

Abstract

Members of the group Archamoebae are free-living or endobiotic amoeboid flagellates and amoebae. They live in anoxic or microoxic habitats, and their mitochondria have been reduced. They were originally thought to lack mitochondria and represent one of the earliest eukaryotes. However, this hypothesis has been refuted, and now it is evident that the Archamoebae belongs to the lineage Conosa within the supergroup Amoebozoa, together with aerobic slime molds (Macromycetozoa) and variosean amoebae and flagellates.

Relatively simple microtubular cytoskeleton is a characteristic feature of Archamoebae. It consists of a single basal body from which a flagellum arises, lateral root, and microtubular cone. Cytoskeleton of aflagellated genera has been completely reduced.

About 350 species names of Archamoebae have been created so far. However, most descriptions were based on inadequate morphological features. The identity of numerous species is uncertain, and many of them are likely synonymous. Another problem is a small amount of available molecular data.

During our project, we have substantially improved the dataset of DNA sequences of archamoebae. On the basis of molecular and morphological data, we described 13 new species. We showed that genus *Rhizomastix* belongs to Archamoebae and displays a new type of the cytoskeletal arrangement within the group. We carried out the first multigene analysis of Archamoebae with reasonable taxon sampling. On the basis of our phylogenetic analysis, we conclude that Archamoebae splits into four major lineages: Entamoebidae, Pelomyxidae, Rhizomastixidae and Mastigamoebidae, the first one being sister to the rest. We showed that *Pelomyxa* forms an internal branch of paraphyletic *Mastigella*. We suppose that the last common ancestor of Archamoebae was free-living, and the parasitism has evolved at least three times independently within the group.