

Abstract:

This bachelor's thesis presents the current knowledge of the size of the genome in protists with a focus on the description and comparison of individual methods that were used to solve this issue. Genome size is a characteristic trait of all living organisms and other physiological features related to genome size are also mentioned. Of the selected methods, the greatest emphasis is placed on the flow cytometry, which is considered reliable and currently provides the most data on the size of protist genomes. In addition to flow cytometry, the contribution of whole genome sequencing to understanding the size of protist genomes is mentioned. Problems with estimating the size of protist genomes results from the heterogeneity of protists as a study group and from the non-uniform procedures within individual methods, which make possible comparisons difficult. Protists are evaluated in the work as an insufficiently studied group, within which the size of the genome varies by approximately 200,000×. The conclusion of the thesis summarizes the current knowledge about the genome size of relatively studied groups of protists.

Key Words: Genome size, C-value, Protists, Flow cytometry, whole-genome sequencing, pulsed field gel electrophoresis, Feulgen densitometry, microspectrophotometry