

# Seasonal variability of conditionally rare taxa in the water column bacterioplankton community of subtropical reservoirs in China

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## Abstract

Conditionally rare bacteria are ubiquitous and perhaps the most diverse of microbial lifeforms, but their temporal dynamics remain largely unknown. High-throughput and deep sequencing of the 16S rRNA gene has allowed us to identify and compare the conditionally rare taxa with other bacterioplankton subcommunities. In this study, we examined the effect of season, water depth, and ecological processes on the fluctuations of bacterial subcommunities (including abundant, conditionally rare, moderate, and rare taxa) from three subtropical reservoirs in China. We discovered that the conditionally rare taxa (CRT) made up 49.7 to 71.8% of the bacterioplankton community richness, and they accounted for 70.6 to 84.4% of the temporal changes in the community composition. Beta-diversity analysis revealed strong seasonal succession patterns among all bacterioplankton subcommunities, suggesting abundant, conditionally rare, moderate, and rare taxa subcommunities have comparable environmental sensitivity. The dominant phyla of CRT were Proteobacteria, Actinobacteria, and Bacteroidetes, whose variations were strongly correlated with environmental variables. Both deterministic and stochastic processes showed strong effect on bacterioplankton community assembly, with deterministic patterns more pronounced for CRT subcommunity. The difference in bacterial community composition was strongly linked with seasonal change rather than water depth. The seasonal patterns of CRT expand our understanding of underlying mechanisms for bacterial community structure and composition. This implies their importance in the function and stability of freshwater ecosystem after environmental disturbance.

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