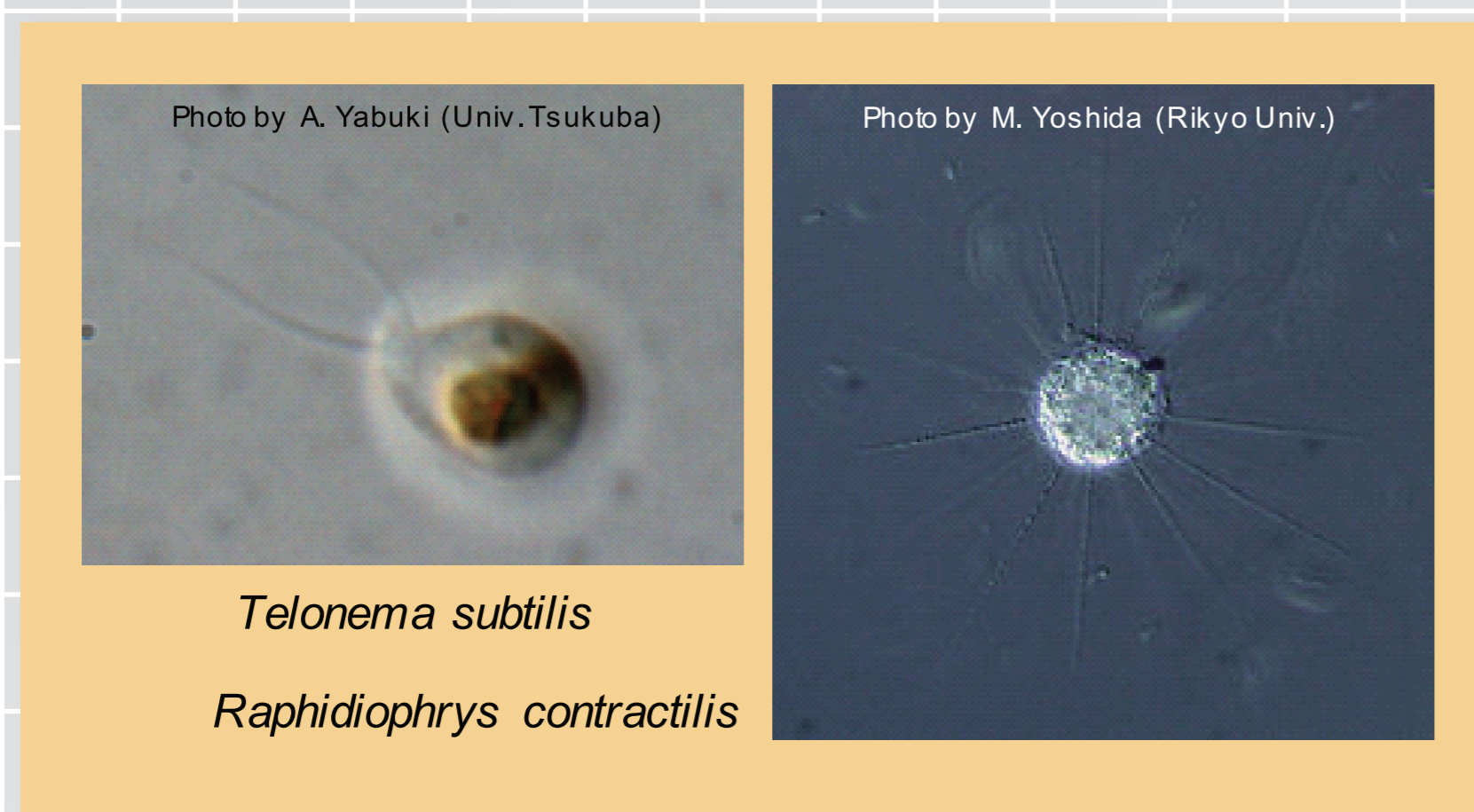# Division of Biological Sciences

Phylogenetic Inference on the Universal Tree of Life

The central focus of our research is to gain insight into origin and early evolution of eukaryotes, one of the most important questions in evolutionary biology. One of the goal of this research is to reconstruct the Universal Tree of Life including diverse organisms on the Earth, based on molecular phylogenetic approach. Since a reliable phylogenetic inference simultaneously requires numerous genes and species, a large scale data analysis using high performance computers plays a key role in our study.

Phylogenetic positions of two enigmatic protist groups, telonemids and centrohelids, inferred from a large scale multigene dataset

Photo by A. Yabuki (Univ.Tsukuba)
Photo by M. Yoshida (Rikyo Univ.)

Telonema subtilis

Raphidiophrys contractilis

Results: We conducted massive expressed sequence tag analyses on the telonemid *Telonema subtilis* and the centrohelid *Raphidiophrys contractilis* using 454 pyrosequencing technology, and generated a 127-gene dataset including 72 taxa and ~30,000 amino acid positions. In the 127-gene analyses, *Telonema* and *Raphidiophrys* constantly grouped with photosynthetic groups, haptophytes and cryptomonads, forming a 'CCTH' clade (shaded in yellow). The CCTH clade was further connected with a clade of stramenopiles, alveolates and rhizarians (shaded in green). Significantly, this large assemblage corresponds to the chromalveolate hypothesis.

Discussion: Our 127-gene analyses successfully provided the first clues for the putative phylogenetic positions of telonemids and centrohelids. Based on the results presented here, these heterotrophic lineages appeared to be critical to elucidate the evolution of red alga-derived plastids in chromalveolates.

Methods: The 127-gene dataset was analyzed by RAxML with the RtRev+Γ+F model, as well as by PhyloBayes with the site-heterogenerous CAT model. Support values (Bayesian posterior probability/ML bootstrap value) were presented on nodes. Closed circles indicated the corresponding nodes are fully supported by both Bayesian and ML analyses.

Reference: Burki et al. "Large-scale phylogenomic analyses revealed that two enigmatic protist lieages, telonemia and Centroheliozoa, are related to photosynthetic chromalveolates." Genome Biology and Evolution 2009 1:231-238.