

**SPATIAL DISTRIBUTION OF BACTERIOPLANKTON LINEAGES ALONG A
MERIDIONAL TRANSECT OF THE PACIFIC OCEAN**

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Abstract

The Pacific Equatorial Divergence Zone is characterized by macronutrient fluxes in excess of the requirement for new primary production, and has been widely studied due to its importance to the global carbon cycle. Understanding the planktonic bacterial community structure in this habitat is an important key to understanding nutrient cycling, carbon flux, and trophodynamics. One way to decipher what ecological niches particular bacterioplankton groups are exploiting is to characterize the bacterial community structure and relate it to the ambient environmental conditions. As part of the Center for Microbial Oceanography: Research and Education (C-MORE) Biogeochemistry of the Upper ocean: Latitudinal Assessment (BULA) cruise, molecular microbial ecology methods were used to investigate the relationship between bacterial communities and the surrounding environment in the Equatorial Pacific Ocean between Suva, Fiji and Honolulu, Hawaii in April 2007 during non-El Nino conditions. At nine latitudes, water column depth profiles spanning the surface to 1000 m were sampled for nucleic acids, inorganic nutrients, conductivity, temperature, oxygen, direct cell counts, and photopigments. Terminal restriction fragment length polymorphism (T-RFLP) and cloning and sequencing of bacterial 16S rRNA gene sequences were used to characterize the bacterial community. Community fingerprint data resulting from the T-RFLP analyses were used to correlate patterns in bacterial community structure with the surrounding environment, and explain the distributions of several abundant bacterial lineages. Surface ocean bacterial communities from approximately 3.0°S latitude to 9.0°N latitude were more closely related to each other than to communities sampled in the gyres north or south of those latitudes. Interestingly, surface ocean bacterial communities from the North and

South Pacific gyres were significantly similar, despite the seasonal difference between hemispheres. The *Alphaproteobacteria* lineage SAR11 subgroup IA dominated the equatorial surface ocean, while SAR11 subgroup II dominated below 100 m. The oxygen minimum zone in the northern hemisphere contained a distinct community, with an abundance of a *Deltaproteobacteria* lineage related to the nitrite oxidizing genus *Nitrospina* and relatives of the uncultured *Gammaproteobacteria* lineage ARCTIC96BD-19.

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