

SPATIAL VARIABILITY IN PLANKTON SIZE STRUCTURE AND COMMUNITY
COMPOSITION ALONG BIOGEOCHEMICAL GRADIENTS IN THE PACIFIC
OCEAN

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ABSTRACT

The size structure of upper ocean plankton assemblages appears to play an important role in determining the efficiency of the biological carbon pump and the resulting magnitude of biologically-mediated carbon export to the deep sea. To evaluate spatial variability in the size structure and community composition of plankton assemblages in the upper ocean measurements of size-fractionated chlorophyll *a* (Chl *a*), phycoerythrin and adenosine 5'-triphosphate (ATP) concentrations along with picoplankton abundances and taxonomic pigment biomarkers were assessed during the BEACH-BASH transect cruise from American Samoa to Honolulu, Hawaii in March 2005. Sampling for this study spanned four different biogeochemical provinces including the oligotrophic South Pacific Subtropical Gyre (SPSG), the relatively nutrient-enriched equatorial upwelling provinces, the Pacific Equatorial Divergence (PEQD) and the North Pacific Equatorial Countercurrent (PNEC), and the oligotrophic North Pacific Tropical Gyre (NPTG). Overall, nutrient concentrations were highest in the PEQD province, coinciding with the strong westerly South Equatorial Current (SEC) and the region of equatorial upwelling, and lowest in the SPSG and NPTG. Chl *a* and phycoerythrin concentrations throughout the transect were overwhelmingly dominated by picoplankton (0.2-2 μm), accounting for 45 - 60 % of the total Chl *a* and 80 - 95 % of the total phycoerythrin throughout the transect. Flow cytometry measurements indicate that the picoplankton community composition was dominated by cyanobacteria of two genera; *Prochlorococcus* spp. and *Synechococcus* spp. and these groups accounted for most of the Chl *a* biomass throughout the transect. Picoeukaryotes also contributed to picoplankton abundances; however

despite the likelihood of many species being present they remain largely unidentified. Total microbial biomass estimates via particulate ATP (P-ATP) measurements showed high variability with the occasional occurrence of larger heterotrophic organisms (>20 μm and 2-10 μm) which are not accounted for in Chl *a* biomass estimates. However, their distribution is sure to play an important role in regulating size structure and food web dynamics. Measurements of taxonomic pigment markers by HPLC confirmed the overwhelming dominance of prochlorophytes and cyanobacteria throughout the transect, however a transition in community composition in the PEQD province was observed. This transition was attributed to the increase in taxonomic pigment markers of chromophyte microalgae (i.e. prymnesiophytes, pelagophytes and diatoms).