

Abstract

Bacterial Community and Its Shaping Mechanisms †

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

Keywords: bacterial; ecology; lakes; metagenomics

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