Metatranscriptomic insights into microbial behavior in the wild

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Community transcriptome analysis, or metatranscriptomics, is providing new insights into microbial behavior in the environment. We are pairing collection of metatranscriptomic time series with population-based bioinformatic analyses. This approach allows us to generate time-resolved whole genome transcriptome profiles of multiple, naturally co-occurring bacterial populations. In this seminar, I will describe the collection and analysis of two high-resolution, multi-day time series of transcriptional activity among microbes in coastal and open ocean surface waters.

In both time series, transcriptional analysis of abundant phytoplankton revealed strong diel periodicity in gene expression. However, the heterotrophic populations of these two environments showed distinct behavioral patterns. In the coastal time series, no obvious diel trends in the transcriptional activity of abundant heterotrophs were detected, but these groups did exhibit synchronous variation in gene expression, suggesting a coordinated response to environmental cues. In the open ocean time series, heterotrophic populations did exhibit diel periodicity in expression of many metabolic transcripts, suggesting entrainment to solar cycles and/or the activities of co-occurring phytoplankton. Together, these data show that microbial community RNA-seq supplemented by analyses that focus on the behavior
of individual taxa can provide significant new insight into microbial community function.