microbial communities in seven different German rivers**

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In the frame of a BMBF-funded project (ReWaM= Regional water management) we investigated the protozoan communities and their role in the microbial food web in seven rivers in Germany (Spree, Havel, Rhine, Moselle, Ruhr, Isar and Ilz) with different hydrological and physico-chemical characteristics. The focus of the project was the elimination of (potentially pathogenic) bacteria by different taxonomic groups of bacteria-consuming organisms. We hypothesized, that protozoa, as main consumers of bacteria, may play a crucial role in the reduction of bacteria. We quantified heterotrophic flagellates and ciliates as well as the abundance of bacteria and phytoplankton at two different times throughout the year (with special emphasis on spring and early summer). Additionally, we assessed the number of metazooplankton organisms at these sampling dates. Taking the data of these analyses into account, we estimated the role of the different members of the microbial food web in the flux of matter of the different rivers. For this, we considered literature data as well as experimental data for food consumption and growth efficiencies of the different groups of organisms. Moreover, for ciliates the portion of bacteria consumed was estimated according to the different functional groups with the help of literature data. Additionally, we considered results of grazing experiments assessing the role of benthic organisms (metazoans and microfauna) regarding the elimination of bacteria. On the poster, we will present exemplary schemes of the potential interactions between the different groups of organisms in the microbial food web of the different rivers investigated. It will be shown, if and in which type of rivers protozoans may play a significant role in the elimination of bacteria and which other groups of organisms may also be responsible for the reduction of bacteria and pathogens.

P25 **Artificially induced versus natural protistan spring bloom dynamics in Lake Zurich**

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Climate warming affects our lakes all over the world. One primary response to rising water temperatures is the strengthening of thermal stratification. This phenomenon leads to a reduction of complete water turnover (mixis) and subsequently to a lack of up-welling nutrients from deep waters. Nutrient depletion results in a fundamental decrease of annual phytoplankton blooms which are the basis of microbial food webs. In Lake Zurich, a series of partial water turnover (from 2013 to 2018) led (i) to a drastic decline of algal spring blooms, and consequently (ii) to discussions about the need of technical measures to maintain the lake's functionality. The idea of artificial turnover emerged to bring nutrient rich deep waters to the surface. In our study, we compared protistan dynamics during a mixing experiment with the *in situ* situation of Lake Zurich during spring 2019.
In the artificial turnover experiment, the increase of nutrients caused indeed a phytoplankton bloom mainly dominated by small centric diatoms. Despite the increase of primary producers only a few herbivorous ciliates, able to grow on a 'nutrient-poor diatom diet', were favored. Thus, the artificially induced phytoplankton bloom caused rather weak cascading effects along the trophic food chain. Surprisingly and in contrast to the previous period, in the year 2019 a natural spring bloom succession was observed again in Lake Zurich. However, dynamics did not mirror the classical scenario known from the past due to unexpected repeated deep mixing events. This repeated up-welling of nutrient rich waters resulted in even three successive phytoplankton blooms, a phenomenon which has not been described for the lake up to now. The *in situ* community composition strongly differed from patterns observed during the artificial turnover experiment. This study demonstrates that technical measures to generate algal spring blooms have to be seen with caution. First, at adequate meteorological circumstances, there is still the internal capacity of the lake to promote spring blooms. Second, effects of artificial turnover on all trophic levels within the microbial food web are not known at all and ask for further detailed experimental studies.

P26 **Biogeographical analyses of SSU and ITS1 sequence diversity reveal differential population substructures and distribution patterns of protist taxa**

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Based on a massive sequencing dataset of 218 European freshwater lakes we investigated geographical restriction of protistan V9-groups and microdiversity of ITS1-substructure within V9-groups. We show that based on V9-groups the geographical restriction and diversity patterns differ for different taxonomic groups as well as between nutritional strategies. Heterotrophic and substrate-bound taxa, like ciliates, Fungi, Apicomplexa or Cercozoa, show a very homogenously distributed diversity across Europe and a more heterogeneous pattern is observable in the predominantly phototrophic Viridiplantae, diatoms and other ochrophytes. Similar to patterns of diversity, pronounced areas of endemism differ between taxa and nutritional strategies. Investigation of ITS1-SWARMS revealed substructuring of V9-groups. Beneath the geographical patterns of the V9-group level a restricted geographical distribution of ITS1-SWARMS within lakes of the associated V9-group can be shown. The ratio of diversification within the SSU-V9-region, as well as the extent of endemism varied between the different taxonomies and nutritional strategies.

P27 **Diagnostic PCR for the identification of endosymbiotic green algae in *Paramecium bursaria* (Ciliophora, Oligohymenophorea)**

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Paramecium bursaria is one of the single-celled model organisms for studying endosymbiosis among ciliates and green algae. Most strains of *P. bursaria* bear either *Chlorella variabilis* or *Micractinium conductrix* as endosymbionts. Both algal genera are unicellular green algae characterized by cup-shaped chloroplasts containing a single pyrenoid and reproduction of autospores. Due to their size and only few morphological characteristics, these green algae are very difficult to discriminate by microscopy. Moreover, it is difficult and time-consuming to cultivate the endosymbionts. Therefore, we developed a diagnostic PCR method for their identification. For comparative studies, we collected about fifty strains of *P. bursaria* from all over the world (new strains and commonly used laboratory strains). For the diagnostic PCR, we designed specific primers for *C. variabilis* and *M. conductrix* and used Chlorellaceae-specific primers for strains, in cases where the species-specific PCRs failed. The genetic variability among the endosymbionts was compared by sequencing of the ITS-2 using different phylogenetic methods. Most strains of *P. bursaria* bear the two known species as endosymbionts. The distribution of *C. variabilis* and *M. conductrix* neither correlate to the geographical origin of *P. bursaria* nor to the syngens (subspecies) of *P. bursaria*.

P28 **Stable isotope probing and confocal raman microspectrometry: a promising toolkit to study predator-prey relationships among protists and prokaryotes**

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Predatory protists are major agents in shaping and controlling bacterioplankton standing stocks and thus play fundamental roles in the food webs and elemental fluxes of aquatic systems. Our project aims to study the interspecies carbon transfer in predator-prey relationships beyond conventional bulk community assays (e.g., grazing rates) on the single-cell level using Stable Isotope Probing (SIP) and Confocal Raman Microspectrometry (CRM). Grazing experiments with 13C-labeled *E. coli* prey cells and the ciliate predator *Tetrahymena pyriformis* were conducted to monitor the label incorporation into the predators' biomass by CRM at unsurpassed subcellular resolution. By comparing SIP-Raman data with cell population dynamics and biomass estimates (predator and prey), we determined feeding and labeling kinetics in this predator-prey system and evaluated SIP-Raman as a quantitative approach to derive single-cell growth rates of protistan predators on a prescribed bacterial diet. As a next step, we performed grazing experiments with 13C-labeled *E. coli* fed to natural protist assemblages in a pristine freshwater lake and detected labeled carbon incorporation in phagotrophic flagellates). We demonstrate that SIP-Raman applied in concert with fluorescence *in situ* hybridization (FISH) can overcome a major challenge in microbial ecology in the future; linking phylogenetic identity with function and rate measurements.

P29 **Modelling approach to describe chaotic dynamics of organisms in chemostat systems**

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The high biodiversity of protistan plankton communities still poses a paradox to science because of the restrictive environmental conditions. Some models showed that non-linear processes could be responsible for the high biodiversity as a key. Particularly deterministic chaos seems to be important for maintaining biodiversity. However, there is still a lack of theoretical and experimental studies indicating chaos in simple systems. With our model system we investigate the appearance of chaotic dynamics in a one-species-chemostat system of a protist species to understand under which circumstances chaotic dynamics may occur. With the help of the results of our model system we plan to improve the theoretical and experimental system to study how chaotic dynamics of a single protist species/trait may affect the coexistence of species/traits in more complex microbial systems.

P30 **Investigating the grazing impact of protists on bacteria assembly and function in the rhizosphere of maize plants**

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A key, but often overlooked, component of microbial interactions in the rhizosphere is the top-down grazing impact of protists on soil bacteria which influences bacterial competition and contributes to the remobilization of nutrients for plant uptake. Understanding these impacts is crucial to the comprehensive representation of the plant holobiome. We hypothesize that increasing species richness of protist grazers leads to increasingly predictable patterns of bacterial community assembly and function in the maize rhizosphere. As a part of the SPP 2089 "Rhizosphere Spatiotemporal Organisation", funded by the German Research Foundation (DFG) we establish a protocol, by which we can investigate changes in the bacterial rhizosphere community as it relates to increasing protist diversity. In doing so, we can assess the impact of protist grazing on bacterial function in maize root systems and overall plant growth.
In a microcosm experiment various combinations of protist species from two functional groups (flagellates and amoeba) will be used to inoculate soil planted with wildtype maize seeds. After three weeks of maize growth, shoots will be harvested and soil samples will be measured for bacterial function, biomass, turnover, respiration and community composition. Using a combination of molecular tools, high-throughput sequencing technology (i.e. Illumina MiSeq), bioinformatics and network analyses, we aim to describe changes in the bacterial community structure with increasing species richness of predators. This study will provide a deeper insight into the complex relationships between plant, protists and bacteria.

P31 **Microscopical studies on *Ministeria vibrans* Tong, 1997 (Filasterea) highlight the cytoskeletal structure of the common ancestor of Filasterea, Metazoa and Choanoflagellata**

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Ministeria vibrans (Filasterea) is a tiny amoeboid species described by Tong in 1997. It has been sporadically found in different habitats, and cultured strains were established. In contrast to other protist groups, there are only few sequences originating from environmental studies that branch with filastereans including *Ministeria*, which might indicate rather infrequent occurrence. *M. vibrans* is well characterised by molecular phylogeny but until now was not ultrastructurally investigated in detail. Here, we provide the ultrastructure for this species based on a new strain isolated from oxygen-depleted water of the Baltic Sea. A thin vibrating flagellum could be observed but no vibrating movement of the cell body and no stalk. Our first ultrastructural study of a filasterean taxon revealed radial microvilli supported by bundles of microfilaments. The cell may contain a special MFOC with retracted bundles of F-actin, probably a temporary F-actin cluster completely used for microvilli rebuilding. For the first time, we received a mostly complete picture of the kinetid structure of a filasterean resembling the same structure as the most ancient kinetid type in sponges. Two centrioles located in the nuclear pit can migrate to the cell periphery and transform into the kinetid: the centriole orthogonal to the kinetosome with a fibrillar root and a basal foot that initiates microtubules. Microvilli in *Ministeria* suggest their presence in the common ancestor of Filasterea and Choanoflagellata. The kinetid structure of *Ministeria* is similar to that of the choanocytes of the most deep-branching sponges, differing essentially from the kinetid of choanoflagellates. Thus, kinetid and microvilli of *Ministeria* illustrate features of the common ancestor of three holozoan groups: Filasterea, Metazoa and Choanoflagellata.


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