

Abstract

The bachelor's thesis focuses on environmental sequencing method and its usage in examining the diversity of microbial eukaryotic organisms. It describes the method, its mechanism, application and the problems associated with it. The work describes the current view of the phylogeny of the major eukaryotic lineages with their closer characteristics. Particular attention is paid to newly discovered groups. The work addresses the relationships inside these groups, summarizes findings of their ecology, food resources, and morphology. A separate chapter is devoted to the occurrence of the protist groups in extreme environmental conditions.

Key words: Diversity of eukaryotes, environmental DNA, sequencing, rRNA, phylogenetics.