

Structure and evolution of mitochondrial genomes in Euglenids

Mitochondria are the cell's powerhouse, present in cells of almost all nucleated organisms - eukaryotes. Formed by endosymbiosis of ancestral eukaryote with bacterium belonging to Alphaproteobacteria, mitochondria determined the evolution and diversity of eukaryotes. One of the remnants of the bacterial past of mitochondria are mitochondrial genomes (mitogenomes) encoding a few dozen proteins and RNAs. Mitogenomes are usually organized into a single, circular DNA molecule. However, many exceptions have been observed among unicellular eukaryotes, also known as protists. The most unusual mitogenomes were identified in the group of protists called Euglenozoa. Mitogenomes in this group are spread among large numbers of circular DNAs. In the case of Kinetoplastida (for example, in trypanosomatids, causative agents of sleeping sickness, Chagas disease or leishmaniasis) form a complicated structure, visible in the light microscope. Members of Diplonemida, the lineage sister to Kinetoplastida, have even larger and more fragmented mitogenomes. Despite the largest known DNA content, mitogenomes in both groups encode surprisingly few proteins and almost no RNAs.

In this project, I aim to investigate the evolution of mitogenomes in the sister lineage of diplomemids and kinetoplastids – euglenids. Recent reports indicate that some euglenids' mitochondrial genomes might be unfragmented. To verify these suggestions and investigate the diversity of euglenids' mitogenomes, I intend to sequence a handful of representative mitogenomes evenly distributed within a group. Short read sequencing will be used to obtain robust sequences of mitogenomes. The structure of selected mitogenomes will be assessed using long-read sequencing and molecular biology techniques. Analysis of acquired sequences and experimental results will allow to identify the structure (linear or circular) and continuity (single or multiple chromosomes) of mitogenomes in euglenids. This information will be mapped on the phylogeny of euglenids and used to determine how structure and gene content have changed during the evolution of euglenids.

Assessing the evolution of mitogenomes in euglenids will contribute to the knowledge of mitogenomes in Euglenozoa and help us reconstruct the evolution of the most bizarre known mitogenomes. It will advance the general understanding of evolutionary processes that take place during endosymbiosis.