

Metagenomic analysis of metabolically active microbial communities of Salenoye Lake # 48 in the Novosibirsk region

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Motivation and Aim: Microbial communities of saline lakes are highly productive in terms of production of organic matter. This is primarily due to the fact that the accumulation of high concentrations of organic matter in cells is necessary to counteract the high osmotic force of the medium. Saline lakes located in the south of western Siberia are interesting for studying for several reasons: they are in a territory with a temperate climate and are subject to constant fluctuations in the concentration of salts and temperatures; they are remote from the most studied saline lakes, which allows us to obtain data about new species. The aim of this study was to investigate phylogenetic and metabolic properties of most metabolic active parts of saline lakes ecosystems.

Methods and Algorithms: As a model object we took the Solenoye Lake # 48 (Bagan district, Novosibirsk region). We have performed a metagenomic sequencing of microbial communities from of microbial mat and top layer of sediments. Libraries for sequencing were prepared by Ph.D. Vasilyev G.V. in the Center for Genomic Research of the ICG SB RAS. Sequencing was carried out by Genetics and Reproductive Medicine Center “Genetico” (Moscow) on the Illumina NovaSeq 6000. The following resources were used for data processing and analysis: fastQC, trmomatics, metaSPAdes, metaQuast, MaxBin, MGrast.

Results: We performed a metagenomic sequencing of the two most active microbial communities of this lake. The total amount of data was 50 GB for each point. This allows us to obtain genomes of microorganisms with a high degree of coverage, a sequence of viral genetic material. In contrast to the 16s rRNA of metagenomic analysis, this approach allowed to obtain information on species diversity without distortion caused by the selection of primers and PCR. In particular, we were able to obtain information on the presence in the microbial communities of diatom algae of the family Phaeodactylaceae. In the report, we will provide information on the phylogenetic diversity and metabolic possibilities of the microbial communities under investigation, as well as on the genomes of microorganisms that will be extracted by that time.

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