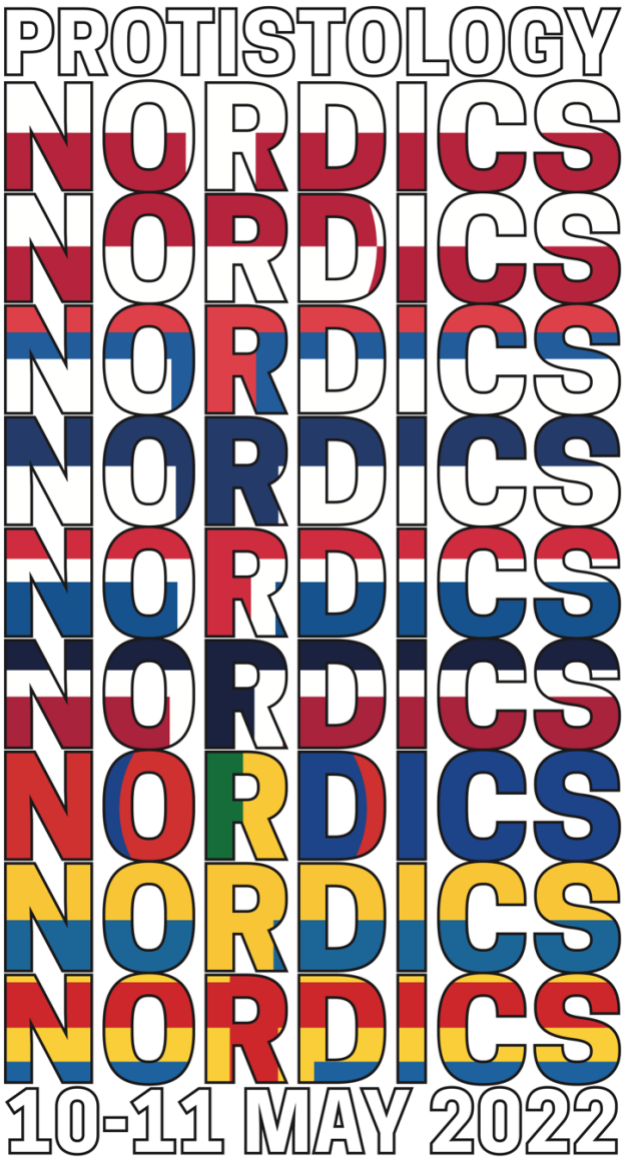
Protistology Nordics

Programme & Abstracts

10–11 May 2022



Dear colleagues,

Protistology Nordics 2022 is designed to promote scientists in Nordic countries that study the genetics, cell biology, ecology, and evolution of protists. The aims of this meeting are to provide a regional forum for early-career and advanced researchers to present their work, and, hopefully, to establish a society that will continue to meet and promote protistan research.

The invited talks will be by Bente Edvardsen (University of Oslo, Norway) and Jon Jerlström-Hultqvist (Uppsala University, Sweden). Twenty-two contributed talks will be presented across four sessions. And six contributed posters will be presented in a single session.

The International Society of Protistologists (ISOP) is supporting Protistology Nordics 2022 by providing funds for travel/housing awards (for students and postdocs who are ISOP members), talk/poster prises, and for general running costs. Talks will be streamed using ISOP's Zoom license.

The Natural History Museum at the University of Oslo is supporting Protistology Nordics 2022 by providing the meeting rooms, and by providing free access to the Zoology and the just-redesigned Geology museums.

The meeting logo was designed by Corey Holt (University of British Columbia).

Kind regards,
Micah Dunthorn & Courtney Stairs & Fabien Burki

ISOP

Natural History Museum

Contents

Organizing Committee

Co-organizers

Micah Dunthorn
Natural History Museum
University of Oslo
Norway

Courtney Stairs
Biology Department
Lund University
Sweden

Fabien Burki
Department of Organismal Biology
Uppsala University
Sweden

Assistant organizers

Anders Alfjorden
Department of Organismal Biology
Uppsala University
Sweden

Karla Iveth Aguilera Campos
Biology Department
Lund University
Sweden

Megan Gross
Department of Ecology
University of Kaiserslautern
Germany

Ioana Onuţ-Brännström
Natural History Museum
University of Oslo
Norway

Programme Overview

	10 May	11 May
09:00	opening remarks	opening remarks
	plenary talk 1	plenary talk 2
10:00	coffee break	coffee break
	contributed talks 1	contributed talks 3
11:00		
12:00	lunch	lunch
13:00		
	contributed talks 2	contributed talks 4
14:00		
15:00	coffee break	coffee break
	posters & beer	
16:00		
17:00		
		dinner talk/poster awards
18:00		
19:00		

Meeting Programme

Tuesday, 10 May

09:00–09:15 **Welcome address**
Hugo de Boer (University of Oslo, Norway)
Micah Dunthorn (University of Oslo, Norway)

Keynote Lecture 1

09:15–10:15 **Bente Edvardsen** (University of Oslo, Norway)
Exploration of protist diversity and distribution in the ocean by a polyphasic approach

10:15–10:45 **coffee break**

Contributed talks 1

Session chair: **Staffan Svärd** (Uppsala University, Sweden)

10:45–11:00 **Markus Hiltunen** (Uppsala University, Sweden)
Genomics of Rhizarian parasites reveal striking similarities to Microsporidia

11:00–11:15 **Julie Boisard** (Lund University, Sweden)
Gregarine genomes deciphering extends our knowledge of apicomplexan diversity

11:15–11:30 **Bart Edelbroek** (Uppsala University, Sweden)
Evolution of microRNAs in Amoebozoa

11:30–11:45 **Jonas Kjellin** Uppsala University, Sweden)
Presence and function of bacterial Rhs toxins in social amoebas

11:45–12:00 **Ioana Onuţ-Brännström** (Uppsala University, Sweden)
A mitosome with distinct metabolism in the uncultured protist parasite Paramikrocytos canceri (Rhizaria, Ascetosporea)

12:00–13:30 **lunch**

Contributed talks 2

Session chair: Fabien Burki (Uppsala University, Sweden)

13:30–13:45	**Daniela Sturm (**Marine Biological Association, United Kingdom) *Metabarcoding reveals spatial differences in protist communities in- and outside a mesoscale meander of the Southern Indian Ocean*
13:45–:14:00	**Luka Supraha** (University of Oslo, Norway) *Biodiversity and biogeography of diatoms from the Svalbard area: community structuring through endemism and dispersal*
14:00–14:15	**Megan Gross** (University of Oslo, Norway) *O Short-branch Microsporidia, Where Art Thou? - Identifying diversity hotspots for future sampling*
14:15–14:30	**Miguel M. Sandin** (Uppsala University, Sweden) *The eco-evolution of microbial eukaryotes inferred from metabarcoding surveys*
14:30–14:45	**Agnes K.M. Weiner** (NORCE, Norway) *Using ancient DNA sequencing to assess the impact of past environmental changes on marine protist biodiversity*
14:45–15:00	**Franck Lejzerowicz** (University of Oslo, Norway) *Protists in the global deep-sea sediment: benthic RNA activity in planktonic DNA deposits*
15:00–15:15	**coffee break**

Posters

15:15–16:45

Poster 1	**Karla Iveth Aguilera Campos** (Lund University, Sweden) *Syntrophic interactions with Arcobacter species are pervasive in breviate protists*
Poster 2	**Christine Lorenzen Elberg** (Aarhus University, Denmark) *Identification of soil protist composition and their effect on bacterial communities*
Poster 3	**Àlex Gàlvez i Morante** (Institut de Biologia Evolutiva, Spain) *Ancestral reconstructions of gene content with Dollo parsimony are incorrect*
Poster 4	**Carolin Peter** (Linnaeus University, Sweden) Changes in the phytoplankton community composition observed in a time series in the Baltic Sea off Sweden's east coast
Poster 5	**Margarita Skamnelou** (Institute of Evolutionary Biology, Spain) *Isolation and characterization of two novel species of choanoflagellates*
Poster 6	**Mara Vizitiu** (Lund University, Sweden) *The Gene They Keep on Giving: lateral gene transfer from protists could enable freshwater sponges to adapt to hypoxia*

Wednesday, 11 May

09:00–09:15 **Opening remarks**
Micah Dunthorn (University of Oslo, Norway)

Keynote Lecture 2

09:15–10:15 **Jon Jerlström-Hultqvist** (Uppsala University, Sweden)
Long-read metagenomics as a tool to understand symbiosis

10:15–10:45 **coffee break**

Contributed talks 3

Session chair: Agnes K.M. Weiner (NORCE, Norway)

10:45–11:00 **Markus Majaneva** (Norwegian Institute for Nature Research (NINA), Norway)
Conducting applied ecology using single-celled eukaryotes

11:00–11:15 **Anna-Lotta Hiillos** (University of Jyväskylä, Finland)
Marine apicomplexan diversity correlations with their potential hosts across benthic communities in the Baltic Sea

11:15–11:30 **Anders Alfjorden** (Uppsala University, Sweden)
Identification of a new gregarine parasite [Apicomplexa, Alveolata] in mass mortality events of freshwater pearl mussels (Margaritifera margaritifera)

11:30–11:45 **Nina Pohl** (University of Cologne, Germany)
The wastewater protist Rhogostoma minus *(Thecofilosea, Rhizaria) is abundant, widespread, and hosts Legionellales*

11:45–12:00 **Wenche Eikrem** (Norwegian Institute for Water Research (NIVA), Norway
Pseudocarteria glaciale *sp. nov. (Chlamydomonadales, Chlorophyceae). An euryhaline flagellate from an Arctic melt pond*

12:00–13:30 **lunch**

Contributed talks 4

Session chair: Courtney Stairs (Lund University, Sweden)

13:30–13:45 **Eva Pyrihová** (University of Stavanger, Norway)
Characterisation of potential glycolytic transporters in Blastocystis

13:45–14:00 **Jeffrey J. Colgren** (University of Bergen, Norway)
Elements of neuronal-like secretion in Choanoflagellates

14:00–14:15 **Seyed Saeed Asadzadeh** (Technical University of Denmark, Denmark)
Hydrodynamic trade-offs in different flagellar arrangements

14:15–14:30 **Sandra Baldauf** (Uppsala University, Sweden)
The Acrasis kona *genome and developmental transcriptomes suggest an early origin of multicellularity in eukaryotes*

14:30–14:45 **Fredrik Söderbom** (Uppsala University, Sweden)
Abundantly expressed class of noncoding RNAs conserved through the multicellular evolution of dictyostelid social amoebas

14:45–15:00 **Staffan Svärd** (Uppsala University, Sweden)
Regulation of encystation in Giardia- *the road to resilience*

15:00–15:15 **coffee break**

Dinner and talk/poster awards

17:30–20:00

Invited Talks

Exploration of protist diversity and distribution in the ocean by a polyphasic approach

Bente Edvardsen (Department of Biosciences, University of Oslo, Norway)

The massive loss of biodiversity due to human activities and climate change is accelerating. We need to know the organisms, who they are, their distribution in time and space and their ecological role in order to be able to conserve biodiversity. We also need to understand the driving forces shaping biodiversity and the community structure to be able to predict the consequences of human activities and mitigate losses. Analyses of phytoplankton communities by light microscopy to study structure, seasonal dynamics and production, and relate this to abiotic factors have been conducted in the Nordic countries for more than a century. Many scientific questions in plankton ecology are the same today as then, and we still ask: who are there? where and how do they occur and what are the driving factors? what are they doing and what are their ecological roles? New technologies have steadily emerged and changed the methodologies and expanded the possibilities what we can discover. DNA-based methods such as metabarcoding have recently become a common method in microbial diversity studies as it provides high taxonomic resolution and may detect also tiny, fragile and rare taxa. Molecular methods may eventually be time-efficient and automated, and do not require specific taxonomic expertise. All methods have however advantages and drawbacks, and one method alone do not give all answers. Further, to be able to link available time series and historical data based on light microscopy to new molecular data, we need to know how they compare. In a polyphasic approach of protist biodiversity studies several methods are combined, such as e.g. light and electron microscopy, molecular biological analyses (e.g. metabarcoding, metatranscriptomics, qPCR), flow cytometry and isolating and culturing strains for morphological, genetic, genomic, physiological and biochemical analyses. By integrating several methods, a more detailed analysis of the community composition, structure, distribution and function can be obtained. In my talk I will show some case studies where a polyphasic approach have been used and discuss challenges and possibilities.

Long-read metagenomics as a tool to understand symbiosis

Jon Jerlström Hultqvist (Department of Cell and Molecular Biology Uppsala University, Sweden)

Anaerobic protists are abundant in diverse low-oxygen environments ranging from marine sediments to animal guts. Comparatively little is known about the diversity in free-living anaerobic protists with respect to their genomes, metabolisms, organelles and symbionts. With the development of inexpensive long-read sequencing technologies, we can now characterize the genomes of diverse anaerobic protists to understand the mechanisms by which they have evolved to inhabit low oxygen. We can also obtain the full genome sequences of associated microbes, including symbiotic bacteria and predict their host-symbiont interactions. *Anaeramoeba* is a newly-described free-living protist with membrane-enclosed bacterial symbionts (*Desulfobacter* sp.) tightly associated with its hydrogen-producing mitochondria-related organelles (MROs). The symbionts reside in deep pits of the host membrane that have connections to the cell-surface. The reconstructed metabolism of the symbiont shows pathways that connect to the end-products of the hosts MRO metabolism. The symbiont encodes a complete vitamin B12 biosynthesis pathway and might serve as a nutritional symbiont for the host. Interestingly, the genomes of *Anaeramoeba* show massive expansions in membrane-trafficking components demonstrated in other organisms to regulate the phagosomal maturation machinery. This suggests that the vacuoles within which the symbionts reside may be modulated and controlled by the host and that this mechanism may be shared by to *Anaeramoeba* species, allowing them to capture, retain and dispose of symbionts.

Contributed Talks

(speaker in bold)

Identification of a new gregarine parasite [Apicomplexa, Alveolata] in mass mortality events of freshwater pearl mussels (*Margaritifera margaritifera*)

Anders Alfjorden (Department of Organismal Biology, Uppsala University, Sweden; National Veterinary Institute, Sweden), Ioana Onut Brännström (Department of Organismal Biology, Uppsala University, Sweden), Niklas Wengström (University of Gothenburg, Sweden; Swedish Anglers Association, Sweden), Mahwash Jamy (Department of Organismal Biology, Uppsala University, Sweden), Arni Kristmundsson (Institute for Experimental Pathology at Keldur, University of Iceland, Iceland), Fabien Burki (Department of Organismal Biology, Uppsala University, Sweden)

Freshwater bivalves play key ecological roles in many lakes and river systems across the world, largely contributing to the good functioning of these ecosystems. The freshwater pearl mussel (FPM) *Margaritifera margaritifera* has a wide range distribution in rivers within the Holarctic region but is globally threatened to extinction due to high sensitivity to environmental changes. FPM has strict requirements for highly oxygenated water, resulting in mass mortality events (MME) from deterioration of water quality such as eutrophication, sedimentation and acidification. In addition to these environmental changes, the role of infectious diseases in MME has not been investigated in most cases. Here, we report the discovery of a novel parasite associated with MME in Swedish populations of FPM using molecular and imaging methods. Phylogenetic analyses revealed that this parasite belongs to one of the terrestrial group of gregarines (Apicomplexa) and is specifically related–but clearly separate– to the tadpole parasite *Nematopsis temporariae*. Cysts detected in gills, and other organs corresponds by morphology to the general description of *Nematopsis* spp. as vermiform single zoites. We propose a tentative life cycle within the FPM host, describing the presumed site of invasion, distribution of different cell forms in host tissues and potential exit from the host into the environment for further spread. We describe this parasite as *Nematopsis margaritifera*, which represents the first report of a parasitic infection in FPM linked to MME and could be linked to the global decline of this mussel species worldwide.

Hydrodynamic trade-offs in different flagellar arrangements

Seyed Saeed Asadzadeh (Centre for Ocean Life, National Institute of Aquatic Resources, Technical University of Denmark, Denmark), Jens H. Walther (Department of Mechanical Engineering, Technical University of Denmark, Denmark), Thomas Kiørboe (Centre for Ocean Life, National Institute of Aquatic Resources, Technical University of Denmark, Denmark)

Flagellates are few-micron sized unicellular organisms equipped with one or a few flagella, and play a key role at the base of oceanic food webs as the main consumers of bacteria and phytoplankton. The beating flagellum propels the organism through the water and generates a feeding current that facilitates prey encounters. At the same time, the stirring generated by the flagellum exposes the cells to their flow-sensing predators. While hydrodynamics of flagella is most often studied in the context of propulsion, efficient foraging is likely a much more important component of their fitness than propulsion per se, giving rise to a great diversity of flagellar arrangements, morphology, and beat kinematics. We hypothesize that the significance of this diversity represents different outcomes of the fundamental trade-offs between resource acquisition, predator avoidance, and propulsion. Using computational fluid dynamics, we study these hydrodynamic trade-offs and investigate how at low Reynolds number, where viscosity impedes predator-prey contact, flagellates yield the necessary feeding current structure and at the same time avoid flow sensing-predators to secure their success and key role in the microbial food webs.

Gregarine genomes deciphering extends our knowledge of apicomplexan diversity

Julie Boisard (Department of Biology, Lund University, Sweden), Evelyne Duvernois-Berthet (Muséum National d'Histoire Naturelle, Centre National de la Recherche Scientifique, Laboratoire Physiologie Moléculaire et Adaptation (PhyMA), UMR7221 CNRS-MNHN, France), Loïc Ponger (Structure et instabilité des génomes (STRING UMR 7196 CNRS/INSERM U1154), Département Adaptations du vivant (AVIV), Muséum National d'Histoire Naturelle, CNRS, INSERM, France), Isabelle Florent (Molécules de Communication et Adaptation des Microorganismes (MCAM, UMR 7245 CNRS), Département Adaptations du vivant (AVIV), Muséum National d'Histoire Naturelle, CNRS, France)

Our current understanding of the evolutionary history of Apicomplexa, eukaryotic unicellular parasites of a wide range of metazoan hosts, is strongly biased toward species infecting humans, such as *Plasmodium* spp (malaria), Toxoplasma gondii (toxoplasmosis) and *Cryptosporidium* spp. (cryptosporidiosis). While the genomes of these highly pathogenic agents are well documented, this is not the case for other apicomplexan lineages such as low pathogenic and non-cultivable gregarines, mostly infecting invertebrate hosts. Yet genomic exploration of such understudied protists is essential to better understand the evolutionary history of apicomplexan parasites and the diversity of their adaptive paths to parasitic lifestyle. Here, we characterize the genome of the marine eugregarine *Porospora gigantea*, extracellular intestinal parasite of Lobsters, remarkable for the macroscopic size of its vegetative feeding forms (trophozoites) as well as its gliding motility speed, the fastest so far recorded for Apicomplexa. From the challenge to isolate from field sampling the biological material in adequate amounts and quality (regarding host or environmental contamination), to the various methodological issues of de novo reconstruction of its genome, we report the discovery of two highly syntenic genomes, *Porospora* cf. *gigantea* A and *Porospora* cf. *gigantea* B. The unexpected extent of genomic diversity and coding capacities among currently known gregarines as well as across well documented apicomplexan groups confirm the importance of studying gregarines. Their understanding will widen our biological and evolutionary view of apicomplexan species diversity, and deepen our knowledge of the molecular bases of key functions such as gliding motility, well known to allow access to the intracellular parasitic lifestyle in Apicomplexa.

Elements of neuronal-like secretion in Choanoflagellates

Jeffrey J. Colgren (Sars International Centre for Marine Molecular Biology, University of Bergen, Norway) & Pawel Burkhardt (Sars International Centre for Marine Molecular Biology, University of Bergen, Norway)

The study of protists, especially within the holozoan clade, is essential for reconstructing the earliest events of animal evolution. Neurons, notably when coupled with muscles, allow animals to move through and interact with their environment in ways unique to life on earth. Though there is not a single defining feature of this ancient cell type, neurons represent an extreme example of tightly regulated secretion, allowing for rapid signaling and communication. Part of this regulation is achieved through a conserved set of proteins involved in coupling calcium signaling with membrane fusion, many of which predate animals. Choanoflagellates, the closest living relative to animals, have polarized cells with an apical flagellum surrounded by a microvilli collar. Here we investigated secretion in these organisms, finding evidence of calcium regulated vesicle fusion at the feeding collar. Taking a targeted approach, we look at the role of the protein complexin (Cplx), a key regulator of calcium mediated secretion in neurons, and find evidence of both conserved and unique function in choanoflagellates. Structural and in vivo studies suggest the choanoflagellate orthologs can bind to the exocytic vesicle fusion machinery and over-expression in the choanoflagellate *Salpingoeca rosetta*, suggests co-localization with vesicle pools, including at the collar. CRISPR-Cas9 mediated disruption of the gene results in a significant increase in cell size with no obvious effects on viability. Visualizing *S. rosetta* Cplx using a genetically encoded epitope tag shows endogenous protein accumulates within the microvilli of the collar. Work is being performed to identify the nature of the size increase as well as identify native interacting proteins to better elucidate the function in *S. rosetta*. Our findings suggest that neuronal like regulation of secretion was present in the last common ancestor of choanoflagellates and animals but likely functioned in diverse contexts and became specialized in the different lineages.

Evolution of microRNAs in Amoebozoa

Bart Edelbroek (Department of Cell and Molecular Biology, Uppsala University, Sweden), Jonas Kjellin (Department of Cell and Molecular Biology, Uppsala University, Sweden), Gernot Glöckner (Center for Biochemistry, University of Cologne, Germany), Angelika A. Noegel (University Hospital Cologne, Cologne, Germany), Ludwig Eichinger (University Hospital Cologne, Cologne, Germany), Pauline Schaap (College of Life Sciences, University of Dundee, United Kingdom), Inna Biryukova (Department of Molecular Biosciences, Stockholm University, Sweden), Marc Friedländer (Department of Molecular Biosciences, Stockholm University, Sweden), Fredrick Söderbom (Department of Cell and Molecular Biology, Uppsala University, Sweden)

MicroRNAs (miRNAs) are important regulators of gene expression in both plants and animals. They are thought to have evolved convergently in these lineages and hypothesized to have played a role in the evolution of multicellularity. In line with this hypothesis, miRNAs have so far only been described in a handful of unicellular eukaryotes. In this study we investigate the presence and evolution of miRNAs in Amoebazoa, focusing on species belonging to *Acanthamoeba*, *Physarum*, and dictyostelid taxonomic groups, representing true unicellular species as well as species where cells go through aggregative multicellularity. Through small RNA sequencing we identified miRNAs which adhere to both the stringent plant and animal miRNA criteria in nearly all examined amoebae, greatly expanding the total number of protists featuring miRNAs. We found conserved miRNAs between closely related species, but the majority of species feature only unique miRNAs. The number and expression of miRNAs seems to vary greatly between related species, and even the mode of targeting appears to differ. This is also reflected in the variable number of genes important for miRNA function, i.e. genes for Dicers and Argonautes. In one of the amoebae that features aggregative multicellularity, *Dictyostelium discoideum*, we observed no effect on the multicellular development when miRNA expression was abolished. Together our results suggest that miRNAs appear to have evolved independently in different amoebazoan lineages where they fulfil specific roles, but they do not seem to play a role in the evolution of multicellularity.

Pseudocarteria glaciale sp. nov. (Chlamydomonadales, Chlorophyceae). An euryhaline flagellate from an Arctic melt pond

Wenche Eikrem (Norwegian Institute for Water Research (NIVA), Norway; Natural History Museum, University of Oslo, Norway), Luka Šupraha, Norwegian Institute for Water Research (NIVA), Norway; Department of Biosciences, University of Oslo, Norway), Jens Wohlmann (Department of Biosciences, University of Oslo, Norway), Daniel Vaulot (Station Biologique de Roscoff, Sorbonne Université, France), Bente Edvardsen (Department of Biosciences, University of Oslo, Norway)

Several chlorophyte flagellates such as *Chlamydomonas nivalis* and *Chlainomonas rubra* thrive at low temperatures and can be found on snow. The present species, Pseudocarteria glaciale sp. nov. was isolated from a freshwater melt-water pond on the sea ice in the Atlantic Arctic, North of Svalbard, at 83.53 oN and 29.7666 oE in August 2018 during a Nansen Leagcy cruise. A strain of this euryhaline alga is currently cultivated in TL30 medium at 4 oC under natural and artificial light. *Pseudocarteria* species are classified in the order Chlamydomonadales and are primarily found in freshwater habitats as plankton. Phylogenetically and morphologically *P. glaciale* sp. nov. belongs to the *Carteria* I lineage. At present there are seven species of *Pseudocarteria* accepted taxonomically and probably some awaiting transfer from *Carteria* to *Pseudocarteria*. Like other Chlamydomonadales-flagellates, *P. glaciale* is characterized by a cell wall with an anterior papilla and four smooth flagella. The flagella bases have a counter clockwise configuration, and the single green chloroplast has an eyespot and a pyrenoid surrounded by starch. Cells divide within the mother cell wall and sexual reproduction has not been observed but is known to occur in other species of the genus. Putative resting spores have also been observed in culture. Our cultured strain, UiO500 is identical in the 18S rRNA gene to the strain RCC2487 isolated from the Beaufort Sea, Canada. Comparison with high throughput sequences of the marker gene 18S rRNA in the metaPR2 database revealed that it is biogeographically restricted to the Arctic.

O Short-branch Microsporidia, Where Art Thou? - Identifying diversity hotspots for future sampling

Megan Gross (Natural History Museum, University of Oslo, Norway; Department of Ecology, Technical University of Kaiserslautern, Germany), Lubomir Rajter (Department of Eukaryotic Microbiology, University of Duisburg-Essen, Germany), Frédéric Mahé (CIRAD, Montpellier, France; PHIM Plant Health Institute, University of Montpellier, CIRAD, INRAE, Institut Agro, IRD, France), David Bass (Cefas, International Centre for Aquatic Animal Health, United Kingdom; Sustainable Aquaculture Futures, Biosciences, College of Life and Environmental Sciences, University of Exeter, United Kingdom; Department of Life Sciences, The Natural History Museum, United Kingdom), Micah Dunthorn (Natural History Museum, University of Oslo, Norway)

The classical, long-branch microsporidia exhibit highly-reduced genomes and highly-specialized polar filaments. The evolution of these unique characteristics remains murky, as accelerated evolutionary rates make it difficult to unravel them. One way to approach this is to evaluate these same characteristics in the short-branch microsporidia. Short-branch microsporidia form a basal grade that consist of partially-characterized and numerous novel environmental lineages. However, identification of the environmental lineages requires knowing where to find and isolate them. To direct future isolation, we used the EukBank database that contains the majority of the publicly available environmental V4 SSU-rRNA sequences of protists. The curated OTU-table and corresponding metadata was used to evaluate the short-branch microsporidia across freshwater, hypersaline, marine benthic, marine pelagic, and terrestrial environments. Presence-absence analyses infer that short-branch microsporidia are most abundant in freshwater and terrestrial environments, and alpha- and beta-diversity measures indicate that focusing our sampling effort on these two environments would cover a large part of the total diversity of short-branch microsporidia. These results can be used to coordinate future isolation and sampling campaigns to better understand the evolution of the microsporidia.

Marine apicomplexan diversity correlations with their potential hosts across benthic communities in the Baltic Sea

Anna-Lotta Hiillos (Department of Biological and Environmental Science, University of Jyväskylä, Finland), Cecilie Petersen (Department of Biological and Environmental Science, University of Jyväskylä, Finland; Roskilde University, Denmark), Sonja Rueckert (School of Applied Sciences, Edinburgh Napier University, United Kingdom) and K. Emily Knott (Department of Biological and Environmental Science, University of Jyväskylä, Finland)

The positive association between species diversity and habitat diversity is well known among free-living organisms. Similarly, due to their dependence on hosts for habitats and resources, parasite species richness has been suggested increase with diversity and abundance of their associated hosts. Additionally, parasite infection patterns (prevalence and infection load) could be affected by the diversity of host communities. Apicomplexans are obligate symbionts for many invertebrates and their diversity has recently been positively correlated to their potential hosts diversity. In this study, combining molecular approaches (metabarcoding for apicomplexans) with traditional sampling (hosts) we assess apicomplexan parasite diversity in seven sites across the Baltic Sea coastal benthos and correlate the diversity with their potential hosts, the benthic invertebrates. Additionally, focusing on a single host species, the polychaete, *Pygospio elegans*, we describe infection patterns of a marine apicomplexan, *Rhytidocystis* sp., and test the association of infection prevalence and load with the diversity of benthic invertebrates. We found that apicomplexan richness (number of observed OTUs) was not correlated with the richness of their potential hosts. However, the infection pattens of *Rhytidocystis* sp. were affected by benthic invertebrate richness: infection load was positively correlated with the abundance of benthic invertebrates, and a negative association was found with host diversity. This could be due to more efficient transmission in homogeneous host community, leading to the higher observed infection loads. While our results contradict with the host richness increases parasite richness hypothesis, further studies are required to draw more general conclusions of determinants of marine apicomplexan richness.

Genomics of Rhizarian parasites reveal striking similarities to Microsporidia

Markus Hiltunen (Department of Organismal Biology, Uppsala University, Sweden), Ioana Onut-Brännström (Department of Organismal Biology, Uppsala University, Sweden), Anders Alfjorden (Department of Organismal Biology, Uppsala University, Sweden), Hana Pecková (Institute of Parasitology, Biology Centre of the Czech Academy of Sciences, Czech Republic), Astrid Holzer (Institute of Parasitology, Biology Centre of the Czech Academy of Sciences, Czech Republic), David Bass (International Centre of Excellence for Aquatic Animal Health, Centre for Environment, Fisheries and Aquaculture Science (Cefas), United Kingdom; Department of Life Sciences, The Natural History Museum London, United Kingdom; Sustainable Aquaculture Futures, Biosciences, College of Life and Environmental Sciences, University of Exeter, United Kingdom), Fabien Burki (Department of Organismal Biology, Uppsala University, Sweden)

Ascetosporea is a eukaryotic group of intracellular parasites of marine invertebrates belonging to the Rhizaria supergroup, which can cause devastating effects on aquaculture. Despite having large socio-economic impact and importance for marine ecosystems, Ascetosporea is one of the most undersampled major groups of parasites. In this project, we sequenced, assembled and annotated the genomes of four species from three classes of Ascetosporea: *Marteilia pararefringens* and *Paramarteilia* sp (Paramyxida), *Bonamia ostreae* (Haplosporida), and *Paramikrocytos canceri* (Mikrocytida). In addition, we sequenced a free-living amoeboid relative to Ascetosporea, so far undescribed as a species and tentatively called M6MM, allowing us to investigate genome evolution during the transition to parasitism in this group. In general, the genomes are highly reduced; both in size, ranging between 12-22 Mb, and gene number, ranging between 2300-5600 genes. The parasite genomes show a reduction in intron length and number, taken to the extreme in P. canceri where no conventional introns could be recovered. In contrast, the M6MM genome is rich in genes and introns. Finally, the mitochondria were also reduced in the parasites, in some cases resembling a mitosome – a stark contrast to M6MM where the mitochondrion was recovered in a single 48 kb contig. This trend of genome reduction is common in parasites, but the degree to which is shown here for Ascetosporea is extreme, and only previously known from Microsporidia, famous for their small and compact genomes. The convergence of genome evolution between these two groups is striking given their evolutionary distance, but suggests that similar parasitic lifestyles lead to similar selective pressures and extreme levels of genome reduction. Our results add genomic data for an important group of parasites, and highlights the drastic consequences a parasitic life style can have on genome evolution.

Abundantly expressed class of noncoding RNAs conserved through the multicellular evolution of dictyostelid social amoebas

Jonas Kjellin (Department of Cell and Molecular Biology, Uppsala University, Sweden), Lotta Avesson (Department of Cell and Molecular Biology, Uppsala University, Sweden), Johan Reimegård (Department of Cell and Molecular Biology, Uppsala University, Sweden), Zhen Liao (Department of Cell and Molecular Biology, Uppsala University, Sweden), Ludwig Eichinger (Center for Biochemistry, University of Cologne, Germany), Angelika Noegel (Center for Biochemistry, University of Cologne, Germany), Gernot Glöckner (Center for Biochemistry, University of Cologne, Germany), Pauline Schaap (College of Life Sciences, University of Dundee, United Kingdom), **Fredrik Söderbom** (Department of Cell and Molecular Biology, Uppsala University, Sweden)

Recent years' discovery of numerous non-coding (nc)RNAs has dramatically changed the view of how organisms control their biological processes. We previously identified an abundant and highly expressed class of ncRNA, 42 – 65 nt long, involved in multicellular development of the social amoeba *Dictyostelium discoideum*. In order to understand if Class I RNAs are unique to *D. discoideum* or also present in other organisms, we searched for Class I RNA genes in genomes from species representing each major group of dictyostelid social amoeba and numerous Class I RNA genes were identified in all of these species. In contrast, genomes from strictly unicellular Amoebozoa showed now evidence of this class of RNA. Analysis of Class I RNAs from the different social amoeba species revealed several conserved features. They harbor a short stem-structure, connecting the 5´ and 3´ ends, and a conserved sequence element. In addition, the genes are preceded by a putative promoter sequence. Our results show that Class I RNA is an ancient class of ncRNAs, likely to have been present in the last common ancestor of Dictyostelia dating back at least 600 million years and we hypothesize that Class I RNAs are involved in evolution of multicellularity in Dictyostelia. Presently we are analyzing mass-spec and RNA-seq data from wt strain and a strain depleted of one Class I RNA gene that we know affect early multicellular development. We expect this study to give insights into the workings of Class I RNA during multicellular development.

Kjellin et al. (2021) Abundantly expressed class of noncoding RNAs conserved through the multicellular evolution of dictyostelid social amoebas. *Genome Res*. 31: 436-447

Presence and function of bacterial Rhs toxins in social amoebas

Jonas Kjellin (Department of Cell and Molecular Biology, Uppsala University, Sweden) & Sanna Koskiniemi (Department of Cell and Molecular Biology, Uppsala University, Sweden)

Bacteria live in complex environments where they have to compete with other microorganisms for resources and protect themselves from predators. To overcome this, many bacteria produce toxins which can either be secreted or delivered to nearby cells in a contact-dependent matter. However, the role of bacterial toxins extends beyond the use as weapons against antagonists. They can also affect the life-style of the toxin producing bacteria by e.g., regulating growth rate and multicellular behavior such as biofilm formation. One such example is found in *Myxococcus xhantus*, which is known for its ability to aggregate together and form fruiting bodies upon starvation. The fruiting bodies normally contains sporulated bacteria. However, if the Rearrangement hotspot (Rhs) toxin is disrupted, a large reduction in the number of spores is detected. Aggregative multicellularity is also found in eukaryotes and have evolved multiple times independently. The most well-studied example is the social amoeba *Dictyostelium discoideum* belonging to Dictyostelia with approximately 150 identified species within Amoebozoa. Almost all social amoebas differentiate into at least two cell types during the development, stalk cells and spore cells. However, in one subgroup, *Acytostelia*, this ability has been lost and instead fruiting bodies contains only spores. Interestingly, an Rhs homologue have been annotated in one of the acytostelids, *Acytostelium subglobosum*. In this study we investigate the presence of Rhs in *Dictyostelia* and attempt to understand its function. By searching for Rhs associated domains in 22 dictyostelid genome assemblies we could identify and validate Rhs presence in one additional amoeba, *Acytostelium digitatum*. Furthermore, PCR-screening indicates that Rhs is present throughout the *Acytostelia* subgroup. Our results indicates that Rhs plays an important role for acytostelids and our ongoing experimental and comparative genomics work aims to elucidate how these toxins affect their life style.

Protists in the global deep-sea sediment: benthic RNA activity in planktonic DNA deposits

Franck Lejzerowicz (Department of Biosciences, University of Oslo, Norway)

Protistan diversity in the deep-sea sediment is amongst the thickest dark matter in biology. Recent studies based on the sequencing of environmental benthic DNA suggest an extremely high diversity structured by oceanic basins, heterogeneity community compositions locally, and key alleged ecological roles. With impending deep-sea mining, it is more than ever pressing to extract useful and accurate knowledge for science to best inform management, notably the in large polymetallic nodule fields of the Clarion-Clipperton Zone (CCZ). Here, I present evidence based on both 18S rDNA and rRNA data, for the uniqueness of the CCZ in terms of protistan diversity and composition, as well as phylogenetic measures based on RNA and DNA read abundances to demonstrate that active protists are tractable and potentially useful indicators. I contextualize my results for the same benthic sites but a different rDNA marker, using complementary comparisons with planktonic sequences from Tara Oceans, to highlight that identifying not only active but also benthic protists is key but necessitates global initiatives. Indeed, as the UN Decade for Ocean Science and its deep-sea flagship research program "Challenger 150" unfold, a data collection and sequencing effort comparable to that of Tara Oceans is necessary for the deep-sea benthic protists. I foresee that advancing deep-sea benthic ecosystem studies in the Nordics will open new avenues for protistology, capacity building and policy globally.

Conducting applied ecology using single-celled eukaryotes

Markus Majaneva (Norwegian Institute for Nature Research (NINA), Norway)

Applied ecology considers the application of concepts, theories, models, and methods of ecology, for example, to the use and management of the environment and biodiversity. Measuring environmental or biodiversity change is thus the essence of applied ecology. Single-celled eukaryotes are ubiquitous and react almost immediately to changes in their environment, and are therefore highly suitable for applied ecological studies. Here, I will present two such studies. The first case is a study in which small lakes in Trondheim were treated with rotenone, a piscicide to eliminate the invasive fish species roach. The second case is a study in which biodiversity of gravel shores was compared in regulated and unregulated lakes near Trondheim. In both cases, biodiversity of single-celled eukaryotes show a clear response to the management actions.

A mitosome with distinct metabolism in the uncultured protist parasite *Paramikrocytos canceri* (Rhizaria, Ascetosporea)

Ioana Onuț-Brännström* (Department of Organismal Biology, Programme of Systematic Biology, Uppsala University, Sweden), Courtney W. Stairs* (Microbiology research group, Department of Biology, Lund University, Sweden) , Karla Iveth Aguilera Campos (Microbiology Research Group, Department of Biology, Lund University, Sweden) , Thijs J. G. Ettema (Laboratory of Microbiology, Wageningen University and Research, The Netherlands), Patrick J. Keeling (Department of Botany, University of British Columbia, Canada), David Bass (CEFAS & Department of Life Sciences, The Natural History Museum & Sustainable Aquaculture Futures, Biosciences, College of Life and Environmental Sciences, University of Exeter, United Kingdom), Fabien Burki (Department of Organismal Biology, Programme of Systematic Biology & Science for Life Laboratory, Uppsala University, Sweden)

*shared authors

Ascetosporea are endoparasites of marine invertebrates that include economically important pathogens of farmed species in aquaculture. Owing to their often-minuscule cell sizes, intracellular lifestyle, lack of cultured representatives and minimal availability of molecular data, these parasites remain poorly studied. Here, we sequenced and assembled the genome and transcriptome of the fast-evolving parasite *Paramikrocytos canceri*, isolated from infected European edible crab *Cancer pagurus*. Using bioinformatic analyses, we propose that *P. canceri* possesses a mitochondrion-related organelle (MRO) with highly reduced metabolism, resembling mitosomes. The organelle lacks a genome and most proteins typically involved in mitochondrial metabolism but, has the complete iron-sulfur cluster (ISC) pathway for Fe-S cluster biosynthesis. However, unlike other mitosomes, the MRO in *P. canceri* is predicted to produce ATP through the last phases of glycolysis, and to synthesize phospholipids de novo through the CDP-DAG pathway. Heterologous gene expression in yeast confirmed that proteins from the ISC and CDP-DAG pathways are targeted to the MRO. This represents a unique combination of metabolic pathways in an MRO, including the first reported case of a mitosome-like organelle able to synthesize phospholipids de novo. Some of these phospholipids, such as phosphatidylserine, are vital in other protist endoparasites that invade their host through apoptotic mimicry.

The wastewater protist *Rhogostoma minus* (Thecofilosea, Rhizaria) is abundant, widespread, and hosts Legionellales

Nina Pohl (Terrestrial Ecology, University of Cologne, Germany), Marcel Dominik Solbach (Terrestrial Ecology, University of Cologne, Germany), Kenneth Dumack (Terrestrial Ecology, University of Cologne, Germany)

Wastewater is treated by concerted actions of the microbial communities within bioreactors. Although protists (unicellular eukaryotes) are good bioindicators and important players influencing denitrification, nitrification, and flocculation, they are the least known organisms in WWTPs. The few recent environmental surveys of the protistan diversity in WWTPs show that the most abundant protistan sequences in WWTPs belong to Thecofilosea (Rhizaria). We re-investigated previously published environmental sequencing data and gathered strains from seven WWTPs to determine which species dominate WWTPs worldwide. We found that all highly abundant thecofilosean sequences represent a single species – *Rhogostoma minus*. Considering that Thecofilosea are frequent hosts for Legionellales, i.e. bacteria linked to waterborne diseases, we confirm that *Rhogostoma minus* functions as a host for Legionellales in WWTPs. Whether the highly abundant *Rhogostoma minus* also serves as a host for known human pathogenic Legionellales requires further attention.

Characterisation of potential glycolytic transporters in *Blastocystis*

Eva Pyrihová (Department of Chemistry, Bioscience and Environmental Engineering, University of Stavanger, Norway; Mitochondrial Biology Unit, University of Cambridge, United Kingdom), Alannah C. King (Mitochondrial Biology Unit, University of Cambridge, United Kingdom), Martin S. King (Mitochondrial Biology Unit, University of Cambridge, United Kingdom), Edmund R. S. Kunji (Mitochondrial Biology Unit, University of Cambridge, United Kingdom), Mark van der Giezen (Department of Chemistry, Bioscience and Environmental Engineering, University of Stavanger, Norway)

Glycolysis is a well-conserved cytosolic pathway that converts glucose into pyruvate, which is subsequently transported via pyruvate carrier into mitochondria and enters the TCA cycle. It was shown that in *Blastocystis* the second part of glycolysis is localised in mitochondria and the pyruvate carrier is missing. Therefore, for *Blastocystis* to perform glycolysis, there has to be another transporter for glycolytic intermediates to trespass the mitochondrial inner membrane. We aim to identify which glycolytic intermediate is transported and also to characterise the novel glycolytic transporter. We found a group of Stramenopile-specific transporters which are not present in any other eukaryotes. We expressed some of these proteins from *Blastocystis* in yeasts and we purified them from yeast mitochondria. We measured their thermostability upon the addition of different substrates. We show that while the addition of glycolytic intermediates does not affect the thermostability of our control proteins, it has a stabilising effect on *Blastocystis*-specific transporters. It indicates that Stramenopiles adapted their transporters to transport glycolytic intermediates. We also investigate the ability of these proteins to transport glycolytic intermediates by measuring the uptake of radioactive substrates using reconstituted proteins into proteoliposomes. We show that *Blastocystis* transporters can bind glycolytic intermediates and are likely responsible for their transport across the mitochondrial membrane. Given that these transporters are Stramenopile specific, they could be exploited as drug targets not only for *Blastocystis* but also for economically important pathogens such as *Saprolegnia* or *Phytophthora*.

The eco-evolution of microbial eukaryotes inferred from metabarcoding surveys

Miguel M. Sandin (Department of Organismal Biology, Uppsala University, Sweden), Fabien Burki (Department of Organismal Biology, Uppsala University, Sweden)

Recent molecular dating analyses suggest that eukaryotes originated more than 2 billion years ago. Following this life-changing event, however, current evidence point to an initial slow diversification process, a period that is sometimes referred to as the “boring billion”. A critical question is thus, what evolutionary processes led eukaryotes to evolve into this incredible diversity that we observe today after the boring billion? In our project, we fit macro-evolutionary models into an ecological perspective to explore the diversification of eukaryotes through geological times at a broad phylogenetic scale. Uniquely, we integrated both long-read and short-read environmental rDNA sequences along with phylogenetically curated references to access the majority of the known eukaryotic molecular diversity. We then combined this phylogeny of eukaryotic diversity, containing more than 100 00 (up to 250 000) OTUs, with 60 established fossil calibrations to date the eukaryotic tree of life and infer diversification patterns throughout the history of eukaryotes. Here, we will introduce this dataset and main challenges found to test the hypothesis that the “boring billion” was perhaps not so boring after all. While early eukaryotic diversification was initially slow, biotic interactions established the main groups that we observe today and set the basis for the later expansion. Only when environmental conditions were more favorable , especially after the second and most pronounced oxygenation event, the standing diversity of eukaryotes became relevant at the global scale to thrive and dominate the biomass.

The *Acrasis kona* genome and developmental transcriptomes suggest an early origin of multicellularity in eukaryotes

Sanea Sheikh (Programme in Systematic Biology, Uppsala University, Sweden), Cheng-Jie Fu (Programme in Systematic Biology, Uppsala University, Sweden), Wei Miao, Institute of Hydrology, Chinese Academy of Science, China) **Sandra Baldauf** (Programme in Systematic Biology, Uppsala University, Sweden)

Multicellular development is remarkably similar in the aggregative multicellular (AGM) amoebae, *Acrasis kona* (Ako) and *Dictyostelium discoideum* (Ddi). However, Ddi and Ako are nearly as distantly related as any two eukaryotes can be (suprakingdoms Amorphea and Discoba, respectively). We have sequenced the acrasid genome and developmental transcriptomes and find that the genome is rich in novel genes, genes acquired by horizontal transfer and multigene families. In fact, nearly half of the proteome clusters into multigene families, and HGT has contributed substantially to this redundancy. Development in A. kona appears to be molecularly much simpler than in Ddi, involving substantially increased expression of nearly 5-fold fewer genes. However, a significant amount of this difference appears to reflect the fact that, unlike developing Ddi, developing Ako does not appear to be starving. In fact, development in the acrasid shows considerable resemblance to both Ddi and clonal (metazoan) development. This includes complex highly conserved pathways for signalling and construction of an extracellular matrix. This suggests that the last common ancestor of eukaryotes may have possessed many of the basic tools for multicellular development.

Metabarcoding reveals spatial differences in protist communities in- and outside a mesoscale meander of the Southern Indian Ocean

Daniela Sturm (Marine Biological Association, United Kingdom), Glen Wheeler (Marine Biological Association, United Kingdom), Colin Brownlee (Marine Biological Association, United Kingdom)

Marine protists include some of the most important primary producers such as diatoms, dinoflagellates, and haptophytes. Especially in the Southern Ocean their distribution and abundance greatly affect biogeochemical cycling and global primary production. Using metabarcoding of the 18S V9 rDNA gene subunit, we describe the composition of protist communities in a mesoscale meander of the southern Indian Ocean. Members of the Alveolata were the most abundant clades and composed mostly of the heterotrophic flagellated Dinophycaea, the parasitic Syndiniales, and the ciliated Spirotrichaea, followed by the photosynthetic Prymnesiophyceae and the heterotrophic stramenopiles MAST. We further found significant differences in the community structure between the centre and the periphery of the occupied meander, which were most likely caused by variations in temperature and salinity. The overall diversity of the protist community was highest at the boundary between the inside and outside of the meander, which may be caused by mixing of productive waters at the meander boundary. Stramenopiles, although not amongst the most abundant taxa, were more successful on the meander periphery, while Dinophycaea were more abundant in the centre. Considering lower nutrient concentrations on the outside of the meander, this result is somewhat surprising as we may expect heterotrophic taxa to outcompete autotrophs under these conditions. However, the area was generally oligotrophic and therefore nutrient concentrations are likely not the main drivers of community composition. Our findings highlight the importance of large-scale oceanographic features on protist abundance and distribution. However, we also suspect that previously reported biases introduced by using non-specific genetic markers have skewed our observed taxa abundances. Many ecologically important taxa, such as coccolithophores, were likely underrepresented in the dataset. Given that similar methods were applied previously in large scale investigations of protist communities, the true abundance of ecologically relevant clades may be much greater than currently recognized.

Biodiversity and biogeography of diatoms from the Svalbard area: community structuring through endemism and dispersal

Luka Supraha (Department of Biosciences, University of Oslo, Norway), Kerstin Klemm (Alfred Wegener Institute, Helmholtz Centre for Polar and Marine Research, German), Sandra Gran-Stadniczeñko (Department of Biosciences, University of Oslo, Norway), Cora Hörstmann (Alfred Wegener Institute, Helmholtz Centre for Polar and Marine Research, German), Daniel Vaulot (Sorbonne Université, CNRS, France; Nanyang Technological University, Singapore), Bente Edvardsen (Department of Biosciences, University of Oslo, Norway), Uwe John (Alfred Wegener Institute, Helmholtz Centre for Polar and Marine Research, Germany)

Diatoms are the key primary producers in the Arctic, both within planktonic and sea ice associated communities. To predict how the ongoing environmental changes may alter their community structure and consequently affect the Arctic ecosystem function, it is crucial to establish a solid framework for their taxonomic identification and understand the processes shaping their biodiversity. In this context, one important question is the relevance of Arctic endemism and dispersal with Atlantic waters for the structuring of Arctic diatom communities. In this work, we combined extensive cultivation of Arctic diatoms, collected from Svalbard fjords during the 2017 cruise HE492 led by Alfred Wegener Institute (AWI, Germany), and their taxonomic characterization using morphological (microscopy) and molecular (18S and 28S rRNA gene sequencing) approaches. Along with the taxonomic characterization, the distribution of each isolated diatom genotype was mapped within the local 18S rRNA metabarcoding dataset spanning five Svalbard fjords and the Hausgarten area and globally, using metaPR2, an extensive compilation of 18S rRNA metabarcoding datasets. We have discovered that Arctic diatoms exhibit a high degree of cryptic biodiversity and that cold-adapted Arctic genotypes are found within major cosmopolitan species complexes. We found that endemism is common among Arctic diatoms and that endemic genotypes are an important component of diatom communities in the area, particularly in the colder, northern fjords. Alongside endemic genotypes, a large proportion of Arctic diatoms are widely distributed in temperate and warm latitudes. We suggest that the distribution of warm-water genotypes in the Svalbard area can be used as an indicator of progressing ocean warming (Atlantification).

Regulation of encystation in *Giardia*- the road to resilience

Staffan Svärd (Department of Cell and Molecular Biology, Uppsala University, Sweden)

Many protists, both free-living and parasitic, form cysts in response to stress responses like starvation. The cysts are resilient and survive for a long time in the environment until conditions get better and the cells can re-start replication. *Giardia intestinalis* is an intestinal protozoan parasite that causes diarrheal infections worldwide. A key process to sustain its chain of transmission is the formation of infectious cysts in the encystation process. We have developed and in vitro encystation protocol for *Giardia* making it possible to study the regulation of this differentiation process. By using deep RNAseq and proteomics we have now a high resolution gene expression map of the process and it shows that it is highly regulated on many different levels by step-wise changes of transcription factors, epigenetic changes and translational regulation. There are many similarities to how human stem cells differentiate into specific cell types, showing that regulation of cell differentiation is conserved in eukaryotic cells.

Using ancient DNA sequencing to assess the impact of past environmental changes on marine protist biodiversity

Agnes K.M. Weiner (NORCE, Norway), Tristan Cordier (NORCE, Norway), Jessica L. Ray (NORCE, Norway), Margit H. Simon (NORCE, Norway), Aud Larsen (NORCE, Norway), Magdalena Łącka (IOPAN, Poland), Joanna Pawlowska (IOPAN, Poland), Dhanushka Devendra (IOPAN, Poland), Małgorzata Szymczak-Żyła (IOPAN, Poland), Magdalena Krajewska (IOPAN, Poland), Mattia Greco (IOPAN, Poland), Ngoc Loi Nguyen (IOPAN, Poland), Marek Zajączkowski (IOPAN, Poland), Jan Pawlowski (IOPAN, Poland), Stijn De Schepper (NORCE, Norway)

Coastal marine ecosystems are highly sensitive to climate change. They are currently being altered by increasing water temperatures, decreasing oxygen levels, anthropogenic stressors and, in the Arctic, changes in sea ice conditions. These rapid changes will inevitably have profound effects on biodiversity and productivity. However, so far, our knowledge on the impact of these changes especially on protist communities remains limited, despite their important roles in food webs and nutrient cycling. In order to understand ongoing and future changes in coastal marine ecosystems, it is essential to assess the response of protist communities to past changes in environmental conditions. To date, such studies are limited to lineages with a fossil record (e.g. Foraminifera), leaving an incomplete picture of the remaining protist diversity. We are now working towards establishing sedimentary ancient DNA sequencing as a new tool for reconstructing past changes in entire protist communities in relation with past environmental changes. In the Polish-Norwegian collaboration project NEEDED, we are focusing on marine sediment cores from the Nordic Seas and assess environmental and biodiversity changes throughout the last 10,000 years. We extract ancient DNA and trace a wide range of protist taxa through time to estimate past changes in diversity and productivity. The paleogenomic data will then be compared to other proxies, changes in sea ice cover and water temperature. In addition, we are adapting ancient DNA sequencing to high-resolution sediment cores from Norwegian fjords to assess the impact of recent environmental and anthropogenic stressors on protist communities.

Posters

Syntrophic interactions with Arcobacter species are pervasive in breviate protists

Karla Iveth Aguilera Campos (Biology Department, Lund University, Sweden), Julie Boisard (Biology Department, Lund University, Sweden), Elena Aramendia Cotillas (Biology Department, Lund University, Sweden), Zhenzhen Yi (Department of Biology, Dalhousie University, Canada; Department of Biology, South China Normal University, China), Shelby K. Williams (Department of Biochemistry & Molecular Biology, Dalhousie University, Canada), Yana Eglit (Department of Biology, Dalhousie University, Canada), Alastair Simpson (Department of Biology, Dalhousie University, Canada), Andrew J. Roger (Department of Biochemistry and Molecular Biology, Dalhousie University, Canada), Courtney Stairs (Biology Department, Lund University, Sweden)

Syntrophy is a type of symbiotic cooperation, performed through metabolic interaction between partners. Syntrophic interactions between prokaryotes are common in anoxic environments, however, whether such interactions exist between microbial eukaryotes (protists) and prokaryotes is much less understood. Previous investigations uncovered a potentially syntrophic interaction between the anaerobic breviate protist *Lenisia limosa* and the bacterium *Arcobacter*. This interaction provides benefits to both partners via hydrogen transfer whereby hydrogen produced by the protist is consumed by *Arcobacter*. The *Arcobacter* symbiont encodes proteins homologous to so-called virulence factors of related pathogenic *Arcobacter* species and these factors are upregulated in the presence of *L. limosa* suggesting they could be key for engaging the syntrophic interaction. The goal of my PhD is to expand our understanding of breviate:*Arcobacter* relationships by studying the molecular features and evolutionary history of syntrophy across the Breviatea phylum. Our preliminary investigation demonstrates that *Arcobacter* species are often found in the same environments and in cultures of other diverse breviate species, indicating that the mutualistic interaction between these two groups of microbes might be pervasive. If so, further investigation may reveal when the breviate:Arcobacter symbioses were first established in the evolutionary history of Breviatea. and the establishment of breviate:*Arcobacter* symbioses happened early in the evolution of the phylum Breviatea.

Identification of soil protist composition and their effect on bacterial communities

Christine Lorenzen Elberg (Department of Environmental Science, Aarhus University, Denmark), Rumakanta Sapkota (Department of Environmental Science, Aarhus University, Denmark), Anne Winding (Department of Environmental Science, Aarhus University, Denmark)

Protist predation on microorganisms in the soil has an important role in shaping the microbiome and leads to an increase of nutrient availability for the plant. These interactions therefore play an important role for crop performance. Although microbial interactions play a vital role in shaping the microbiome structure, understanding of the predator-prey interactions between protists and bacteria are limited. The aim of this study is to identify if the protists communities in wheat and test how different protist species select for specific bacteria as nutrient source. Bulk and rhizosphere soil from four wheat cultivars grown for in a growth chamber were collected and protists were isolated by dilution and culturing. Mono-cultures consisting of one protist species growing on co-isolated bacteria in a bacterial broth were obtained. The isolated protists were identified using Sanger sequencing and bacterial communities will be profiled using metabarcoding of 16S ribosomal DNA. The results will increase our understanding of the protist communities in the wheat rhizosphere and guide us for protists role in rhizosphere microbiome. We believe that such knowledge on microbe-microbe interactions will lead us towards developing solutions for environmentally sustainable crop production.

Ancestral reconstructions of gene content with Dollo parsimony are incorrect

Àlex Gàlvez i Morante (Institut de Biologia Evolutiva, Spain), Laurent Gueguen (Universite Claude Bernard - Lyon I, France), Paschalis Natsidis (University College London, United Kingdom), Max Telford (University College London, United Kingdom), Daniel J. Richter (Institut de Biologia Evolutiva, Spain)

Ancestral reconstruction of gene content is a technique to study the evolution of form and function associated with transitions across the tree of life. Ancestral reconstructions can be based on different phylogenetic inference methods like maximum likelihood or Bayesian inference, but most current studies are based on Dollo parsimony. Even though ancestral reconstruction of gene content is a powerful technique, the results and conclusions that can be extracted from it depend on the accuracy of the reconstruction method that has been applied. Therefore, the aim of this project is to compare different ancestral reconstruction inference methods. We hypothesize that Dollo parsimony assumptions are not appropriate for ancestral reconstruction inferences based on sequence homology (i.e., BLAST), as it is based on the idea that a complex character can only be gained once. This premise does not accurately model molecular sequence evolution and could lead to distortions in phylogenetic studies. In order to test our hypothesis, we first compared the performance of the different methods with real and simulated genomic datasets, and then we reconstructed protein domain evolution on a phylogeny representing known eukaryotic diversity. We observed several overestimations produced by Dollo parsimony, especially in ancestral nodes closer to the root of the tree. This led us to the conclusion that, confirming our hypothesis, Dollo parsimony is not an appropriate method for ancestral reconstruction studies based on sequence homology.

Changes in the phytoplankton community composition observed in a time series in the Baltic Sea off Sweden's east coast

Carolin Peter (Biology and Environmental Science, Linnaeus University, Sweden), Hanna Farnelid (Biology and Environmental Science, Linnaeus University, Sweden), Elin Lindehoff (Biology and Environmental Science, Linnaeus University, Sweden), Emil Fridolfsson (Biology and Environmental Science, Linnaeus University, Sweden), Catherine Legrand (Biology and Environmental Science, Linnaeus University, Sweden)

The Baltic Sea is predicted to undergo a series of changes in meteorological as well as chemical characteristic due to global climate change. An important resource, which helps to improve the predictions of what effect these changes might have on the ecosystem, are monitoring efforts. The Linnaeus Microbial Observatory time series, which consists of biweekly samplings off the coast of Öland (Sweden) reveals unexpected trends in the phytoplankton community composition. It was predicted that the combination of increased temperature and inherently high nutrient availability, especially phosphate, will lead to an increase in summer blooms of filamentous, diazotrophic cyanobacteria. Over the past five years, however, this was not observed. The ratio between dinoflagellates and diatoms didn’t increase, as predicted, either and instead decreased significantly. On the other hand, higher temperatures did correlate with significant changes in the phytoplankton community composition. While the proportion of cyanobacteria and chlorophytes increased, the proportions of chrysophytes, cryptophytes, dinoflagellates and haptophytes decreased. An observed increase in the ratio between ammonium and nitrate, was correlated to an increase in dinoflagellate biomass. Climate change is going to not only affect the phylogenetic composition of the community but also its size structure. The forecasted increases in temperature and ammonium to nitrate ratio, are predicted to favour small cells over larger ones. These correlations can be observed in the present dataset. Over the past five years, however, the biomass of larger cells above 20µm ESD increased, while the biomass of smaller cells between 20µm and 5µm ESD decreased. These findings highlight that the natural dynamics are far more complicated and intricate than currently predicted in simple models.

Isolation and characterization of two novel species of choanoflagellates

Margarita Skamnelou (Institute of Evolutionary Biology (IBE), Spain) , Luis Javier González Galindo (Department of Biology, University of Oxford, UK) , Cédric Berney (Station Biologique de Roscoff, France), David Moreira (Université Paris-Sud, France), Purificación López García (Université Paris-Sud, France), Daniel J. Richter (Institute of Evolutionary Biology (IBE), Spain)

Choanoflagellates are small unicellular and colonial heterotrophic protists with significant ecological impact on microbial food webs. Their conserved morphology consists of a cell body with a single flagellum surrounded by a collar of microvilli. Along with their similar structure and function with the choanocytes in sponges, recent phylogenetic and metatranscriptomic studies place choanoflagellates as the closest unicellular relative of metazoans and unravel the existence of "animal" gene families in their genome, highlighting further their evolutionary significance. Considering their key role in evolution and ecology, expanding our knowledge on their diversity and biology is of utmost importance. Here we describe the isolation of two novel choanoflagellate species from Mijet, Croatia (CRO20CHO1) and Lanzarote, Spain (LJO2) and the characterization of their morphological properties by using various imaging approaches like fluorescent confocal microscopy and Transmission/Scanning Electron Microscopy (TEM/SEM respectively). 18S rRNA sequencing and subsequent phylogenetic analysis placed CRO20CHO1 as closely related to the *Hartaetosiga* genus and LJO2 to the Stagondoeca genus. Fluorescent labelling revealed that the surface of CRO20CHO1 species is characterized by a carbohydrate coat, called the glycocalyx. TEM analysis further demonstrated closed fitting and flexibility within the coat. On the other hand, LJO2 was shown to be surrounded by an organic covering called theca, which extends to a pedicel. Super-resolution imaging demonstrated a relaxed theca fitting, with a unique shape resembling a "Nolan amphora" (common artifact of Greek pottery). In addition to these structural characteristics, SEM analysis also shed light into aspects of their distinct life stages, with a notable example being the formation of stalked colonies by CRO20CHO1. Finally, aiming to further characterize these species, we are currently in the process of de novo assembling their transcriptome. In the long term, the study of these unknown organisms will serve towards further understanding aspects of eukaryotic evolution and diversity.

The Gene They Keep on Giving: lateral gene transfer from protists could enable freshwater sponges to adapt to hypoxia

Mara Vizitiu (Biology Department, Lund University, Sweden), Julie Boisard (Biology Department, Lund University, Sweden), Courtney Stairs (Biology Department, Lund University, Sweden)

The mitochondrial electron transport chain represents a key component of the cellular respiration process, being comprised of a series of subunits known as "complexes", electron donors, acceptors, and carriers. In aerobic conditions, the molecule ubiquinone (UQ) plays the role of electron carrier, receiving electrons from complexes I and II and transferring them further to cytochrome c; however, under anaerobic conditions, this carrier is instead replaced by an analogous molecule, called rhodoquinone (RQ), that transfers electrons between complexes I and II in its reduced form. RQ-utilizing species are spread throughout the tree of life and two distinct RQ biosynthesis pathways have been identified. In metazoans, RQ is biosynthesized via a modified UQ biosynthesis pathway that is dependent on a splice variant of the *coq2* gene. The second possible way to synthesize RQ involves a protein known as RQUA, which has thus far been characterized in bacteria and protists. Using genome and transcriptome sequencing data we were able to identify three species of sponges (phylum Porifera) belonging to three different genera of the family Spongillidae, that also encode the gene *rquA*, this representing the first instance in which the gene has been described in Opisthokonts. Moreover, based on phylogenetic data, we hypothesize that these freshwater sponges acquired *rquA* via lateral gene transfer from a donor lineage within Euglenida. Our findings do not only suggest that freshwater sponges could employ this protist-specific strategy to adapt to hypoxia, but also highlight once more the significance of unicellular eukaryotes in the evolution of anaerobic metabolism.

Participants

Karla Iveth Aguilera Campos
Lund University
Sweden

Anders Alfjorden
Uppsala University
Sweden

Seyed Saeed Asadzadeh
Technical University of Denmark
Denmark

Sandra Baldauf
Uppsala University
Sweden

Marit Bjorbækmo
University of Oslo
Norway

Julie Boisard
Lund University
Sweden

Fabien Burki
Uppsala University
Sweden

Jeffrey Colgren
University of Bergen
Norway

Hugo de Boer
University of Oslo
Norway

Micah Dunthorn
University of Oslo
Norway

Bart Edelbroek
Uppsala University
Sweden

Bente Edvardsen
University of Oslo
Norway

Wenche Eikrem
University of Oslo
Norway

Christine Elberg
Aarhus University
Denmark

Àlex Gàlvez i Morante
Institut de Biologia Evolutiva
Spain

Megan Gross
Technical University Kaiserslautern
Germany

Khrystyna Gryn
University of Oslo
Norway

Anna-Lotta Hiillos
University of Jyväskylä
Finland

Markus Hiltunen
Uppsala University
Sweden

Jon Jerlström-Hultqvist
Uppsala University
Sweden

Jonas Kjellin
Uppsala University
Sweden

Emily Knott
University of Jyväskylä
Finland

Anders Kristian Krabberød
University of Oslo
Norway

Franck Lejzerowicz
University of Oslo
Norway

Markus Majaneva
Norwegian Institute for Nature Research
Norway

Quentin Mauvisseau
University of Oslo
Norway

Miguel Mendez Sandin
Uppsala University
Sweden

Ioana Onut Brännström
University of Oslo
Norway

Carolin Peter
Linnaeus University
Sweden

Nina Pohl
University of Cologne
Germany

Eva Pyrihová
University of Stavanger/ University of Cambridge
Norway

Margarita Skamnelou
Institute of Evolutionary Biology
Spain

Fredrik Söderbom
Uppsala University
Sweden

Courtney Stairs
Lund University
Sweden

Daniela Sturm
Marine Biological Association
United Kingdom

Luka Supraha
University of Oslo
Norway

Staffan Svärd
Uppsala University
Sweden

Mara Vizitiu
Lund University
Sweden

Agnes Weiner
NORCE
Norway