

Title:

Global freshwater mitochondrial genome atlas sheds light on (micro)eukaryotic diversity and evolution

Authors:

Lucas Serra Moncadas, Adrian-Stefan Andrei

Institution(s):

University of Zurich, Dep. of plant and microbial biology. Limnological station

Abstract (300 words maximum): :

Eukaryotes play key roles in aquatic ecosystems by contributing to nutrient cycling and maintaining overall environmental health. Larger eukaryotes, such as fish, help to regulate microbial population growth and contribute to nutrient cycling through feeding and excretion. Meanwhile, smaller eukaryotes such as phytoplankton drive primary production via photosynthesis, facilitate nutrient transfer within the food web, and serve as bioindicators of ecosystem health. Given their ecological significance, understanding the processes shaping the eukaryotic diversity—as well as the impact of climate change upon it—is essential. Recovering eukaryotic genomes from environmental samples poses significant challenges due to their inherent genomic complexity and the difficulties posed by their size and cultivation. While traditional approaches, such as 18S rRNA studies, provide valuable insights into their diversity, they often fall short of achieving species-level resolution. To circumvent these limitations, we compiled a global metagenomic dataset of freshwater lakes and aimed to recover environmental mitochondrial genomes. Their typically small, compact, and multi-copy nature makes them ideal candidates for metagenomic recovery. By employing this cultivation-free approach, we successfully recovered nearly 20'000 environmental mitochondrial genomes. In contrast to the existing mitochondrial reference databases dominated by metazoan and plant mitochondrial genomes, our study expanded the representation of undersampled (micro)eukaryotic taxa, including SAR, Cryptophyceae, and Haptista. These three lineages accounted for up to 13'049 of the recovered genomes, despite having only 333 representatives in the current databases. Overall, our findings highlight the potential of mitochondrial genomes as a powerful tool for freshwater biodiversity monitoring and assessing the ecosystems' responses to contemporary stressors, such as climate change and pollution.