

Description for the general public:

Circular DNA molecules (eccDNA) are commonly found in eukaryotic cells. Aside from the genetic material of semi-autonomous organelles: mitochondria and chloroplasts (mtDNA, cpDNA) circular DNA molecules derived from canonical, linear chromosomal loci are also present in Eukarya. The formation of circular DNA is strongly associated with plasticity of the genomes. Some of them are present in the cell constantly, while the others appear as a result of disease or in response to stress.

High diversity of these molecules, their variable size, and the presence of regions containing repeats make it difficult to align and analyze DNA circular sequences. The reads originating from these molecules usually remain underrepresented or rejected as information noise in datasets obtained as a result of whole genome sequencing. For this reason, knowledge about the resource of circular DNA in cells, their biological functions and mechanisms of their formation remains obscure, even though eccDNA has long been a known phenomenon. In the case of euglenids (Euglenida, Euglenozoa, Excavata), the current informations are very scarce.

The main scope of the project is to examine the repertoire of circular DNA molecules within a given species as well as between two metabolically different representatives of euglenids – phototrophic *Euglena gracilis* and *E. longa*, which has lost the ability to photosynthesis. The eccDNA molecules present in cells under optimal culture conditions as well as under the influence of oxidative stress induced by UV irradiation will be characterized in the proposed study. The project will exploit innovative methods of preparation and recently developed algorithmic tools. The obtained data will also be verified experimentally.

The accomplishment of this project will significantly enrich the knowledge about the organization of genetic material of euglenids and the dynamics of their genomes. We strongly believe that the results obtained during this project will contribute to a better understanding of the mechanisms responsible for biogenesis and diversification of eccDNA. They will also contribute to better understand the factors affecting the plasticity of eukaryotic genomes – especially in clonal organisms, such as the euglenids.