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# Phylogenetic Diversity of Microorganisms from Chemocline of the Meromictic Soda Lake Doroninskoe (Zabaikalie, Russia)

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## 1 Introduction

Many soda and salt lakes are characterized by the formation of the meromictic conditions under which a part of the water column is not involved in the annual process of mixing (MacIntyre, Melack, 1982). This creates an ideal environment for the growth of anoxic phototrophic and chemoautotrophic microorganisms in the border between mixo- and monimolimnion (chemocline). Because of these unique bacteria activity, sulfur is cycled through the chemocline (Parkin, Brock, 1981). It is well known that actively functioning anoxic phototrophic microorganisms in this layer makes it brightly purple color (Overmann, 1997; Gorlenko, 2010).

Lake Doroninskoe is meromictic soda lake located in East Transbaikalia (N51º25'; E112º28') in the permafrost zone. It is characterized by a distinct chemocline with high concentration of sulfate and sharp gradient of oxygen and sulfide (Zamana, Borzenko, 2007), that positively correlates with the distribution of bacteria (Gorlenko et al., 2010). A distinctive peculiarity of the lake from the two other meromictic Siberian lakes Shira and Shunet

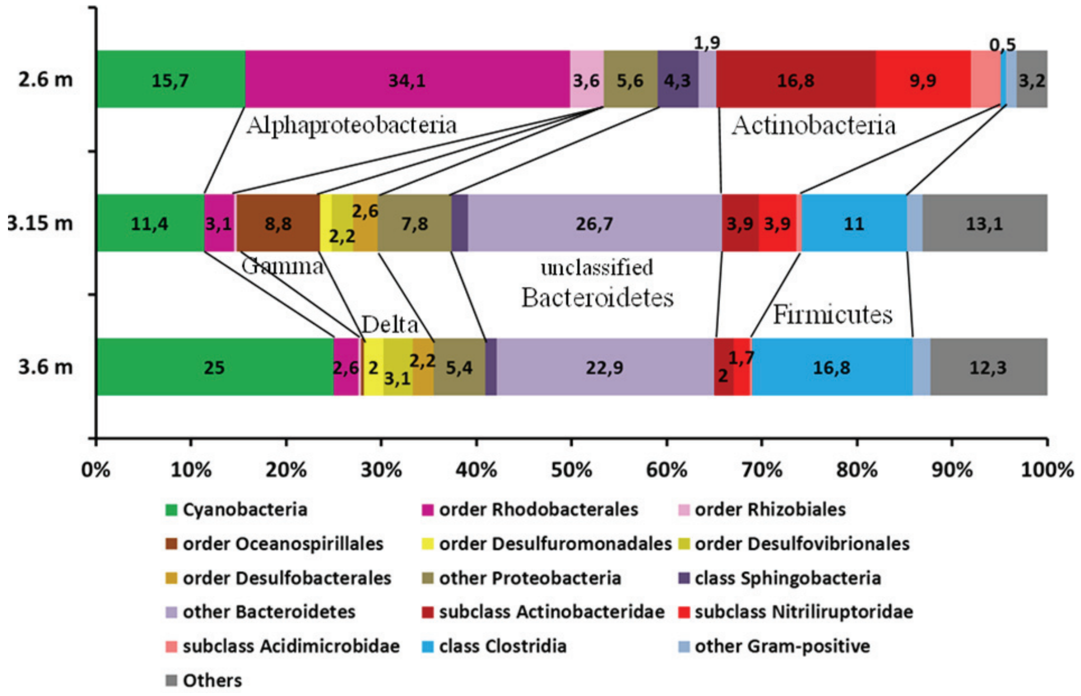

Fig. 1. Dynamic of changes in the structure of microbial communities in the contact zone of aerobic and sulfide layers of the water column of Lake Doroninskoe (March, 2013)

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(Rogozin et al., 2010) is a low level of light penetration into the chemocline zone, which is 0.001%, and the lack of bright colored water in this zone. The latest one phenomenon is of particular interest in the study of microbial community of the lake.

Phylogenetic diversity of microbial communities has been studied from three zones of Lake Doroninskoe: the upper aerobic (2.6 m), narrow redox (3.15 m), and lower sulfide zone (3.6 m), at a total depth of 6.2 m in March 2013 by 16S rDNA amplicon pyrosequencing.

Metagenome analysis of the microbial communities of the zones of the water column revealed the representatives of 11 major Eubacteria phyla: Cyanobacteria, Acidobacteria, Actinobacteria, Proteobacteria, Verrucomicrobia, Tenericutes, Firmicutes, Bacteroidetes, Planctomycetes, Spirochaetes, Deinococcus-Thermus, 5 fantom phila: TM7, SR1 , BRC1, WS3, OD1, and one phyla of Archaea – Euryarchaeota (Figure 1). Herein the fraction of unidentified sequences was 0.5–5.3%. Dominant at different depths were: Cyanobacteria, Proteobacteria, Bacteroidetes, Actinobacteria and Firmicutes.

Dominant group of oxygenic phototrophic chlorophyll "a" containing cyanobacteria was represented by the only phantom GpIIa genus of the corresponding family. It has been shown a high content in the hydrogen sulphide and redox zones of the lake, probably due to the process of cell sedimentation from the surface layers. Taking into account that the level of illumination on the 2.6 m was less than 50 lux, and in the redox zone was about 1–5 lux, at this light intensity only green sulfur bacteria belonged to family Chlorobiaceae of all prokaryotic organisms could function as phototrophs (Marschall et al., 2010).

Dominant classes of the phylum Proteobacteria were Alpha-, Gamma-, and Deltaproteobacteria, whose fraction in the microbial communities differed significantly (Figure). Rhodobacterales and Rhizobiales of the class Alphaproteobacteria have been dominant at a depth of 2.6 m, but their fraction decreased in the chemocline and sulfide layer. The main representatives of this group were purple non-sulfur bacteria, which are able to grow anaerobically with the light or aerobically in the dark used various organic compounds both as an electron donor and a nitrogen source. They were represented in the microbial community by the families Rhodobacteraceae and Beijerinckiaceae, with dominant genera *Rhodobaca* and *Chelatococcus*, respectively. Representatives of Oceanospirillales (Gammaproteobacteria) were found only in the chemocline zone, their fraction in the microbial community was 8.7 %, with dominant genus *Marinospirillum* and *Nitrincola* (Oceanospirillaceae). Detection *Desulfuromusa* (Desulfuromonadales), *Desulfonatronum, Desulfonatronovibrio* (Desulfovibrionales), and *Desulfurivibrio* (Desulfobacterales) of Deltaproteobacteria in the chemocline and sulfide layer indicated the presence of active processes of sulfur cycling - sulfate-reduction.

Unidentified representatives of the phylum Bacteroidetes have been detected in all layers with predominance at depths of 3.15 and 3.6 m. Negative correlation have been shown between this group and class Sphingobacteria of the same phylum. Genera *Gracilimonas* and *Sediminibacterium* as well as unidentified members of the family Chitinophagaceae were dominated at a depth of 2.6 m. Negative correlation was found in the distribution of the two major phyla of Gram positive bacteria Actinobacteria and Firmicutes. So, at a depth of 2.6 m the subclasses Actinobacteridae, Nitriliruptoridae, and Acidimicrobidae of the phylum Actinobacteria were dominated, while in the chemocline zone and lower – class Clostridia of the phylum Firmicutes.

Analysis of the functional diversity of microorganisms from chemocline zone have been revealed the presence of both "strict specialists" whose presence is limited with specific only for them micro-environments, and "generalists", adapted to the unstable conditions and existing versatile metabolism.

Among the identified microorganisms from chemocline, anoxic phototrophs were found as a dominant "generalists". They belonged to non-sulfur purple bacteria of the families Rhodospirillaceae and Rhodobacteraceae class Alphaproteobacteria. A characteristic feature of these bacteria was the ability to skip from phototrophic to aerobic chemotrophic metabolism.

It is interesting to note that chemotrophic bacteria with known functional genes for the anoxic photosynthesis-key enzyme of the Calvin cycle (Rubisco) have been detected in chemocline microbial community with a maximum in the oxygen layer. But they could be relevant to the minor part of the "generalists". These bacteria belong to genera *Bradyrhizobium, Paracoccus*, and *Rhodobacter,* class Alphaproteobacteria, heterotrophs of the families Oceanospirillaceae, class Gammaproteobacteria, and Burkholderiaceae, class Betaproteobacteria. At the same layers bacteria with an alternative photosynthesis with actinorhodopsin genes belonged to family Microbacteriaceae, phylum Actinobacteria have been detected.

In general, the microbial community of meromictic Lake Doroninskoe in the contact zone of aerobic and sulfide-containing layers have been characterized by high microbial diversity with dominance of bacteria with a universal type of metabolism such as non-sulfur purple bacteria of the families Rhodospirillaceae and Rhodobacteraceae, class Alphaproteobacteria.

**Key words**: Diversity, Soda Lake, Meromixis, Lake Doroninskoe, 16S rRNA Gene; Phylogeny.