

# Microbial community diversity in hot springs of the Baikal rift zone

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**ABSTRACT.** The taxonomic diversity of the microbial community of the Baikal rift zone hot springs has been studied. The hot springs were characterized by different temperature (from 34 to 77 °C), hydrogen sulfide concentration (from 0.02 to 12.75 mg/L), and silica (from 89 to 144 mg/L). pH values varied from 8.1 to 9.7. The dominance of distinct phyla was revealed depending on the spring water temperature. Microbial communities in bacterial mat developing at higher temperatures (53 - 58 °C) were similar by taxonomic composition. The community at 34-51 °C was very different from the high-temperature regions. *Nitrospirae* и *Deinococcus-Thermus* dominated in the microbial mats community with temperature 65 °C, but phyla *Atribacteria*, *Nitrospirae*, *Chloroflexi* prevailed in at 53-65 °C. *Proteobacteria* and *Cyanobacteria* dominated at temperatures 34-51 °C.

**Keywords:** Microbial community, taxonomic diversity, environmental factors, hot spring, Baikal rift zone

## 1. Introduction

Terrestrial hot springs are extreme ecosystems and convenient model system for studying the ecology of prokaryotes by the constancy of chemical composition and temperature (Sand, 2003; Coman et al., 2013; Badhai et al., 2015).

Hot springs of the Baikal Rift Zone (BRZ) are characterized by high temperatures and high pH values favorable for the development of thermophilic and alkaliphilic prokaryotes (Zaitseva et al., 2004; Kublanov et al., 2009; Lavrentieva et al., 2009; 2018; Namsaraev et al., 2010; Radnagurueva et al., 2016).

Metagenomic analysis of a microbial community let to characterize the composition and structure of microbial communities in natural environments, to identify the dominant physiological groups of microorganisms, and to determine the metabolic potential of microorganisms and the community as a whole.

This study aimed to characterize the hot springs microbial communities of BRZ hot springs depending on environmental factors.

## 2. Material and methods

The objects of the study were hot springs (from 34 to 77 °C) Alla, Garga, Seyuya, Umkhei, Kuchiger and Goryachinsk located in the Baikal Rift Zone. The samples of water, bottom sediments, and microbial mats were collected in the summer-autumn seasons of 2013 -2015.

Physico-chemical characteristics of hot springs was carried out at the sampling sites using portable instruments and standard methods (Reznikov et al., 1970).

Total DNA was isolated by use commercial kits "DNA-sorb" (AmpliSens, Russia) and «Bacterial Genomic DNA kit» (Axygen, USA). Metagenomic analysis of V3-V4 variable regions of 16S rRNA was carried out using a MiSeq sequencer (Illumina, USA) at the Genomics Shared Use Center (Novosibirsk).

Raw sequences were analyzed with UPARSE pipeline (Edgar, 2013) using Usearch v8.1. The UPARSE pipeline included merging of paired reads; read quality filtering; length trimming; merging of identical reads (dereplication); discarding singleton reads; removing chimeras and OTU clustering using the UPARSE-OTU algorithm. The OTU sequences were assigned a taxonomy using the RDP classifier 2.11 (Wang, 2007).

## 3. Results and Discussion

The temperature at the sampling varied from 34 to 77 °C, the hottest water were observed in Garga and Alla hot springs. The pH water changed from 8.1 to 9.7, the Eh varied from -333 to +55 mV. All hot springs were characterized by low mineralization (from 0.18 to 0.74 g/L), hydrogen sulfide contents (from 0.02 to 12.75 mg/L), and silica (from 89 to 144 mg/L).

*Nitrospirae* and *Deinococcus-Thermus* were dominant in the microbial community at 65 °C, while *Chloroflexi* and *Atribacteria* - at 53-58 °C. The

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*Chloroflexi*-bearing community began to prevail in the temperature range 53-58 °C, (Seyuya, Alla - station 3). The bacterial community of Alla spring mat (station 1, 55 °C) is taxonomically diverse, where no phylum is dominant. When the temperature dropped to 45-50 °C, *Proteobacteria* representatives (Goryachinsk, Garga) were the dominant phylum. Representatives of *Cyanobacteria* were co-dominant. The number of their sequences was inversely related to the sequences of the phylum *Chloroflexi*.

It is known that in the community of microbial mats, where photosynthetic *Chloroflexi* and *Cyanobacteria* are present, *Chloroflexi* bacteria usually switch to photoheterotrophic metabolism due to organic compounds synthesized by *Cyanobacteria*, rather than compete with *Cyanobacteria* for inorganic carbon. This is especially specifically for microbial mats in alkaline springs, where the CO<sub>2</sub> content of the water is limited (van der Meer *et al.*, 2003).

Representatives of *Proteobacteria* was approximately 70% of whole community at 34 °C (Alla, station 5).

The phylum *Aquificae* was found in minor amounts in almost all microbial mats of the springs, except Goryachinsk (45 °C), and Umkhei (43 °C), as well as in the low-temperature zone of the Alla spring (station 5, 34 °C). This group is known to include extremely thermophilic bacteria capable of multiplying at temperatures up to 95 °C.

The bacterial community of hydrothermal stations with mesophilic temperatures (34-43 °C) is characterized by the appearance and increase of heterotrophic bacteria of the phyla *Proteobacteria*, *Acidobacteria*, *Bacteroidetes*, *Chlorobi*, *Planctomycetes*.

Comparative analysis of the composition of dominant taxa showed significant differences depending on the place of sampling and revealed the spatial stratification of the community. Bacterial communities in microbial mats developing at higher temperatures (53 - 58 °C) were similar in terms of the qualitative taxonomic composition. Whereas the community of the mat at 34-51 °C was very different from the high-temperature regions.

Thus, if phylogenetically diverse groups of *Atribacteria*, *Nitrospirae*, *Chloroflexi* prevailed in the high-temperature region, *Proteobacteria* dominated with decreasing temperature. No thermophilic representatives of phyla such as *Atribacteria*, *Nitrospirae*, and *Deinococcus-Thermus* specific for the community of high-temperature mat were found in the low-temperature mat.

#### 4. Conclusions

The species richness and diversity of the microbial community of the hydrothermal waters of the Baikal Rift Zone were higher in microbial mats and bottom sediments than in water. Diversity of bacteria increased with temperature decrease in hydrothermal fluids. The phyla *Atribacteria*, *Nitrospirae*, *Chloroflexi* prevailed in the community of microbial mats developing at temperatures of 53-65 °C. Representatives

of *Proteobacteria* and *Cyanobacteria* dominated, and the number of bacteria of the phyla *Acidobacteria*, *Bacteroidetes*, *Chlorobi*, *Planctomycetes* also increased at 34-51 °C.

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