



Abstract

# The Bacterial Community and Its Shaping Mechanisms <sup>†</sup>

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**Abstract:** Bacterial activities drive most of the Earth's biogeochemical cycles and, thus, much effort has been devoted to understanding the mechanisms governing their community assemblies in nature. In freshwater ecosystems, selection has been found to be the main driver shaping bacterial communities. However, its relative importance compared with other processes (including dispersal, drift, and diversification) may depend on the spatial heterogeneity and the dispersal rates within a metacommunity. Here, we investigate the main ecological processes modulating bacterial assembly in the eutrophic shallow lakes of the pampa plain (Argentina) across spatial scales (regional, watershed, and local). To do this, 52 shallow lakes with contrasting limnological features and alternative states were studied. The bacterial composition was analysed using high-throughput sequencing (*Illumina Miseq* technology) of the 16S rDNA V4 region, and statistical inferences based on the phylogenetic and taxa turnover were applied. Based on this analysis, ASVs (amplicon sequence variants, unique DNA sequences obtained from massive sequencing) with a strong association with hypersaline environments and turbid water regimes were observed. In addition to this, processes such as dispersal and drift had a greater importance than that of selection, as expected in theory.

**Keywords:** bacterial; ecology; lakes; metagenomics



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