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## **Genomic view on origin of foraminifera and their relationships with other amoeboid protists**

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Until recently the molecular phylogeny of eukaryotes was mainly based on analyses of single or very few genes. The availability of genomic sequences from a broad range of eukaryotic phyla brought new perspectives and provided a more reliable view of the evolutionary relationships among eukaryotes. In particular, the phylogenomic analyses helped to resolve the eukaryote tree into a topology with a rather small number of major groups. Nevertheless, the evolutionary relationships of many groups of protists, including foraminifera, are yet to be confirmed.

Based on rRNA sequences, foraminifera were at first thought to be an early diverging lineage among eukaryotes. This view has been challenged by analyses of actin, polyubiquitin and RNA polymerase sequences, which consistently demonstrated phylogenetic affinities of foraminifera to Cercozoa, a heterogeneous assemblage of filose testate amoebae, cercozoans, amoeboflagellates, chlorarachniophytes, gromiids, as well as certain protistan parasites Plasmodiophoriida (plants) and Haplosporidia (invertebrates). Among these groups, foraminifera appear to be most closely related to Gromiida, Plasmodiophoriida and Haplosporidia. Later studies showed that foraminifera and Cercozoa are sister group to radiolarians (Polycystinea & Acantharea) and a new supergroup Rhizaria comprising radiolaria, foraminifera, and Cercozoa was established.

Although Rhizaria has been well accepted as being one of the major groups of eukaryotes, their representatives are missing in all the multigene phylogenies published yet. To fill this gap we sequenced around 1900 Expressed Sequence Tags (ESTs) from the freshwater naked foraminiferan *Reticulomyxa filosa*. Using our foraminiferan EST dataset as well as the other ESTs available for a chlorarachniophyte, *Bigelowiella natans*, we constructed a 96 gene eukaryote phylogeny which includes for the first time the supergroup Rhizaria. The overall topology of our trees is in agreement with previously published studies, showing the split between opisthokonts (animals + fungi) and bikonts

(Plantae, Stramenopiles, Alveolates, Excavates), and with Amoebozoa branching close to the root of eukaryotes. Our results confirm the monophyly of Rhizaria (Foraminifera + Cercozoa) with very high statistical support in all analyses. Furthermore, Rhizaria branch consistently as sister group of the Stramenopiles, which includes, among others, the diatoms, the brown algae and the actinophryid heliozoans.