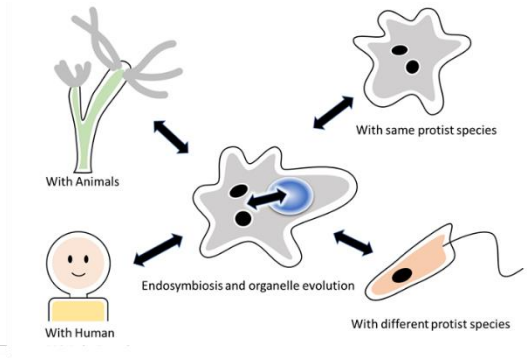
Symposium 5
Molecular basis for interactions between protists and other organisms

Organizers: Toshinobu Suzaki (Kobe University, Japan) and Federico Buonanno (University of Macerata, Italy)



Synopsis: Since protists are single-celled organisms, one might think that these organisms live a solitary life, independent of other organisms. In reality, however, many protists develop complex interrelationships with other unicellular and multicellular organisms. For example, predatory protists recognize and capture other organisms as prey. On the other hand, to escape from predators, they need to recognize their enemies correctly. Some protists recognize cells of the same species of different cell types for sexual reproduction. Some are symbiotic with other eukaryotes or prokaryotes in their cells, and some are symbiotic in the bodies of other larger organisms. There are also protozoa that can infect animals and cause disease. Recent studies have revealed the mechanisms by which protists recognize other organisms. As a result, we have gained many unique insights into the molecular mechanisms of cellular interactions between protists and other organisms, and the aspects of biological evolution driven by these interactions. This symposium will highlight the cell-cell interactions of protists, especially from their molecular and evolutionary perspectives, and will present the latest research results.

S5-1

Talk Title The offensive-defensive strategies adopted by ciliated protists

Federico Buonanno and Claudio Ortenzi (Laboratory of Protistology and Biology Education, Department of ECHT, University of Macerata, Italy)

In the last 30 years, a lot of studies have been devoted to describe the predator-prey interactions among unicellular eukaryotic organisms like protists. Especially in ciliates, a particular attention has been focused on the significant role of specialized ejectable membrane-bound organelles, generally called extrusomes, used in the immobilization and capture of prey, and in defense from predators. Essentially, two types of strategies are adopted by ciliates in predator–prey interactions: the first is mediated by mechanical mechanisms involving some subpellicular non-toxic extrusive organelles (for example the trichocysts), while the second is mediated by toxic secondary metabolites (contained in different kinds of chemical extrusomes) used for offense or defense by a number of ciliate species. These interactions are mainly studied in unicellular predator-prey models but, recently, some researches have also focused their attention on analyzing predation or defensive strategies against metazoans. With regard to these strategies, the interactions between ciliates and microinvertebrates seem to indicate that the evolution of chemical-behavioral machinery in micro-ecosystems can be compared, in terms of variations and complexity, with those characterizing macro-ecosystems.

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S5-2

Genome analysis reveals interactions and evolution in *Hydra-Chlorella* symbiosis

Mayuko Hamada (Ushimado Marine Institute, Okayama University, Japan)

Symbiosis with microalgae is a general biological phenomenon found in various organisms. In Cnidarian, it can be observed in many species in corals, jellyfish, sea anemones and hydras. In particular, the symbiosis between green hydra and its symbiotic algae has been the subject of

research since decades. To understand principles of symbiogenesis and their links to evolution at the molecular- and the genome-level, we decoded genomes of the green hydra *Hydra viridissima* A99 and its symbiotic algae *Chlorella* sp. A99, and focused on the specific features in their genomes. In the symbiosis of green hydra, the symbiotic alga requires nitrogenous amino acids derived from the host, and the host acquires photosynthetically fixed carbon from the algae in the form of maltose. The alga is unable to grow outside the host, indicating loss of autonomy during establishment of the dependent relationships. In the symbiotic *Chlorella* genome, degeneration of inorganic nitrogen assimilation system and duplication of amino acid transporter genes were observed, reflecting metabolic dependency of the symbiont on the host. On the other hand, in the green hydra genome, innate immune genes are specifically increased and their domain structures are further complicated, compared to non-symbiotic hydra. These characteristics are also seen in corals, and may contribute to defence and maintenance of the symbiotic environment in common. In this symposium, I will present the findings obtained from the comparative genome analyses of green hydra and its symbiotic algae, and discuss the generality and diversity of animal-algal symbiosis.
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S5-3

***Paulinella micropora* KR01 genome reveals dominant host contribution and role of novel genes in primary plastid endosymbiosis**

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Eukaryotic photosynthetic organelles, plastids, are the powerhouses of many aquatic and terrestrial ecosystems. The canonical plastid in algae and plants originated >1 billion years ago and therefore offers limited insights into the initial stages of organelle evolution. To address this issue, we focus here on the photosynthetic amoeba *Paulinella micropora* strain KR01 (hereafter, KR01) that underwent a more recent (ca. 124 Mya) primary endosymbiosis of a photosynthetic organelle, termed the chromatophore. Phylogenetic analyses using four gene markers revealed three distinct lineages of photosynthetic *Paulinella* species. We generated the complete chromatophore genome sequences from *P. longichromatophora* and *P. micropora* KR01/NZ27. Our analysis suggests that when a basal split occurred among photosynthetic *Paulinella* species ca. 60 Mya, only 35% of the ancestral orthologous gene families from the cyanobacterial endosymbiont remained in chromatophore DNA. Analysis of genomic and transcriptomic data resulted in a high-quality draft assembly of size 707 Mbp and 32,358 predicted gene models. A total of 287 chromatophore targeted long-proteins were predicted in silico, 206 of which comprise the ancestral organelle proteome in photosynthetic *Paulinella* species with functions in nucleotide metabolism and oxidative stress response. Gene co-expression analysis identified networks containing known high light stress response genes as well as a variety of putative “dark” genes of unknown function. We characterized diurnally rhythmic genes in this species and found that over 51% are dark. Our results demonstrate the massive amount of genetic innovation needed to domesticate a photosynthetic organelle and identify a storehouse of novel genes implicated in the transition from a heterotrophic lifestyle to photoautotrophy.
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S5-4

Protein trafficking and parasite-derived membrane structures in *P. falciparum*-infected erythrocytes.

Hideyuki Iriko (Division of Global Infectious Diseases, Department of Public Health, Graduate School of Health Sciences, Kobe University, Japan)

Malaria is caused by *Plasmodium* parasites that are transmitted to humans through the bite of infected Anopheline mosquitoes. In the human body, malaria parasites undergo repeated cycles

of erythrocyte invasion, proliferation within the cell and egress. Of the five species that infect humans, the most pathogenic species is *Plasmodium falciparum*. *P. falciparum* modify infected erythrocyte membrane by the export of parasite proteins. The modifications in cell adhesion, deformability, and permeability properties of infected erythrocytes contribute to parasite survival and immune evasion. Malaria parasites export hundreds of proteins into the erythrocytes. In infected erythrocyte of *P. falciparum*, the individual steps of protein export are associated with parasite-derived membranes. The intra-erythrocytic parasites are surrounded by a lipid bilayer membrane referred to as parasitophorous vacuole membrane (PVM). To reach the erythrocyte cytosol, all parasite-exported proteins should cross PVM through a protein translocon called *Plasmodium* Translocon of EXported proteins (PTEX). Then the proteins are transported to the Maurer's clefts. Maurer's clefts are parasite-derived structures within the host cell cytoplasm that are thought to function as a sorting compartment between the parasite and the erythrocyte membrane. In this symposium, I will present an overview of the protein trafficking and the parasite-derived membrane structures in *P. falciparum*-infected erythrocytes.

iriko@koala.kobe-u.ac.jp Abstract (Hideyuki Iriko)