

Variation in coastal Antarctic microbial community composition at sub-mesoscale : spatial distance or environmental filtering?

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Abstract

Spatial environmental heterogeneity influences diversity of organisms at different scales. Environmental filtering suggests that local environmental conditions provide habitat-specific scenarios for niche requirements, ultimately determining the composition of local communities. In this work, we analyze the spatial variation of microbial communities across environmental gradients of sea surface temperature, salinity and photosynthetically active radiation and spatial distance in Fildes Bay, King George Island, Antarctica. We hypothesize that environmental filters are the main control of the spatial variation of these communities. Thus, strong relationships between community composition and environmental variation and weak relationships between community composition and spatial distance are expected. Combining physical characterization of the water column, cell counts by flow cytometry, small ribosomal subunit genes fingerprinting and next generation sequencing, we contrast the abundance and composition of photosynthetic eukaryotes and heterotrophic bacterial local communities at a submesoscale. Our results indicate that the strength of the environmental controls differed markedly between eukaryotes and bacterial communities. Whereas eukaryotic photosynthetic assemblages responded weakly to environmental variability, bacteria respond promptly to fine-scale environmental changes in this polar marine system..

Keywords

Spatial variation, Antarctica, Microbial community, Environmental filtering, Submesoscale, Community composition.