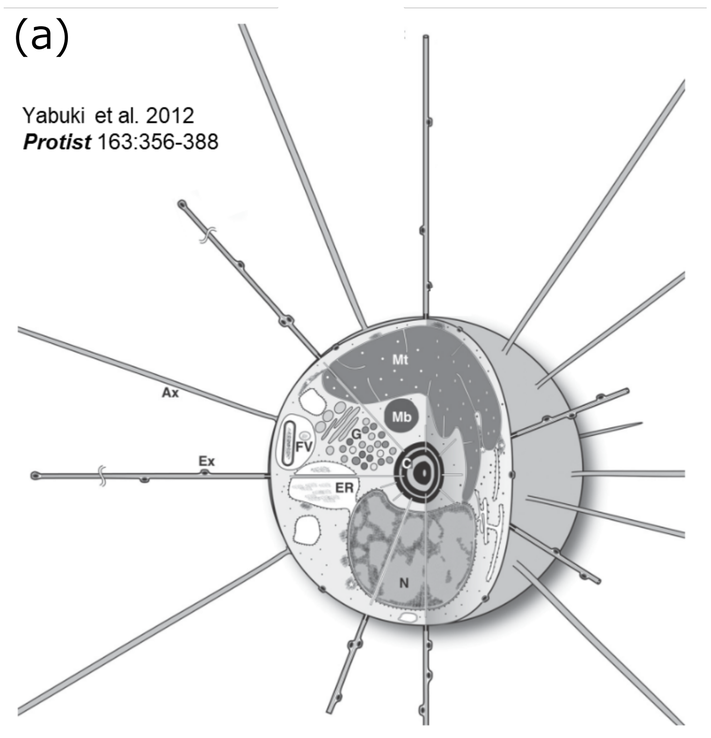
Biological Sciences

338-gene analyses resolved the phylogenetic affiliation of a microeukaryote *Microheliella maris.*

Previously published phylogenetic studies failed to elucidate the phylogenetic position of a heliozoan microeukaryote *Microheliella maris*. Thus, we took a “phylogenomic” approach to place *M. maris* in the global tree of eukaryotes with accuracy. In the phylogeny inferred from an alignment containing 338 genes, *M. maris* branched at the base of the clade of a diverse collection of microeukaryote collectively called Cryptista with high statistical support.



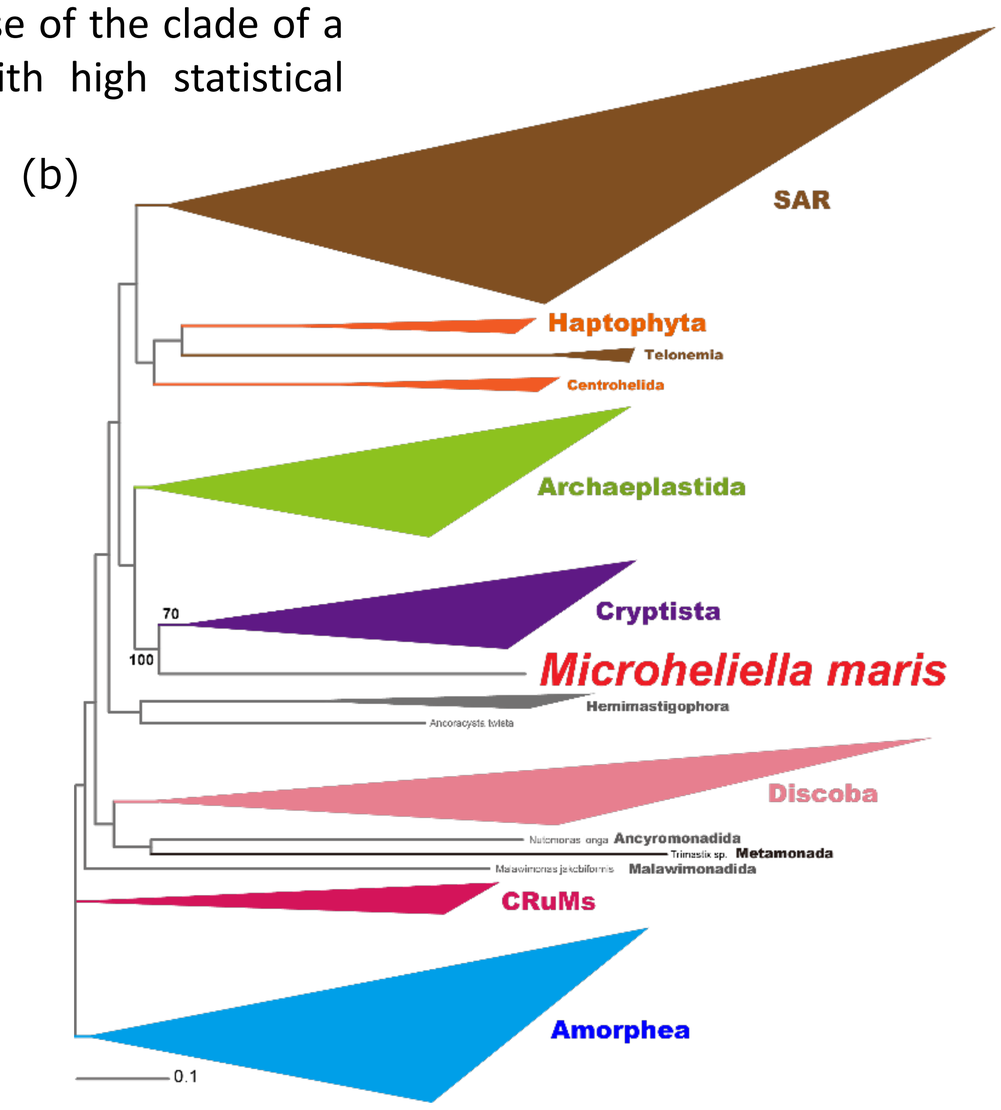


Fig. 1a: Schematic cell drawing of *Microheliell maris*.

Fig. 1b: Maximum likelihood phylogeny inferred from the 338-gene alignment.

In silico structural modeling and analysis of translation elongation factor 1α proteins

Translation elongation factor-1α (EF-1α) interacts with tRNA during protein synthesis. Some eukaryotes appeared to possess highly divergent EF-1α (^{div}EF-1α), implying that these proteins lack the ability to interact with tRNA. We modelled the tertiary structures of ^{div}EF-1α and validated their model structures by molecular dynamics simulations. We found that the molecular surfaces of ^{div}EF-1α are negatively charged partly, suggesting that they may not interact with negatively charged tRNA as strongly as the canonical EF-1α with the positively charged surfaces.

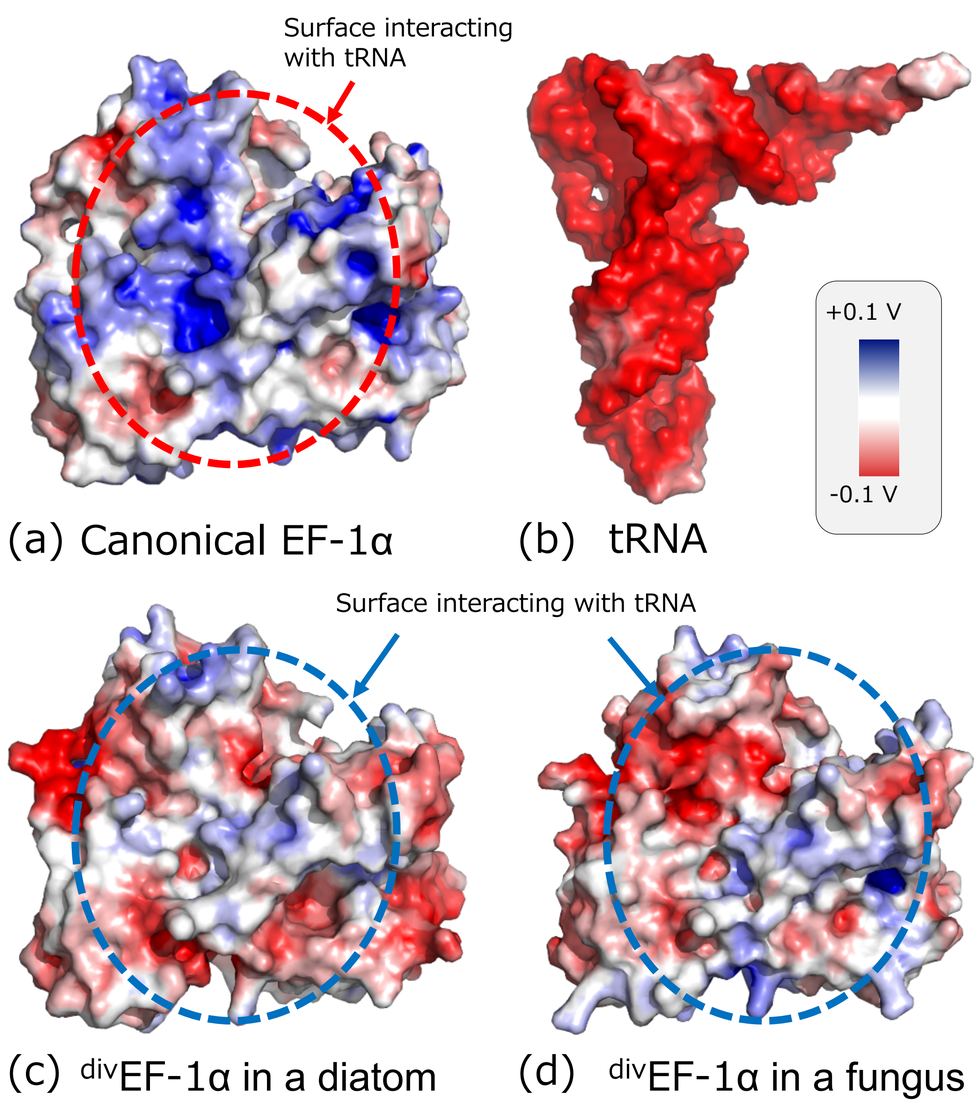


Fig. 2: EF-1α and tRNA structures and surface electrostatic distribution. (a) EF-1α structure of an archaeon (PDB ID: 3WXM). (b) tRNA structure (PDB ID: 1EHZ). (c & d) ^{div}EF-1α models. Dotted lines in (a), (c) and (d) indicate the surfaces interacting with tRNA.

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