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An Integrated Study to Analyze Salt Lake Microbial Community Structure (Novosibirsk Oblast, Russia)

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Salt Lake is one of the lakes in the system, consisting of a huge amount of salt and bitter-salty lakes in Novosibirsk Oblast and Altai Krai. These lakes are unique and highly unstable systems where the parameters of geochemical environments can vary markedly during season, month, week or even day. This leads primarily to changes in the composition and structure of microbial community. Moreover, these lakes are investigated geochemically and microbiologically only partially, and the Salt Lake was investigated for the first time.

From 2008 to 2010 we used methods of molecular biology (Ligation Independent Cloning (SLIC); fluorescence in situ hybridization (FISH)), light and electron microscopy, and methods of classical microbiology to study the microbial communities of Salt Lake. Taxonomic structure of the communities was studied by parallel amplicon sequencing of the variable region V3-V5 of 16S rRNA gene and metagenomic sequencing of total DNA of communities. Simultaneously hydro-chemical parameters of water (pH, Eh, cationic/anionic composition, gas components) were studied. Mineralization of water in the lake was 230 g/l. The chemical composition is shown in the article (Lazareva et al., 2012).

As a result, the number of different physiological groups of microorganisms has been investigated in the water, in the microbial mat and in the bottom sediments of the Salt Lake. By seeding it was found that the amounts of aerobic proteolytic and amylolytic bacterial decomposers

in water layer are 2×10^4 and $2 \times 10^4 - 3 \times 10^5$ CFU/ mL respectively. A high number of microorganisms (5×10^5 CFU/mL) capable of growing on organic media at both high pH (more than 10) and in the presence of NaCl (25%) was revealed. The vertical distribution of bacterial decomposers in the sediment core was investigated. It is shown that in general, changes in the numbers of different groups of microorganisms-decomposers in sediment core layers were significant and reached for organisms grown in LB medium - $8,4 \times 10^4$ CFU/ mL, for amylolytics - $1,1 \times 10^5$ CFU/mL, for proteolytics - $8,3 \times 10^4$ CFU/mL and lipolytics - $1,0 \times 10^5$ CFU/mL. Observed fluctuations in the number can be explained by physical and chemical gradients, existing and/or resulting from microbial activity in different layers of sediments.

A study of the microbial communities' structure was conducted by fluorescence in situ hybridization and quantitative composition of archaea, bacteria, cyanobacteria and algae was obtained. Overrepresentations of bacteria in the plankton community and cyanobacteria in the microbial mat were established. Archaea represented a small part of the community.

During the pilot cloning over 200 clones were received. Analysis of the 16S rRNA gene sequences revealed representatives of such groups as Cyanobacteria, Deltaproteobacteria, Alphaproteobacteria, Bacteroidetes and Firmicutes. A unique composition of cyanobacterial community represented by species of the genera *Leptolyngbya*, *Gloeocapsa*, *Geitlerinema* is marked. The greatest number of clones (26) was obtained for the genus *Cymbella* (Diatoms), 17 clones were obtained for the

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phylum Bacteroidetes, 12, 10 and 9 were obtained for genera *Marinobacter*, *Desulfosarcina* and *Haloanaerobium* respectively.

By pyrosequencing it was found that the dominant group in the microbial mat of the lake consists of representatives of Proteobacteria (59%), Gammaproteobacteria and Alphaproteobacteria classes. 11% percent of the sequences were representatives of Cyanobacteria, 10% - Bacteroidetes. 6% of sequences belonged to eukaryotic organisms, mainly diatoms (Bacillariophyta). Representatives of the Archaea (Euryarchaeota) in conjunction with other types of bacteria were insignificant.

The study of halophilic microbial community of Salt Lake using a whole range of methods allowed ensuring accuracy and completeness of the results. For the first time the taxonomic structure of the community was identified

and analyzed.

Key words: Salt Lake, microbial community, Novosibirsk Oblast.

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References

- Lazareva, E.V., Bryanskaya, A.V., Taran, O.P., Kolmogorov, Y.P., Malup, T.K., Peltek, S.E. and Zhmodik, S.M., 2012. Investigation of element distribution between components of a salt-lake system by SR-XRF. *Journal of Surface Investigation-X-Ray Synchrotron and Neutron Techniques*, 6 (6): 1009-1018