

Molecular evolution of microtubule system of protist symbionts of termites

Shigeharu Moriya,^{*1,*2} Moriya Ohkuma,^{*1,*2} and Toshiaki Kudo^{*1,*2}

^{*1}Microbiology Laboratory, RIKEN

^{*2}Bio Recycle Project, JST



S. Moriya

Termites harbour unique eukaryotic flagellates, which belong to the class Parabasalea (including the orders Trichomonadida and Hypermastigida) and the order Oxymonadida. These protist symbionts are of interest as model organisms for the study of the early evolution of eukaryotic cells because they have a simple and primitive cellular system. In this aspect, we analyzed the phylogenetic relationship of these protist symbionts using two different protein sequences to understand the early evolution of the microtubule system.

Recently, molecular phylogenetic studies have suggested that the protist symbionts of termites are one of the most earliest eukaryotes.¹⁻³ Previous findings suggested that the structural simplicity of these protists⁴ may have originated from the primitive features of those early eukaryotes. Therefore, we consider that these protists are good model organisms for the studying of the early evolution of eukaryotic cellular systems. Termites harbor protists that are classified into two phyla, namely Parabasalids and Oxymonads⁵ (Fig. 1). Although protists of both phyla are considered early eukaryotes, they have different cellular systems. For example, protists of both phyla have a large bundled microtubule system known as axostyle. In contrast to the locomotive axostyle of oxymonads, parabasalids have the un-locomotive axostyle.⁴ These findings suggested that the microtubule systems of these protists are under different evolutionary constraints even though these protists are assigned to the same early stage of eukaryotic evolution.¹⁻³ Here, we show some examples.

Based on the phylogenetic tree (Fig. 2) of EF-1 α one of the commonly used phyletic markers, protists of the two phyla mentioned above were in the early branching position of eukaryotic evolution.⁶ However, the results shown in Fig. 3 and those previously reported⁶ show that the phylogenetic tree of α -tubulin, a phyletic marker of the microtubule system, suggested that has two large lineages, namely, an “animal-fungi” clade and a “plant-protists” clade. Interestingly, the parabasalian α -tubulin was assigned to the early stage of the “animal-fungi” clade and the oxymonad α -tubulin was assigned to the early stage of the “plant-protists” clade.⁶ This topology is completely inconsistent with the EF-1 α phylogeny. These results suggest that the α -tubulin protein of protists of both phyla has different functional or structural roles in each of these taxonomic groups. It appears that some specific functional or structural constraints imposed on the microtubule system may have driven the evolution of the α -tubulin gene in the early stage of evolution of eukaryotic or-

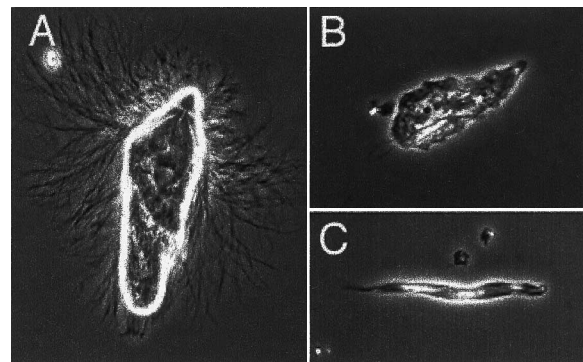


Fig. 1. Protist symbionts of *Reticulitermes speratus*. A: Palabasalid protist, *Trichonympha agilis*. B: Oxymonad protist, *Pyronympha grandis*. C: Oxymonad protist, *Dinonympha exilis*.

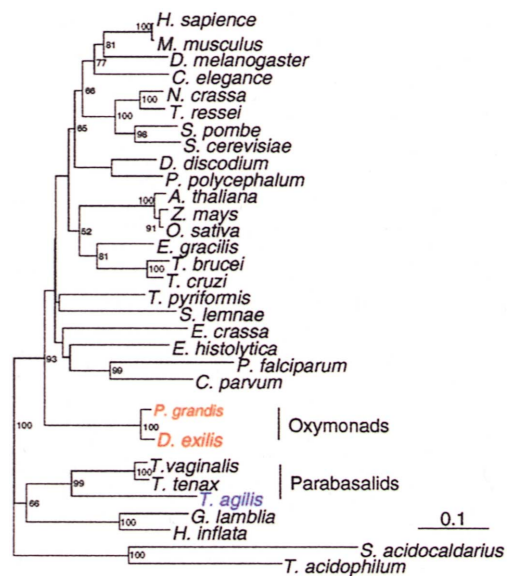


Fig. 2. Phylogenetic tree based on EF-1 α sequences.

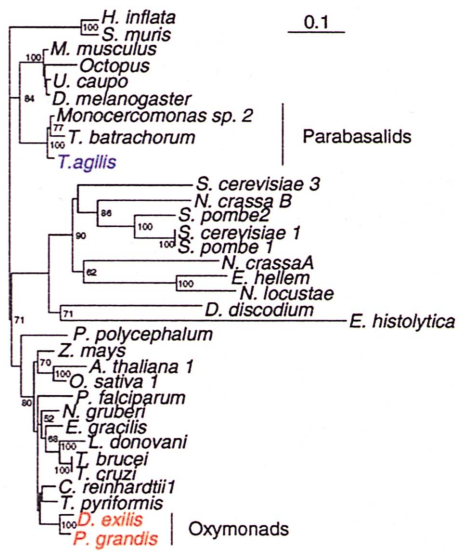


Fig. 3. Phylogenetic tree based on α -tubulin sequences.

ganisms.

We conclude that two clades of the microtubule system, the “animal-parabasalids” clade and the “plant-protists-oxymonads” clade were generated in the earliest stage of eukaryotic evolution. In the future, phylogenetic analysis of more proteins will provide more line of evidence of other special functional or structural constraints. This will contribute to solving the entire complex issue of early eukaryotic evolution.

References

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