

THE STRUCTURE OF PLANKTONIC BACTERIAL COMMUNITIES FROM THE
NUTRIENT RICH COAST OF CHILE TO THE ULTRA OLIGOTROPHIC SOUTH
PACIFIC SUBTROPICAL GYRE

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ABSTRACT

Despite the presence of steep temperature and nutrient gradients hypothesized to influence microbial communities, the South East Pacific remains one of the most sparsely sampled oceanic regions from a biological and biogeochemical perspective. In this study, DNA samples collected from the upper 1000 meters from the coast of Chile to Easter Island during the Biogeochemical Gradients: Role in Arranging Planktonic Assemblages cruise were sequenced on the Illumina MiSeq platform. A total of 10,106,053 quality 16S rRNA gene sequence reads are contained within this Illumina dataset. Sequence analyses using the Quantitative Insights Into Microbial Ecology pipeline showed that *Gammaproteobacteria* (24.5%), *Cyanobacteria* (23.0%), *Alphaproteobacteria* (16.0%), and *Bacteroidetes* (12.0%) were the most abundant bacterial groups in the South East Pacific. Statistical analysis revealed differences in microbial communities of the euphotic zone (0.1% photosynthetically available radiation level and above) and aphotic zone (below 0.1% photosynthetically available radiation level) (PERMANOVA: $P < 0.0001$). Additionally, pairwise analyses between sampling stations across the cruise transect revealed greater differences between stations in the euphotic zone than the aphotic zone. The results open up the possibility of conducting studies focusing on individual microbial groups and their roles in biogeochemical cycles.