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TAXONOMIC STRUCTURE OF BACTERIOPLANKTON
OF THE KUIBYSHEV RESERVOIR
(Volga River, Russia)

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The Kuibyshev Reservoir was created in 1957 after the Volga River was dammed near the cities of Zhigulevsk and Togliatti. Since Reservoir inception, heterotrophic bacterioplankton investigation have been conducting. These studies have yielded long-term data on changes in its abundance and biomass. However, until recently, its true taxonomic structure remained unexplored, as only a small portion of the bacterial community is culturable. In 2021, 2023, and 2024, we studied bacterioplankton in the lower part of the reservoir, including both classical methods and metabarcoding based on sequencing data from the hypervariable V4 region of the 16S rRNA gene. Over the entire study period, 3061 non-cyanobacterial OTUs were detected; individual samples contained between 327 and 1349 OTUs (average 782). The combined library recorded 45 phyla of the kingdom Bacteria according to Silva's taxonomy; nine of these included more than 100 OTUs each, but 17 minor phyla contained 5 or fewer OTUs. 283 OTUs remained unassigned even to the phylum level. Based on read abundance, the community was dominated by Pseudomonadota, Bacteroidota, Actinomycetota, Verrucomicrobiota, and Planctomycetota, which together accounted for 90% of non-cyanobacterial sequences. The large proportion of Verrucomicrobiota and Planctomycetota phyla is not typical for large freshwater lakes and reservoirs and is a specific feature of the Kuibyshev Reservoir. The 905 OTUs, whose abundance exceeded 0.1% in at least one sample, clearly constituted the bulk of the bacterioplankton in the studied reservoir. The dominant OTU complex included typical freshwater lineages: *Planktophila*, *Nanopelagicus* (Nanopelagicaceae: Actinomycetota), *Fonsibacter* (Pelagibacteriales: α -proteobacteria), *Limnohabitans* (Comamonadaceae: β -proteobacteria), *Massilia* and several other Oxalobacteraceae (β -proteobacteria). Additionally, taxa associated with various phytoplankton species and cyanobacterial blooms, such as strain UKL13-3 (NS11-12: Bacteroidota), proteobacteria *Roseomonas* and *Sphingorhabdus*, and members of Planctomycetaceae, were prominent. Spatiotemporal analysis revealed no distinct site- or date-specific clusters of bacterial OTUs. The PERMANOVA analysis showed that bacterioplankton taxonomic structure was approximately equally and independently affected by *Chl-a* concentration and sampling month. According to microscopy data, throughout the study period, bacterioplankton biomass (34–361 $\mu\text{g C/L}$) and abundance ($1.5\text{--}12.7 \cdot 10^6$ cells/mL) varied significantly. On average, both indicators increased seasonally from May to August and decreased by September. Solitary free-living cells prevailed in bacterioplankton. Bacteria associated to varying degrees with individual cells or colonies of phytoplankton, were recorded in July–August at all stations. The total bacterial biomass and abundance significantly correlated with the *Chl-a* concentration.

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