## Spatial and Temporal Patterns of Free-Living Microbial Community Diversity in Narragansett Bay, RI

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Microbes play pivotal roles in marine ecosystems such as in biogeochemical cycling (i.e carbon and nitrogen cycles) along with animal and human health. Narragansett Bay is a well-mixed estuary that supports diverse habitats from salt marshes to shellfish reefs and is both ecologically and economically important. While many of the important processes occurring in the bay are mediated by microbes, little is known about the taxonomic composition or function of the microbial communities. Here, we apply 16S rRNA community profiling to examine the spatial and temporal patterns of microbial diversity in the surface waters throughout Narragansett Bay. The free-living fraction of microbes (0.22-5.0 micron) in the water column was sampled from seven sites across the mid and lower bay from September 2017 to August 2018. The V4 region of the 16S rRNA gene was targeted using Illumina MiSeq sequencing for the identification of community profiles. From this study, several major taxa were identified across all samples, including the Alphaproteobacteria, Gammaproteobacteria, Bacteroidetes, and Verrucomicrobia. Initial results indicate potential correlations of the alpha and beta community diversity with sampling months rather than sites. Although only one year of sampling has been completed, a potentially reproducible community structure (by season) through beta diversity analyses has been identified that calls for additional analysis. Ongoing analyses include the identification of abundant and variable taxa by month. For example, there is a significantly higher relative abundance of the genus Vibrio in the month of August. Understanding the identity of the microbes in Narragansett Bay is the first step in elucidating their functions in ecologically and economically relevant processes.