

Characterization of bacteriophage diversity in Narragansett Bay, RI during a winter-spring algal bloom

Faith Brown, Zachary Pimentel, Alexa Sterling, David Banks-Richardson, Bethany Jenkins, Tatiana Rynearson & Ying Zhang

University of Rhode Island

Bacteriophages (viruses that infect bacteria) play important roles in regulating community dynamics of ecologically important bacteria in marine ecosystems. However, little is known about the dynamics of bacteriophage communities in Narragansett Bay (NBay), RI. Previous analysis of NBay bacterial communities during a historically large winter-spring phytoplankton bloom in 2018 revealed decreased bacterial community diversity in response to the bloom. Here we examine the community response of bacteriophage through the same bloom period. In order to evaluate the structure of bacteriophage communities, VirFinder was applied to a shotgun metagenomic co-assembly from the 0.2 -5 μm fraction of surface waters during a winter-spring algal bloom in 2018. Of all of the assembled contigs, 22% (over 300,000) were predicted to be from bacteriophages. Across all 12 samples in the co-assembly, there was a mean bacteriophage relative abundance of $16.2 \pm 2.1\%$. Similar to what was observed in bacterial communities, decreased alpha diversity, measured with Shannon and Simpson diversity indices, was observed during the bloom. Further work to profile the taxonomic identity and functional potential of these bacteriophages will help to reveal their significance to the ecologically and economically important NBay ecosystem.