**Influence of Habitat on Diversity and Evolution of Surface Ocean Microbes**

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**Project Goals:**
The development of computational tools to assess and compare marine metagenomic samples on the basis of phylogenetic and functional diversity, and to examine genome level adaptations to resource availability in different size classes of marine bacteria. The Global Ocean Survey (GOS) continues to sample and analyze marine microbial life around the world from the Sorcerer II research vessel. Comparisons of microbial populations in the Indian Ocean to those found during GOS phase I have resulted in a better understanding of variation in ecological niches available in marine surface waters.

**Abstract:**
In open ocean pelagic ecosystems bacterial cells account for approximately half of the organic biomassand bacterial activity is responsible for consumption of a large fraction of photosynthetically-derived carbon. Genomic adaptations that underlie bacterial physiological adaptations to environmental gradients such as latitude, temperature, productivity, and particle association have not been clearly elucidated on a large scale. Through analyses of metagenomic data derived from size-fractionated bacterial communities, large scale phylogenomics, and genome size-normalized analyses of genomic contents we elucidate several fundamental adaptations to environmental gradients in the surface ocean. Our results show that marine bacterioplankton in the surface ocean adapt to environmental variability in three ways; molecular-level alterations, changes in overall genomic content, and transitions in community structure. We report on the influence of habitat on genomic properties such as estimated genome size, gene family composition, transporter repertoire, and carbon to nitrogen ratio of the predicted proteome. Small free-living picoplanktonic open-ocean bacterioplankton compared to coastal, larger size-class, or particle associated bacteria have smaller genomes that are enriched for transporters, depleted in regulatory components and encode a proteome with relatively less nitrogen content. Overall patterns of diversity and richness are significantly higher for bacterial communities collected on larger pore-size filters. Intra- and inter-relationships between sites based on diversity measures suggest

that larger size class or particle-associated bacterial communities and those that inhabit more productive waters are significantly more variable.

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