PROTISTOLOGY NORDICS LUND 2023

Programme & Abstracts

2-3 May 2023

Dear Colleagues,

Following the success of Protistology Nordics 2022 in Oslo, we are excited to announce that Protistology Nordics 2023 will be held in Lund, providing another opportunity for scientists in Nordic countries to come together and showcase their research on the genetics, cell biology, ecology, and evolution of protists.

Our aim for this meeting is to continue promoting a supportive environment for both early-career and advanced researchers to present their work and connect with others in the field. We hope that Protistology Nordics 2023 will strengthen the community dedicated to promoting and advancing protistan research.

We are delighted to announce that Mahwash Jamy from Swedish University of Agricultural Sciences will deliver the plenary talk. Six talks will be presented across two sessions, with an additional three flash talks in session one.

The meeting will take place in Kulturen, a unique open-air museum that provides an immersive experience of the cultural heritage of the Skåne region. Attendees will have the opportunity to explore the museum's several exhibitions, providing an immersive experience of the past.

We look forward to seeing you all at Protistology Nordics 2023 and continuing to grow and strengthen our community of protistologists in the Nordic region.

Kind Regards,
The organizing committee

Mara Vizitiu, Sofia Paraskevopoulou, Courtney Stairs, Micah Dunthorn, and Fabien Burki

Organizers

Courtney Stairs
Biology Department
Lund University
Sweden

Sofia Paraskevopoulou
Biology Department
Lund University
Sweden

Mara Vizitiu
Biology Department
Lund University
Sweden

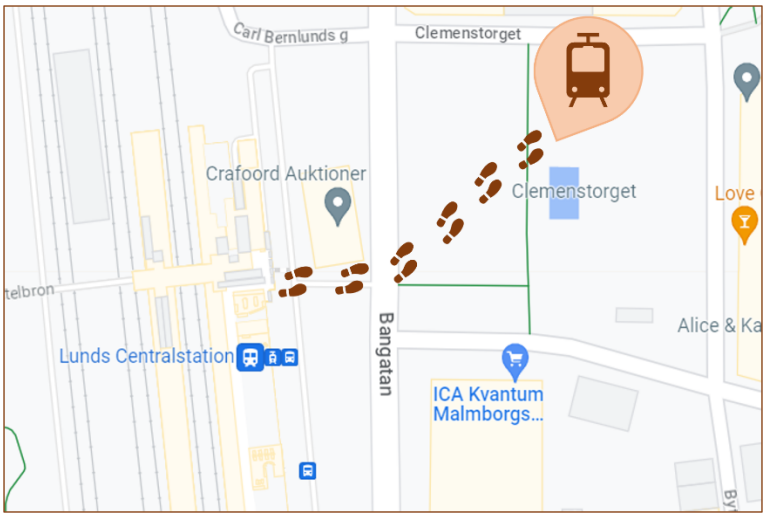
Micah Dunthorn
Natural History Museum
University of Oslo
Norway

Fabien Burki
Department of Organismal Biology
Uppsala University
Sweden

Premises

2 May

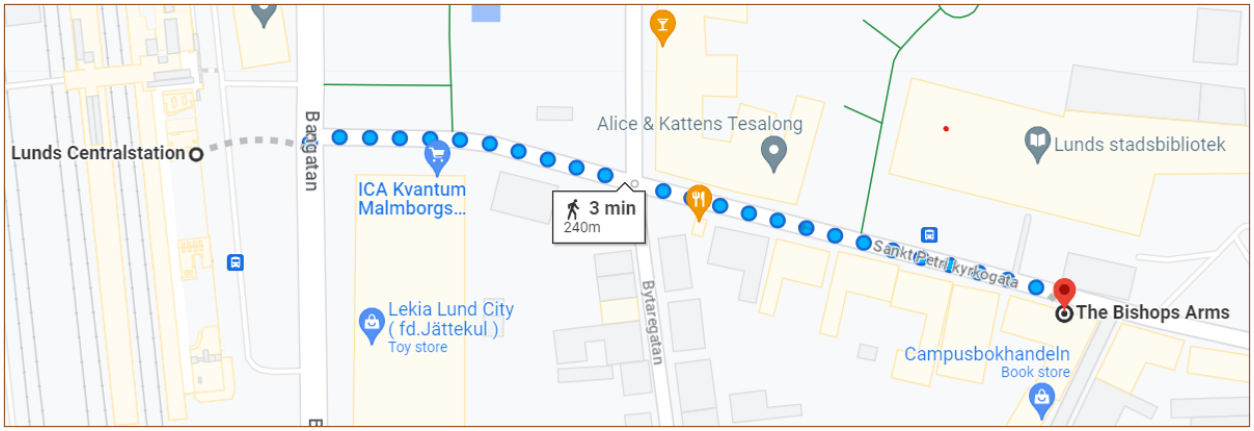
Microscope activity: Biologihuset - Sölvegatan 35, Lund



- Walk to the tram station Lund C
- Take Tram 1 towards ESS
- Go two stops until Lund LTH
- The tram will leave you right outside Biologihuset

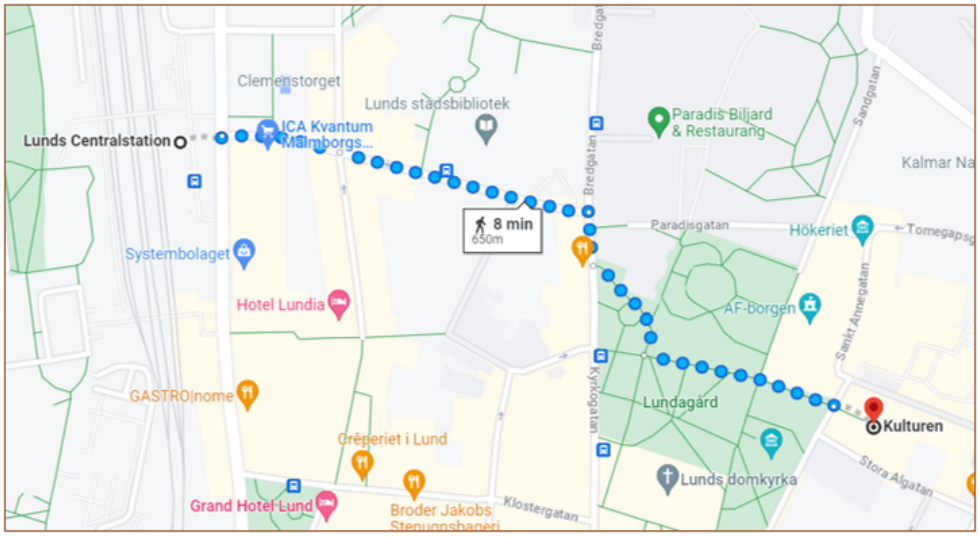
Information about tickets: https://www.skanetrafiken.se/biljetter/kopbiljett/

Pub mingle: The Bishop's Arms, S:t Petri Kyrkogata 7, Lund

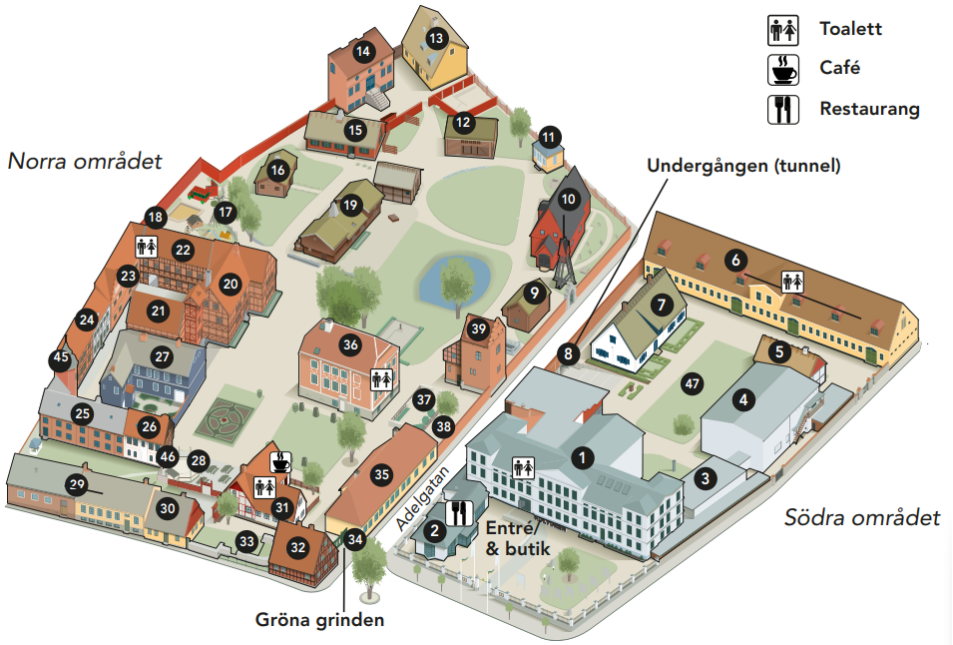


3 May

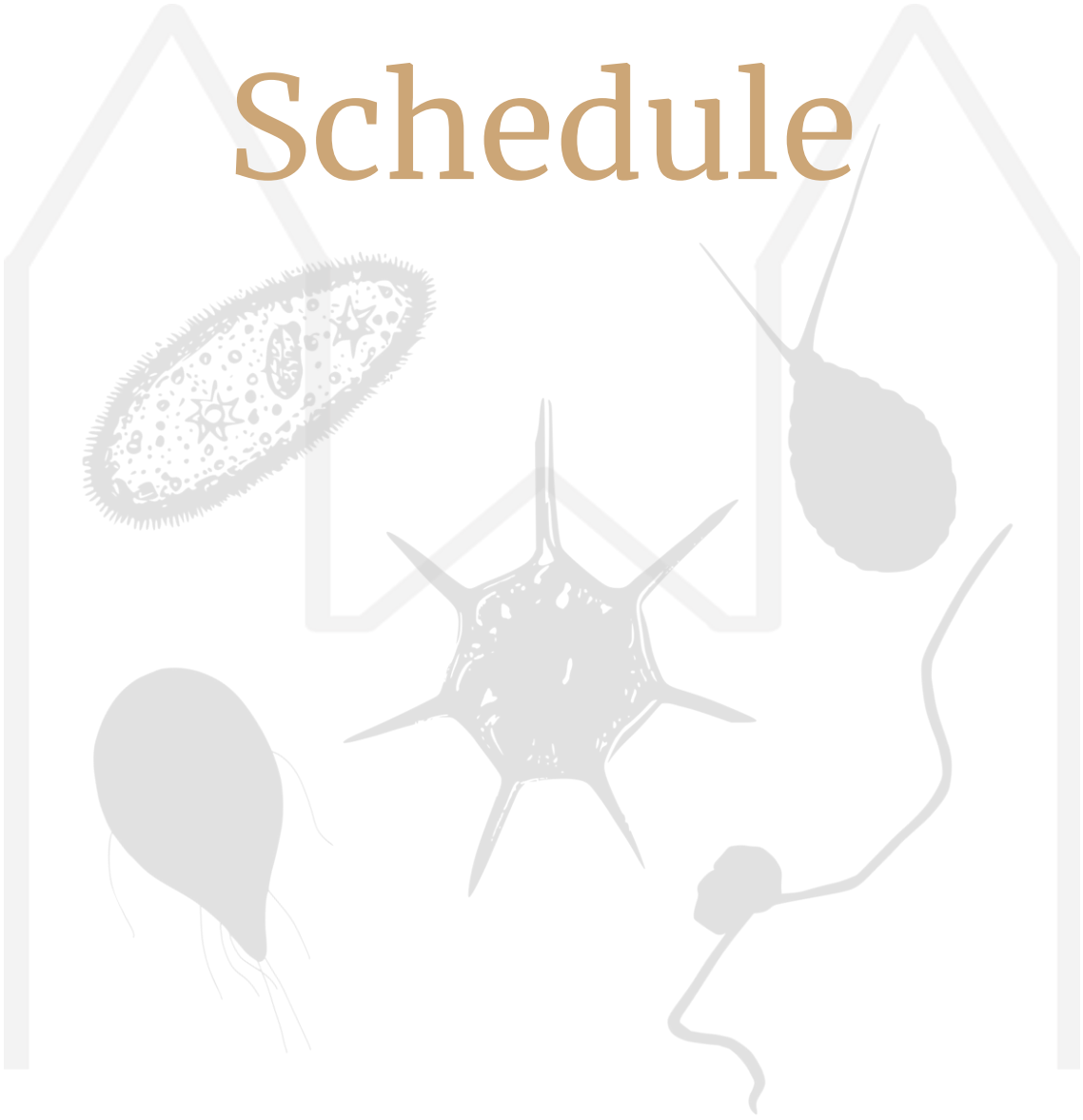
Meeting location: Kulturen, Tegnérsplatsen 6, Lund



More information available at: https://www.kulturen.com/vara-besoksmal/kulturen-i-lund/hitta-till-kulturen/



Schedule



Programme overview

2 May

14:00 – 16:30	*Microscopy session* Biologihuset Sölvegatan 35
18:00 -	*Pub night* Bishop's arms Sankt Petri kyrkogata 7

3 May

Kulturen, Tegnérsplatsen 6

9:00 - 9:15	Registration
9:15 - 9:30	Welcome address
9:30 - 10:15	Plenary talk
10:15 - 10:45	Fika (coffee + snacks)
10:45 - 11:30	Contributed talks
11: 30 - 11:45	Flash talks
12:00 - 13:00	Lunch
13:15 – 14:00	Contributed talks
14:00 - 15:30	Free time (explore Kulturen)
15:30 -	Drinks + society discussion

Detailed schedule

2 May

14:00 – 16:30 *Microscopy session* (drop-in)
Location: Biologihuset, Sölvegatan 35, Lund
Coffee and snacks will be provided

18:00 - *Pub night*
Location: The Bishop's Arms, S:t Petri Kyrkogata 7, Lund

3 May

Location: Kulturen, Tegnérsplatsen 6, Lund

09:15 - 09:30 *Welcome address*
Courtney Stairs (Lund University)
Micah Dunthorn (University of Oslo)

PLENARY TALK

Chair: Courtney Stairs

09:30 - 10:15 Mahwash Jamy (Swedish University of Agricultural Sciences)
Long Reads and rRNA Databases: Exploring Protist Diversity and Evolution through Metabarcoding

10:15 - 10:45 Fika (coffee and snacks) at Kulturen

CONTRIBUTED TALKS 1

Chair: Staffan Svärd

10:45 - 11:00 **Micah Dunthorn** (University of Oslo)
The Number of Free-living Ciliate Species

11:00 - 11:15 **Megan Gross** (Rheinland-Pfälzische Technische Universität Kaiserslautern-Landau)
Digital PCR as a New Cutting-edge Tool for Measuring Ciliate Abundance

11:15 - 11:30 **Yash Pardasani** (Uppsala University)
Investigating Paulinella Amoebas to Understand the Origin of Photosynthetic Eukaryotes

FLASH TALKS

Chair: Mara Vizitiu, Sofia Paraskevopoulou

11: 30 - 11:35 **Nina Pohl** (Uppsala University)
Picozoa and the Origin of Plastids

11: 35 - 11:40 **Constance Choquel** (Lund University)
Evaluating 3D Morphometrics Changes in Calcite Shells Using a Multistressor Experimental Approach (Stress^{3D})

11:40 - 11:45 **Anders Alfjorden** (Uppsala University)
Hidden Oyster Flagellate Makes an Entrance

12:00 - 13:00 Lunch at Kulturen

CONTRIBUTED TALKS 2

Chair: Micah Dunthorn, Sofia Paraskevopoulou

13:15 - 13:30	Staffan Svärd (Uppsala University) *Giardia - a Parasite with Two Faces*
13:30 - 13:45	Jon Jerlström Hultqvist (Uppsala University) *Three-dimensional Structure of a Protist Symbiosis*
13:45 - 14:00	Courtney Stairs (Lund University) *Hacking the Electron Transport Chain to Live without Oxygen*
14:00 - 15:30	Free time – explore Kulturen
15:30 -	Drinks and discussion about creating a Protistology society

Abstracts

Plenary talk

Long Reads and rRNA Databases: Exploring Protist Diversity and Evolution through Metabarcoding

Mahwash Jamy[1,2]

[1]*Department of Aquatic Sciences and Assessment, Swedish University of Agricultural Sciences, Uppsala, Sweden*
[2]*Natural History Museum, University of Oslo, Oslo Norway*

Metabarcoding studies have transformed our understanding of environmental protist diversity and ecology by generating millions of short-read fragments (<500 bp) of the 18S gene. However, these short reads are limited in their phylogenetic signal and the processed sequences are rarely available in a standardized format. In this talk, I will present two recent advances that address these issues: (1) long-read metabarcoding, and (2) the emergence of ribosomal RNA (rRNA) databases such as metaPR2.

The first part of my talk focuses on long-read metabarcoding, which allows us to obtain longer sequences (~ 4500 bp) spanning the 18S and 28S genes. These longer sequences can be used to infer robust 18S-28S phylogenies of environmental diversity, and crucially, enable investigation of evolutionary questions. Specifically, I will present how long-read metabarcoding enabled us to investigate the evolution of habitat preferences across the eukaryotic tree of life.

The second part of my talk focuses on metaPR2 (https://shiny.metapr2.org). This database contains taxonomically annotated 18S rRNA metabarcodes from 59 datasets, including over 6,200 samples and 93,000 ASVs. I will provide examples of how metaPR2 has been used to investigate protist diversity and chart future developments, particularly those related to functional annotations.

Enjoyed this talk? Find the speaker here: mahwash.jamy@slu.se

Contributed talks

The Number of Free-living Ciliate Species

Micah Dunthorn[1]

[1]*Natural History Museum, University of Oslo, Norway*

Wilhelm Foissner was right, or nearly-right, about a lot of things. And even when he was wrong, his ideas were at least easily testable. One example of where Foissner was right, was his view that the number of free-living ciliate species is a lot higher than commonly thought. He came to his high species numbers based on his deep understanding of the morphological diversity within the ciliates (including minutely observing characteristics of both cells and cysts), and on his extrapolations from his novel observations when he explored environments usually ignored by ciliatologists. In line with Foissner's views, using available metabarcoding data from EukBank (part of the international UniEuk initiative), 19,000 OTUs were inferred from world-wide samples that were sequenced for the V4 region of SSU-rRNA. This number of free-living ciliate OTUs will likely become much higher as more and more environments are sequenced, especially from terrestrial communities.

Enjoyed this talk? Find the speaker here: micah.dunthorn@nhm.uio.no

Digital PCR as a New Cutting-edge Tool for Measuring Ciliate Abundance

Megan Gross[1], Micah Dunthorn[2], Thorsten Stoeck[1]

[1]Department of Ecology, Rheinland-Pfälzische Technische Universität Kaiserslautern-Landau, Kaiserslautern, Germany
[2]Natural History Museum, University of Oslo, Oslo, Norway

Observing the abundances of ciliates is pivotal to understanding their ecological importance in different ecosystems. Although numerous morphological and molecular methods have been developed to estimate microbial abundances, we still lack a standardized technique for accurate and precise estimations of ciliate abundances. The novel digital PCR (dPCR) technology has recently been successfully used to analyze copy number variation among different groups of organisms. Here, we show that dPCR is not only applicable for the estimation of copy number variations in ciliates, but can also be used to quantify their relative abundances. Single-cell analysis of rDNA copy number variation within the model ciliate *Paramecium tetraurelia* showed that dPCR is a precise and easy to handle tool to quantify intraspecific copy number variations of ciliates. Despite these variations, we found that digital PCR was able to successfully detect increasing cell numbers of mock communities. Our results demonstrate that digital PCR can be applied to future environmental studies that aim to quantify abundances of individual ciliate species.

Enjoyed this talk? Find the speaker here: megross@rhrk.uni-kl.de

Investigating Paulinella Amoebas to Understand the Origin of Photosynthetic Eukaryotes

Yash Pardasani[1], Fabien Burki[1,2]

[1]Department of Organismal Biology (Systematic Biology), Uppsala University, Uppsala, Sweden
[2] Science for Life Laboratory, Uppsala University, Uppsala, Sweden

The primary endosymbiosis event (engulfment of cyanobacteria by heterotrophic eukaryote) that led to the origin of plastids in Archaeplastida happened more than 1.5 billion years ago. As such, the intermediate stages of plastid establishment in ancestral Archaeplastida are very difficult to reconstruct.

Strikingly, an independent primary endosymbiosis event occurred relatively very recently, around 60-90 million years ago, in an entirely different eukaryotic lineage, the genus of rhizarian filose testate amoeba *Paulinella*. The resulting evolution of chromatophores (the photosynthetic organelles in photosynthetic *Paulinella* species) is currently the only known case in which primary photo-endosymbiosis was repeated.

These amoebae are found in freshwater, brackish, and marine waters but their diversity in environmental surveys is poorly known. Unlike Archaeplastida, several heterotrophic lineages of *Paulinella* are known, some of which have been shown to eat cyanobacteria. The existence of close living heterotrophic relatives makes *Paulinella* an outstanding model for unravelling the early stages of primary endosymbiosis and represents a unique opportunity to study the process of plastid establishment.

During my PhD, I will work on heterotrophic *Paulinella* species and investigate the genetic changes that occur during the transition from heterotrophy to photoautotrophy. The talk will provide an overview to my PhD project and our preliminary findings on the diversity, phylogeny, and habitats of these intriguing protists. The findings from my project will contribute to wider understanding the processes that led to the transition of endosymbiont to an organelle and will expand our comprehension of the post symbiotic genome evolution of both the plastid and the host.

Enjoyed this talk? Find the speaker here: yash.pardasani@ebc.uu.se

Giardia - a Parasite with Two Faces

Staffan Svärd[1]

[1]*Department of Cell and Molecular Biology, Uppsala University, Sweden*

Giardia intestinalis is a non-invasive, protozoan parasite infecting the upper small intestine of most mammals. Symptomatic infections cause the diarrheal disease giardiasis in humans and animals, but at least half of the infections are asymptomatic. However, the molecular underpinnings of these different outcomes of the infection are still poorly defined. We studied the early transcriptional response to *G. intestinalis* trophozoites, the disease-causing life-cycle stage, in cellines (differentiated Caco-2 cells) and human enteroid-derived, 2-dimensional intestinal epithelial cell (IEC) monolayers. Parasites induce a robust initial inflammatory response in Caco-2 cells but trophozoites preconditioned in media that maximise parasite fitness triggered only neglectable inflammatory transcription in the IECs from enetroids during the first hours of co-incubation. By sharp contrast, "non-fit" or lysed trophozoites induced a vigorous IEC transcriptional response, including high up-regulation of many inflammatory cytokines and chemokines. Furthermore, "fit" trophozoites could even suppress the stimulatory effect of lysed trophozoites in mixed infections, suggesting active *G. intestinalis* suppression of the IEC response. By dual-species RNA-sequencing, we defined the IEC and *G. intestinalis* gene expression programs associated with these differential outcomes of the infection. Taken together, our results show how *G.* intestinalis infection can lead to such highly variable effects on the host, and pinpoints trophozoite fitness as a key determinant of the IEC response to this common parasite.

Enjoyed this talk? Find the speaker here: staffan.svard@icm.uu.se

Three-dimensional Structure of a Protist Symbiosis

Jon Jerlström Hultqvist[1]

[1]*Department of Cell and Molecular Biology, Uppsala University, Uppsala, Sweden*

Symbiotic relationships drive evolutionary change and are important sources of novelty. Here we investigate a highly structured syntrophic symbiosis between species of the anaerobic protist *Anaeramoeba* (Anaeramoebae, Metamonada) and its bacterial symbionts. *Anaeramoeba flamelloides* have *Desulfobacteraceae* symbionts that are found in membrane structures internal to the amoebae. Here we use Focused Ion Beam Scanning Electron Microscopy (FIB-SEM) to visualize the symbiont – hydrogenosome structure in *Anaeramoeba flamelloides*. Reconstruction of the three-dimensional structure of symbionts, hydrogenosomes and symbiont-enclosing compartments show that the symbionts are housed in a loosely connected network with thin connections between symbiont compartments. Gene families encoding membrane-trafficking components that regulate the phagosomal maturation machinery are notably expanded in *Anaeramoeba* spp. and may be involved in organizing and/or stabilizing the symbiosomal membrane system. Overall, the Anaeramoebae have evolved a dynamic symbiosome comprised of a vacuolar system that facilitates positioning and maintenance of sulfate-reducing bacterial ectosymbionts.

Enjoyed this talk? Find the speaker here: jon.jerlstrom.hultqvist@icm.uu.se

Hacking the Electron Transport Chain to Live without Oxygen

Mara Vizitiu[1], Sofia Paraskevopoulou[1] and Courtney Stairs[1]

[1]Department of Biology, Lund University, Sweden

Eukaryotic microbes (protists) and animals that occupy low-oxygen environments often have drastically different mitochondrial metabolism compared to their aerobic relatives. A common theme among the metabolism of anaerobic protists and animals is modifications of the electron transport chain (ETC). In animals, this can involve remodeling of the ETC complexes under low-oxygen/anoxic conditions to promote oxygen-independent energy conservation, while in protists, we often observe the loss of genes encoding different components of the ETC. In both animals and protists, these ETC modifications co-occur with the use of alternative electron carriers such as the ubiquinone analog, rhodoquinone (RQ). Interestingly, it seems like animals use a different strategy to synthesize RQ when compared to protists and bacteria suggesting that RQ biosynthesis has evolved at least twice across the tree of life. Here, we will discuss the diversity of the ETC across the tree of eukaryotes and review hypotheses for how ETCs are modified, and ultimately lost, in protists. We will report preliminary evidence that suggests some animals may have acquired the gene encoding the protist-specific RQ synthesis protein by lateral gene transfer from anaerobic protists. We find that while protists have converged to some of the same metabolism as anaerobic animals, there are clear protist-specific strategies to thrive without oxygen.

Enjoyed this talk? Find the speaker here: courtney.stairs@biol.lu.se

Flash talks

Picozoa and the Origin of Plastids

Nina Pohl[1]

[1]*Department of Organismal Biology, Uppsala University, Sweden*

Plastids and the emergence of photosynthetic eukaryotes marked a crucial turning point in evolution and paved the way for life as we know it today. It is now understood that plastids originated from a process called primary endosymbiosis. In this process a photosynthetic cyanobacterium was engulfed by a protist. Over time, the bacterium was reduced and integrated into the host's metabolism. This primary endosymbiosis is known to have occurred in two lineages: the Archaeplastida, which include land plants and a wide variety of micro and macro algae, and testate amoebae from the genus *Paulinella*.

The evolution of plastids in Archaeplastida is commonly believed to have resulted from a single event in their last common ancestor. However, recent findings have cast doubt on this theory with the placement of the marine heterotrophic flagellate phylum Picozoa within Archaeplastida as sister to Rhodophyta (red algae) and Rhodelphidia. Although the Rhodelphidia still possess remnants of plastids, there is currently no evidence of any plastid residue in known Picozoa. Complete plastid loss is exceedingly rare and has not yet been observed in any free-living species. This raises the possibility that Picozoa never had plastids at all and challenges the notion that plastids in Archaeplastida originated from a single event.

In my PhD project, I aim to investigate the possibility of Picozoa having had a plastid in order to shed light on the origin of plastids in Archaeplastida. To achieve this, I plan to explore the diversity of this relatively unknown phylum and search for evidence of a plastid using genomics, transcriptomics, and CARD-FISH microscopy.

Enjoyed this talk? Find the speaker here: nina.pohl@ebc.uu.se

Evaluating 3D Morphometrics Changes in Calcite Shells Using a Multistressor Experimental Approach (Stress^{3D})

Constance Choquel[1], Elsa Muller[1], Sam Dupont[2], Emmanuelle Geslin[3], Helena L. Filipsson[1]

[1]Department of Geology, Lund University, Sweden
[2]Department of Marine Ecology, Sven Lovén Centre for Marine Sciences, University of Gothenburg, Kristineberg, Sweden
[3]Université d'Angers, Nantes Université, Le Mans Université, Angers, France

Marine environmental challenges such as warming, acidification and oxygen depletion in the world's oceans are some of the biggest issues we face today. These challenges are all interconnected and linked to the rise in atmospheric carbon dioxide pressure (pCO_2). Although the oceans play a crucial role as a sink for carbon dioxide and atmospheric temperature, the consequences of this sink are apparent as seawater temperatures continue to rise, and the pH and oxygen levels in the oceans decline.

These three stressors can have complex and poorly understood concurrent effects on calcifying marine microorganisms e.g., survival rate, and shell (test) calcification. Specifically, we conducted an experiment using one of the most important marine calcium carbonate-secreting microorganisms – foraminifera. Our experimental setup was designed to culture several species of benthic foraminifera from the Gullmar Fjord in controlled aquariums under different conditions with lowered pH and oxygen conditions and also with increased water temperature.

Before the experiment, the specimens were labeled with calcein to distinguish between newly formed chambers and pre-existing calcite, then CellTracker Blue was used to label the specimens post-experiment to determine their viability. To complement survival and test calcification, we will use synchrotron light-based X-ray (µCT) to explore 3D shell morphological variations (thickness, pore patterns, surface/volume ratio) as indicators of environmental changes.

Enjoyed this talk? Find the speaker here: constance.choquel@geol.lu.se

Hidden Oyster Flagellate Makes an Entrance

Anders Alfjorden[1]

[1]*EBC, Institute of Organismal biology, Uppsala University, Sweden*

Marine bivalves are filter feeders that constantly consume or filter a vast array microorganism, including protists. However, some protists can survive within the host's intestinal system, utilizing released resources or other microorganisms, and occasionally turn parasitic under certain conditions. Hexamitinae are Diplomonads that include both free living and parasitic flagellate species. Many are also intestinal parasites of different vertebrates and invertebrate hosts such as oysters. The exact role of Hexamita spp. in oysters remains unresolved, with studies from 1950-1980 debating their classification as parasites or commensals. One species found in oysters, *Hexamita nelsoni*, is known from morphological work as well as 18S rDNA sequencing, however to our knowledge no lasting culture is available. *H. nelsoni* displays seasonality, mainly found in the colder period of the year and therefore also well adapted to Nordic climate. Despite this, there is limited knowledge about its role within the oyster host. We will present preliminary results on potential survival strategies within the host where no flagellated stages are detected. Histology and cell cultivation are employed to identify the presence of flagellated trophozoite stages.

Enjoyed this talk? Find the speaker here: anders.alfjorden@ebc.uu.se