# Microbial Community Structure in the Amazon River Plume

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## Abstract

The Amazon River discharges more than 200,000 m3 s-1 into the Western Tropical Atlantic Ocean from May to June. The low salinity surface plume extends more than 1800 km from the mouth and covers an area greater than 1 million square kilometers. We hypothesize that the plume exhibits distinct microbial community assemblages driven by plume age, nutrient supply, and light availability. We collected samples for nutrients and flow-cytometry measurements to investigate the spatial variability of the cyanobacteria Prochlorococcus spp. and Synechococcus spp., picoeukaryotes, and heterotrophic bacteria. Overall the surface salinity of the water we sampled ranged from 15.5 ppt at the southernmost station to 36.3 ppt in the open ocean station. The surface nitrate and soluble reactive phosphorus concentrations ranged from below detection limit to  $3.3 \,\mu\text{M}$  and  $2 \,\mu\text{M}$ , respectively. Generally, in the freshest surface plume waters (15-28 ppt) we found the highest abundances of Synechococcus spp., picoeukaryotes, and hetrotrophic bacteria with little or no Prochlorococcus spp. In the transition of surface salinities from 28 ppt to 32 ppt, a population of Prochlorococcus spp. began to form below the surface plume while Synechococcus spp. abundances at the surface remained unchanged and picoeukaryotes, and heterotrophic bacteria abundances decreased. As the surface salinity climbed over 32 ppt, the Prochlorococcus spp. abundance was uniformly high throughout the euphotic zone. On the other hand, as surface salinities increased over 32 ppt Synechococcus spp. abundances at the surface gradually decreased, while picoeukaryote and hetrotrophic bacterial abundances remained constant. We will discuss changes in the microbial community composition as a function of nutrient and light availability, as well as plume age in the Amazon Plume-Ocean continuum in both surface and deep chlorophyll maximum assemblages.

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