2019

Surveying Apicomplexan Diversity and Dynamics in Narragansett Bay

Evelyn Spencer
evelynspencer11@my.uri.edu

Follow this and additional works at: https://digitalcommons.uri.edu/srhonorsprog

Part of the Biodiversity Commons, Bioinformatics Commons, Biology Commons, and the Genetics and Genomics Commons

Recommended Citation
https://digitalcommons.uri.edu/srhonorsprog/710

This Article is brought to you for free and open access by the Honors Program at the University of Rhode Island at DigitalCommons@URI. It has been accepted for inclusion in Senior Honors Projects by an authorized administrator of DigitalCommons@URI. For more information, please contact digitalcommons@etal.uri.edu.
INTRODUCTION:
Parasites play an important role in marine ecosystems and their diversity is generally understudied. Apicomplexans, a group of parasitic protists in the phylum Alveolata, infect a wide variety of animal hosts and are abundant in ecosystems spanning from Polar Regions to Neotropical rainforests. Previous data generated from marine sediments in Antarctica, Naples Bay, and off the coast of Oslo, exhibit high diversity and numbers of apicomplexans. The effects apicomplexans have on their hosts can be dramatic. The genus of Plasmodium causes Malaria, a leading contributor to human mortality with an estimated 430,000 deaths in 2015 alone. While we know many species inhabit soil environments, a full investigation into their biodiversity is necessary.

OBJECTIVES:
Abundance and diversity of these protists are unknown for Narragansett Bay, despite the fact that they infect many commercially important species. To determine abundance of apicomplexans in Rhode Island marine ecosystems, sediment samples were collected from 10 sites from Charlestown to Newport. These data were used as a baseline analysis for Rhode Island marine sediments and were compared to other areas of the world to determine where apicomplexan abundance and diversity is highest in Rhode Island.

Of the species of apicomplexans observed in sediment communities in Narragansett Bay, gregarines (Figure 1) are a subclass that are generally understudied. Looking at these species of apicomplexans, fluorescence in situ hybridization (FISH) probes will be designed to specifically target small portions of the gregarine genome.

METHODS:
Sediment and water samples were collected from fifteen sites around Narragansett Bay and the Matunuck to Charlestown coastline. Samples were filtered through 12.0 and 0.4 micron polycarbonate membrane filters using a peristaltic pump and placed into DNA/RNA shield.

DNA extracted using the NucleoSpin Soil Kit by Macherey-Nagel.

The V3 region of the 18S RNA gene was amplified from the DNA using PCR protocols designed specifically for a clade that includes Stramenopiles, Alveolata, and Rhizaria (SAR).

Amplified DNA was sequenced on the Illumina MiSeq Next Generation Sequencing.

Data analyzed using QIIME2 (vr. 2018.8), SILVA (vr.128), and R (vr.3.5.1).

REFERENCES:

ACKNOWLEDGMENTS:
Sequencing of some material was funded by the National Science Foundation under EPSCoR Cooperative Agreement #OIA-1655221 and a scholarship awarded by the Undergraduate Research and Innovation Office.
Abundance and diversity of apicomplexans, parasitic protists in the phylum Alveolata, are unknown for Narragansett Bay despite the fact that they infect almost all commercially important species. Sediment samples were collected from 10 locations across Charlestown to Newport and filtered through a peristaltic pump. DNA was extracted and the V3 region of the 18S gene was amplified using primers specifically for a clade including Stramenopiles, Alveolata, and Rhizaria (SAR). Figure 1 includes photos of two sampling locations and an image of a microscopic gregarine, an understudied group of apicomplexans. Figure 2 visualizes diversity of the SAR clade at each of the 10 sampling locations, highlighting apicomplexan abundance. The abundance of apicomplexan sequence reads found in the bay sediment data ranged from 0-60% of SAR, depending on filtration methods and location. Matunuck beach and Charlestown Breachway exhibited the highest abundance of apicomplexan sequence reads, and both locations consisted of a sand/silt sediment mix and were located in an estuarine environment. Charlestown beach, King's beach, and Hulls cove in Jamestown showed the lowest abundance of apicomplexans in their sandy, rocky sediment environments. The species composition of the apicomplexans at each site are displayed in Figure 3, with Novel Apicomplexa Class 1 exhibiting the highest abundance in Charlestown Breachway, GSO pier, Matunuck Beach, and Ninigret Pond. Future research to identify undescribed apicomplexans within host species is ongoing and will help model parasite dynamics among commercially relevant species.