

Short communication

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Ecology of estuarine waters in small rivers of Southern Baikal in 2018

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ABSTRACT. We conducted comprehensive studies in small rivers and estuarine water areas of Southern Baikal during the under-ice (March) and summer (July) periods of 2018. The chemical composition of water, the number of microorganisms, their diversity and metabolic potential in the studied areas correlated with the geographic location of the rivers, their flow and the degree of anthropogenic impact.

Keywords: Lake Baikal small tributaries, estuarine basins, chemical composition, ice and water microbial communities, dark CO₂ assimilation, biodiversity

River ecosystems are used as sources of drinking water, for irrigation, industries and hydropower, and as transport and tourist routes; therefore, they are the most vulnerable aquatic ecosystems. Microorganisms that ensure the biochemical processes, as well as biodegradation and biotransformation of various pollutants, play a key role in the recovery and preservation of the state of these ecosystems (Kirchman, 1994; Bai et al., 2014; Ruiz-González et al., 2015; Wang et al., 2018). To date, much research has been done to assess the impact of domestic sewage on river ecosystems (Dugdale et al., 2013), which is also relevant for the tributaries of Lake Baikal (Drucker et al., 1993; Maksimov, 1995; Shtykova et al., 2016; Malnik et al., 2019). Small Baikal tributaries show an increase in the concentrations of phosphorus and nitrogen compounds as well as mass development of algae nonspecific for the littoral zone of Lake Baikal (Kravtsova et al., 2014; Khanaev et al., 2016; Timoshkin et al., 2016).

Using different approaches: cultivation, targeted sequencing of 16S rRNA genes, the metabolic activity of communities using radioactively labelled substrates, non-metric multidimensional scaling, and correlation analysis, we analysed chemical and microbiological data on the small rivers of Southern Baikal during the under-ice (March) and summer (July) periods of 2018. The obtained data demonstrate metabolic and taxonomic differences in bacterial communities between the river and estuarine water areas as well as in communities from southeastern and southwestern water areas of Lake Baikal.

Chemical parameters, total bacterial count

(TBC) and the number of various physiological groups of microorganisms in rivers and their estuarine water areas formed several clusters that correlated with the geographic location of the rivers, their flow and the degree of anthropogenic impact (Sinyukovich and Troitskaya, 2000; Zemskaya et al., 2019). As before, atmospheric precipitation enriched with the emissions of nitrogen oxide and sulphur from nearby thermal power stations affects the chemical composition of the rivers on both sides of Southern Baikal, which leads to the change in pH of water (Khodzher et al., 2002; Sorokovikova et al., 2002; Obolkin et al., 2016; Tomberg et al., 2016). The conducted studies have revealed that water in these rivers water does not undergo significant acidification that affects the vital activity of the bacterioplankton and phytoplankton communities (Bukin et al., 2020). Analysis of the data on the dark CO₂ assimilation, TBC, the number of organotrophic, thermotolerant and faecal bacteria indicated the most polluted river and assessed the metabolic activity of communities depending on environmental conditions. During the under-ice period, the dark CO₂ assimilation values were higher in the river and estuarine communities of microorganisms in the southeastern part of the lake compared to those in the southwestern part of Lake Baikal. In summer, we recorded higher values of this indicator: the rivers in the southwestern part of Southern Baikal, as well as the estuarine water areas in the southeastern part of Southern Baikal, showed the highest metabolic activity of microbial communities. The rivers and their estuarine water areas in the southwestern part of the lake are the

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most potentially hazardous for drinking purposes, where in different studied seasons, the number of coliform bacteria and spores of sulphate-reducing bacteria exceeded the ISO 9308-1, 2000 standards (Drucker et al., 1993; Maksimov, 1995; Shtykova et al., 2016; Malnik et al., 2019). The use of targeted sequencing of 16S rRNA genes for the analysis of communities of aquatic microorganisms allowed us to fully access the pollution sources, complementing the traditionally used indicators (for example, *E. coli*, enterococci) often used in monitoring programmes. As a positive point, we can indicate a decrease in the bacterial diversity in the estuarine areas, which can be due to the dilution of river waters with the Baikal waters, where we recorded less diverse composition of bacterial communities, as well as the death of allochthonous microflora exposed to other conditions.

Using the Illumina MiSeq platform, we studied the diversity of microorganisms in rivers, estuarine water areas and the pelagic zone during the under-ice and summer periods. In different seasons, the studied microbiomes showed the dominance of *Cyanobacteria*, *Actinobacteria*, *Proteobacteria*, *Bacteroidetes*, and *Verrucomicrobia*, which are widespread in other freshwater ecosystems (Newton et al., 2011). In the communities, we detected microorganisms involved in various stages of the transformation of organic and inorganic substances. The report will also discuss the difference in the taxonomic composition of microbiomes in the river and estuarine water areas.

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