

Oceanography Seminar

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“Towards Four Dimensional Microbial (Eco)Systems Biology in the Sea”

Microbial communities regulate the cycling of energy and matter in the marine environment, yet the details of how they interact with one another, respond to environmental change, and how their activities vary in space and time, are not well understood. Genomic methods and allied technologies are now providing new perspective on the distribution of microbial taxa, genes, and processes in the marine environment. One of the larger challenges remaining is defining the dynamics and interactions of microbial taxa, gene and process distributions on appropriate spatial and temporal scales. How do microbial metabolic activities and interactions of specific planktonic microbial populations vary over the course of minutes, hours, days and weeks? Over what spatial scales? Put another way, exactly what does a typical “day in the life” of wild planktonic microbial species look like? We are leveraging Lagrangian survey strategies that employ robotic sampling techniques, and coupling these surveys with community-wide microbial gene expression analyses in wild planktonic microbial populations, to help answer some of these questions. Results using such approaches show that in surface waters, individual populations, as well as very different bacterial and archaeal species, display remarkably similar, time-variable patterns of synchronous gene expression over extended periods of time. These new results suggest that specific environmental cues may elicit cross-species coordination of gene expression among diverse microbial groups, that has potential to enable multispecies coupling of metabolic activities. We are currently trying to understand how such temporal compartmentalization of metabolism among different species might regulate matter and energy flux and biogeochemical cycles over time. Our results suggest that coupling genome-enabled technology with new robotic approaches in observational oceanography has great potential to advance understanding of the inner workings of complex planktonic microbial communities.

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