

University of Tsukuba | Center for Computational Sciences

HPC for Phylogenetic Tree Inference

Phylogenomics analyses revealed a novel microeukaryote strain SRT308 is a basalbranching eugolenozoan.

We isolated a novel microeukryote strain SRT308 (Fig. 1a) from marine sediment sample collected in Republic of Palau. In a phylogenetic analysis of small subunit ribosomal DNA sequences, SRT308 shows no strong affinity with major eukaryotic lineages (data not shown). However, our phylogenomic analysis using 153 protein-coding genes placed SRT308 at the base of



Euglenozoa with strong statistical support, suggesting this organism is the most basal-branching member of Eugolenozoa known to date (Fig. 1b).



Photo by Dr. T. Shiratori (Univ. Tsukuba)

Fig. 1a: Microeukaryote strain SRT308.

Fig. 1b: ML phylogeny based on a 153-protein alignment (38,592 amino acid positions). MLBP (above) and BPPs (below) are shown at nodes. The nods with full MLBP and are highlighted by dots.

Mitochondrial genome of strain SRT308: the ancestral features of eugolenozoan mitochondrial genomes?

rpl19

rpI35

sdh3

sdh4

tufA



genomes. Euglenozoa 15JULD BOTTON BS Several and a several LOADOO 210 John Stand rps12 nad7 nad8 atp1 nad2 nad4L cox1 cox2 nad6 cox3 cob nad3 sdh2 nad11 nad1 nad4 nad9 nad5 nad13 cox11 rps10 rps19 rpl14 ccmC rps11 rpl2 rpl16 ccmF rps13 rpl5 rpi11 rps14 rpl6 rps8 tatC rps1 rpl10 rpl20 rpl31 rpl34 cox15 secY

Fig. 2b: Venn diagram of

protein-coding genes in

euglenozoan mitochondrial

Euglenozoa is a large protist assemblage comprising Euglenida, Diplonemea and Kinetoplastea, of which mitochondrial (mt) genomes are multiple linear/circular chromosomes coding restricted numbers of proteins. On the other hand, SRT308 mt genome is a single circular chromosome with ~61 Kb in length (Fig. 2a), and codes the union of proteincoding genes found in the euglenozoan mt genomes studies so far (Fig. 2b). These characteristics likely coincide with the position of SRT308, which is basal to the Euglenozoan clade (Fig. 1a).

in orange. Structural RNA genes are shown in blue.





