Society of Eukaryotic Microbiology

44th Annual Meeting

11-14 February 2025, Neuchâtel, Switzerland

Book of abstracts

GORDON AND BETTY MOORE FOUNDATION

Hydrobiologie-Limnologie-Stiftung für Gewässerforschung

ISOP International Society of Protistologists

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Hydrobiologie-Limnologie-Stiftung für Gewässerforschung

ISOP International Society of Protistologists

Gesellschaft für Eukaryotische Mikrobiologie e.V.
Society of Eukaryotic Microbiology

unine Université de Neuchâtel

ZEISS

Dear Colleagues and Friends,

Welcome in Neuchâtel!

On behalf of the Society for Eukaryotic Microbiology and the organizing committee, it is a great pleasure to welcome you to the 44th meeting of the Society for Eukaryotic Microbiology.

I would like to thank our sponsors, the Society for Eukaryotic Microbiology and the local team for making this meeting possible.

We hope you will enjoy the meeting as well as the beautiful millennial city of Neuchâtel.

With kindest regards,

Pr. Edward MITCHELL

Local Organizing Committee

Pr. Edward MITCHELL

Dr. Guillaume LENTENDU

Robin CALISTI

Arnaud DANO

Benjamin ORY

Camille VOEGELI

Scientific Committee

Pr. Edward MITCHELL

Dr. Guillaume LENTENDU

Prof. Jens BOENIGK

Dr. Yana EGLIT

Dr. Laure GUILLOU

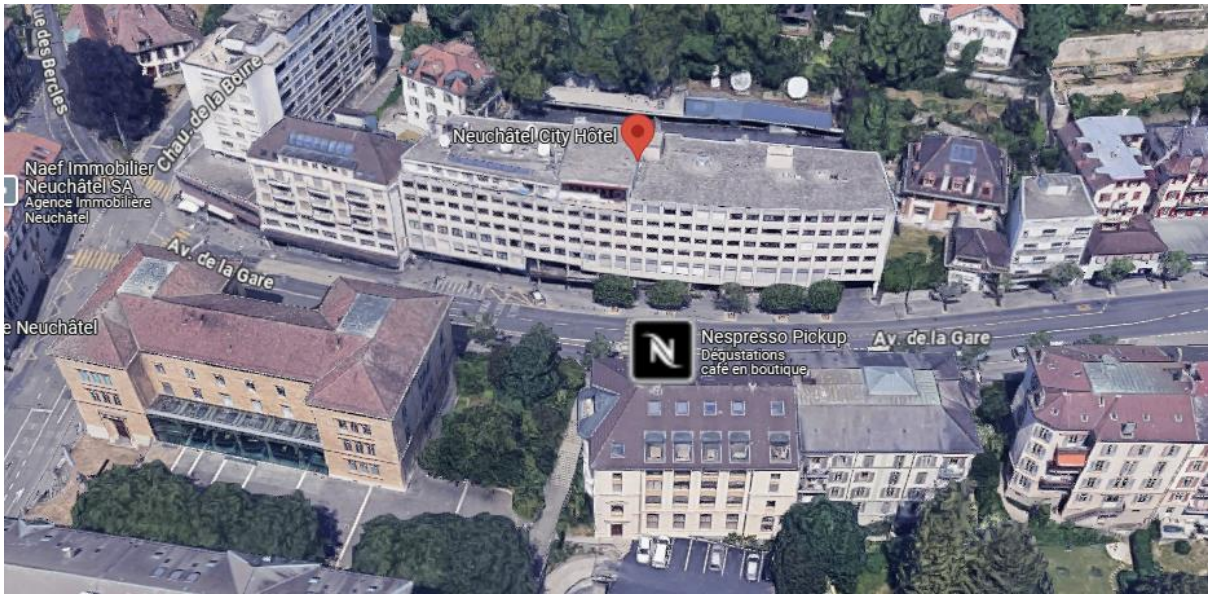
Dr. Elisabeth HEHENBERGER

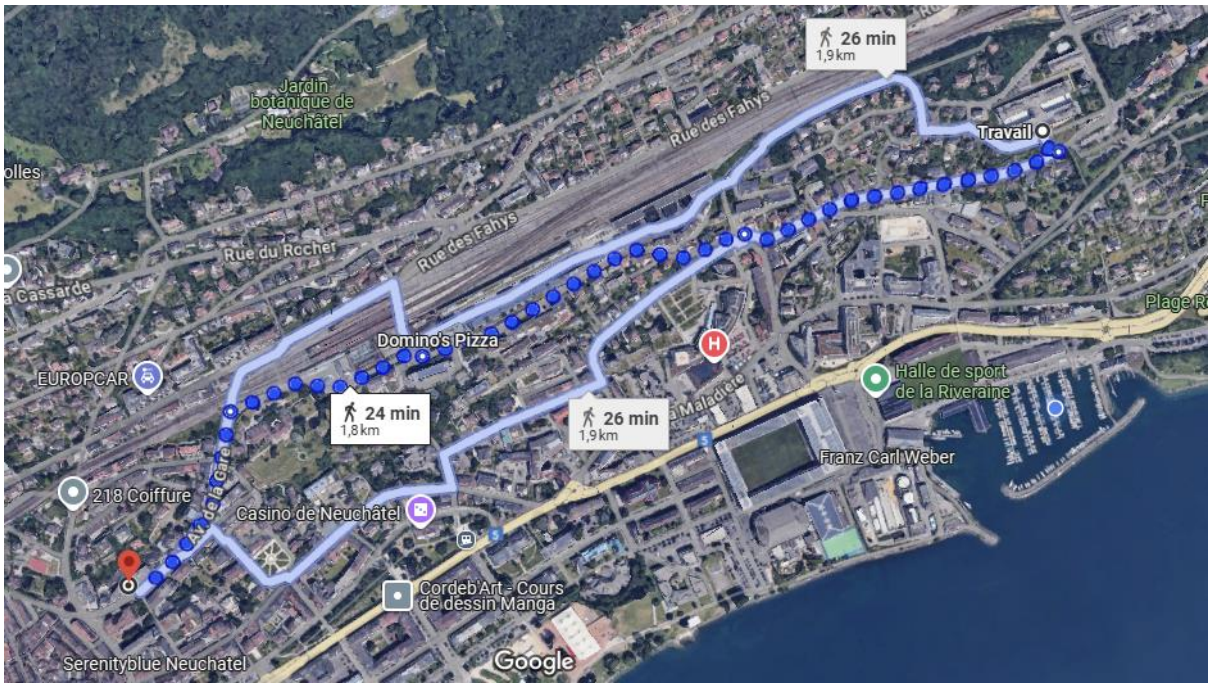
Dr. Thomas POSCH

Content

Hotel

15 -17 AVENUE DE LA GARE
2000 NEUCHÂTEL



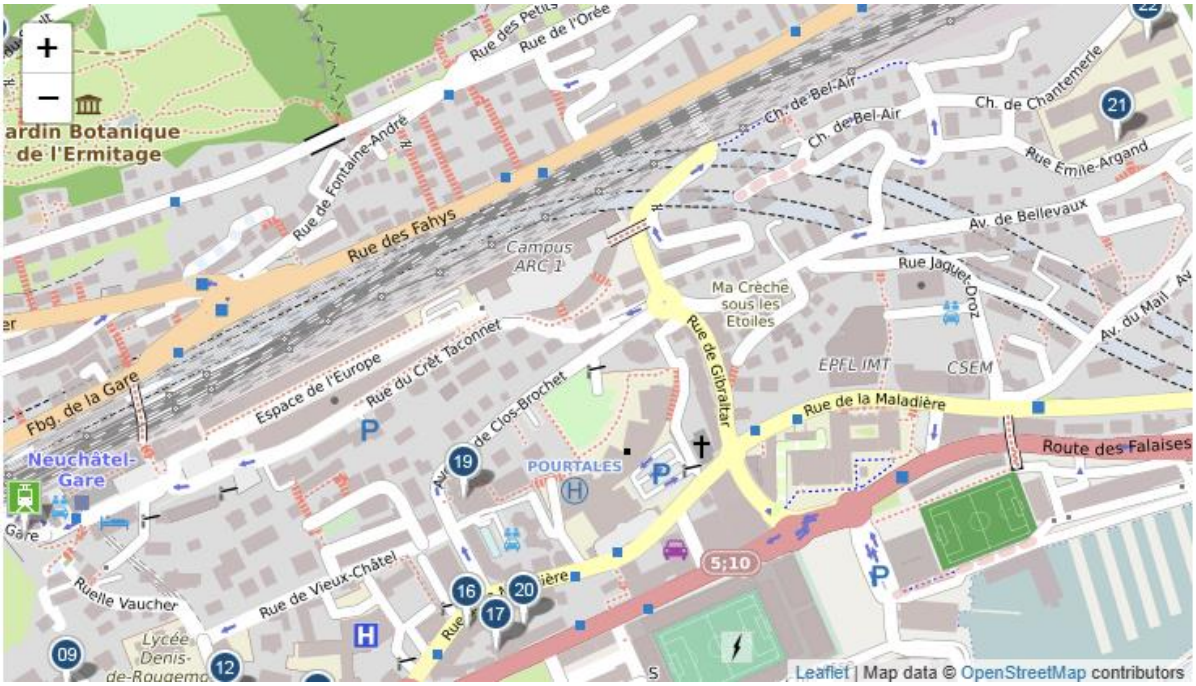


Way from train station to conference venue

Conference and workshop venue

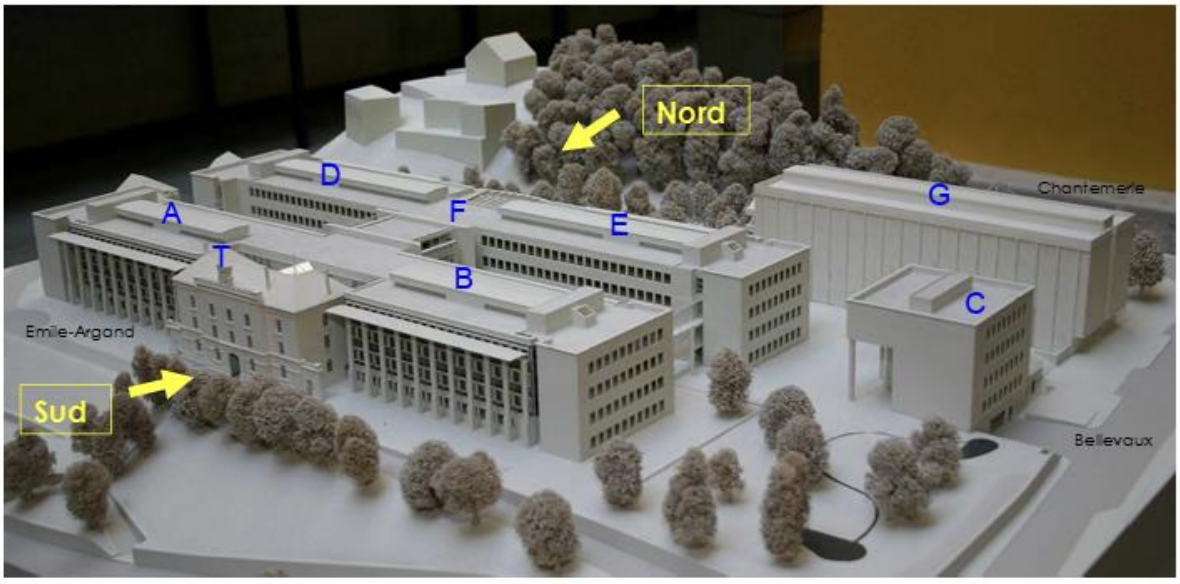
University of Neuchâtel
UniMail building = Science Building
⇨ nr 21 on the map

The train station is on the left (Neuchâtel Gare)



University

Université de Neuchâtel - Faculté des sciences - Site UniMail



Public transport

If you have booked in a hotel, you have free public transport within the limits of Neuchâtel

Useful websites

Swiss trains:
https://www.sbb.ch/en

Neuchâtel public transport (in French only):
https://www.transn.ch/

Descriptions of excursions

Latenium

The largest archaeological museum in Switzerland
https://latenium.ch/en/
Located on the shores of Lake Neuchâtel, the museum and its archaeological park tell you about 500 centuries of regional history, from the Middle Palaeolithic to Modern Times

Centre Dürenmatt Neuchâtel

Museum dedicated to one of Switzerland's major writers right next to the wonderful botanical garden of Neuchâtel
https://www.cdn.ch/cdn/en/home.html
Friedrich Dürrenmatt (1921–90), the world-renowned writer and playwright, was also an avid painter and illustrator his whole life. The Centre Dürrenmatt Neuchâtel (CDN) showcases his paintings as they relate to his literary works in a permanent exhibition. The museum also stages temporary exhibitions and events, and offers guided tours, workshops for schools, publications, a podcast and virtual tours. Designed by Mario Botta around Dürrenmatt's former home, the CDN showcases parts of the writer and painter's living space.

Laboratoire Temps-Fréquence

How the World's most precise atomic clocks are produced and what this means for our everyday life
https://www.unine.ch/ltf/home.html
The Time and Frequency Laboratory constitutes one of the nine key areas of research and innovation of the University of Neuchâtel. The Time-Frequency and Optical Metrology Centre explores and pushes the frontiers in time measurements, photonics, and metrology and participate to the international efforts to define the international atomic time TAI with primary frequency standards, with the development of the unique atomic fountain clock FOCS-2 that operates with a continuous beam of cold cesium atoms.

Old city of Neuchâtel

1000 years of history, castle and collégiale (cathedral) and more
https://www.j3l.ch/en/Z10771/destinations/cities/city-of-neuchatel
Millennial city with lots of charm, Neuchâtel will enchant you with its elegant yellow-ochre buildings and its privileged location at the largest entirely Swiss lake.

Workshops program

Workshop 1 - Room D008

Dung-dwelling Protists

Tristan Henderson
Mississippi State University, U.S.A.
https://amoeba.msstate.edu/

The evolutionary transition from aquatic to terrestrial environments marks a pivotal event in Earth's history, enabling organisms to exploit new niches and driving the emergence of novel adaptive strategies. As multicellular organisms like plants and animals adapted to terrestrial environments, they created or became novel microhabitats for microbes. One fascinating and largely underexplored microhabitat is dung.

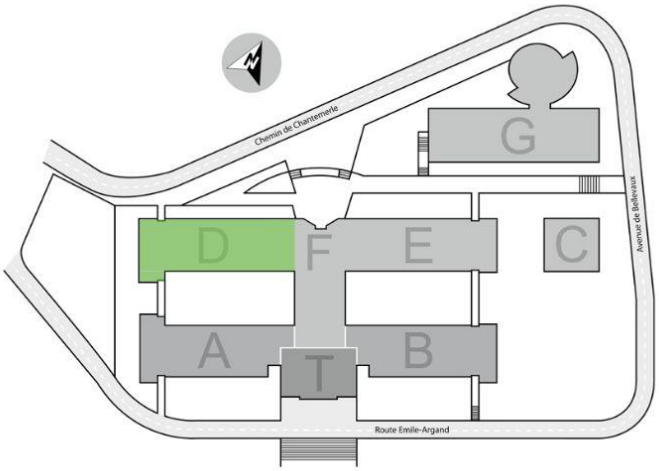
Dung is a rather unique microhabitat to evolve to. Its timing, placing, and very composition depends on the animal and their diet. Dung is considered “ephemeral” meaning it has a short window of bioactivity, much like carrion or rotten fruit, yet in many cases it supports a diverse and rich community of organisms. From butterflies to beetles, and bacteria to protists, this workshop will briefly cover what is known about the ecology and growing prevalence of dung, with a focus on domesticated ruminants (cattle and horses). In a modern context, cow dung is particularly interesting due to the global expansion of cattle farms on deforested areas, and thus the spread of dung-specific organisms.

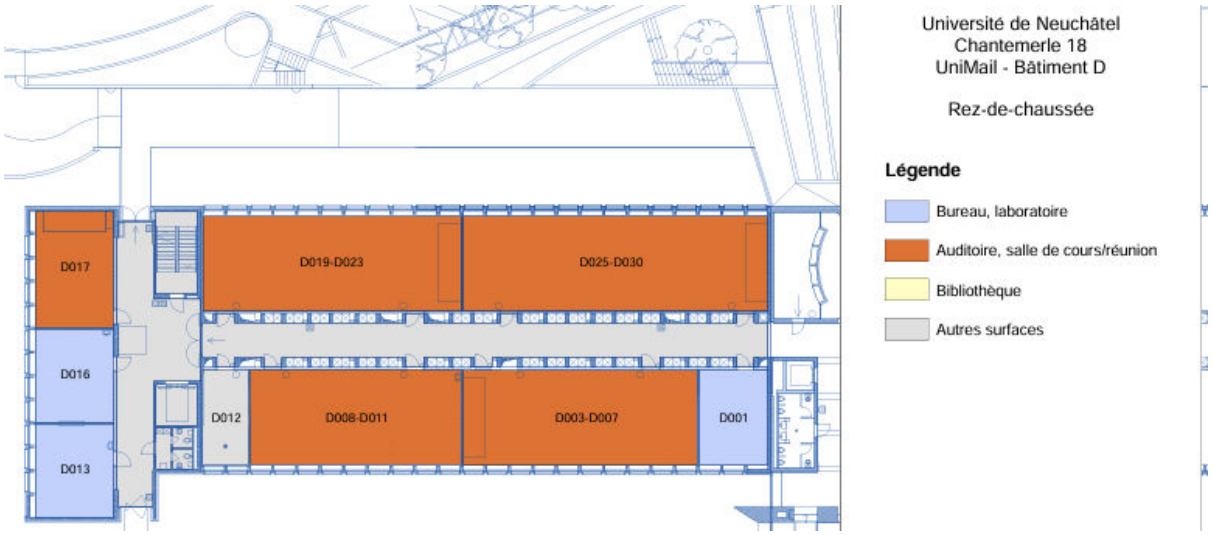
While we will cover the overall protist diversity found in dung environments, a major theme in this workshop is collective behavior. Three protists from herbivore dung exhibit a “social” life cycle similar to dictyostelids, but are phylogenetically distant, belonging to different supergroups (*Copromyxa protea* [Amoebozoa], *Sorodiplophrys stercorea* [Stramenopiles], and *Guttulinopsis vulgaris* [Rhizaria]). Another protist, *Sappinia pedata* (Amoebozoa), has been observed displaying aggregative behavior on dung but it has not been

investigated. We will use insights from studying these four species to learn methods of researching dung-dwelling protists overall.

In this workshop we will cover:

- Evolution, ecology, and growing prevalence of dung
- [potentially] Parasites related to cattle and dung
- Diversity of protists inhabiting dung and their unique behaviors
- How to find, isolate, and culture several protists from dung
- Current methods to study dung-dwelling protist behavior





Room nr D008

Workshop 2 - Room E026

Analyses of barcoding and metabarcoding amplicon sequencing datasets

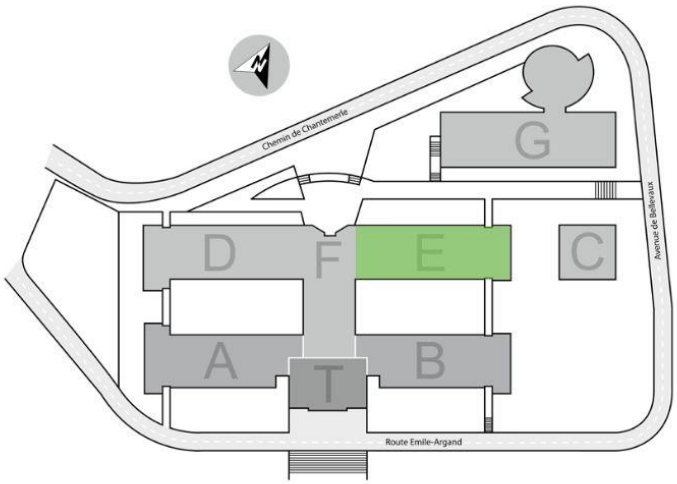
Guillaume Lentendu
University of Neuchâtel, Switzerland

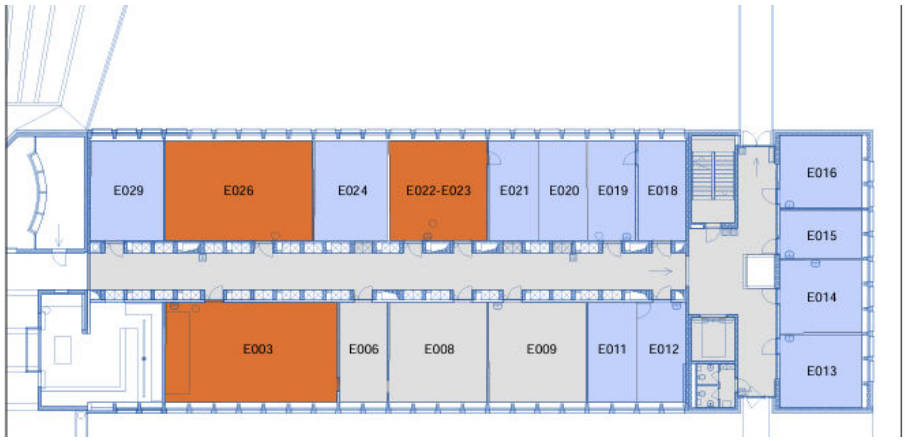
https://www.unine.ch/biolsol/home/collaborators/Guillaume_Lentendu-1.html

High-throughput sequencing has become the standard in biodiversity, ecology and phylogenomics research, but most researchers lack a comprehensive overview of these different approaches as well as the bioinformatic requirements and databases availability to process such datasets. This workshop intends to shed light on some of these high-throughput sequencing techniques (Illumina, PacBio, Nanopore), their benefit, cost, ease of application and bioinformatic processing.

The workshop will include hands-on sessions in which we will analyse a metabarcoding dataset from Illumina MiSeq, but other type of datasets (e.g. Nanopore, PacBio) could be investigated too depending on the demand (please vote at registration). We will test different tools for sequence manipulation, sequence quality reporting, primer and barcodes removing, denoising, clustering and taxonomic annotation. I will cover the common issues and how to solve them: low quality at the end of reads, error model-based correction of raw reads, cross-contamination (tag jumping), general contamination, sequencing depth bias. I will stress the need for positive controls (e.g. MOCK communities) and negative controls at DNA extraction, PCR and sequencing steps. The workshop will also provide hands-on experience with a high-performance computer (HPC).

A minimum knowledge of bash and R scripting would help to the good conduction of this workshop. Introduction lectures and tutorials can be found here and there for bash, and here and there for R.
Computers with all needed software will be provided. No support to install software on personal computers will be provided.





Rez-de-chaussée

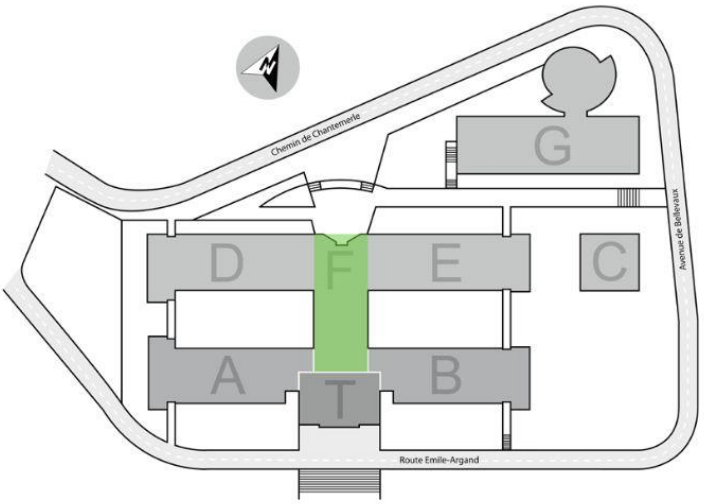
Légende

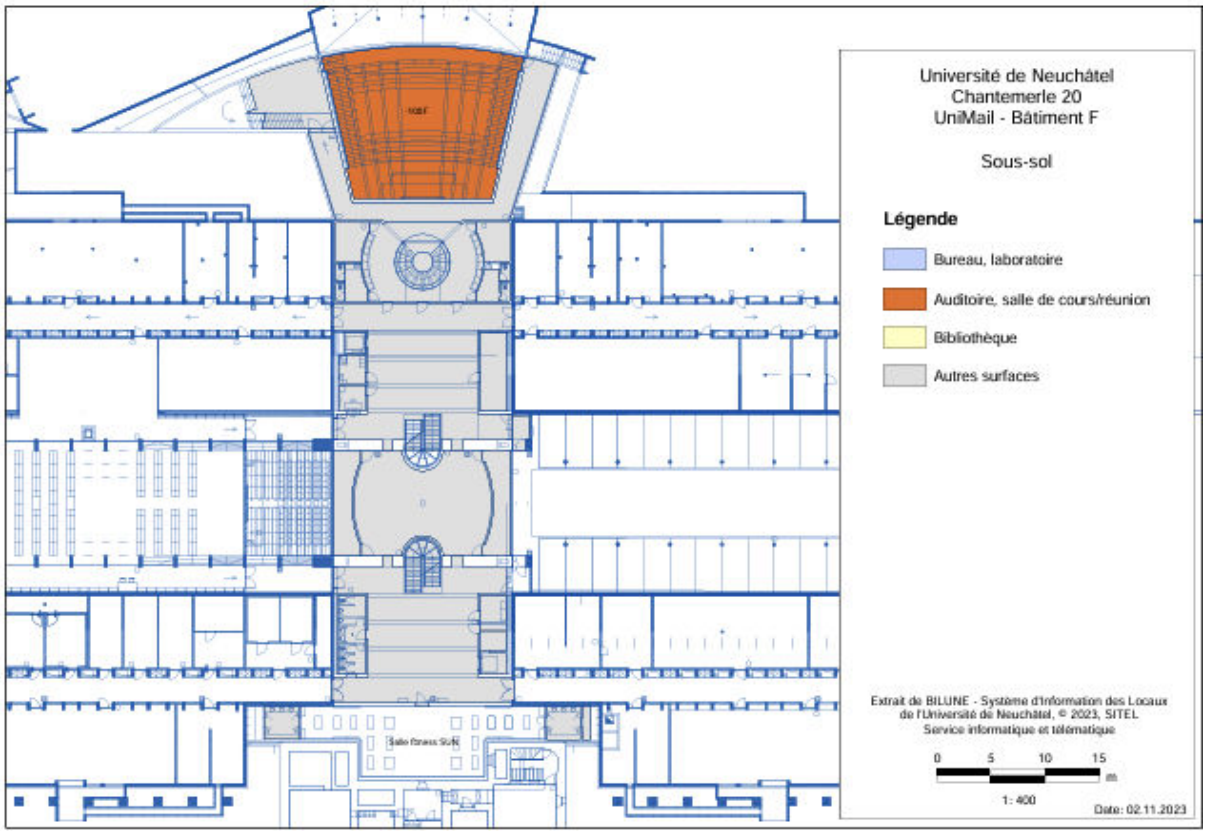
- Bureau, laboratoire
- Auditoire, salle de cours/réunion
- Bibliothèque
- Autres surfaces

Room nr E026

Conference

Auditoire F-100





Program Overview

TUESDAY 11.02.2025 - Workshops

8:30-9:00	**Welcome & Registration**	
9:00-9:30	Introduction to workshop 1 **High-throughput analysis of soil protist diversity**	**Guillaume LENTENDU**
9:30-10:00	Introduction to workshop 2 **Dung-dwelling Protists**	**Tristan HENDERSON**
10:00-10:30	Break	
10:30-12:15	Workshop - avanced lectures on the workshop topic	G. LENTENDU / T. HENDERSON
12:15-13:30	Lunch	Tunisian cuisine (Tebbsi Restaurant)
13:30-15:30	Workshop - practicals (parallel sessions)	G. LENTENDU / T. HENDERSON
15:30-16:00	Break	
16:00-17:00	Workshop -C6:C14 discussions (parallel sessions)	G. LENTENDU / T. HENDERSON
Evening	Registration - Get together apero-meal	Swiss traditional buffet (Buffet paysan)

WEDNESDAY 12.02.2025 - Morning

8:30-8:45	**Welcome & Registration**	
Session 1	**Biotic intereactions and bio**	**Chair : Jens BOENIGK**
8:45-9:30	**Keynote Lecture**	**Laure GUILLOU**
9:30-9:45	Hitchhiking Bacteria: Diverging effects of different tyre wear particles on microbial biofilm composition	Dana BLUDAU
9:45-10'00	Detection of peat in growing substrate based on testate amoeba communities	Camille VOEGELI
10:00-10:15	Spatio-temporal patterns of *Tetrahymena* and other protists at the edge of chaos	Johannes WERNER
10:15-10-30	Bioaccumulation of Rare Earth Elements, Iron, and Aluminium in three *Tetrahymena* species	Jana KOHL-CHANDRAMOHAN
10:30-11:00	Break	
Session 2	**Trophic interactions and ecosystem functioning**	**Chair : G. LENTENDU**
11:00-11:15	Using testate amoebae as bioindicators of greenhouse gas fluxes in peatlands	Robin CALISTI
11:15-11:30	Under the cover of darkness: how *Plasmodiophora brassicae* affects Arabidopsis thaliana physiology during the night	Andrea GARVETTO
11:30-11:45	A taxonomic monograph of hyalospheniid testate amoebae (Amoebozoa: Arcellinida: Hyalospheniformes)	Edward MITCHELL
11:45-12:00	Assessing protistan communities from agricultural soils with nanopore Technologies	David SINGER
12:00-12:15	Structure and function of soil protist communities across soil microhabitats and their response to land-use change	Gennuo WANG
12:15-13:30	Lunch	Middle Eastern cuisine (Chef Falafel)

WEDNESDAY 12.02.2025 - Afternoon

13:45-14:00	**Announcements**	**Edward MITCHELL**
Session 3	**Parasites and symbionts**	**Chair : T. HENDERSON**
14:00-14:45	**Keynote Lecture**	**Elisabeth HEHENBERGER**
14:45-15:00	Revisiting the diversity of freshwater gregarine species	Anthony ALLAN-CARDOSO
15:00-15:15	R-bodies of *Paramecium* endosymbiont *Caedimonas varicaedens* and various non-endosymbiotic bacteria are diverse in both morphology and expansion kinetic behavior	Lennart DÖRR
15:15-15:30	*Blastocystis* (Stramenopila) – parasite or commensal ?	Julia WALOCHNIK
15:30-15:45	Cultivation of anaerobic ciliates with respiratory endosymbionts	Linus Matz ZELLER
15:45-16:00	Towards a better understanding of gregarine-host relationships	Sonja RÜCKERT
16:00-16:30	Break	
16:30-17:15	**Grell Prize Lecture**	T.B.A.
17:15-19:00	**Poster session**	
19:00-20:30	Dinner	Tunisian cuisine (Tebbsi Restaurant)

THURSDAY 13.02.2025 - Morning

8:30-8:45	**Welcome**	
Session 4	**Phylogeny and evolution**	**Chair : L. GUILLOU**
8:45-9:30	**Keynote Lecture**	**Yana EGLIT**
9:30-9:45	Contributed talkImpact of pig cadavers on forest soil cercomonads (Rhizaria: Cercozoa: Cercomonadida), assessed by high-throughput sequencing	Arnaud DANO
9:45-10:00	A revised classification of the testate amoeba family Euglyphidae based on scale morphology and DNA barcoding	Clément DUCKERT
10:00-10:15	Keeping the balance in Kareniaceae (Dinoflagellata): *Gertia stigmatica* never replaced its peridinin plastid, while Karlodinium ballantinum replaced it twice	Kacper MACISZEWSKI
10:15-10-30	Disentangling the cryptic *Rhynchomonas* morphospecies complex by combining phylogenetic, morphological and autoecological methods	Julian WAGENHOFER
10:30-11:00	Break	
Session 5	**Cell biology and physiology**	**Chair : E. MITCHELL**
11:00-11:15	Distinct Transcriptional Mechanisms in *Paramecium tetraurelia*: Exploring the Roles of DSIF and Spt6 in Pol II-driven Processes	Franziska DREWS
11:15-11:30	Beyond Dictyostelids: Unveiling the Hidden Lives of Other Social Amoebae	Tristan HENDERSON
11:30-11:45	Unveiling the mitochondrial architecture of Gastrotricha: insights into evolution and lineage-specific adaptations	Anush KOSAKYAN
11:45-12:00	Analysis of Ptiwi proteins in the exogenous RNAi pathway in *Paramecium tetraurelia* reveal so far unknown involvements in RNAi by Feeding	Marcello PIRRITANO
12:00-12:15	The untapped value of moss herbaria for protist biodiversity and biogeography : examples from tropical Sphagnum and description of a new *Centropyxis* species from Peru	Benjamin ORY

THURSDAY 13.02.2025 - Afternoon

12:15-12:30	**Announcements**	**Edward MITCHELL**
12:15-13:30	Lunch	Indian cuisine (Paprika Restaurant)
13:30-16:30	**Excursions**	
16:30-17:15	**Honorary member lecture**	**Martin SCHLEGEL**
17:20-19:00	**Society of Eukaryotic Microbiology Meeting**	
19:00-01:00	Conference dinner and party	Gala dinner (Silex Restaurant)

Location of the gala dinner: **Restaurant Le Silex** https://lesilex.ch/

Address: Chemin du Port 2, 2068 Hauterive

Location on **map**: Google Map LInk

How to get there **by public transport**:

Walk down the stairs and road to “Bas du Mail” bus stop.

Take bus ne 101 direction “Marin”

https://maps.app.goo.gl/rwR1iDUumJH3qgFW7

The last buses back

Bus 101: 23:42

Bus: 107: 00:31 but note that it’s ca. 1km walk to the bus, stop, give yourself 20’ extra

FRIDAY 14.02.2025 - Morning

8:45-9:00	**Welcome**	
Session 4	**Ecology and biodiversity (Alka-Selzer session)**	**Chair : E. HEHENBERGER**
9:00-9:45	**Keynote Lecture**	**Jens BOENIGK**
9:45-10:00	Insights into Unexplored Protist Diversity through Long-read 18S rRNA gene Metabarcoding	Alice ADLER
10:00-10:15	Metabarcoding of soil protists in the third-generation sequencing era	Guillaume LENTENDU
10:15-10-30	Integrating High Throughput Molecular and Optical Methods to Study Protistan Abundances in Groundwater Ecosystems	Nadine MÖBIUS
10:30-10:45	Occurrence of ciliates in the sediment of the Southern Baltic	Anja SCHERWAß
10:45-11:15	Break	
Session 5	**Taxonomy and evolution**	**Chair : Y. EGLIT**
11:15-11:30	A metagenomic roadmap to global freshwater mitochondrial diversity	Adrian-Stefan ANDREI
11:30-11:45	Charting the landscape of cytoskeletal diversity in microbial eukaryotes	Omaya DUDIN
11:45-12:00	From single cells to shells: Lorica formation in the model tintinnid genus *Schmidingerella* (Alveolata, Ciliophora)	Maximilian GANSER
12:00-12:15	Arcellinida metabarcoding, a new tool for environmental health evaluation in lentic systems	Enrique LARA
12:15-12:30	**Announcements**	**Edward MITCHELL**
12:30-13:30	Lunch	Cosmopolitan cuisine (Tennis Restaurant)
End of meeting		

Keynote Abstracts

Stability of microbial food webs in a changing world

Authors

Jens Boenigk

Biodiversity, University of Duisburg-Essen, Essen, Germany
https://www.uni-due.de/biodiversitaet/mitarbeiter-staff.shtml

Abstract:

Ecosystems are affected by multiple stressors and these stressors often interact in complex, nonlinear ways to impact negatively on biodiversity and ecosystem functions. Therefore, predictions about changes in biodiversity and ecosystem function are difficult, yet critically important. Of particular concern are increasing frequency and intensity of heatwaves driven by climate change, but salinization and other stressors also significantly impact microbial communities and community function. As microbial food webs and in particular the regulation of bacterial density and community composition through protistan grazing stabilize the basis of any food web, they critically contribute to ecosystem stability. The high diversity of microbial communities and a presumably high level of functional redundancy of morphologically similar flagellate taxa can buffer community functions and ecosystem services despite a high species turn-over. This particularly also accounts for grazing interactions between protists and bacteria as structuring element for bacterial communities. The turn–over of differently adapted cryptic species with presumably similar feeding preferences may stabilize microbial ecosystem functions facing environmental change.

Exploring unseen cellular and behavioural diversity through cultivation

Authors

Yana Eglit

Botany Department, University of British Columbia, Vancouver, Canada,
soon University of Geneva, Switzerland
https://www.researchgate.net/profile/Yana-Eglit

Abstract:

Much of the novel major lineage discovery over the past 20 years involved cultivation of isolates of interest identified by light microscopy. I have used this approach to characterise several phylogenetically significant lineages of eukaryotes, including a super-group-level clade comprised of Hemimastigophora, *Meteora*, and "Protist X". These novel cultured representatives allow for improved phylogenetic reconstruction and general morphological characterisation; moreover, they can be a source of curious cell biological and behavioural observations -- particularly among eukaryotrophs, or protists that predate upon other protists. I will present a few such organisms, of varying phylogenetic importance, that also exhibit peculiar cellular and/or behavioural phenomena observed (primarily) under light microscopy.

In short, come for the trees, stay for the microbial feasting (or vice versa)!

Unseen Ecological Drivers: The Role of Marine Parasites in Ecosystem Dynamics and their Unexpected Biology

Authors

Laure Guillou

Roscoff Biological Station, CNRS & Sorbonne University, Roscoff, France
https://cv.hal.science/laure-guillou

Abstract:

Earth's biodiversity is entering a sixth mass extinction, marked by unprecedented extinction rates. Parasites, which are believed to account for half of all species richness, could represent the unseen majority of species extinctions. While parasites are often viewed through an anthropocentric lens—as biological agents causing diseases in humans, animals, or plants—they play essential ecological roles. They limit species invasions, control the growth of opportunistic species, and mediate biomass transfer between trophic levels. Consequently, their preservation is critical for the resilience of ecosystems.

Although extensively studied as human pathogens and threats to human interests, parasites have largely been overlooked in microbial aquatic ecology, particularly in marine environments. Marine Alveolates (MALVs) were identified as one of the most hyperdiverse lineages in the metabarcoding dataset collected during the Tara Oceans expedition. Despite their diversity, only a few species within the MALV lineage have been formally described. Most are obligate aplastidial parasitoids, intracellular biotrophs, meaning the host remains alive during the infection but eventually kills.

This diverse group encompasses a wide range of specialized parasites, each adapted to infect specific host types. However, collectively, MALVs can infect a broad array of marine hosts, from unicellular organisms like dinoflagellates, ciliates, and radiolarians to larger multicellular animals such as crustaceans and fish. MALVs significantly impact marine ecosystems and industries: some species cause devastating epizootics that affect fisheries and aquaculture, while others drive the collapse of toxic algal blooms, reshaping phytoplankton community dynamics.

In this conference, we will provide an overview of the current knowledge of these lineages from both ecological and biological perspectives, highlight major discoveries made in recent years, and explore what remains to be uncovered, with the aim of inspiring future researchers to investigate these remarkable marine parasites.

(Core) Dinoflagellates - Never stop shopping for plastids

Authors

Elisabeth Hehenberger

Biology Centre, Czech Academy of Sciences, České Budějovice, Czech Republic
https://protistomics.eu/hehenberger/

Abstract:

Dinoflagellates are a highly diverse, abundant and widespread group of unicellular eukaryotes with several fascinating characteristics, including genomes so gigantic they are packed into permanently condensed, liquid-crystalline chromosomes in a nucleus called dinokaryon. Also, regarding their plastids, dinoflagellates follow an uncommon trajectory – their plastid evolution is likely the most dynamic of all plastid-bearing eukaryotes. Several dinoflagellate lineages have replaced their ancestral dinoflagellate plastid (the “peridinin” plastid) with new permanent plastids from various algal donors but up to now this behavior seems to have been restricted to core dinoflagellates – comprising all dinoflagellates with the typical dinokaryon. Here I will present our microscopic, phylogenomic and transcriptomic analyses of several dinoflagellate lineages newly reported to have replaced their ancestral plastid, including a lineage outside of the core dinoflagellates, and discuss how these results impact our view of plastid evolution.

Oral presentation Abstracts

Insights into Unexplored Protist Diversity through Long-read 18S rRNA gene Metabarcoding

AUTHORS

Aline Adler [1], David Singer [2], Sarah Wegmüller [1], Sarah Scotton [1], Thierry Heger [2], Alexandre Kuhn [1]
[1] Laboratory of Molecular Biology, School of Engineering, University of Applied Sciences and Arts Western Switzerland, Sion, Switzerland
[2]. Changins, School of Viticulture and Enology, University of Applied Sciences and Arts Western Switzerland, Nyon, Switzerland
aline.adler@hevs.ch

ABSTRACT

Sustainable agriculture requires tools for precise prediction of soil and plant health. The soil microbiome, and particularly protists, are promising bioindicators of environmental quality. However, the approach based on short DNA fragments from soil protists faces limitations in achieving identification at the species or strain level. Third-generation sequencing addresses this challenge by providing longer DNA fragments, thereby enhancing phylogenetic resolution. Yet, this novel approach lacks extensive validation and standardized protocols, which are crucial for ensuring robust and reproducible results. In this study, a molecular profiling approach based on Oxford Nanopore long sequences (18S rRNA gene) was compared to an approach based on Illumina short sequences (V4 region of the 18S rRNA gene) using DNA extracted from six vineyard soil samples. This approach involves amplifying and sequencing approximately 4,500 bp of the ribosomal operon (18S, ITS, 5.8S, and 28S). Taxonomic assignment was performed on the 18S (V4–V9) region of the operon by comparison with the PR2 database. Taxonomic assignment dissimilarities were analyzed to determine whether they stemmed from sequencing errors or biological diversity. Surprisingly, most of the additional diversity observed with the long sequences reflected genuine biological variation rather than sequencing errors, providing more precise and robust assignments compared to the short sequences. It resulted in the detection of significantly higher protist diversity than that revealed by the V4 region alone. This is one of the first glimpses into the untapped protist diversity, highlighting the potential of long-read sequencing to uncover previously overlooked ecological complexity of protists communities in Swiss vineyard soils.

Revisiting the diversity of freshwater gregarine species

Authors:

Anthony Allan-Cardoso, Lucas Arnold, Sonja Rückert
Department of Eukaryotic Microbiology, University of Duisburg-Essen, Essen, Germany

Abstract:

As an ancestral group of symbionts infecting invertebrates, gregarines are supposed to have an important position for understanding the evolutionary development of parasitism in the phylum Apicomplexa. However, due to their lack of direct clinical significance to humans, gregarines have been largely overlooked in research.

Most known species have barely been examined since their initial descriptions, which often predate the advent of modern sequencing and electron microscopy techniques. As a result, only a fraction of gregarine species has been documented with ultrastructural or molecular data, with this gap being particularly pronounced among those infecting freshwater hosts. Compounding this issue is the significant underrepresentation of freshwater ecosystems in protist metagenomic surveys, leading to a scarcity of environmental sequences from freshwater gregarines.

To address this, the present project has screened through over 60 common freshwater invertebrate species in both degraded and close to natural stream systems in North Rhine-Westphalia. So far over a dozen gregarine species have been identified. SSU DNA sequences have been retrieved for phylogenetic analyses to explore their relationships. Additionally, SEM micrographs have been produced for several of these newly sequenced species to comprehensively characterize a small collection of freshwater gregarines.

Hitchhiking Bacteria: Diverging effects of different tyre wear particles on microbial biofilm composition

Authors:

Dana Bludau [1, 2, 3], Sophie Volkenandt1, Julian Wagenhofer4, Frank Nitsche [4], Hartmut Arndt [4], Jens Boenigk [1, 2]

[1] Department Biodiversity, University of Duisburg–Essen, Essen, Germany
[2] Center for Water and Environmental Research, University of Duisburg–Essen, Essen, Germany
[3] Department of Engineering and Natural Sciences, Westphalian University of Applied Sciences, Recklinghausen, Germany
[4] Department of General Ecology, Institute of Zoology, University of Cologne, Cologne, Germany

Abstract:

Tyre wear particles (TWP) are an emerging form of microplastic pollution in freshwater systems, providing surfaces for microbial colonization while potentially altering microbial communities. We investigated how TWP size, wear condition, and intended vehicle use influence microbial biofilm composition. Over four weeks, TWP were incubated in the Rhine River alongside size-matched sediment controls, followed by 16S V4 rRNA amplicon sequencing.

Our results reveal significant differences in microbial composition between TWP and sediment biofilms, with TWP exhibiting markedly reduced biodiversity. Particle size played a crucial role: larger TWP further decreased biodiversity compared to smaller particles. Interestingly, Aquabacterium and Ketobacter were strongly enriched on TWP suggesting a selective advantage under these conditions.

These findings reveal the effects of TWP on microbial biofilm communities, emphasizing their potential role in altering freshwater microbial ecosystems. Given the widespread release of TWP, understanding their ecological impact is crucial for assessing their role in aquatic pollution and ecosystem functioning.

Testate amoebae : a powerful, multi-faceted group of bioindicators for peatland management

AUTHORS

Robin CALISTI [1], Edward A.D. Mitchell [1]

[1] Laboratory of Soil Biodiversity, University of Neuchâtel, Switzerland

ABSTRACT

Boreal peatlands are increasingly threatened by climate change and anthropogenic disturbances, such as drainage, which lead to a decline in their water table, promoting peat decomposition and turning these C-sinks into sources of carbon dioxide (CO_2). Conversely, peatlands with higher water tables (natural or restored) tend to release methane (CH_4), a process driven by anoxic methanogenic Archaea living in the water-saturated peat. Given the significant role of peatlands in the global carbon cycle, developing effective methods for monitoring water table (WT) dynamics and associated greenhouse gas (GHG) fluxes is crucial for quantifying their contribution to climate change, informing restoration strategies and providing reliable data for carbon credits assessments. Peatland restoration aims both to restore biodiversity and minimize C loss or ideally fix C but concomitant releases of CH4 need to be quantified as well.

Testate amoebae (TA), a paraphyletic group of shelled protists, are highly diverse and abundant in boreal peatlands. These microorganisms are commonly used as bioindicators of water table depth through the application of transfer functions. This modelling approach relies on extensive datasets of TA community and associated environmental variables, from which species-specific preferences and tolerances are derived. By applying these transfer functions, TA can be utilized to infer past and present hydrological conditions in peatlands. Here, we present several case studies illustrating the application of TA in assessing peatland WT and evaluating the effects of peatland hydrological restoration through water table depth reconstruction.

As water table depth is a key driver of GHG fluxes we developed a transfer function using TA as bioindicators of greenhouse gas fluxes (CO_2 and CH_4) in peatland ecosystems. We collected GHG flux data from four peatlands in the Jura Mountains from chamber measurements and correlated these fluxes with TA communities to build transfer functions. The transfer function for CH4 show better performance than the one for CO2 for which more data will be needed. This approach offers a cost-effective and time-efficient alternative to direct GHG flux measurements, providing a valuable tool for assessing peatland C dynamics and optimizing renaturation strategies.

Impact of pig cadavers on forest soil cercomonads (Rhizaria: Cercozoa: Cercomonadida), assessed by high-throughput sequencing

AUTHORS

Arnaud Dano [1], Chistophe V.W. Seppey [1], Ildikò Szelecz [1], David Singer [1], Isacco Darini [1], Edouard Cattin [1], Edward A.D. Mitchell [1], Guillaume Lentendu [1] & Clément Duckert [1]

[1] Laboratory of Soil Biodiversity, University of Neuchâtel, Rue Emile-Argand 11, 2000 Neuchâtel, Switzerland

ABSTRACT

Cadavers decomposing in a natural setting modify the soil abiotic and biotic characteristics. Several studies have described the temporal patterns of cadaver impact on soil chemistry and organisms with the aim to develop (bio-)indicators of the post-mortem interval (PMI), but detailed studies on specific groups of soil protists are scarce. We conducted a long-time experiment (ca. 3 years) in a Swiss deciduous forest where soil samples we collected under pig cadavers and control plots with the goal to study the cercomonads, and abundant and widespread group of bacterivorous soil zooflagellates. Cercomonads are known to respond quickly to changes in microenvironmental conditions, and we therefore hypothesized that they would strongly respond to decomposing cadavers. Given the high impact of cadaver fluids we hypothesised that indicators of cadaver presence would likely represent novel lineages. The soil DNA was extracted and the SSU ribosomal RNA gene was amplified between the V4 and V9 regions targeting the cercomonads. The resulting amplicons were sequenced using the Single Molecule, Real-Time technology from Pacific Biosciences (PacBio). A total of 679 operational taxonomic units (OTUs) were obtained, of which 121 were cercomonads. A maximum likelihood (ML) phylogenetic analysis showed that these cercomonad OTUs belonged to all known genera of this order (i.e. Cercomonas, Eocercomonas, Paracercomonas, Metabolomas, Nucleocercomonas, Cavernomonas and Brevimastigomonas) but some also seemed to belong to new clades. Ca. 13% (16) OTUs in genera Cercomonas, Eocercomonas and Paracercomonas were significantly related to cadaver presence. Some strongly declined in abundance in the early stages of decomposition while some reached highest abundance at specific decomposition stages. These results suggest that cercomonads could be used as forensic bio-indicators (indicators of cadavers at least at one stage or indicators of cadaver absence) in forests to assess the (past) presence of a cadaver or to estimate the PMI.

R-bodies of Paramecium endosymbiont Caedimonas varicaedens and various nonendosymbiotic bacteria are diverse in both morphology and expansion kinetic behavior

Authors:

Lennart Dörr [1], Robin Ghosh [2], Michael Schweikert [3]

[1] Department of Biobased Materials, Institute of Biomaterials and Biomolecular Systems, University of Stuttgart, Pfaffenwaldring 57, 70569 Stuttgart, Germany
[2] Department of Bioenergetics, Institute of Biomaterials and Biomolecular Systems, University of Stuttgart, Pfaffenwaldring 57, 70569 Stuttgart, Germany. Present address: Department of Biophysics, Institute of Biomaterials and Biomolecular Systems, University of Stuttgart, Pfaffenwaldring 57 and Institute of Energy Efficiency in Production, University of Stuttgart, Nobelstr. 12, 70569 Stuttgart, Germany
[3] Department of Biobased Materials, Institute of Biomaterials and Biomolecular Systems, University of Stuttgart, Pfaffenwaldring 57, 70569 Stuttgart, Germany and SRF Advanced Materials Innovation and Characterization (AMICA), University of Stuttgart, Pfaffenwaldring 31, 70569, Stuttgart, Germany

Abstract:

R-bodies are coiled proteinaceous ribbon structures, present in a variety of gram-negative bacteria, and are responsible for the so-called ‘killer-effect’ in paramecia. They are approx. 200500 nm in width and can reversibly transition from their coiled resting state into an approx. 310 µm long rod under certain conditions, e.g. a decrease in pH. Whereas the R-bodies of Paramecium endosymbiont Caedibacter taeniospiralis are well-characterized in their morphology and kinetic behavior, those of other bacteria, such as the paramecial endosymbiont Caedimonas varicaedens or those of many non-endosymbiotic bacteria, have only been sparsely characterized, and not in a genomic context. Using light- and electronmicroscopic methods, including high frame-rate video recordings of the R-body shape-transitions, we analyzed the R-body morphologies of six different proteobacteria, as well as their kinetic behaviour and induction. These data were compared to available genetic information to extract systematic defining features.

Distinct Transcriptional Mechanisms in Paramecium tetraurelia: Exploring the Roles of DSIF and Spt6 in Pol II-driven Processes

Authors:

Franziska Drews [1], Rebekka Obermann [1], Ignasi Forné [2], Axel Imhof [2], Martin Simon [1]

[1] Molecular Cell Biology and Microbiology, Faculty of Mathematics and Natural Sciences, University of Wuppertal, Germany
[2] ZfP, Ludwig-Maximilians-University of Munich, Planegg-Martinsried, Germany

Abstract:

The regulation of genes is critical for cells to adapt quickly to changing environmental conditions while maintaining homeostasis. This regulation involves the swift activation or repression of gene transcription, primarily controlled at the level of mRNA synthesis by the multi-subunit RNA Polymerase II (Pol II) complex. The largest Pol II subunit, Rpb1, is one of the most extensively studied structures in terms of transcriptional regulation, a mechanism that involves sequential phosphorylation at the carboxy-terminal domain (CTD) of Rpb[1] This phosphorylation is orchestrated by various consecutively assembling factors which guide the activity and efficiency of Pol II.

In Paramecium tetraurelia, not only does the Pol II CTD lack the characteristic structure described for other model organisms but moreover, database mining approaches reveal that several subunits of transcriptional regulatory complexes are either fully absent or significantly divergent. Thereby, Paramecium serves as an intriguing model for studying RNA transcription and the epigenetic machinery, probably operating through fundamentally distinct mechanisms compared to other eukaryotes.

Here we focus on two factors being crucial for transcriptional elongation and termination: the DSIFcomplex composed of SPT4/Spt5 and the histone chaperone Spt[6] Spt5 is a universally conserved elongation factor that interacts with Pol II and has been described to be involved in ncRNA transcription during Paramecium sexual development while its role in mRNA transcription in vegetative growth remains elusive. Furthermore, preliminary RNAi experiments revealed Spt6 being crucial for cell viability, probably due to its indispensable function in gene regulation. Thereby, interactions between Pol II and the described factors in Paramecium are particularly compelling, as they highlight both conserved and organism-specific features. This contributes to a more comprehensive understanding of the evolution of transcriptional regulation and will reveal unique adaptations of the machinery in ciliates in future.

A revised classification of the testate amoeba family Euglyphidae based on scale morphology and DNA barcoding

AUTHORS

Clément Duckert, Edward A.D. Mitchell, Enrique Lara & Ralf Meisterfeld

ABSTRACT

The family Euglyphidae (Rhizaria : Cercozoa : Euglyphida), characterized by one or several rows of conspicuous serrated scales surrounding the aperture, is one the most iconic groups of testate amoebae. However, the knowledge of their taxonomy is still very incomplete, which prevents them from being used as ecological proxies despite their presence and abundance in most terrestrial or freshwater habitats. Furthermore, despite evidence that the current taxonomic framework is inadequate, this group has not been critically reviewed since Decloitre's monograph in 1962. As such, the taxonomic literature of Euglyphidae is a taxonomic and nomenclatural mess. Here we re-evaluate the systematics of the group, and propose a new classification based on scanning electron microscopy, DNA barcoding and a critical review of the literature. We describe 23 new species and invalidate most taxa that were described before the onset of scanning electron microscopy as a taxonomy tool. Finally, we define sections for use as a simplified taxonomic framework to study and report observations of Euglyphidae based on light microscopy as generally done by (paleo)ecologists as identification at higher taxonomic resolution is considered hopeless leading to inconsistencies among analysts and confusion in the (palaeo)ecological litterature.

From single cells to shells: Lorica formation in the model tintinnid genus Schmidingerella (Alveolata, Ciliophora)

AUTHORS:

Maximilian H. Ganser, Birgit Weißenbacher, Sabine Agatha
Department of Environment and Biodiversity, Paris Lodron University Salzburg, Salzburg, Austria

ABSTRACT:

Tintinnid ciliates are marine planktonic protists distinguished by their characteristic tube- or vase-shaped shells called loricae. Since their first documented observations over 230 years ago, the loricae and the process by which these unicellular organisms construct them has fascinated scientists. Despite significant interest, several aspects of lorica formation remain unclear, and no documentation exists detailing the entire process—from material production via secretion to assembly. During daily cell division, tintinnids produce substantial quantities of material, which the daughter cell uses to construct its own lorica following transverse fission. We investigated lorica formation in the model genus Schmidingerella Agatha & Strüder-Kypke, 2012. Using monoclonal culture material, we examined living cells as well as chemically and cryofixed specimens to study morphological and ultrastructural changes of the organisms and the biomaterial across the cell cycle through light and electron microscopy. For the first time, we reconstructed the cellular process of lorica material production, elucidating its genesis, timing, and distribution during cell division. Additionally, we estimated the final material volume generated for constructing a new lorica. Finally, detailed live observations revealed the secretion process, providing unprecedented insights into the interplay between tintinnid cell behaviour and the self-assembly dynamics of this unique biomaterial.

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Under the cover of darkness: how Plasmodiophora brassicae affects Arabidopsis thaliana physiology during the night

AUTHORS

Andrea Garvetto [1], Michaela Hittorf [1], Freia Benade [2], Susann Auer [2], Jutta Ludwig-Müller [2], Sigrid Neuhauser [1]

[1] Institut für Mikrobiologie, Universität Innsbruck, Innsbruck, Tirol, Österreich
[2] Institut für Botanik, Technische Universität Dresden, Dresden, Deutschland

ABSTRACT

As sessile and light-dependent organisms, plants are inherently attuned to diel cycles of night and day. Among many other processes, diel cycles have been shown to influence the interactions of plants with pathogenic microbes, mostly by means of oscillations in the expression of genes involved in energy allocation and defenses. Specialized plant pathogens evolved to fit host rhythms and/or to act as zeitgebers, modifying the plant rhythms to counter defenses, to better tap into host resources and to carve their own niche. Here, for the first time we produced a circadian RNA-seq dataset of the obligate biotrophic rhizarian parasite Plasmodiophora brassicae (Phytomyxea, Rhizaria) and its host Arabidopsis thaliana in the early (14 days) and late (21 days) phases of clubroot infection. In our first exploratory investigation of this multilayered dataset, we focus on the effects of infection on the plant physiology in daytime and nighttime. We observe a high proportion of genes differentially expressed in the night, which decreases with the host age. GO term analyses show that these genes are mostly enriching processes also influenced during the day, pointing at a previously unrecognized more intense manipulation of the host physiology during the night. Finally, we detect and discuss instances of infection-driven night-specific processes and alterations of night-day rhythms, providing a first temporal atlas of clubroot gene expression.

Beyond Dictyostelids: Unveiling the Hidden Lives of Other Social Amoebae

AUTHORS

Tristan Henderson

ABSTRACT

Organisms that achieve multicellularity display a high degree of cooperation and coordination amongst genetically kin cells in a world where individuals often need to compete for limited resources. For this reason, the innovation of multicellularity and the mechanisms that drive cooperative behaviors have captivated biologists for centuries. However, the array of model organisms we use to understand these biological processes is skewed towards a few select taxa, typically members of Opisthokonta. Yet we know that evolutionary transitions, like multicellularity and collective behaviors, have arisen many times across the tree of life. In this talk, I will provide insights from work on non-dictyostelid social amoebae in their proper context, terrestrial microhabitats. The members of social amoebae are phylogenetically distant, hinting that the biological processes underpinning their collective behavior evolved independently. Differences in their biology become more apparent the more we observe them. Here, I will introduce innovations in culturing techniques of two dung-dwelling species, Copromyxa protea, and Guttulinopsis vulgaris. Our findings show that the life cycles of these social amoebae possess deeper complexities, from bacterial interactions to cellular suicide. With timelapse microscopy and experimental evidence, this talk will briefly explore how careful observation and altering culture conditions can reveal hidden biology in these often-ignored organisms.

Unveiling the mitochondrial architecture of Gastrotricha: insights into evolution and lineage-specific adaptations

AUTHORS

Anush Kosakyan [1,2] , Agata Cesaretti [1], Francesco Saponi [1,2,3], Leandro Gammuto [4], Valentina Serra [5], Giulio Petroni [5], M. Antonio Todaro [1,2]
[1] Department of Life Sciences, University of Modena and Reggio Emilia, via G. Campi, 213/D, 41125, Modena, Italy
[2] Ntional Biodiversity Future Center (NBFC), Piazza Marina 61, 90133 Palermo, Italy
[3] Department of Earth and Marine Sciences, University of Palermo, Via Archirafi, 22, 90123 Palermo, Italy
[4] Department of Biology and Biotechnology "L. Spallanzani". Via A. Ferrata 9, 27100, Pavia, Italy
[5] Department of Biology, University of Pisa, 56126, Pisa, Italy

ABSTRACT

Studies of mitochondrial genomes have significantly advanced our understanding of eukaryotic life, its diversity and complexity. Despite the generation of mtDNA sequences for thousands of specimens, mitochondrial genomic data remains limited or entirely absent for many taxonomic groups. One such group is the phylum Gastrotricha, comprising free-living microscopic aquatic worms with diverse adaptations to both marine and freshwater environments and a fascinating array of reproductive strategies. Of the 900 known gastrotrich species, mitogenome data is available for only two, hindering the comprehensive understanding of the group's deep evolutionary history. In this study, we present the mitochondrial genomes of 20 gastrotrich species to investigate their molecular architecture across different lineages and to identify potential evolutionary events related to the biology and ecology of these organisms. Our analyses reveal a distinct separation between the two gastrotrich orders in terms of mitochondrial genome structure, gene number, and rearrangement. Our data suggest that gastrotrich mitogenomes are lineage-specific, presenting unique adaptations from a genomic perspective. Additionally, our study proposes a fast and reliable methodology to obtain multiple sequences from single microeukaryotes with high success rates. This is particularly important when dealing with specimens that have low genomic material. Therefore, this methodology can be successfully applied also to protists many of which lack genomic datasets.

A taxonomic monograph of hyalospheniid testate amoebae (Amoebozoa: Arcellinida: Hyalospheniformes)

AUTHORS

Anush Kosakyan, Ralf Meisterfeld, Enrique Lara, Clément Duckert, Edward A. D. Mitchell

ABSTRACT

Taxonomic monographs on groups or protists are rare and testate amoebae are a good example of this. Since Georges Deflandre published his monograph on the genus Nebela in 1936 no systematic revision of this beautiful group of testate amoebae had been done. In the meantime, the genus was split into several genera, and many new species were described. A taxonomic revision was clearly overdue.

In this monograph, we present a taxonomic revision of the sub-order Hyalospheniformes (Amoebozoa, Arcellinida), which includes a single family, the Hyalospheniidae. The monograph includes taxonomic keys to genera and species. A total of 14 genera, and 97 species are presented in detail with detailed descriptions of every taxon: light and scanning electron microscopic pictures and/or original line drawings for each species, diagnostic criteria and morphological and morphometrical characteristics notes on the ecology, geographical distribution, taxonomy and molecular data where available. Annotated lists of dubious and incertae sedis species and synonymous names are provided and each case is discussed to make future taxonomic work easier.

This book is designed to benefit protistologists in general, and particularly ecologists and palaeoecologists, by assisting with the ease and accuracy of identification of hyalospheniid testate amoeba species, many of which are useful bioindicators. We also hope that this book will serve as a useful basis for future work regarding the taxonomy, biogeography, and ecology of these beautiful organisms.

Joseph Leidy famously once wrote “How can life be tiresome sol long as there is still a new rhizopod undescribed?” There is no shortage of new Hyalospheniformes awaiting to being described. We hope this book will make the life of passionate taxonomists easier!

Bioaccumulation of Rare Earth Elements, Iron, and Aluminium in three Tetrahymena species

Authors:

Jana Kohl-Chandramohan [1], Michael Schweikert [1,2], Tobias Junginger [3], Ingo Hartenbach [5], Marie-Louise Lemloh [2,4]

[1] University of Stuttgart, Institute of Biomaterials and Biomolecular Systems, 70569 Stuttgart, Germany
[2] University of Stuttgart, SRF AMICA, 70569 Stuttgart, Germany
[3] University of Stuttgart, IWS, Research Facility for Subsurface Remediation (VEGAS), 70569 Stuttgart, Germany
[4] University of Stuttgart, Materials Testing Institute, 70569 Stuttgart, Germany
[5] University of Stuttgart, Institute of Inorganic Chemistry, 70569 Stuttgart, Germany
*Jana.kohl@bio.uni-stuttgart.de

Abstract:

Understanding how organisms can deal with critical elements in their environment is becoming increasingly important with the growing use of high-tech materials and their occurrence in the environment. The unicellular eukaryotic ciliate Tetrahymena can tolerate high concentrations of toxic heavy metals and is known to have developed several detoxification strategies – one of which is the intracellular bioaccumulation and transformation of dissolved heavy metals in their environment into solid intracellular metal-containing particles, with subsequent excretion of the particles into the surrounding media [1].

In our recent research, we investigated the process of tolerance, cellular uptake and bioaccumulation of several metals (La, Ce, Sm, Eu, Gd, Dy, Fe and Al) in tree ciliate species of Tetrahymena using light and electron microscopy (SEM-EDX) as well as quantitative analytical methods (ICP-OES). Exposure of the cells of the tree species to dissolved metals in their organic growth medium resulted in the uptake of the metals and an intracellular bioaccumulation with the formation of biogenic metal-containing particles inside the food vacuoles of the cells. The particles are excreted into the surrounding medium within a few hours. They consist of the respectively added metal in an organic matrix. The Tetrahymena species depending size of the particles varies between [2]4-[3]1 µm. A depletion rate of 45-97 % of the respective rare earth element concentrations in the medium of the cells was observed after 48 h. [2]

Microbial bioaccumulation pathways are a promising approach to discover new bio-inspired strategies for recycling or remediation. Furthermore, the study of bio-composite materials, such as these metalcontaining particles, is of interest for novel applications in medicine, chemistry or materials science [3].

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Bioaccumulation of Rare Earth Elements, Iron, and Aluminium in three Tetrahymena species

Authors

Jana Kohl-Chandramohan [1], Michael Schweikert [1,2], Tobias Junginger [3], Ingo Hartenbach [5], Marie-Louise Lemloh [2,4]

[1] University of Stuttgart, Institute of Biomaterials and Biomolecular Systems, 70569 Stuttgart, Germany
[2] University of Stuttgart, SRF AMICA, 70569 Stuttgart, Germany
[3] University of Stuttgart, IWS, Research Facility for Subsurface Remediation (VEGAS), 70569 Stuttgart, Germany
[4] University of Stuttgart, Materials Testing Institute, 70569 Stuttgart, Germany
[5] University of Stuttgart, Institute of Inorganic Chemistry, 70569 Stuttgart, Germany
*Jana.kohl@bio.uni-stuttgart.de

Abstract

Understanding how organisms can deal with critical elements in their environment is becoming increasingly important with the growing use of high-tech materials and their occurrence in the environment. The unicellular eukaryotic ciliate Tetrahymena can tolerate high concentrations of toxic heavy metals and is known to have developed several detoxification strategies – one of which is the intracellular bioaccumulation and transformation of dissolved heavy metals in their environment into solid intracellular metal-containing particles, with subsequent excretion of the particles into the surrounding media [1].

In our recent research, we investigated the process of tolerance, cellular uptake and bioaccumulation of several metals (La, Ce, Sm, Eu, Gd, Dy, Fe, and Al) in three ciliate species of Tetrahymena using light and electron microscopy (SEM-EDX) as well as quantitative analytical methods (ICP-OES). Exposure of the cells of the three species to dissolved metals in their organic growth medium resulted in the uptake of the metals and an intracellular bioaccumulation with the formation of biogenic metal-containing particles inside the food vacuoles of the cells. The particles are excreted into the surrounding medium within a few hours. They consist of the respectively added metal in an organic matrix. The Tetrahymena species depending size of the particles varies between 2.5-3.2 µm. A depletion rate of 26-87 % of the respective rare earth element concentrations in the medium of the cells was observed after 48 h. [2]

Microbial bioaccumulation pathways are a promising approach to discover new bio-inspired strategies for recycling or remediation. Furthermore, the study of bio-composite materials, such as these metal-containing particles, is of interest for novel applications in medicine, chemistry or materials science [3].

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Arcellinida metabarcoding, a new tool for environmental health evaluation in lentic systems

AUTHORS

Enrique Lara [1], Rubén González Miguéns [2], Carmen Soler Zamora [1,3]
[1] Real Jardín Botánico-CSIC, Madrid, España
[2] Institut de Biologia Evolutiva (CSIC-Universitat Pompeu Fabra), Barcelona, España
[3] Eurofins Cavendish, Ctra. Bailén-Motril, Parcela 102-B, Pol. Juncaril 18210 Peligros, Granada, Spain

ABSTRACT

Bioindication, the evaluation biological responses to environmental perturbations, is crucial for assessing environmental health. Traditionally, bioindication in freshwater ecosystems relied on macroscopic organisms such as arthropods. Nowadays, the technological leap forward brought by massive sequencing and applied to environmental DNA (eDNA) allows using protists as bioindicators without the need of morphological identification. We propose here a novel eDNAbased approach using Arcellinida, a group of top predators among protists, to monitor freshwater ecosystems quality. In that purpose, we firstly apply a specific eDNA protocol to evaluate their diversity and the connectivity between sites. Then, we characterized the Arcellinida diversity over one year at three different points of the Lake Sanabria, an ancient glacier lake known to be subjected to anthropogenic disturbances, and compared this diversity with an undisturbed control site. Results indicate limited connectivity between the different ecosystems, and an edge effect in the flood zone in the shore of Lake Sanabria. Disturbed freshwater ecosystems exhibited reduced Arcellinida diversity at both specific and infraspecific levels, providing valuable insights into recent perturbations. Arcellinida-based bioindication provides a sensitive, accurate and easy to interpret protocol for monitoring disturbances in freshwater ecosystems. It represents a valuable tool for environmental assessments and conservation strategies.

Integrating High Throughput Molecular and Optical Methods to Study Protistan Abundances in Groundwater Ecosystems

Authors:

Dr. Nadine Möbius [1,2], Dr. Susanne Dunker [2,3], Dr. Anna Maria Fiore-Donno [4], Prof. Antonis Chatzinotas [2,5], Prof. Martin Schlegel [2,6], Dr. Martina Herrmann [2,7]

[1] FSU Jena, Institute of Biodiversity
[2] German Center for Integrative Biodiversity Research (iDiv) Halle Jena Leipzig
[3] Helmholtz Centre for Environmental Research-UFZ, Department Physiological Diversity
[4] University of Cologne, Institute of Zoology
[5] Helmholtz Centre for Environmental Research-UFZ, Department of Applied Microbial Ecology University of Leipzig
[6] University of Leipzig, Institute of Biology, Biodiversity and Evolution
[7] FSU Jena, Institute of Biodiversity

Abstract:

Heterotrophic bacterivorous protists play a pivotal role in microbial food webs. However, their impact on groundwater bacterial communities and organic carbon transfer to higher trophic levels remains largely unknown. Assessing their role in trophic interactions using molecular techniques has been limited by the variability in 18S rRNA gene copy numbers, complicating the quantification of protists.
Our study introduces a novel approach integrating high-throughput molecular and optical methods to accurately estimate protistan abundances. Our key objective is the establishment of protist enumeration by Multispectral Imaging Flow Cytometry (MIFC), combined with qPCR assays and 18S rRNA gene targeted amplicon sequencing, to derive taxon-specific correction factors, facilitating precise estimation of key taxa abundances from molecular data. In addition, we aim to compare protistan communities between carbonate-rock (Hainich Critical Zone Exploratory) and sandstone aquifers (Saale-Elster-Sandstone Observatory) located in Thuringia, using molecular and cultivation-dependent approaches. Protistan monocultures were used to successfully generate initial reference image datasets using MIFC, covering sizes from 3 to 50 µm and various morphotypes. Convolutional neural network (CNN) training achieved over 85% precision in predicting protistan morphotypes. Enrichments of groundwater protistan communities initially exhibited predominance of nanoflagellates (3-
15 µm) and flagellates (15-20 µm), followed by successional changes in favor of ciliates and amoebae (Acanthamoeba, Hartmannella, Vahlkampfia) within 1-2 weeks. By 4-6 weeks, occasional heliozoans and Aspidisca sp. emerged.

Our results demonstrate that MIFC can effectively distinguish protistan taxa based on morphological features, enabling high-throughput automated quantification. Ciliate abundance in distinct groundwater sites have been estimated based on first taxon-specific correction factors identified using qPCR. Abundance estimations along with improved community assessment by metatranscriptomics will help to advance our understanding of microbial food web structure in aquifers from diverse geological settings.

Charting the landscape of cytoskeletal diversity in microbial eukaryotes

AUTHORS

Felix Mikus [1], Armando Rubio Ramos [2], Hiral Shah [1], Marine Olivetta [3], Susanne Borgers [2], Jonas Hellgoth [1], Clémence Saint-Donat [1], Margarida Araújo [1], Chandni Bhickta [1], Paulina Cherek [4], Jone Bilbao [5], Estibalitz Txurruka [5], Nikolaus Leisch [4], Yannick Schwab [1,6], Filip Husnik [7], Sergio Seoane [5], Ian Probert [8], Paul Guichard [2], Virginie Hamel [2], Gautam Dey [1], Omaya Dudin [3].
[1] Cell Biology and Biophysics, European Molecular Biology Laboratory (EMBL), Heidelberg, Germany.
[2] University of Geneva, Department of Molecular and Cellular Biology, Faculty of Sciences, Geneva, Switzerland.
[3] University of Geneva, Department of Biochemistry, Faculty of Sciences, Geneva, Switzerland.
[4] Mobile Laboratories Facility, European Molecular Biology Laboratory (EMBL), Heidelberg, Germany.
[5] Department of Plant Biology and Ecology, Faculty of Science and Technology, University of the Basque Country, UPV/EHU, Leioa, Spain.
[6] Electron Microscopy Core Facility, European Molecular Biology Laboratory (EMBL), Heidelberg, Germany.
[7] Okinawa Institute of Science and Technology Graduate University, Okinawa, Japan.
[8] Sorbonne Université, CNRS, FR2424, Roscoff Culture Collection, Station Biologique de Roscoff, Roscoff, France.

ABSTRACT

Microbial eukaryotes are small and often resistant to standard labelling and imaging techniques, and therefore remain understudied – despite their critical ecological importance - with the exception of a few established models. Here, we use Ultrastructure Expansion Microscopy (U-ExM) to carry out high-resolution volumetric imaging of over 200 cultured planktonic eukaryotes across major lineages. By combining U-ExM with pan- and specific immuno-labelling, we reveal novel microtubule and centrin-containing elements and assign molecular identities to enigmatic cytoskeletal structures observed previously only by electron microscopy. Our investigation represents the first systematic survey of the extensive cytoskeletal diversity on display across the eukaryotic tree, including the major species groups of dinoflagellates, haptophytes, ciliates, euglenids, cryptomonads, and green algae. Our U-ExM approach extends to mixed environmental samples, paving the way for environmental cell biology at ultrastructural resolution and unprecedented scale, a crucial step towards understanding and protecting complex ecosystems in the face of biodiversity loss.

The untapped value of moss herbaria for protist biodiversity and biogeography: examples from tropical Sphagnum and description of a new Centropyxis species from Peru

AUTHORS

Benjamin Ory [1], Ferry Siemensma [2], Michelle Price [3], Edward A. D. Mitchell [1]

[1] Laboratory of Soil Biodiversity, University of Neuchâtel, Switzerland
[2] Julianaweg 10 1241VW, Kortenhoef, the Netherlands
[3] Conservatoire et Jardin Botaniques de Genève, Switzerland

ABSTRACT

Moss herbaria represent an underutilized resource for exploring protist biodiversity and biogeography. These collections, which include over billions of moss specimens globally, offer temporal and spatial records spanning centuries, allowing the reconstruction of past ecosystems and biodiversity patterns. Until recently, their potential for studying testate amoebae and other protists was unexplored.

Recent studies have demonstrated how herbarium mosses can reveal long-term shifts in protist communities and environmental conditions. Using herbarium material opens research possibilities in areas that are now inaccessible or that have been heavily altered or destroyed by human activities.

We present the discovery of a new Centropyxis species from a tropical Sphagnum sample from in Peru from the Geneva Botanical Garden collection. The new species is characterised by distinctive morphological features: sharp, regularly spaced tooth-like projections on the ventral half of the aperture. Based on these morphological characteristics, which we analysed by light and scanning electron microscopy this morphotype is clearly a new species belonging to the genus Centropyxis.

The study also illustrates how herbarium-based research can provide new insights into the diversity and geographical distribution of protist species. Our methodology, which includes rehydration and gentle centrifugation to preserve delicate moss structures, ensures minimal sample damage, critical when working with rare or irreplaceable specimens. This approach opens the door to a large-scale survey of protist diversity in herbarium collections worldwide.

Analysis of Ptiwi proteins in the exogenous RNAi pathway in Paramecium tetraurelia reveal so far unknown involvements in RNAi by Feeding

Authors:

Pirritano, Marcello [1], Drews, Franziska [2], Franzenburg, Sören [3], Simon, Martin [4]

[1] Molecular Cell Biology and Microbiology, Faculty of Mathematics and Natural Sciences, University of Wuppertal, Wuppertal, Germany
[2] Molecular Cell Biology and Microbiology, Faculty of Mathematics and Natural Sciences, University of Wuppertal, Wuppertal, Germany
[3] Competence Centre for Genomic Analysis, Christian-Albrechts-University Kiel, 24118 Kiel, Germany
[4] Molecular Cell Biology and Microbiology, Faculty of Mathematics and Natural Sciences, University of Wuppertal, Wuppertal, Germany

Abstract:

RNAi by Feeding described a phenomenon where exogenous dsRNA is taken up via the food vacuole and processed into primary siRNAs. These siRNAs can engage in base paring with mRNA molecules, promoting their degradation or blockage of translation, leading to a phenotypical silencing of the target gene. Using the attacked mRNA as a template, secondary siRNAs can be produced.

This function of siRNAs has to be mediated by proteins, the so called argonautes. They load the produced siRNAs, scan the mRNA population within the cell to find the target molecules, and mediate the degradation of the mRNA molecule. However, they can also translocate in the cell's nucleus and establish chromatin modifications using the loaded siRNA as a guide to the gene locus, preventing the production of mRNA in the first place.

In Paramecium tetraurelia, a total of three different argonaute proteins, called Ptiwis, are reported to be involved in this pathway. Speculations are that Ptiwi13 associates with primary siRNAs, while Ptiwi12 and 15 load secondary siRNAs.

In this work, we analyzed the association of the three different Ptiwis with primary and secondary siRNAs to shed light on the involvement of the three Ptiwis in the exogenous RNAi process. We included Ptiwi14 in the analysis, described as not involved in the pathway, intended as a negative control, revealing some surprising new aspects about Ptiwi14's involvement in paramecium RNAi mechanisms.

Towards a better understanding of gregarine-host relationships

Authors:

Sonja Rückert

Department of Eukaryotic Microbiology University of Duisburg-Essen, Essen, Germany

Abstract:

Gregarines are known as obligate parasites in the taxon Apicomplexa, although their relationship with their hosts is often unknown or assumed to be neutral. In this talk I will provide an overview of recent advancements in developing gregarine-host model systems to elucidate the complex interactions between these apicomplexan symbionts and their invertebrate hosts. Gregarines exhibit a dynamic relationship with their hosts, that ranges on the spectrum from mutualism to parasitism, influenced by environmental factors such as nutrient availability or environmental stressors. Fluctuating conditions, can shift these interactions, altering host fitness, development, and survival. This can have knock-on effects, if host organisms play essential roles in their ecosystems like e.g. *Gammarus pulex*, an amphipod integral to maintaining the structure and function of freshwater ecosystems. This emphasizes the need for integrative models to study gregarine-host relationships under natural and experimental conditions.

Hidden biodiversity – challenge in abundance

Authors:

Martin Schlegel
Institue of Biology, Leipzig University

Abstract:

We applied metabarcoding with group-specific primers for a comprehensive assessment of the diverse protist phyla Cercoza (Rhizaria) and Oomycota (Stramenopiles) across all ecological compartments from forest soils to the canopy region in a temperate and tropical biome.

In the Leipzig floodplain forest, we detected distinct communities of ~ 400 Oomycota OTUs and >700 Cercozoa OTUs. Most variation in beta diversity was explained by microhabitat differences within tree canopies. We observed obligate biotrophic species, showing tree canopies to be a hitherto overlooked reservoir for parasitic protists. In addition, we found a high diversity in air samples. In spring, heterogeneity within alpha diversity was high during initial colonization. Subsequently, communities underwent compositional changes in autumn, reflecting recurring phenological changes during colonization.

In a tropical rainforest in the northeast of Papua New Guinea we detected distinct communities of 652 and 283 OTUs for Cercozoa and Oomycota, in three autochthonous tree species. In Cercozoa most taxa corresponded to those known from temperate zones. However, in Oomycetes, approximately 50% of all OTUs showed a sequence identity of less than 70% to any reference sequence, pointing to a substantial unknown diversity of microbial eukaryotes.

In a metatranscriptomic approach we assessed the entire living canopy bark microbiome in the Leipzig floodplain forest. With almost 1500 genera, we found a high microbial diversity on three tree species with distinct bark textures (Quercus robur, Tilia cordata), both with rough bark, and maple (Acer
pseudoplatanus) with smooth bark. Regarding Cercoza and Oomycota we found a broad taxonomic overlap with our metabarcoding data. Core co-occurrence network analysis revealed a rich food web dominated by algal primary producers, and bacterial and fungal decomposers, sustaining a diverse community of consumers, including protists, microscopic Metazoa and predatory bacteria. Co-occurring algae and fungi highlight the importance of algal-fungal lichen symbioses even at the microscopic scale.

A metagenomic roadmap to global freshwater mitochondrial diversity

Authors:

Lucas Serra Moncadas, Adrian-Stefan Andrei
Limnological Station, Department of Plant and Microbial Biology, University of Zurich

Abstract:

Freshwater resources make up just [3]5% of Earth's water, with only 0.25% readily accessible in lakes, yet they play an outsized role in sustaining life. Despite their limited surface area, these lakes drive global carbon cycling, support high biodiversity, and provide essential resources—including drinking water, irrigation, fisheries, and recreation. Their microbial communities underpin nutrient cycling and water quality but face increasing threats from pollution, extreme weather, and rising temperatures linked to climate change.
Among these microorganisms, eukaryotic plankton (EP) stands out for fuelling primary production and aquatic food webs. While metabarcoding analyses have advanced our grasp of EP diversity and community dynamics, they often lack species-level resolution and phylogenetic signals crucial for deeper evolutionary or biogeographic insights—and for effective long-term monitoring. Recovering EP genomes from environmental samples is also challenging, given the size and complexity of EP nuclear chromosomes, and the dominance of prokaryotic DNA in shotgun sequencing runs.
To address these hurdles, we recovered EP mitochondrial genomes via a cultivation-free, genome-resolved metagenomic approach, directly analysing EP genomic data from freshwater samples. In a proof-of-concept study, we assembled a globally distributed database of ~3,400 metagenomes, and applied a machine learning model (9[4]8% sensitivity, 99.83% accuracy) to identify ~80,000 candidate mitochondrial genomes. Rigorous curation yielded ~20,000 EP mitochondrial genomes, 81% of which were taxonomically classified. Compared with reference databases (RefSeq 224) dominated by metazoan and plant lineages, our dataset expanded EP taxonomic diversity by up to 24-fold (Cryptophyceae) and phylogenetic diversity by up to 52-fold (SAR). We further increased representation of historically undersampled EP lineages— particularly SAR, Cryptophyceae, and Haptista—totalling 13,049 recovered genomes versus only 333 representatives in current databases. These findings underscore the power of mitochondrial metagenomics to illuminate EP diversity, guide conservation, and predict how environmental shifts may alter freshwater ecosystems.

Occurrence of ciliates in the sediment of the Southern Baltic

Authors:

Anja Scherwaß
Huth Svenja, Arndt Hartmut

Abstract:

The talk presents results from a study of protozoans (here with focus on ciliates) in the sediment of the Baltic Sea in the area of the German Baltic Sea coast. The results are part of a study examining the possible impact of trawling on organisms in the sediment in the Baltic Sea. The trawling areas as well as areas which were unaffected of trawling were sampled in several sampling sessions. Various species of protozoa were isolated from these samplings, with previously unknown species also being discovered. In the talk, the results of these analyzes will be presented and the possible influence of trawling on protozoological colonization will be discussed. We also address different tolerances to salinity of the species found, because different salinities are characteristic for the Baltic Sea and could be also detected during the sampling campaign.

Assessing protistan communities from agricultural soils with nanopore Technologies

Authors

David Singer [1], Aline Adler [2], Sarah Scotton [2], Sarah Wegmüller [2], Alexandre Kuhn [2], Thierry J. Heger [1]

1. Changins, HESSO University of Applied Sciences and Arts Western Switzerland, Switzerland
2. School of Engineering, HES-SO Valais-Wallis, HEI, HES-SO University of Applied, Sciences and Arts Western Switzerland. Contact: david.singer@changins.ch

Abstract

Soil protists play multiple roles in agricultural environments. For example, Plasmodiophora brassicae, the causative agent of clubroot, is a growing issue for the cultivation of Brassica crops across the world. Monitoring protist diversity, including pathogenic species, is essential for the early identification of potential plant health threats. Early detection of soilborne plant pathogens could contribute to the development of efficient and sustainable agricultural management practices.
Molecular methods offer a promising approach for developing such detection tools. Advances in sequencing technology now enable the recovery of long DNA fragments such as the full length of the ribosomal operon. These fragments provide high phylogenetic resolution and facilitate the characterization of protist taxa at the species or strain level. Nevertheless, further research is needed to optimize reliable and efficient monitoring methods.
In this project, we developed a protocol using Oxford Nanopore sequencing technology for assessing protists diversity in agricultural soils. We developed and tested a bioinformatic pipeline using DNA sequences from several protist cultures. NanoClust workflow was used to form consensus sequences and PR2 was used for taxonomy assignments. The resulting consensus sequences were up to 100% identical to the culture reference sequences. This dataset will then be compared to similar ones obtained from and Illumina NextSeq platform. Finally, we tested the efficiency of our protocol to detect P. brassicae from infested field soil samples. Altogether, this study highlights the potential of Oxford Nanopore sequencing technology to characterize protist diversity and detect protist pathogens.

Detection of peat in growing substrate based on testate amoeba communities

Authors:

Camille Voegeli, Serge Zaugg, Lena Märki, Clément Duckert, Edward Mitchell

Abstract:

Peat has been the most important growing media component for decades. However, due to the ecological impacts of peat extraction, such as greenhouse gas emissions and biodiversity loss, there is a strong incentive to reduce and eventually eliminate its use. If bans are pronounced, tools are needed to assess if substrates are indeed peat-free, but no such method is available.

To address this, we developed a novel method utilizing peat-specific testate amoeba (TA) species. TA are unicellular microorganisms living in aquatic and terrestrial habitats that produce a shell which is characteristic for each species and allows identification. They are commonly used as bioindicators of present and past environmental conditions in peatlands.

The method is a decision support system based on deep learning to detect peat specific TA within extensive collections of microscopy images from commercial growing media. We identified a shortlist of species exclusive to peatlands. Samples of peat were analysed, and present TA were photographed. These images were then used to train the machine learning system. The species Archerella flavum was found in all peat samples, and Amphitrema wrightianum was also frequent. Both species were absent in non-peat samples.

The proof of concept for this method has been successfully established, enabling the detection of peat in a sample. Our next step is to improve the robustness of the method by expanding the dataset of images and developing a quantification tool to measure the proportion of peat in samples. Additionally, we plan to include samples of cultivated Sphagnum moss to determine if the TA they harbour are different from natural peat.

Disentangling the cryptic Rhynchomonas morphospecies complex by combining phylogenetic, morphological and autoecological methods

Authors:

Wagenhofer Julian, Nitsche Frank, Arndt Hartmut

University of Cologne, Biozentrum, General Ecology, Zülpicher Str. 47b, 50674 Cologne

Abstract:

The Rhynchomonas morphotype has been observed almost globally, with strains isolated from marine, brackish, freshwater, and soil habitats, showcasing its ubiquitous distribution. Rhynchomonas nasuta (Stokes) Klebs was first described in 1888 and renamed in 189[2] Since then, isolates resembling this highly successful and widespread morphotype have been attributed to Rhynchomonas nasuta, which currently remains the only valid and thoroughly described species. However, phylogenetic studies on the Neobodonida have recognized the large genetic variability within this morphospecies complex and have called for a taxonomic revision. This study undertook a taxonomic revision using an integrative approach that combined phylogenetic (18S and 28S rDNA; 90 strains), morphological (DIC and SEM; 16 strains), and autoecological (salinity tolerance; 16 strains) methods. Furthermore, it nearly doubles the number of Rhynchomonas-like 18S rDNA sequences (>1500 nucleotides) by adding 42 new strains to publicly available databases. The phylogenetic results reveal a clear pattern, separating the different strains into six distinct clades. The salinity experiments further support this separation, showing significant differences in tolerance levels among the sub-clades, which contain strains from different environments. Certainly, the isolation of new strains from undersampled habitats will lead to the discovery of additional phylogenetic lineages and further refinement of the current phylogenetic tree.

Blastocystis (Stramenopila) – parasite or commensal?

Authors:

Julia Walochnik, Renate Schneider, Birgit Wagner, Wilhelm Ludwig, Ursula Wiedermann

Institute for Specific Prophylaxis and Tropical Medicine, Center for Pathophysiology, Infectiology and Immunology, Medical University of Vienna
*julia.walochnik@meduniwien.ac.at

Abstract:

Blastocystis is the most prevalent intestinal protist in humans, with assumedly more than one billion individuals colonized, most of them, however, without any symptoms. It lives in the large intestine and divides by binary fission. Blastocystis is regarded as part of the healthy gut microbiota, being more common in normal weight individuals compared to obese and being associated with higher bacterial richness in the gut. Long-term colonization with the same strains seems to be common. However, high Blastocystis density is usually associated with diarrhea and some studies have suggested that Blastocystis may antagonize beneficial gut bacteria.

Blastocystis is a species complex with currently 32 genetic subtypes (ST1-32), ST1-4 being the most prevalent ones in humans. Interestingly, while ST1, ST2, and ST3 seem to have a world-wide distribution, ST4 seems to be restricted to Europe. Most subtypes have a low host-specificity, can infect a wide range of vertebrates and can also be isolated from the environment. The trophozoites are round and have a huge central vacuole, which gave the genus its name. However, it was not until 1991, that a true cyst stage was discovered, which is the only form that can pass through the stomach. Blastocystis also has an amoeboid form, which is found particularly in individuals with symptomatic infections. Despite mainly living anaerobically, Blastocystis does have mitochondrion-like organelles.

At our institution, approximately 10% of the stool samples are positive for Blastocystis by microscopy. While the vast majority of patients have very light infections, we see around 150 cases of moderate and around 50 cases of heavy Blastocystis infections per year. The latter are often associated with other infections or underlying diseases. Genetic subtypes ST1/2 and ST3/4 are approximately equally represented. Treatment, which mostly relies on metronidazole, rarely results in clearance and may be entirely unsuccessful.

Structure and function of soil protist communities across soil microhabitats and their response to land-use change

AUTHORS

Gennuo Wang [1], Zheng Zhou [2], Yan Zhang [1], Stefan Scheu [1] and Valentyna Krashevska [3]

[1] Johann Friedrich Blumenbach Institute of Zoology and Anthropology, University of Göttingen, Göttingen, Germany
[2] Department of Ecology of Tropical Agricultural Systems, University of Hohenheim, Hohenheim, Germany
[3] Senckenberg Biodiversity and Climate Research Centre, Functional Environmental Genomics, Frankfurt, Germany

ABSTRACT

The litter layer and the rhizosphere are the key habitats where resources are provided to the soil food web. However, little is known about how changes in land use affect the community composition of these habitats. In this study, protists, as key regulators of soil microbial diversity and nutrient cycling, are used to investigate ecological roles of litter- and root-associated communities and their response to the conversion of rainforests into plantation systems. Using high-throughput sequencing, we investigated protists in different microhabitats (litter, rhizosphere, and soil) across four land-use systems, i.e., rainforest, shrubland, rubber plantations, and oil palm plantations. Protists in the rhizosphere responded most sensitively to land-use changes, with significantly higher α-diversity and distinct protist community compositions in oil palm plantations compared to the other land-use systems. Soil abiotic factors, including pH, carbon concentration, nitrogen concentration, and water content, as well as biotic factors, including bacterial, fungal, and nematode diversity, jointly regulated protist diversity and community composition, with biotic factors being more important in the rhizosphere than in the litter. Dominance of habitat generalists suggests that the protist community in litter is less sensitive to land use change compared to the rhizosphere. However, compared to litter neither the diversity of specialists in the rhizosphere nor in soil was increased. The findings highlight the key role of different microbial habitats in shaping protist communities, with rhizosphere protist communities more sensitively responding to land-use changes than protist communities in litter. By investigating the responses of protist communities to land-use changes and identifying the drivers in the main soil compartments, this study provides new insights into the mechanisms of how land-use changes alter soil microbial communities.

Keywords: Tropical soil protists, soil compartments, Land-use change, abiotic and biotic factors, High-throughput sequencing, ecological niches, and food web interactions

Spatio-temporal patterns of Tetrahymena and other protists at the edge of chaos

Authors:

Johannes Werner, Hartmut Arndt

Department of General Ecology, Institute of Zoology, University of Cologne, Zuelpicher Straße 47b, D50674 Cologne, Germany.

Abstract:

Spatio-temporal dynamics in microbial communities are crucial for ecosystem functioning and biodiversity maintenance. We designed a microfluidic platform with interconnected habitat patches to investigate spatial ecology at the microscale. Using this tool, we focused on the single-species system of Tetrahymena pyriformis, revealing complex spatio-temporal patterns without external forcing. Our automated analyses documented pattern formation, including chaotic dynamics, across 50 interconnected patches. The system exhibited characteristics of being at the "edge of chaos," displaying a mixture of chaotic and ordered dynamics. This suggests that complexity and unpredictability are fundamental properties of living systems. Different initial conditions led to changes in patterns, highlighting the complexity and inherent unpredictability of self-organized pattern formation. A model incorporating stochastic fluctuations verified the deterministic nature of these patterns.

To demonstrate the utility of the microfluidic chip, we conducted proof-of-concept experiments including a predator-prey interaction between Tetrahymena and the heliozoan ambush predator Raphidiophrys ambigua, and a two-species competition experiment with Tetrahymena and Blepharisma americanum. These experiments highlight the capacity of the chip to identify the behavior of single- and multi-species systems. The platform's ability to track individual cells in real-time or retrospectively using video analysis expands the potential for studying spatial ecology at both individual and population levels. This approach bridges the gap between theoretical models and experimental observations and may reveal general insights into the fundamental nature of living systems and their spatio-temporal organization.

Cultivation of anaerobic ciliates with respiratory endosymbionts

Authors:

Linus M. Zeller [1], Louison Nicolas-Asselineau [1], Bram Vekeman [2], Carolin Otersen [1], Kateřina Koštířová [3], Ondřej Pomahač [3], Ivan Čepička [3], Boran Kartal [1], Jana Milucka [1]

[1] (Biogeochemistry Department, Max Planck Institute for Marine Microbiology, Bremen)
[2] (Department of Microbiology and Ecosystem Science, University Vienna, Vienna)
[3] (Department of Zoology, Charles University, Prague)

Abstract:

The acquisition of obligate bacterial endosymbionts was a fundamental event in the evolution of eukaryotes, giving rise to mitochondria and consequently higher forms of life. The discovery of ‘Candidatus Azoamicus ciliaticola’, a gammaproteobacterial endosymbiont of an anaerobic plagiopylean ciliate (Graf et al. 2021), shows that some extant eukaryotes may also host and possess other 'respiratory' endosymbionts to supplement or even replace their mitochondria. The Azoamicaceae endosymbionts are ubiquitously distributed in various aquatic habitats around the world, including ground-, fresh-, and wastewater. Despite their phylogenetic diversity the symbionts’ hosts appear to be constrained to a single clade of uncultured ciliates within the class Plagiopylea.

Here, we describe a new cultivation approach that has resulted in a successful enrichment of plagiopylean hosts of respiratory endosymbionts. For this, two continuous anoxic bioreactors were specifically designed and set up with sludge samples from a local wastewater treatment plant. These bioreactors have been running for over one year and are continuously supplied with nitrate-replete minimal medium. Subsamples from these bioreactors were used as an inoculum for anoxic batch cultures in which growth of small ciliates (10-20 µm) could be observed after a few weeks. These cultures are subcultivated monthly and are dominated by one or two ciliate morphotypes which reach abundances of up to 1000 cells mL-[1] Using specific primers we could show that these morphotypes belong to this uncultivated plagiopylean clade, comprising at least 3 undescribed ciliate species. Combining specific 18S and 16S FISH probes confirmed that the enriched ciliates are associated with respiratory endosymbionts.

This work thus represents the first ever reported cultivation of plagiopylean ciliates with respiratory endosymbionts, paving way for establishing these ciliates as a model system for protist-bacteria interactions. Furthermore, our work highlights the immense potential of continuous bioreactors as means to specifically enrich so far uncultivated protists.

Poster Abstracts

Effects of salinity and temperature on the growth of freshwater diatoms

Authors:

Alina Becker, Bank Beszteri, Sara Beszteri

Universität Duisburg-Essen, alina.becker@stud.uni-due.de, bank.beszteri@uni-due.de, sara.beszteri@uni-due.de

Abstract:

The global environment changes rapidly due to the anthropogenic climate change. Especially freshwater ecosystems are exposed to many interacting stressors like temperature and salinity. These stressors are also influenced by the consequences of the anthropogenic climate change. They have effects on the composition and biomass of diatoms. Diatoms are one of the most important primary producers on this planet, because they are the foundation of many aquatic food webs. With selected diatom strains, the effect of the combined factors: temperature and salinity on the growth rate was tested. The tested tolerance ranges could indicate which species can tolerate certain changes, such as raised temperature or/and salinity, and which species can't. Different requirements for temperature and salinity can explain the difference between the growth rates of the tested diatoms. Diatoms are known for their affinity of lower temperatures, compared to other algae. In this study the species Cymbella incurvata, Navicula gregaria and Nitzschia linearis were tested. The gathered data shows the affinity of these diatoms for lower temperatures. All species grew best at temperatures from 10 °C to 20 °C, in combination with lower salinity. With increasing salinity, the growth rates decreased at all observed temperatures. At 25 °C the growth rates for N. linearis were the highest. For C. incurvata and N. gregaria the threshold of their tolerance was reached at 25 °C. A threshold or part of a tolerance range for salinity and temperature can be seen for all three tested species. Regarding the data it can be said that with increasing salinity and temperature of freshwater bodies, not all species of diatoms will be able to survive. After passing a certain interspecific threshold, the biodiversity of diatom communities could be rapidly decreasing. This loss of biodiversity can also affect other levels of ecosystems.

Investigation of bioaccumulation in Tetrahymena pyriformis under different cell culture conditions

AUTHORS

Beate Britz [1], Jana Kohl-Chandramohan [2], Marie-Louise Lemloh [1,3]

[1] University of Stuttgart, Materials Testing Institute, 70569 Stuttgart, Germany
[2] University of Stuttgart, Institute of Biomaterials and Biomolecular Systems, 70569 Stuttgart, Germany
[3] University of Stuttgart, SRF AMICA, 70569 Stuttgart, Germany
Beate.Britz@mpa.uni-stuttgart.de

ABSTRACT

The ciliate Tetrahymena pyriformis can tolerate high concentrations of toxic heavy metals including the rare earth element gadolinium (Gd) by exploiting its ability of cellular uptake and intracellular bioaccumulation, to form intracellular particles in food vacuoles and excrete the metal-containing particles into the medium.1,2

In order to evaluate the conditions under which this process of bioaccumulation can be observed, the parameters of the cell culture were varied. Different media (organic and non-organic) were tested as an alternative growth medium to the standard proteose peptone (PP) medium.3 These media were also tested with regard to the maintenance of the ability to bioaccumulate artificial added Gd. Further, several environmental samples from a teaching and research sewage treatment plant were tested with additional elements. The process of bioaccumulation was observed and characterized by using various microscopic techniques, such as light microscopy, scanning electron microscopy (SEM), and energy-dispersive X-ray spectroscopy (EDS).

The pH range in PP in which sufficient cell population growth could be observed was determined with pH 5-10. Bioaccumulation was observed for different cell culture media as well as for environmental samples.

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New heterotrophic flagellates from the pelagial of the Atlantic Ocean

Authors:

Pauline Mische, Manon Dünn, Hartmut Arndt

University of Cologne, Institute of Zoology, Department of Ecology, Zuelpicher Str. 47b, 50674 Cologne, Germany

Abstract:

Protists are the most abundant and diverse eukaryotes in the oceans, yet our understanding of their vertical distribution throughout different ocean depths is limited. We already know that throughout different ocean depths and even in the deep sea, they can maintain a high level of genetic diversity despite challenging environmental conditions such as the absence of light, low temperatures, high pressure levels and low levels of nutrients. Recent studies of the sediments of the deep-sea basins of different oceans have shown that benthic protist communities differ considerably from one another and a high degree of endemism has been found. However, it is still unknown whether benthic communities are exchanged via the pelagial. The aim of the present study is to analyze newly found pelagic taxa of heterotrophic flagellates morphologically and phylogenetically and to determine whether they can be associated with benthicassociated protists of the deep sea or whether a distribution via the pelagial is irrelevant.

The samples examined in this study were collected from the pelagial of the North Atlantic with a focus on the vertical and horizontal distribution of protist communities. All samples were obtained during the cruise of R/V Maria Sibylla Merian, MSM 112/2 from November to December 202[2] Cultures were established from samples collected from the surface to the abyssal depth of 4000m. The work included the isolation, cultivation and phylogenetic and morphological examination of heterotrophic nanoflagellates communities. A morphological and phylogenetic analysis of the taxa identified in these pelagic samples and a comparison with those recorded in deep-sea benthic and pelagic genotype libraries are presented and discussed.

Multigene approach and notes on morphology in the delimitation of the genus Tetmemena (Ciliophora, Hypotrichia, Dorsomarginalia)

Authors:

Maxwell Juti Owuor [1,2], Ulrike Koll [2], Nadia Kostner [2], Elijah Lelmen [3], Alexey Potekhin [2], Thomas Pröschold [2], Geoffrey Odhiambo Ong'ondo [3], Bettina Sonntag [2]

[1] Department of Biochemistry and Molecular Biology, Egerton University, P.O. Box 536, 20115, Egerton, Kenya
[2] Research Department for Limnology, Mondsee, University of Innsbruck, A-5310 Mondsee, Austria
[3] Department of Biological Science, Egerton University, P.O. Box 536, 20115 Egerton, Kenya

Abstract:

Currently, six species and two subspecies are assigned to the genus Tetmemena. However, their phylogenetic analysis, especially based on 18S rRNA, is not robust while their morphological taxonomy is always limited by morphoplasticity and cryptic species. Based on a multigene approach, i.e., 18S rRNA, ITS1 and ITS2 and Cytochrome Oxidase 1 (CO1) the six Tetmemena species were delimited, and results confirmed with morphological data. The results show that the Tetmemena genus is polyphyletic and has five lineages (clusters). Three lineages include T. bifaria and T. polymorpha; T. indica and T. saprai; and T. pustulata and T. vorax. Morphologically, these three lineages would be delimited based on cyst structure and dorsal kinety 4 (DK 4): with spiny cyst and incomplete DK4 in T. bifaria/polymorpha; smooth cyst and incomplete DK4 in T. saprai/indica, and spiny cyst and bipolar DK4 in T. pustulata/vorax. The compensatory base exchange (CBC) confirmed the lineages but not the species. However, T. pustulata (AF508775) from North America was on its own cluster indicating misidentification. The unique cluster of Onychondromus grandis within the Tetmemena subclade is difficult to explain except by ontogenesis.

Eukaryome Dynamics in the Red Coral Corallium rubrum in a Warming Mediterranean Sea

AUTHORS

Camille Prioux [1,2 3], Christine Ferrier-Pagès [3], Denis Allemand [3], Romie Tignat-Perrier [2,3]

[1] Sorbonne Université, Collège Doctoral, Paris, France

[2] Unité de Recherche sur la Biologie des Coraux Précieux CSM - CHANEL, Centre Scientifique de Monaco, 8 Quai Antoine 1er, MC 98000, Monaco, Principality of Monaco

[3] Centre Scientifique de Monaco, 8 Quai Antoine 1er, MC 98000, Principality of Monaco

ABSTRACT

The Mediterranean Sea is warming at a rate 20% faster than the global average, with climate change significantly increasing the frequency and intensity of marine heatwaves (MHWs). These extreme events are wreaking havoc on marine ecosystems, particularly affecting habitat-forming species. Iconic Mediterranean octocoral species, such as Corallium rubrum, are now increasingly vulnerable to temperature-induced diseases and mass mortality.

This study investigates the response of C. rubrum to global warming, focusing on the often-overlooked eukaryome. By combining laboratory experiments with field sampling during the unprecedented MHWs of 2022, we assessed the physiological health of coral hosts, including tissue loss, mortality, and stress-related gene expression. Additionally, we characterized the eukaryome composition through 18S rRNA gene sequencing under varying conditions of control, heat stress, and recovery. To enhance detection of microeukaryotes, we developed novel UnNonMet primers, minimizing interference from host genetic material.

Under normal conditions, the C. rubrum eukaryome was predominantly composed of Dino-Group I, Licnophoridae, and Labyrinthulomycetes. However, under heat stress, dramatic shifts in eukaryome composition occurred, with notable increases in the relative abundance of Ephelotidae, Exobasidiomycetes, Corallicolidae, Labyrinthulomycetes, and Phaeophyceae epibionts. These microbial shifts were observed before any signs of host health decline, and were strongly linked to depth, stress intensity, and colony condition. After two weeks of recovery, coral stress lessened, and the eukaryome largely reverted to its baseline state. Yet, subtle changes persisted, underscoring the potential long-term impacts of repeated MHWs. This highlights the urgent need to understand how successive heatwaves could increase stress on marine organisms, amplifying the threat of ecosystem degradation. These findings significantly enhance our understanding of the ecological consequences of MHWs, underscoring the critical need for immediate climate action to protect C. rubrum and other at-risk Mediterranean coral species.

Multiple origin of coccoid Ulvophyceae (Chlorophyta) discovered by the usage of an integrative approach

AUTHORS

Thomas Pröschold and Tatyana Darienko

Research Department for Limnology Mondsee, University of Innsbruck

ABSTRACT

Coccoid Ulvophyceae are often overlooked despite their wide distribution. They occur as epiphytes on marine seaweeds or grow on stones or on shells of mussels and corals. Most of the species are not easy to identify based solely on morphology. Most marine coccoid and sarcinoid green algal species have traditionally been placed within genera dominated by species from freshwater or soil habitats. For example, the genera Chlorocystis and Halochlorococcum contain exclusively marine species; however, their familial and ordinal affinities are unclear. They are characterized by a vegetative cell with lobated or reticulated chloroplast, formation of quadriflagellated zoospores. They were integrated into the family Chlorochytriaceae of the Chlorophyceae which embraces all coccoid green algae with epi- or endophytic life phases. Later, they were excluded from the family of Chlorophyceae based on studies of their life histories in culture, and transferred to their newly described order, Chlorocystidales of the Ulvophyceae. Both genera form a “Codiolum”-stage that serves as the unicellular sporophyte in their life cycles. Phylogenetic analyses of SSU and ITS rDNA sequences confirmed that these coccoid taxa belong to the Chlorocystidales, together with the sarcinoid genus Desmochloris. Interestingly, two other lineages reproducing by quadriflagellated zoospores were discovered using this approach. Symbiochlorum hainanense represented together with the terrestrial coccoid Ignatius tetrasporus the order Ignatiales of the Ulvophyceae. Surprisingly, the strain SAG 2662 isolated from a hypersaline artificial lake in Solotvyno, Ukraine, formed a new monophyletic lineage among the Ulvophyceae, which is highly supported in all of the bootstrap and Bayesian analyses and approximately unbiased tests of user-defined trees and can tolerate a high variation of salinities. Considering our results, the new genus Solotvynia and the new order Solotvyniales were proposed. All biflagellated coccoid strains were members of the genus Sykidion, which represented its own order, Sykidiales among the Ulvophyceae.
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The planktonic freshwater ciliate Balanion planctonicum (Ciliophora, Prostomatea): a cryptic species complex or a ‘complex species’?

Authors:

Martina Schalch-Schuler, Barbara Bassin, Adrian-Stefan Andrei, Gianna Dirren-Pitsch, Katherine Waller, Cyrill Hofer, Jakob Pernthaler and Thomas Posch
Kilchberg Limnological Station

Abstract:

The globally distributed ciliate Balanion planctonicum is a primary consumer of phytoplankton spring blooms. Due to its small size (~20 µm), identification and quantification by molecular tools is preferable as an alternative to the laborious counting of specimen in quantitative protargol stains. However, previous sequencing of the 18S rDNA V9 region of B. lanctonicum from Lake Zurich (Switzerland) and subsequent quantification by fluorescence in situ hybridization yielded significantly lower cell numbers than using morphotype counting. This raised the question of whether B. planctonicum shows a cryptic diversity or whether it is just ‘complex species’ with intra-clonal polymorphisms. Over three years, we established numerous monoclonal cultures, and long-read sequencing of rDNA operons revealed four distinct dominant haplotypes (BpHs 1 – 4). The gene sequences of BpHs 1 and 3 differed by 6% and did not share intra-clonal polymorphisms, providing evidence for two distinct clades. Furthermore, phylogenetic analyses corroborate the sister relationship between Balanion and Askenasia (plus Hexasterias and Radiosperma). Morphologically, the two Balanion clades are nearly indistinguishable with small differences in macronucleus size and in the cell length to width ratio. CARD-FISH analyses indicated that the diversity of B. planctonicum is even more extensive with still unidentified clades.

Geographic origin or phylogeny – what determines the ecophysiology of Prymnesium parvum?

Authors:

Xenia Schefer, Anna Hahn, Sára Beszteri, Christina Bock
University of Duisburg-Essen, Germany

Abstract:

The euryhaline and eurytherm haptophyte Prymnesium is a toxic microalga with a cosmopolitan distribution found in various aquatic habitats: marine, brackish, and freshwater. Within the genus Prymnesium, the species Prymnesium parvum is of particular interest due to its genetic diversity, which arises from the existence of multiple cryptic species. Prymnesium has been reported as responsible for harmful algal blooms (HABs) since the 1920s, but there has been a notable increase in the frequency and intensity of these events in recent decades.

Growth of different Prymnesium strains isolated from diverse geographical origins was assessed to observe individual tolerance limits to environmental factors relevant for bloom formation. Therefore, batch culture experiments were performed under varying combinations of temperature and salinity conditions to monitor how the origins of the strains affect their growth responses to these stressors. Whereas algal strains investigated exhibited a relatively wide tolerance range as expected, individual tolerance limits were observed. These could be linked either to distinct geographical origins, the existence of cryptic species within Prymnesium with unique ecophysiological characteristics, or a combination of both.

These findings contribute to the comprehension of the factors that facilitate the occurrence and intensity of toxic algal blooms and provide a foundation for projections of future bloom abundances in aquatic ecosystems.

Exploring the efficacy of metabarcoding and non-target screening for detecting treated wastewater

Authors:

Guido Sieber [1,2], Felix Drees [3], Manan Shah [1,4], Tom L. Stach [2,4] Lotta Hohrenk-Danzouma [3], Christina Bock [1,2], Maryam Vosough [2,3], Mark Schumann [5], Bernd Sures [2,5,6], Alexander J. Probst [2,4,7], Torsten C. Schmidt [2,3], Daniela Beisser [1,2], Jens Boenigk [1,2]

[1] Biodiversity, University of Duisburg-Essen, Universitätsstraße 5, 45141 Essen, Germany
[2] Centre for Water and Environmental Research, University of Duisburg-Essen, 45141 Essen, Universitätsstraße. 5, Germany
[3] Instrumental Analytical Chemistry, University of Duisburg-Essen, 45141 Essen, Universitätsstraße 5, Germany
[4] Environmental Metagenomics, Research Center One Health Ruhr of the University Alliance Ruhr, Faculty of Chemistry, University of Duisburg-Essen, 45141 Essen, Germany
[5] Aquatic Ecology, University of Duisburg-Essen, 45141 Essen, Universitätsstraße. 5, Germany
[6]. Research Center One Health Ruhr of the University Alliance Ruhr, University of Duisburg-Essen, 45141 Essen, Universitätsstraße 5, Germany
[7]. Centre for Medical Biotechnology (ZMB), University of Duisburg-Essen, Universitätsstraße 5, 45141 Essen, Germany

Abstract:

Wastewater treatment processes can eliminate many pollutants, yet remainder pollutants contain organic compounds and microorganisms released into ecosystems. These remainder pollutants have the potential to adversely impact downstream ecosystem processes, but their presence is currently not being monitored. This study was set out with the aim of investigating the effectiveness and sensitivity of non-target screening of chemical compounds, 18S V9 rRNA gene, and full-length 16S rRNA gene metabarcoding techniques for detecting treated wastewater in receiving waters. We aimed at assessing the impact of introducing 33 % treated wastewater into a triplicated large-scale mesocosm setup during a 10-day exposure period. Discharge of treated wastewater significantly altered the chemical signature as well as the microeukaryotic and prokaryotic diversity of the mesocosms. Non-target screening, 18S V9 rRNA gene, and full-length 16S rRNA gene metabarcoding detected these changes with significant covariation of the detected pattern between methods.

The 18S V9 rRNA gene metabarcoding exhibited superior sensitivity immediately following the introduction of treated wastewater and remained one of the top-performing methods throughout the study. Full-length 16S rRNA gene metabarcoding demonstrated sensitivity only in the initial hour, but became insignificant thereafter. The non-target screening approach was effective throughout the experiment and in contrast to the metabarcoding methods the signal to noise ratio remained similar during the experiment resulting in an increasing relative strength of this method. Based on our findings, we conclude that all methods employed for monitoring environmental disturbances from various sources are suitable. The distinguishing factor of these methods is their ability to detect unknown pollutants and organisms, which sets them apart from previously utilized approaches and allows for a more comprehensive perspective. Given their diverse strengths, particularly in terms of temporal resolution, these methods are best suited as complementary approaches.

Coleps – The Protist of the Year 2025

Authors:

Bettina Sonntag [1], Marie-Louise Lemloh [2], Thomas Pröschold [1], Michael Schweikert [2]

[1] Research Department for Limnology, Mondsee, University of Innsbruck, Austria
[2] Department of Biobased Materials, University of Stuttgart, Germany

Abstract:

Coleps is a widespread and common ciliate in lakes, ponds and in marine environments. The cells are about 40 – 80 µm long and barrel-shaped. These ciliates have a very peculiar armor made of calcium carbonate plates with teeth, windows, and ciliary outlets. Coleps is currently used in research to investigate processes during biomineralization. There are several species in the genus Coleps which feed on diverse organisms such as bacteria and other protists, as well as on detritus which is usually colonized by microorganisms. Coleps therefore is often very colorful when food is digested in food vacuoles. The resulting orange-reddish color in Coleps appears when algal food is acidified during digestion. Coleps can additionally live in a facultative symbiosis with green algae and then appears grass-green. The algal endosymbionts provide the ciliate with nutrients, which they produce through photosynthesis. The combination of ingested food and the possession of endosymbionts is called mixotrophy. Further, when dying or dead organisms such as ciliates or copepods are present in the environment, entire swarms of Coleps come to feast on the carrion. Even cheese is an attractive food for these ciliates. Another specificity is that many species of Coleps can only be distinguished genetically, as they cannot be differentiated microscopically (cryptic species). These features make Coleps an exciting subject of research and this is why this ciliate is the Protist of the Year 202[5]

Food selection of interception feeding heterotrophic flagellates focusing on surface charge of the prey.

Authors:

Maite Sütthoff, Simone Engelskirchen, Jens Boenigk, Christina Bock

Abstract:

Being the most important predators for bacteria heterotrophic flagellates shape the adaption and composition of occurring bacteria communities through selection. They form the microbial food webs and connect it to higher trophic levels. Moreover, suspended sediments such as clay and other suspended particles that do not serve as food are widely found in freshwater ecosystems, causing significant environmental harm. It is unclear how heterotrophic flagellates discriminate between food and non-food particles.

Heterotrophic flagellates can select their food based on different prey characteristics. One of these is the surface charge. So far, no clear selection based in surface charge of bacteria is known, but this might be due to the interference of other prey characteristics such as cell size, motility and other surface parameters. However, using only artificial non-food particles, negative selection is known for strongly negatively charged surfaces. Environmental factors like salt concentration can affect selectivity and charge of the particles. In this work the food selection of various heterotrophic flagellates is investigated using differently charged fluorescent particles. The differences in food preferences between two particles will be compared so that differences in feeding rates based on food selection can be recognized. Furthermore, the influence of salinity stress on selectivity is investigated.

List of participants

Aline	ADLER	School of Engineering, University of Applied Sciences and Arts Western Switzerland	alice.adler@hevs.ch
Anthony	ALLAN-CARDOSO	Department Eukaryotic Microbiology, University of Duisburg Essen	anthony.allancardoso@uni-due.de
Adrian-Stefan	ANDREI	Limnological Station, Department of Plant and Microbial Biology, University of Zurich	stefan.andrei@limnol.uzh.ch
Alina	BECKER	Universität t Duisburg-Essen	alina.becker@stud.uni-due.de
Saskia	BINDSCHEDLER	Laboratory of Microbiology, University of Neuchâtel	saskia.bindschedler@unine.ch
Quentin	BLANDENIER	Laboratory of Soil Biodiversity, University of Neuchâtel	quentin.blandenier@gmail.com
Dana	BLUDAU	University of Duisburg-Essen	dana.bludau@uni-due.de
Jens	BOENIGK	University of Duisburg-Essen	jens.boenigk@uni-due.de
Beate	BRITZ	University of Stuttgart, MPA/AMICA	beate.britz@mpa.uni-stuttgart.de
Anna	BUSCH	University of Cologne	anna.busch@uni-koeln.de
Robin	CALISTI	Laboratory of Soil Biodiversity, University of Neuchâtel	robin.calisti@unine.ch
Arnaud	DANO	Laboratory of Soil Biodiversity, University of Neuchâtel	arnaud.dano@unine.ch
Lennart	DÖRR	University of Stuttgart	lennart.doerr@bio.uni-stuttgart.de
Franziska	DREWS	University of Wuppertal	drews@uni-wuppertal.de
Clément	DUCKERT	Laboratory of Soil Biodiversity, University of Neuchâtel	cduckert@outlook.fr
Omaya	DUDIN	Department of Biochemistry, University of Geneva	omaya.dudin@unige.ch
Yana	EGLIT	Biochemistry Department, University of Geneva	yeglit@dal.ca
Emilie	FAVRE	Laboratory of Soil Biodiversity, University of Neuchâtel	emilie2.favre@unine.ch
Maximilian	GANSER	Paris Lodron University Salzburg	maximilian.ganser@plus.ac.at
Andrea	GARVETTO	Universität Innsbruck	andrea.garvetto@uibk.ac.at
Laure	GUILLOU	Station Biologique de Roscoff, CNRS/Sorbonne Université	lguillou@sb-roscoff.fr
Elisabeth	HEHENBERGER	Biology Centre, Czech Academy of Sciences	elisabeth.hehenberger@paru.cas.cz
Tristan	HENDERSON	Mississippi State University	tch318@msstate.edu
Sebastian	HESS	Technical University of Darmstadt	hess@bio.tu-darmstadt.de
Tarja Tamara	HOFFMEYER	Universität zu Köln, Institut für Zoologie	thoffme3@uni-koeln.de
Jon	KAYE	Moore Foundation	jon.kaye@moore.org
Jana	KOHL-CHANDRAMOHAN	Universität Stuttgart	jana.kohl@bio.uni-stuttgart.de
Anush	KOSAKYAN	University of Modena and Reggio Emilia	anna.kosakyan@gmail.com

Lucile	LAMY	Laboratory of Soil Biodiversity, University of Neuchâtel	lucile.lamy@aol.com
Enrique	LARA	Real Jardín Botánico-CSIC	enrique.lara@rjb.csic.es
Marie-Louise	LEMLOH	University of Stuttgart	marie-louise.lemloh@amica.uni-stuttgart.de
Guillaume	LENTENDU	Laboratory of Soil Biodiversity, University of Neuchâtel	guillaume.lentendu@unine.ch
Caroline	LINHART	Laboratory of Soil Biodiversity, University of Neuchâtel	caroline.linhart@unine.ch
Kacper	MACISZEWSKI	Laboratory of Genomics and Diversity of Protists, Institute of Parasitology, Biology Centre, Czech Academy of Sciences	kacper.maciszewski@paru.cas.cz
Pauline	MISCHE	University of Cologne, Institute of Zoology, Department of Ecology	pmische@smail.uni-koeln.de
Edward	MITCHELL	Laboratory of Soil Biodiversity, University of Neuchâtel	edward.mitchell@unine.ch
Nadine	MÖBIUS	Friedrich Schiller University Jena Institute of Biodiversity Aquatic Geomicrobiology	nadine.moebius@uni-jena.de
Maren	NOTHOF	RPTU Kaiserslautern	nothofm@rptu.de
Armand	NZOKO	Laboratory of Soil Biodiversity, University of Neuchâtel	armand.nzoko@unine.ch
Benjamin	ORY	Laboratory of Soil Biodiversity, University of Neuchâtel	benjamin.ory@unine.ch
Maxwell	OWUOR	Department of Biochemistry and Molecular Biology, Egerton University, P.O. Box 536, 20115 Egerton, Kenya	maxwelljuti@gmail.com
Marcello	PIRRITANO	Bergische Universität Wuppertal	pirritano@uni-wuppertal.de
Caroline	PLANCHE	Laboratory of Soil Biodiversity, University of Neuchâtel	caroline.planche@unine.ch
Thomas	POSCH	Limnological Station, University of Zurich	posch@limnol.uzh.ch
Camille	PRIOUX	Centre Scientifique de Monaco	cprioux@centrescientifique.mc
Thomas	PRÖSCHOLD	Research Department for Limnology Mondsee, University of Innsbruck	thomas.proeschold@uibk.ac.at
Renate	RADEK	Freie Universität Berlin	renate.radek@fu-berlin.de
Sonja	RÜCKERT	Department of Eukaryotic Microbiology, University of Duisburg-Essen	rueckert.sonja@googlemail.com
Martina	SCHALCH-SCHULER	Limnological Station Kilchberg	martina.schuler@limnol.uzh.ch
Xenia	SCHEFER	Biodiversity, University Duisburg-Essen	xenia.schefer@stud.uni-due.de
Anja	SCHERWAß	University of Cologne	anja.scherwass@uni-koeln.de
Martin	SCHLEGEL	Institute fo Biology, Leipzig University	schlegel@uni-leipzig.de
Michael	SCHWEIKERT	University of Stuttgart	michael.schweikert@bio.uni-stuttgart.de
Guido	SIEBER	University of Duisburg-Essen	guido.sieber@uni-due.de

Martin	SIMON	Molecular Cell Biology and Microbiology	masimon@uni-wuppertal.de
David	SINGER	HES-SO Changins	david.singer@changins.ch
Bettina	SONNTAG	Research Department for Limnology, Mondsee, University of Innsbruck	bettina.sonntag@uibk.ac.at
Christian	SPANNER	Research Department for Limnology, Mondsee	christian.spanner@uibk.ac.at
Maite	SÜTTHOFF	Biodiversity, University Duisburg-Essen	maite.suetthoff@stud.uni-duisburg-essen.de
Andrea	VALDEAVELLANO CAMPUSANO	Laboratory of Soil Biodiversity, University of Neuchâtel	andrea.valdeavellano@unine.ch
Camille	VOEGELI	Laboratory of Soil Biodiversity, University of Neuchâtel	camille.vogeli@unine.ch
Julian	WAGENHOFER	University of Cologne	jwagenh1@uni-koeln.de
Julia	WALOCHNIK	Medical University of Vienna	julia.walochnik@meduniwien.ac.at
Gennuo	WANG	Georg-August-Universität Göttingen	gennuo.wang@uni-goettingen.de
Johannes	WERNER	Institute of Zoology, University of Cologne	johannes.werner@uni-koeln.de
Linus Matz	ZELLER	Max Planck Institute for Marine Microbiology	lzeller@mpi-bremen.de