

Letters of Intent: Endeavour
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Biogeochemistry of Methane at Deep-Sea Hydrothermal Vents; a Comparative Study at Juan de Fuca and EPR vents

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Abstract:

Hydrothermal venting is a major source of methane to the ocean. Endmember concentrations for methane in vent fluids from hydrothermal vents (e.g., East Pacific Rise, Galapagos Spreading Center, Guaymas Basin, and Southern Juan de Fuca Ridge) can range from 10^5 - 10^7 times higher than methane concentrations in ocean bottom water. Being less dense than the surrounding seawater, hydrothermal fluids from high temperature "black smokers" form buoyant plumes that rise until neutral buoyancy is achieved, usually hundreds of meters above the sea bottom. However, previous studies have shown CH₄/3He ratios in lateral plumes have shown that plume CH₄ is lost more rapidly than can be accounted for by dilution with ambient seawater along the length of the plume's path, indicating that methane oxidation may be responsible for the removal of methane. Methanotrophic bacteria are the only organisms known to be capable of converting methane into cell carbon or CO₂. While methane oxidation has been measured in the hydrothermal plumes of Endeavour Segment of the Juan de Fuca Ridge have been reported, little is known about the abundance, diversity, or growth and metabolism of the microorganisms responsible for this important phenomenon,

We propose a comparative study of methane dynamics and methanotroph diversity at hydrothermal vent habitats at Juan de Fuca and East Pacific Rise (EPR). We will use a variety of gas probe devices deployed from submersibles for multiple measurements of in-situ dissolved methane gas concentration gradients in deep-sea water columns. These will be taken in conjunction with concurrent un-decompressed sample collections (in sealed cylinders) for measurement of methane oxidation rates and molecular analyses of methanotrophs. Corresponding collection of samples will allow for studies of the molecular ecology of methanotrophic bacteria based on methanotroph-specific 16S rRNA gene and functional gene sequences.

The key scientific questions to be addressed in this proposal include:

- What are the sources and concentrations of methane supporting the methanotrophic bacterial communities? - What are the incidence and phylogenetic diversity of methanotrophic bacteria in methane-rich hydrothermal plumes under different temperatures, redox potentials, and methane concentration gradients?
- How do the methanotrophic bacterial communities change over time with variations in temperature, redox potentials, tidal perturbations and other temporal cycles?

Methanotrophic bacteria are an environmentally important group due to their role in the global methane cycle and potential for use in climate change mitigation efforts. Their role in methane cycle of deep-sea hydrothermal vents has been implicated by measurements of methane oxidation, but little is known about their distribution relative to methane concentrations, their diversity and relative importance in the vent ecosystems. In depth studies of methane concentrations and oxidation rates, as well as methanotroph diversity at the group and genus level are now possible with advances in sampling and molecular analyses. The comparative and collaborative research proposed here will make significant contributions to our understanding of the diversity and abundance of these organisms in the vent environment and provide estimates of the importance of CH₄ cycling in the deep-sea.