

Abstract

Here I am presenting a novel deep-branching organism, flagellate SUM-K. SUM-K is morphologically inconspicuous protists that occurs in two distinctive forms, immotile “sun-like” form and motile, flagellated form. Sun-like cells are rounded approximately 5 μm big cells that produce numerous thin radial projections artificially resembling Heliozoans. Based on ultrastructure analysis and light microscopy observations we classified these projections as novel type of extrusomes with putative function of prey predation. Flagellate state moves with one anterior, posterolaterally directed flagellum. The posterior end of the cell bears a long extrusion that resembles a flagellum but is not motile. Based on these morphological characteristics organism can't be classified into any of the establish eukaryotic supergroups. Likewise, phylogenetic analysis based on SSU rDNA failed to resolve its evolutionary position, placing it to relation with *Ancoracysta twisti*, an orphan lineage similarly unclassifiable to any of current eukaryotic supergroups. Robust analysis based on 206 orthologous genes placed SUM-K to relation with Hemimastigophora. Even though the morphology of currently described Hemimastigophoreans and organism SUM-K is incongruent, its relation presents interesting prospective of evolution of ancient Diaphoretickes. Energetic metabolism of protist SUM-K is also compelling. We are routinely cultivating it under anoxic and microoxic conditions but transcriptomic data shows a rich set of enzymes of aerobic metabolism in addition to pathways typical for anaerobes, such as pyruvate:ferredoxin oxidoreductase (PFO), alternative oxidase (AOX) or pyruvate formate lyase (PFL). A common theme among anaerobic protists is the serial loss of components of the electron transport chain, which also applies for SUM-K, seemingly absent of complex I. Furthermore, its mitochondrial genome is surprisingly complex, coding first ever described homolog of gen *secA*, remnant of ancestral alphaproteobacterial pathway of protein secretion.

Key words: extrusomes, eukaryotic diversity, electron transport chain, anaerobic metabolism, mitogenome