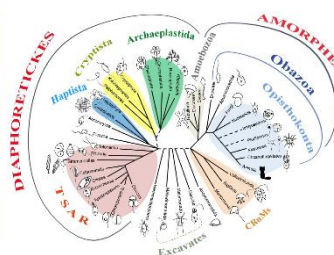
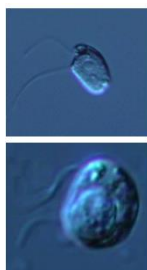


Symposium 3

Biology of heterotrophic and parasitic protists

Organizers: Denis Tikhonenkov (Russian Academy of Science, Russia) and Kevin Wakeman (Hokkaido University, Japan)

Synopsis: Protists represent diverse phylogenetic lineages, and contain a large number of species that possess ancestral cellular and genomic characteristics in relation to their multicellular relatives. Phylogenetic data on heterotrophic and parasitic protists are extremely important in terms of reconstructing the universal tree of life.



The basal or intermediate evolutionary positions occupied by these organisms make them particularly important for elucidating the origin, diversity, and evolution of model organisms. Within the framework of the proposed symposium, we will be looking at (1) new data on novel, deep-branching lineages of heterotrophic protists and (2) phylogenomic reconstructions uniting Archaeplastida and Cryptista supergroups. Also, protists are a compulsory link in microbial food webs and provide effective pathways for the transformation of matter and energy in aquatic ecosystems. They possess a full range of trophic and life strategies seen across eukaryotes, albeit on a microscopic scale. Many protists are secondary-heterotrophic and non-photosynthetic. They have descended from photosynthetic ancestors and reverted to solely heterotrophic lifestyles. In this context (3), an investigation of secondary-heterotrophic protists and their peculiar metabolism and genomic organization will be presented. Finally, a considerable number of protists have evolved independently into a parasitic lifestyle, many of which are notorious pathogens that have an impact on public health and ecology. Here, current views on (4) patterns of evolution and diversity of marine Apicomplexa and parasitic dinoflagellates will be presented. One of the major aspects of protozoan biology is symbiotic relations with prokaryotes, which date back at least two billion years ago to the origin of mitochondria. A broad view of (5) bacterial and archaeal symbioses associated with protist hosts, focusing on their evolution, ecology, and cell biology will be present.

S3-1

Novel deep-branching lineages of heterotrophic protists and their evolutionary significance

Denis Tikhonenkov (Papanin Institute for Biology of Inland Waters, Russian Academy of Sciences, Borok, 152742, Russia)

Recent investigations and findings of new species, high-level taxa and even previously unknown phylogenetic lineages of eukaryotes demonstrates that heterotrophic (especially predatory) flagellates remain extremely poorly studied, but often represent the most important deep-branching lineages of eukaryotes. They often form a sister groups to giant eukaryotic clusters on phylogenetic trees, and illustrate an ancestral state of one or another supergroup of eukaryotes. Recent studies of predatory flagellates, have provided new data revealing the early stages of evolution of Opisthokonta, Alveolata, and Archaeplastida supergroups; leading to the revision of the eukaryotic tree and ideas on mitochondrial evolution and the root of the tree of all eukaryotic organisms; demonstrating the ways of the emergence and development of unique cellular and genomic innovations that led to the formation of multicellularity, photosynthesis, and parasitism. Further investigations of predatory flagellates are important for understanding the role of phagotrophy in the origin of symbiogenetic organelles – plastids and mitochondria, and will also help to clarify the evolution of major eukaryotic supergroups and resolve their relationships.

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S3-2

***Microheriella maris* units Archaeplastida and Cryptista in phylogenomics**

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There are still many "orphan" protists of which phylogenetic affiliation has not yet been determined by previous studies in the eukaryotic tree. Determining their phylogenetic positions has the potential to fill the gaps in eukaryotic diversity and it contributes to reveal true phylogenetic relationships among major lineages that still remain to be resolved well. *Microheliella maris* was originally described as a member of the phylum Heliozoa, but previous large-scale phylogenetic analyses have not been able to confidently place this organism within any previously described species or lineages. In this study, we analyzed the alignment of 319 genes and demonstrated that *M. maris* represents the basal lineage of Cryptista. Here, we propose a new clade name "Pancryptista", which includes *M. maris* and Cryptista. In addition, the results of the analysis of 319 genes showed that *M. maris* is an important taxon to recover the monophyly of Archaeplastida and the sister relationship between Archaeplastida and Pancryptista, so we call this assemblage "CAM clade" here. Cryptista tends to be attracted to Rhodophyta depending on the taxon sampling in phylogenomic alignments, and this phylogenetic "signal" may have prevented the stable recovery of Archaeplastida monophyly in previous studies. Based on our detailed molecular phylogenetic analyses using 319 genes, we hypothesize that many genes in Cryptophyceae, the internal lineage of Cryptista, have been partly recombined with homologous genes transferred from red algal endosymbionts during secondary endosymbiosis and have a faint phylogenetic affinity with the genes of Rhodophyta.

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S3-3

To be algae or not to be algae: losses of photosynthesis in diatoms

Ryoma Kamikawa (Graduate School of Agriculture, Kyoto University, Japan)

The first photosynthetic plastid has emerged through the primary endosymbiosis between a photosynthetic cyanobacterial cell and a heterotrophic eukaryotic cell in the common ancestor of Archaeplastida. Currently, plastids distribute in phylogenetically diverse eukaryotic lineages, through multiple eukaryote-eukaryote endosymbioses. In contrast to horizontal transfers of photosynthetic ability, many eukaryotic species have lost photosynthesis independently. Some of those species are now parasitic or predatory, the others are osmotrophic. It remains unclear how the lifestyles affect genome evolution after loss of photosynthesis. Diatoms, one of the main oceanic primary producers, include multiple osmotrophic species that have lost photosynthesis. In this study, the draft genome of the non-photosynthetic diatom *Nitzschia putrida*, was determined and compared with those of parasitic eukaryotes that have lost photosynthesis secondarily. The genome size and the number of genes in *N. putrida* are comparable to those of photosynthetic diatoms. In silico prediction suggests retention of a variety of plastid metabolic pathways regardless of massive reduction of the plastid proteome in *N. putrida*. In addition to the non-photosynthetic plastid proteome, the peroxisome proteins for photorespiration were not encoded in the *N. putrida* genome, suggesting loss of plastid-peroxisome metabolic interaction. Although light is utilized in diatoms not only for photosynthesis but also for regulation of gene expression and cell division, growth experiments and comparative transcriptome analyses suggest that *N. putrida* is less dependent on light dark cycles. The genome of *N. putrida* enriches particular gene families such as genes for certain transporters and secreted proteins, both of which are likely important for osmotrophic lifestyles. Genes for those proteins were appeared to be less abundant in parasitic eukaryotes that have lost photosynthesis than in their photosynthetic relatives, suggesting distinct genome evolution after loss of photosynthesis between osmotrophic and parasitic species.

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S3-4

Patterns of evolution and diversity of marine apicomplexans and parasitic dinoflagellates

Kevin C. Wakeman (Institute for the Advancement of Higher Education, Hokkaido University, Japan)

The alveolates are a diverse group of single-celled eukaryotes (protists) that have been traditionally defined by three major groups: apicomplexans, dinoflagellates, and ciliates. More contemporary work on select alveolate lineages (i.e., early diverging parasitic lineages) has let researchers in this field revisit some of the earliest stages of alveolate evolution. In this talk, I will give a brief introduction to alveolate lineages, covering some of the recent advances in the field that have been brought about in this age of genomics. In particular, I will discuss on-going themes related to the early diversification and host specificity of parasitic alveolates within the genera *Lankesteria*, *Haplozoon*, and *Platyproteum*. Here, I will present some preliminary work that highlights coevolutionary patterns (host specificity) between these parasites and their hosts. I will also cover some of the character evolution of these groups that make them intriguing models for understanding the early evolution of alveolates, in particular, fundamentally understanding the repeated and independent evolutionary transition of alveolates from a free-living (photosynthetic) ancestor to an obligate parasitic niche.

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S3-5

Bacterial and archaeal symbioses with protists

Filip Husnik (Okinawa Institute of Science and Technology, Okinawa, Japan)

Most of the genetic, cellular, and biochemical diversity of life rests within single-celled organisms — the prokaryotes (bacteria and archaea) and microbial eukaryotes (protists). Very close interactions, or symbioses, between protists and prokaryotes are ubiquitous, ecologically significant, and date back at least two billion years ago to the origin of mitochondria. However, most of our knowledge about the evolution and functions of eukaryotic symbioses comes from the study of animal hosts, which represent only a small subset of eukaryotic diversity. In this talk, I will take a broad view of bacterial and archaeal symbioses with protist hosts, focusing on their evolution, ecology, and cell biology, and also explore what functions (if any) the symbionts provide to their hosts. With the immense diversity of protist symbioses starting to come into focus, we can now begin to see how these systems will impact symbiosis theory more broadly.

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