1 Introduction

Prokaryotes are key organisms in aquatic ecosystems as they play an important role in the biogeochemical cycling of elements. Investigations on the relationships between the diversity of microbial community and environmental factors offer useful information that both leads to understanding of the process of element cycling and offers the possibility to predict ecosystem responses to environmental changes (Fuhrman et al., 2006). In fact, bacterial diversity is clearly affected by certain environmental factors, such as pH, water temperature, water chemistry, nutrient condition, geographical and seasonal variations (Lindstrom et al., 2005; Hahn, 2006; Zeng et al., 2009). However, to predict and describe microbially mediated processes, spatial and temporal patterns of diversity at multiple levels could be investigated. Because of the high diversity of microbial communities, the ability to characterize their fine-scale vertical distribution has only become achievable within the past decade (Scholz et al., 2012). Next-generation ‘-omics’ technologies such as high-throughput amplicon sequencing allow collection of thousands to millions of sequences (Green et al., 2008; DeLong, 2009) and following bystatistical methods detection of numerically dominant as well as uncommon organisms in a system (Bent, Forney, 2008; Gonzalez et al., 2012). The first ones are seem to be responsible for the majority of metabolic activity and energy flux, but uncommon organisms serve as a reservoir of genetic and functional diversity (Yachi, Loreau, 1999; Nandi et al., 2004), often play key roles in ecosystems (Phillips et al., 2000), and can become numerically important if environmental conditions change (Bent, Forney, 2008).

The main aim of the present study was identification of microbial diversity of Lake Doroninskoe by high-throughput 16S rDNA amplicon sequencing to search vertical distribution of major bacterial taxa and to find uncommon bacterial groups.

2 Object and Methods

Lake Doroninskoe is meromictic soda lake located in East Transbaikalia (N51°25′; E112°28′) in the permafrost zone. It is characterized by an alkaline values of pH (9.72), a relatively elevated water and sediments mineralization (32.3 g/l) and a permanent chemocline at a depth of 3.0–3.75 m separating the aerobic epilimnion from the anaerobic, sulfidogenichypolimnion (Zamana, Borzenko, 2007); those positively correlate with the distribution of bacteria (Gorlenko et al., 2010).

Samples of water were collected in March 2013, filtered through 0.22 um polycarbonate filters (Millipore), and stored at −20°C before further treatment. DNA isolation was done with Bacterial Genomic DNA isolation kit (Axygen), 16S rDNA amplicons sequencing was done at Novosibirsk center “Genomika”. Bioinformatics’ analysis was done at the Ribosomal Database Project web site (https://rdp.cme.msu.edu/index.jsp) (Cole et al., 2014; Wang et al., 2007).

3 Results and Discussion

The water body of Lake Doroninskoeis structured into three distinct zones: the oximixiolimnion (from surface to the depth of 3.0–3.75 m), a narrow chemocline (width of 0.15–0.20 m), and the anoxic monimolimnion (from the depth of 3.15–3.75 to the bottom with maximum of 6.2
Metagenomic analysis revealed five dominant phyla: Proteobacteria, Bacteroidetes, Actinobacteria, Cyanobacteria, and Firmicutes (Fig. 1). The negative correlation of two bacterial groups was determined in the maximum abundance at the different zone of the lake. The first group consisted of Proteobacteria and Actinobacteria, whereas the second ones included Bacteroidetes, Firmicutes, and Cyanobacteria.

Proteobacteria are numerically dominant phylum, and Rhodobaca makes the main contribution to its vertical distribution with the maximum coinciding with the presence of light and deposition of organic matter. Additional input to the maximum at 3.15 m makes by Nitrincola. The distribution of Desulfonatronum depends on water chemistry. Uncommon representatives are Serratia, having more or less uniform distribution through the water column of the lake (Fig. 2). The vertical distribution of Firmicutes has been dependent on the presence of known representatives Dethiobacter, Tindallia, and Saccharofermentans.

Uncommon representatives of phyla Bacteroidetes and Actinobacteria have been influenced to their vertical distribution in Lake Doroninskoe, whereas cultivated Sediminibacterium and Gracilimonas have negative distribution with the maximum coinciding with the presence of light and deposition of organic matter. Additional input to the maximum at 3.15 m makes by Nitrincola. The distribution of Desulfonatronum depends on water chemistry. Uncommon representatives are Serratia, having more or less uniform distribution through the water column of the lake (Fig. 2). The vertical distribution of Firmicutes has been dependent on the presence of known representatives Dethiobacter, Tindallia, and Saccharofermentans.

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**Fig. 1.** Distribution of main bacterial taxa through water column.

**Fig. 2.** Distribution of Proteobacteria, Rhodobaca, Serratia, Nitrincola, and Desulfonatronum through water column of Lake Doroninskoe (March, 2013).

**Fig. 3.** Distribution of Bacteroidetes, Sediminibacterium, Gracilimonas (A) and Nitriruptor, Ilumatobacter (B) through water column of Lake Doroninskoe (March, 2013).
correlation with their maxima (Fig.3,A). Nitriliruptor and Ilumatobacter of the phyla Actinobacteria have been shown the uniform distribution through the water column of the lake (Fig. 3, B).

**Key words:** Soda Lake Doroninskoe, Bacterial Diversity, 16S rRNA Gene, High-Throughput Amplicon Sequencing.

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