Division of Life Science: Molecular Evolution Group

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Phylogenetic analysis of major phylogenetic groups in eukaryotes: It has been proposed that eukaryotes can be divided into roughly six major phylogenetic groups. We use molecular phylogenetic analysis with multiple gene sequences to infer whether each major phylogenetic group is truly monophyletic and how closely related the groups are. We are also studying the methods for phylogenetic analyses to make unbiased inferences. We are also interested in symbiosis between two distinct unicellular organisms, as multiple symbiotic events played a major role in the early evolution of eukaryotes. We are challenging to elucidate the mechanism underlying symbiotic events by assessing genomic data sampled from diverse organisms.

Earth is inhabited by a wide variety of organisms. For example, we humans have a spine, move our own bodies, and consume foods (other organisms) to survive. The human body is made up of many cells. Although plants are also made up of many cells, their way of life differs significantly from ours. Plants do not move by themselves and do not need to eat food. Instead, they live by photosynthesis, which is based on light energy. Although we do not always realize it, there are a vast number of other species on the planet that we cannot see with the naked eye. These organisms have a wide variety of appearances and lifestyles. All of these organisms on Earth have evolved over a long period of time from a single primitive organism to their present forms. Our research group focuses on eukaryotes—organisms with nuclei in their cells—and aims to understand the evolutionary relationships among the major phylogenetic groups of eukaryotes and their evolutionary paths. We know that in the evolutionary process of eukaryotes, there have been multiple instances where organisms from completely different phylogenetic lineages have evolved symbiotically in cells and become part of the cells. Such symbiotic events are thought to have contributed substantially to the diversification of eukaryotic organisms, but the mechanism whereby two separate organism lineages fuse into a single organism remains largely unknown. We are working to understand the principles of symbiosis that led to the current diversity among eukaryotes using genomic information and other data.

Research Topics

We endeavor to understand the evolutionary path of eukaryotes by inferring their phylogenetic relationships and performing comparative genomic analyses based on data regarding gene (DNA) sequences and protein amino-acid sequences of existing species. Furthermore, there are many "new" organisms in the natural environment that have yet to be studied, and these undiscovered organisms may hold the key to solving various problems in eukaryotic evolution. We are investigating such organisms that are evolutionarily important but have not yet been investigated. To this end, we are analyzing each organism's evolutionary characteristics by acquiring large-scale genetic and genomic information from eukaryotes from various phyla.
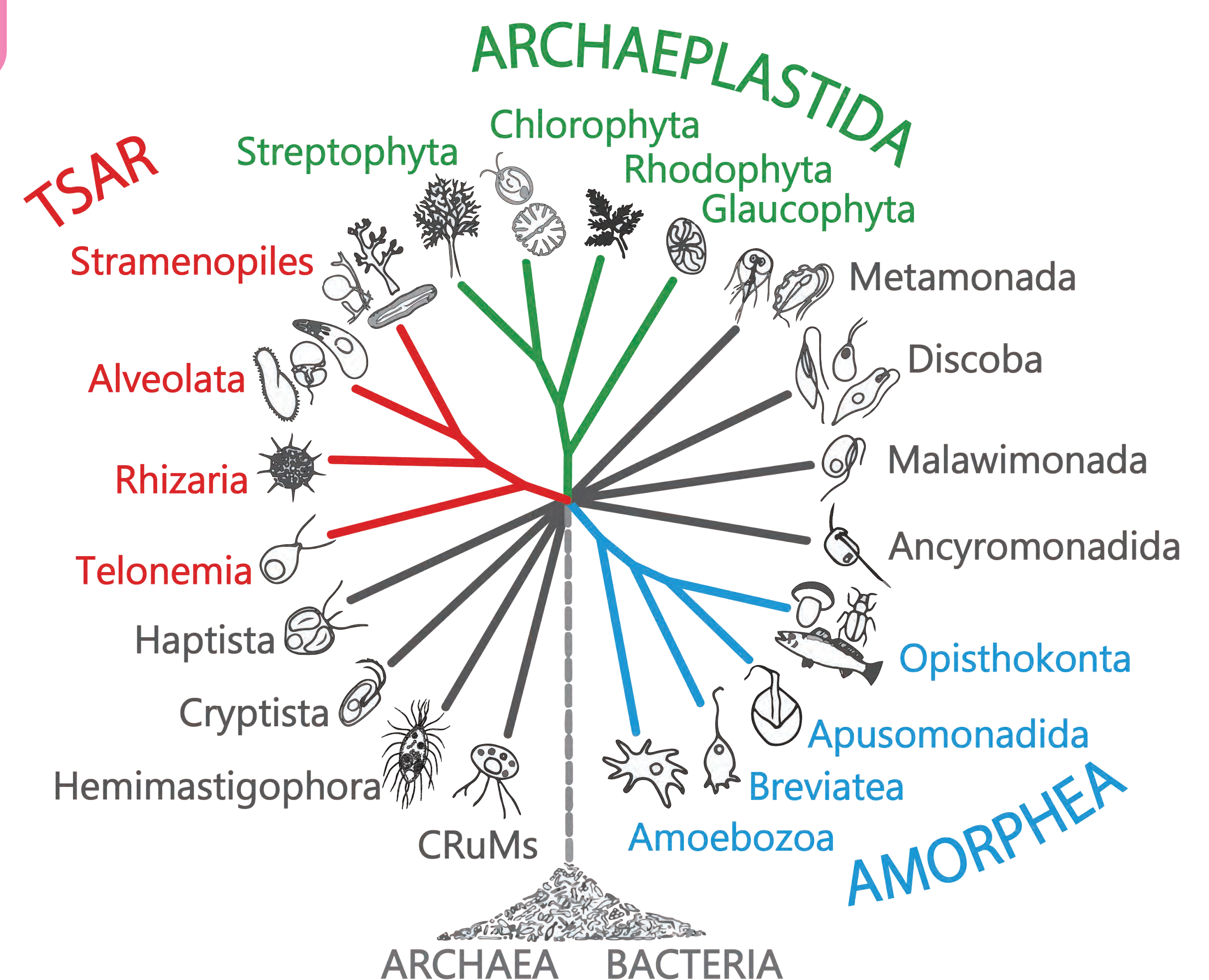

Fig.1 Main lineages of eukaryotes

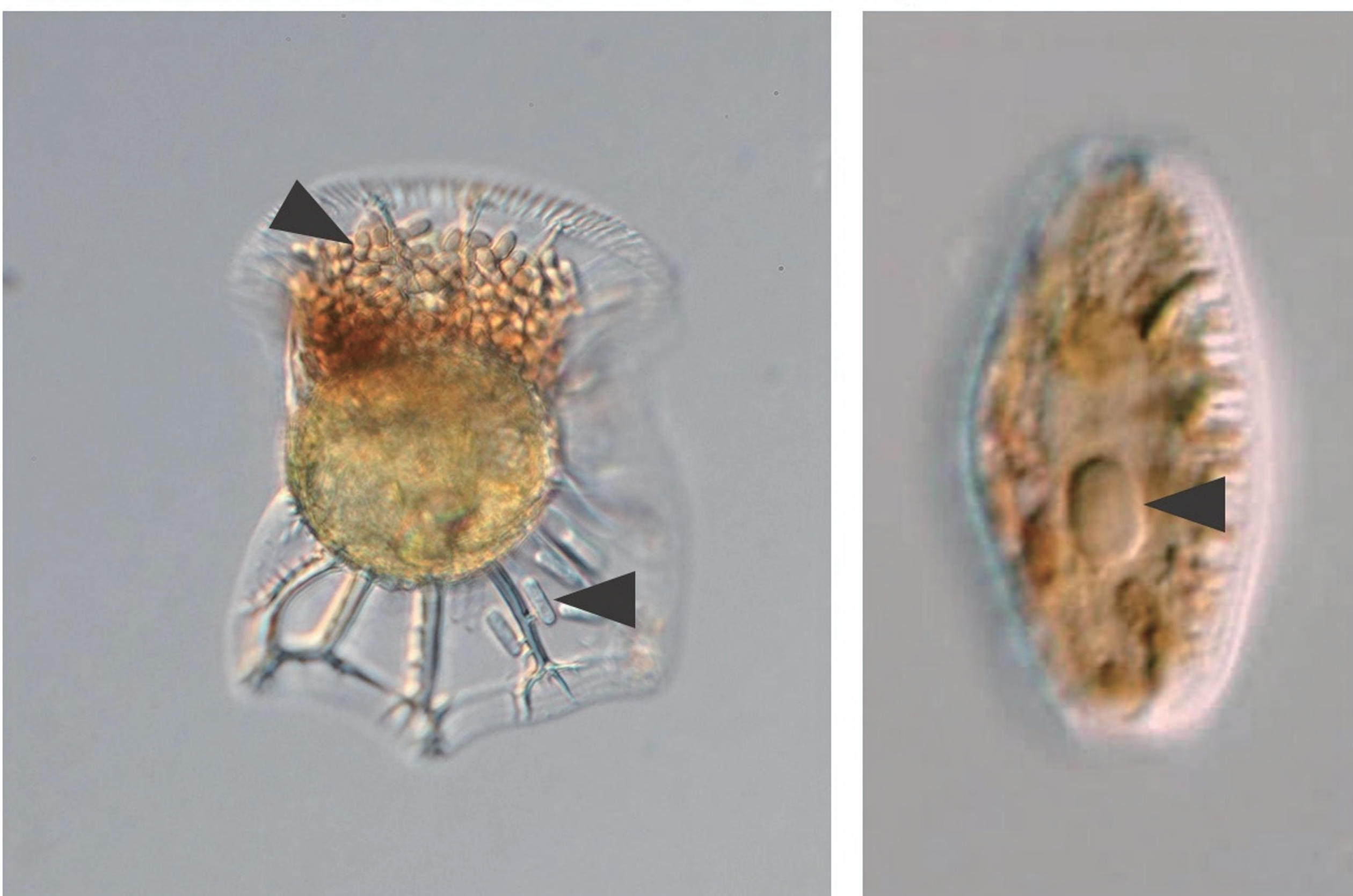**Dinoflagellate (left) and diatom (right) with cyanobacterial symbionts**

Fig.2 Example of a unicellular eukaryote that coexists with bacteria (arrows)

Molecular phylogenetic analysis requires statistical processing using the maximum likelihood method, and computers are used for this purpose. In a nucleotide or amino-acid sequence, "signals" corresponding to past evolutionary events and random changes (called "noise") have accumulated during the evolutionary process. The problem lies in the fact that the amount of noise in the sequence increases over time, while the amount of signal decreases. Therefore, to accurately infer the relationship between major eukaryotic phylogenetic groups that may have diverged in the distant past, it is necessary to analyze large amounts of sequence data. We are using supercomputers to analyze transcriptome data and genome data to handle large amounts of data containing complex genetic information.