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Exploring the Effects of Hypoxia on Sulfate Reducing Anaerobes

Annaliese K. Jones

Sponsor: Bethany Jenkins, Cell and Molecular Biology

As a student about to graduate with a degree in Biological Sciences, I find myself faced with the need to find my own independent research interests and scientific voice. As a result of my interests in the fields of both microbiology and ecology, I am drawn to questions surrounding the role and behavior of microorganisms in the environment. With climate change being an issue capturing the attention of a large portion of the scientific community, I have chosen to focus my attention on environmentally active microbes that reside in estuarine sediments, specifically Narragansett Bay, RI. These microbes may be affected by periods of marine hypoxia (defined by the Environmental Protection Agency as oxygen concentrations lower than 2 mg of O₂/L of H₂O). Hypoxia results from a combination of factors including nutrient loading, and stratification of the surface water from freshwater riverine inputs and warm surface water temperatures. These conditions promote phytoplankton blooms and subsequent oxygen depletion when dead phytoplankton biomass falls to sediments and is consumed by microorganisms that respire O₂ as part of their metabolism. Climate change has been shown to exacerbate the problem of hypoxic ocean waters by increasing stratification and warming as well as by causing large changes in rainfall patterns, enhancing runoff of freshwater and nutrients to coastal ecosystems. Microbes residing in marine sediments impacted by hypoxia are responsible for a significant portion of the global cycling of nutrients, processes critical for life on land as well as in the ocean. Given these facts, I am particularly interested in how hypoxia impacts microbes that are involved in the cycling of sulfur (S) and in the cycling of nitrogen (N) in sediments from Narragansett Bay that experience seasonal hypoxia.

Previous research conducted in Dr. Jenkins' lab has revealed that a gene involved in N fixation, *nifH*, is highly expressed only during periods of hypoxia. When this gene was sequenced it was discovered that the environmental samples from Narragansett Bay were most closely related to those from groups of sulfate reducing bacteria. This led me to question the effects of hypoxia on sulfate reducing bacteria, if the processes of nitrogen fixation and sulfate reduction would display a link, and to determine the phylogenetic relationship of active S reducers to active N fixers.

With this previous research serving as a point of comparison, I have chosen to examine the presence and expression of *dsrB*, a gene involved in the sulfate reduction pathway, during periods of seasonal hypoxia in Narragansett Bay, RI. I have done this by using molecular techniques (examining both the presence (DNA) and expression (RNA) of *dsrB*) to account for change bacterial sulfate reduction during periods when nitrogen fixers are expressing their genes. Sequence data from this gene (*dsrB*) was also used to identify the organisms responsible for sulfate reduction in Greenwich Bay. Results show a relationship between communities responsible for both processes based on gene expression and comparative community composition.

Keywords: environmental microbiology, nutrient cycling bacteria, gene expression, hypoxia, climate change