Oysters and Microbes and Narragansett Bay, Oh My!

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Oysters are keystone species in the coastal environment and play a crucial role in nutrient cycling and improving water quality for other marine organisms and humans. As estuarine organisms, they are subject to fluctuating environmental conditions, including nutrient loading, runoff, pollution, and anoxia, that impact their health and function. A potential mechanism of acclimation in oysters is the recruitment of diverse microbial communities.

Our research seeks to characterize adult oyster microbiomes and health at 7 sites along an estuarine nutrient gradient in Narragansett Bay using histology, qPCR detection of specific pathogens, and 16S rRNA amplicon sequencing. Adult oysters were collected from ambient conditions at all 7 sites, along with oysters treated with additional fertilizer (to simulate nutrient loading) at 2 of the sites located in Point Judith Pond. Tissues (gut, inner and outer shell biofilms) were processed and DNA was extracted for disease analysis and microbiome sequencing. As expected, a strong North to South estuarine gradient was observed in the Bay, with increasing salinity, pH, and dissolved oxygen, and decreasing nitrate, nitrite, and phosphate concentrations. Differences in several oyster health parameters, including prevalence of the parasite *Perkinsus marinus,* were detected between sites, and the highest disease levels were seen at the site with the highest ammonium concentration and salinity. Within the Point Judith sites, oysters exposed to a high nutrient load showed a significant change in their ability to denitrify, as well as changes in the microbial composition in oyster gut, suggesting that this change in denitrification is mediated by the gut microbiome.

Further analysis is focused on determining: a) how the oyster host and its microbiome interact to respond to estuarine conditions; b) how microbial composition and function differ within different tissues of an oyster using metatranscriptomics; and c) changes in expression of microbial genes associated with nitrogen cycling processes.