

Metagenomic approach in studying of bacterial communities in Lake Baikal

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Lake Baikal, the most ancient and deep lake on the Earth, is characterized by the highest hydrobiont diversity among freshwater reservoirs. Microorganisms, in spite of their key role in biogeochemical processes and in the functioning of the Lake, remain insufficiently studied. Metagenomics, or community genomics, is a new approach to study microbial community structure analyzing the genomic content without cultivation.

In this study we compared microbial diversity and structure of communities of different parts of Lake Baikal. Six analysis sites, three in pelagic area of different basins of the Lake and three in littoral zone were chosen for sampling. Pelagic area is characterized as oligotrophic, while the offshore bays are well-warmed, mesotrophic tourist-recreational areas experiencing enhanced anthropogenic load. Pyrosequencing of 16S rRNA genes from environmental DNA as power tool to reveal the diversity of the microbial community was applied.

Pyrosequencing data showed that pelagic communities of three basins of the lake have similar taxonomic composition with the dominance of phylum Cyanobacteria. Representatives of phyla Proteobacteria and Actinobacteria consist up to 10% in the plankton communities. In total, pyrosequencing revealed 9 bacterial phyla in Southern Baikal, 11 – in Central Baikal and 10 – in the Northern Baikal. Pelagic communities of Lake Baikal basins had similar taxonomic composition. Littoral communities were characterized by higher number of bacterial phyla. The maximum number of phyla (26) was revealed in the coastal area of Southern Baikal dominated by three bacterial phyla: Bacteroidetes, Actinobacteria and Proteobacteria. In the littoral zone of Central Baikal in Gulf Mukhor 20 phyla were found, dominated by Cyanobacteria, Actinobacteria and Proteobacteria. In the Gulf of Turka were found 18 phyla, dominated by Cyanobacteria and Proteobacteria. Offshore communities were different in composition of taxa. Alpha-diversity was evaluated in the bacterial

community. Bacterioplankton of the pelagic zone was characterized by low values of OTU, for littoral communities values of observed and calculated OTU were 4-10 times higher. Evaluation of beta-diversity was produced by UniFrac analysis. Pelagic communities clustered together, while the littoral ones formed remote branches.

Thus, metagenomic analysis revealed and characterized a variety of bacterial taxa in Lake Baikal. It has been shown that the bacterial community of open Baikal is more stable compared to the littoral ones and species diversity correlates with trophic condition of water.

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