

Structure of bacterial, archaeal and microeukaryotic communities of upper sediment in Lake Vorota, Pole of Cold (Yakutia)

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ABSTRACT. Upper layer of the bottom sediment is important as an area where freshly deposited sediment is remineralized. In this work we have described structure and diversity of bacterial, archaeal and microeukaryotic communities from upper sediment of Lake Vorota (Yakutia). According to high-throughput sequencing of 16S fragment, most common bacteria are Cyanobacteria, Deltaproteobacteria, Bacteroidota and Desulfobacteriota; archaeal community is dominated by Halobacteriota. Analysis of 18S sequences from microscopic eukaryotes has revealed the predominance of Diatomea.

Keywords: Surface sediments, bacteria, archaea, microeukaryotes, high-throughput sequencing

1. Introduction

High-altitude and high-latitude lakes are covered by ice for more than 40% of the year. The existence of winter season affects ecology and metabolism of freshwater microorganisms. Lake Vorota is situated at the junction of Suntar-Khayata Range and Oymyakon Plateau at the altitude of 1014 m, near the Northern Pole of Cold (Rusanov et al., 1967; Atlas..., 1989). Microscopy has shown that a photic layer of this lake is inhabited in summer by five divisions of microalgae: Cyanoprokaryota, Cryptophyta, Chrysophyta, Bacillariophyta, and Chlorophyta (Tomberg et al., 2017). Electron microscopy has allowed detecting a high diversity of silica-scaled chrysophytes (Bessudova et al., 2019), as well as a diatom *Lindavia minuta* (Skvortzow) T. Nakov et al. (Usoltseva et al., 2020) which was previously thought to be an endemic of Lake Baikal. These three papers are all that was published about the algae of this lake, and information about its bacterial and archaeal communities is altogether absent.

The goal of this work was to study the taxonomic composition of bacterial, archaeal and microeukaryotic communities of upper sediment in oligotrophic Lake Vorota using high-throughput sequencing

2. Material and methods

Samples were taken in ice period (June, 2017) in littoral zone of Lake Vorota (Yakutia) from a depth

of 5 m. The sample of surface sediment was taken by scuba divers in sterile flask and stored. Total DNA was extracted according to the standard method (Shubenkova et al., 2005). To determine the taxonomic structure, V3-V4 fragments of 16S rRNA gene of bacteria and archaea, and V4 fragment of 18S rRNA gene of eukaryotes were amplified and sequenced on Illumina MiSeq system in Evrogen (Moscow). Analysis of obtained data was performed in Usearch v. 10 (Edgar, 2010) and Mothur 1.44.2. Reads were clustered into operational taxonomic units (OTUs) at 97% gene similarity using Silva v.138.

3. Results

The sequencing has produced 74490 bacterial reads clustered into 974 OTUs; 61505 archaeal reads clustered into 167 OTUs; and 78835 eukaryotic reads clustered into 384 OTUs. In the sediment surface sample from Lake Vorota the highest number of reads (25% of the library) was assigned to phylum *Proteobacteria*. Numerous OTUs belonged to *Crenothrix*, *Methylibium*, *Steroidobacteraceae*, *Comamonadaceae*, and *Sutterellaceae*. Phylum *Cyanobacteria* covered 23% of the reads, including such genera as *Cyanobium*, *Synechocystis*, and *Geminocystis*. Phyla *Bacteroidota* and *Desulfobacteriota* made up 13% of the library each; *Chloroflexi* and *Actinobacteriota* – 10% each; *Verrucomicrobiota* – 7%; *Acidobacteriota* – 6%; *Spirochaeta* – 3%; *Gemmatimonadota* – 2% (Fig.).

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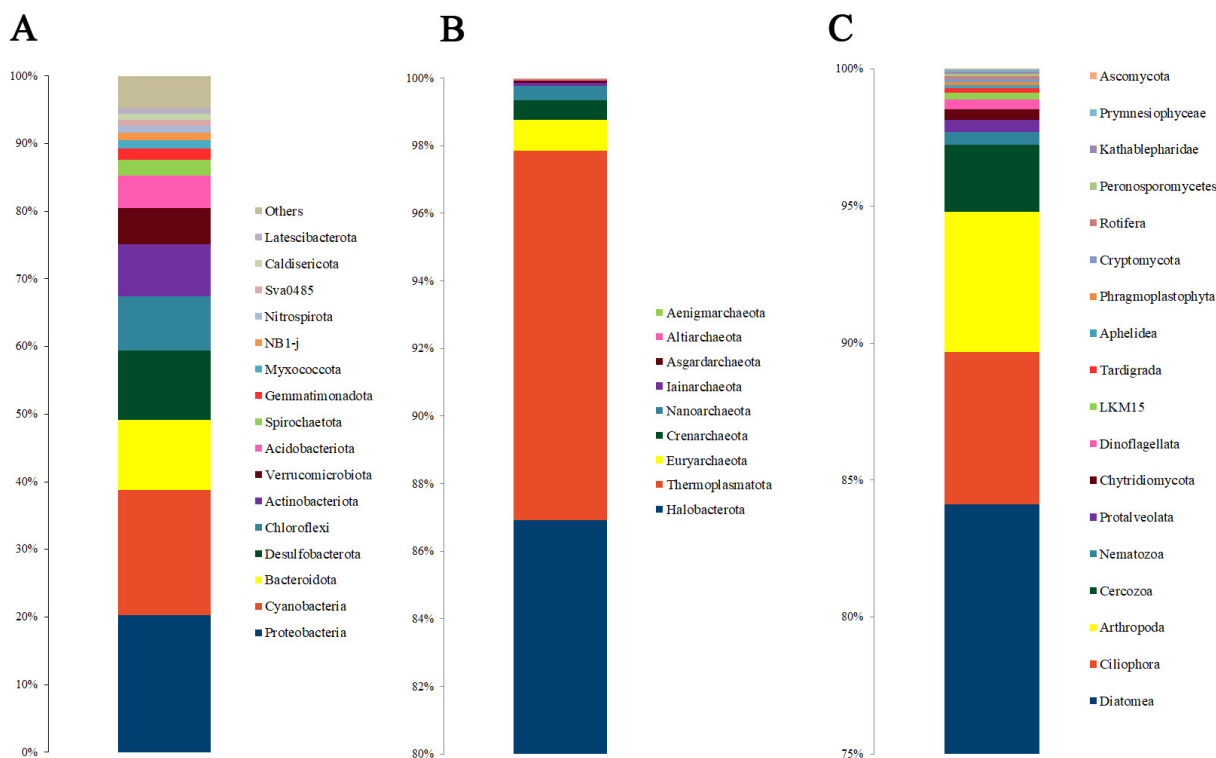


Fig. Taxonomic composition of sediment surface community in Lake Vorota according to the high-throughput sequencing of fragments of 16S and 18S rRNA genes. A – bacteria; B – archaea; C – eukaryotes.

Other phyla included less than 2% reads each. Among the archaea, the majority was assigned to phylum *Halobacterota* (87%), with its most common OTUs being *Methanoregula* and *Methanosaeta*. Phylum *Thermoplasmata* had 11% of the reads; other phyla had less than 1% reads each. Eukaryotic community was dominated by *Diatomea* (84%). Most common OTUs were representatives of *Fragilariiales*, *Staurosira*, *Neidium*, and *Navicula*. *Ciliophora* made up 5.5% of the library; *Arthropoda* – 5; *Cercozoa* – 2.5%. Most numerous OTUs belonged to subclass *Haptoria*, subtype *Intramacronucleata*, and order *Podocopida*.

4. Discussion and conclusions

Analysis of high-throughput sequencing data has allowed us to document taxonomic composition of sediment surface community from Lake Vorota. Most common bacterial genera, *Crenothrix* and *Methylibium*, are methane- and methylotrophic (Nakatsu et al., 2006; Oswald et al., 2017). *Methanoregula*, which are most common among archaea, are strictly anaerobic methanogens (Zinder and Bräuer, 2015). Diatom genera *Staurosira*, *Neidium*, and *Navicula*, as well as order *Fragilariiales*, are benthic dwellers of the Arctic (Schmidt et al., 2004; Paull et al., 2008), as well as cold oligotrophic lakes such as lake Baikal (Pomazkina and Rodionova, 2003).

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