

Evolutionary changes of the mitochondrial genome among amoebae of the order Vannellida (Amoebozoa, Discosea)

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Mitochondrial genes and complete mitochondrial genomes are a powerful tool for molecular phylogeny and evolutionary reconstructions. This tool is not widely applied among Amoebozoa because the number of sequenced mitogenomes is limited in this group; all yet sequenced ones represent just a few branches of the evolutionary tree of Amoebozoa. For the present study we have sequenced five mitochondrial genomes of amoebae belonging to the order Vannellida. These data represent two named vannellid genera: *Vannella* and *Clydonella* and two new genus-level basal branches of vannellids, not yet named. We compared gene content, gene order and level of synteny between these genomes and ones belonging to other groups of Amoebozoa and performed phylogenetic analysis using 20 mitochondrial genes shared by nearly all sequenced mitochondrial genomes. Results show high evolutionary rate of amoebozoan mitochondrial genomes and confirm relatively low level of synteny between the mitogenomes of species belonging to distant clades of amoebozoan tree, while closely related species show many common characters in gene content and order of genes. This study evidences that the structure and gene order of the mitochondrial genome may be highly useful for reconstruction of relationships between the major amoebozoan clades. Supported with RSF 17-14-01391 grant.