Influence of Nutrients and Currents on the Genomic Composition of Microbes across an Upwelling Mosaic

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Project Goals:
Our basic research program focused on acquisition and analysis of marine microbial metagenomic data and development of genomic analysis tools for broad, external community use. Our Marine Metagenomic Diversity effort generated and analyzed shotgun sequencing data from microbial communities sampled from >260 sites around the world. Starting in the summer 2007 and continuing until the winter of 2008, we initiated a series of sampling efforts focused on the Southern California Bight and California Current Ecosystem in collaboration with several groups. In the summer of 2007, this cruise was done in collaboration with the California Cooperative Oceanic Fisheries Investigations (CalCOFI) group to evaluate metagenomics at select areas characterized by coastal upwelling. These samples are a contrast to the primarily open ocean sites of the GOS expedition due to the upwelling of nutrient rich deep waters that enable an increase in primary production at the surface.

Abstract:
Metagenomic datasets were generated from samples collected along a coastal to open ocean transect between Southern California Bight and California Current waters during a seasonal upwelling event, providing an opportunity to examine the impact of episodic pulses of cold nutrient rich water into surface ocean microbial communities. The dataset consists of approximately 5.8 million predicted proteins across seven sites, from 3 different size classes: 0.1-0.8μm, 0.8-3.0μm, and 3.0-200.0μm. Taxonomic and metabolic analyses suggest that sequences from the 0.1-0.8μm size class correlated with their position along the upwelling mosaic. However, taxonomic profiles of bacteria from the larger size classes (0.8-200μm) were less constrained by habitat and characterized by an increase in Cyanobacteria, Bacteroidetes, Flavobacteria, and dsDNA viral sequences. Functional annotation of transmembrane proteins indicate that sites comprised of organisms with small genomes have an enrichment of transporters with substrate specificities for amino acids, iron and cadmium; whereas, organisms with larger genomes have a higher percentage of transporters for ammonium and potassium. Eukaryotic-type

glutamine synthetase (GS) II proteins were identified and taxonomically classified as viral, most closely related to the GSII in Mimivirus, suggesting that marine Mimivirus-like particles may have played a role in the transfer of GSII gene functions. Additionally, a Planctomycete bloom was sampled from one upwelling site providing a rare opportunity to assess the genomic composition of a marine Planctomycete population. The significant correlations observed between genomic properties, community structure, and nutrient availability provide insights into habitat-driven dynamics among oligotrophic versus upwelled marine waters adjoining each other spatially.

Publications:

In Press Lisa Zeigler Allen, Eric E. Allen, Jonathan H. Badger, John P. McCrow, Ian T. Paulsen, Liam D. H. Elbourne, Mathangi Thiagarajan, Doug B. Rusch, Kenneth H. Nealson, Shannon J. Williamson, J. Craig Venter, Andrew E. Allen. Influence of nutrients and currents on the genomic composition of microbes across an upwelling mosaic. *ISME Journal.*

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