

# The composition of the communities of green algae and microeukaryotes at the sites of Lake Baikal contrasting in anthropogenic pressure

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**ABSTRACT.** The taxonomic diversity of the algae communities and their associated microeukaryotes from the Lake Baikal regions contrasting in anthropogenic impact was studied using the high-throughput sequencing methods. The 18S rDNA (V4 region) and ITS2 were chosen as markers. The main differences were observed in the taxonomic compositions of green algae and fungi from the communities studied. The taxonomic composition of the members of the SAR group was similar in the studied communities but differed in the abundance of their taxa.

**Keywords:** green algae, microeukaryotes, metagenome, 18S rDNA (V4 region), ITS2, Lake Baikal

## 1. Introduction

The ecosystem of Lake Baikal experiences large-scale changes accompanied by the death of Baikal endemics, such as sponges, replacement of dominants in phytobenthos, and wide distribution of the members of the genus *Spirogyra*. Anthropogenic pollution, in particular, pollution of groundwater with wastewater, an increase in the amount of ballast water discharge, etc, and global warming are among the causes of this phenomenon (Timoshkin et al., 2018). Microeukaryotes, as well as green algae, are among the first to react to the environmental changes. In this regard, clarification of the taxonomic composition in the modern communities of green algae and microeukaryotes at the Lake Baikal regions contrasting in the anthropogenic impact is of fundamental importance for characterizing of its ecological state.

## 2. Material and methods

Algae and their associated microeukaryotes were sampled taking into account the vertical zonation in the distribution of algae at ten localities of Lake Baikal with the assistance of scuba divers: Onokochanskaya Bay (a locality with a massive growth of filamentous algae and visually clear), Irinda, Boro-Elga, Khara-

Murin, Emelyanovka, Listvyanka, Kultuk, Baikalsk, and Maksimikha, at depths from 0.5 to 10 m. DNA was extracted according to the modified Doyle and Dickson technique (Doyle and Dickson, 1987). Amplification and subsequent high-throughput sequencing of the 18S rDNA (V4 region) and ITS2 markers using the Illumina MiSeq platform were carried out at the SB RAS Genomics Core Facility (Novosibirsk, Russia). Contigs with 97% similarity were classified as a single operational taxonomic unit (OTU).

## 3. Results and discussion

The datasets obtained for the 18S rDNA and ITS2 markers were grouped into 351 OTUs and 332 OTUs of the species rank, respectively. The group of green algae (79-95%) was the most representative in all studied communities. Only in communities from Kultuk, the proportion of green algae was 39%, and near Onokochanskaya Bay it was 49%. The low percentage of green algae at these localities can be due to the predominance of sandy bottoms that do not contribute to the development of benthic algae. In comparison with the data on the long-term profiling from 1963 to 1988 (Izhboldina et al., 2017a; 2017b), the taxonomic composition of green algae in the communities studied has undergone some changes. Thus, at the Boro-Elga

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and Kultuk, the diversity of green algae has increased. At the same time, at the Maksimikha and Khara-Murin, the taxonomic compositions of communities of green algae have not shown significant changes.

The communities studied differed in the predominance of taxonomic units of the SAR group. They were the most massive in the community from the Boro-Elga site. The main proportion belonged to ciliates (Ciliophora) (97%). The group of stramenopiles was presented by diatoms and chrysophytes represented, but their ratios differed at different sampling localities.

Fungi and fungus-like organisms ranged from 1 to 36% in the communities studied. At the localities under the anthropogenic impact (Baikalsk and Listvyanka), we detected the members of Zoopagomycota.

#### 4. Conclusions

The taxonomic composition of algae and fungi revealed by the sequences of the 18S rDNA (V4 region) was less diverse than those based on the ITS2 marker. However, the 18S rDNA marker provided a detailed characterization of the diversity of the SAR group in the communities studied. The metagenomic analysis detected the key members in the communities. Among green algae, these were the members of the cosmopolitan genera *Stigeoclonium*, *Cladophora*, *Ulothrix*, and *Spirogyra* as well as the Baikal endemic genus *Draparnaldioides*. The communities from different regions of Lake Baikal mostly differed in the spectrum of fungi.

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