

Taxonomic and Functional Profiling of the Microbiome of the Eastern Oyster, *Crassostrea virginica*

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As an ecosystem engineer in marine environments, the reef-forming eastern oyster, *Crassostrea virginica*, provides habitat to other organisms and is involved in the deposition of organic matter to the surrounding sediments. Therefore, oyster population dynamics have profound impacts on the nutrient cycling and carbon flow to coastal sediments and higher trophic levels. Despite their high filtration rate (and hence high rate of encountering microbes from the water column), eastern oysters harbor a distinct microbiota from the surrounding seawater. While the taxonomic composition of the microbiota has been explored in prior studies, little is known about the tissue-specific composition of oyster microbiomes and the potential functional roles they play in mediating the health of oyster populations.

Using 16S rRNA sequencing to profile tissue-specific microbial communities of individual oysters carrying varying loads of the protozoan pathogen *Perkinsus marinus*, we first identified core taxa associated with different tissue types and observed potential correlations between taxa abundance and *P. marinus* infections. Global analysis of the taxonomic profiles also revealed a more distinct microbiome in the digestive tract compared to the gill, mantle, shell, hemolymph, and pallial fluid. In order to probe the functional roles of the digestive tract microbiome, shotgun metagenomic sequencing was then performed which led to the identification of over 200 metagenomic bins, including two high quality metagenome assembled genomes (MAGs) representing uncultured strains of Mollicutes and Chlamydiae. Detailed functional analysis of the MAGs revealed genes involved in potential host associations, with machinery in the Mollicutes MAG mediating binding to the host epithelium layers and genes in the Chlamydiae MAG mediating interactions with the host immune system.

Further study of host-microbe interactions will enable our understanding of host physiology, population dynamics, and ecosystem processes related to oyster microbiome functions in Rhode Island's coastal waters.