



Bacterioplankton community composition of two eutrophic Siberian reservoirs

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Bacterioplankton are among the most abundant and important components of aquatic ecosystems. The taxonomic composition of bacterial assemblages and their spatiotemporal dynamics in freshwater lakes and reservoirs are likely to be of major importance in determining the role of bacteria in aquatic food web and biogeochemistry. The study of bacterial diversity in water habitats has strongly advanced with the recent introduction of molecular techniques.

Using 16S rRNA partial gene sequence analyses we have investigated the bacterial diversity of winter bacterioplankton of two neighbouring eutrophic Siberian reservoirs. The reservoirs are similar in phytoplankton community composition in spring and autumn but tend to differ in summer in exhibiting cyanobacterial bloom. Forty-eight groups of unique partial 16S rRNA gene sequences (OTUs) retrieved from both clone libraries were mostly affiliated with the class Actinobacteria, beta subdivision of the class Proteobacteria, and the phylum Cytophaga-Flavobacterium-Bacteroides. A significant number of bacterial 16S rRNA gene clones including dominant clones were closely related to uncultured freshwater bacteria previously found in different and geographically isolated aquatic ecosystems such as Lake Vostok accretion ice (Antarctica), Toolik Lake (Alaska), high-mountain oligotrophic Crater Lake (Northern America) and Lake Gossenköllesee (Austria), and Lake Baikal deep waters.

Further, during summer seasons of 2000-2001 seasonal dynamics of species composition of free-living bacterioplankton were studied in these reservoirs using 16S rDNA PCR-DGGE technique. Surprisingly, the cluster analysis of the DGGE data did not show any specific difference between bacterioplankton communities of blooming and non-blooming reservoirs. During two summer seasons dominating bacterioplankton

clones were the same in both reservoirs. Sequence analysis revealed that they were similar to the previously detected Crater Lake clone relative and other typical freshwater bacteria. Thus, we can conclude that the development of cyanobacterial bloom in the studied small freshwater reservoir did not cause changes of the composition of dominant heterotrophic bacterioplankton species. It resulted only in a certain increase of diversity of the pelagic bacterial community at the expense of some subdominant bacterial ribotypes.

As found in our studies, species composition of free-living non-cultivated freshwater bacterioplankton appeared to be surprisingly conservative. For instance, similar ribotypes were found in the two eutrophic Siberian reservoirs and diverse aquatic ecosystems, both eutrophic and oligotrophic, of Europe, Antarctica, and Alaska, in unique North American Crater Lake, and Lake Baikal (depth 400 m). Rather different temperature and nutritional conditions, as well as the composition of other biota, yet, don't result in a great difference of bacterial species composition. This striking fact might be due to a great capacity of bacteria for very wide adaptation. This may be also a possible interpretation of our finding that dominant free-living bacterioplankton species are independent of significant ecological changes accompanying cyanobacterial bloom.