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Microbial ecology of seafloor communities at deep-sea hydrothermal seamounts

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Circulation of hydrothermal fluids and seawater occurs within the upper 500 m of porous oceanic crust and provides a rich environment for microbial growth in the seafloor. Enrichment cultures, geochemical indicators, and sequence analyses of PCR amplicons of ribosomal RNA genes demonstrate that these crustal fluids host a microbial community composed of organisms indigenous to the seafloor, including anaerobic thermophiles and mesophilic sulfur oxidizers, and organisms from other deep-sea habitats, such as seawater. However, the seafloor microbial communities remain undersampled and our knowledge of what microbes are present and how they are distributed in this dynamic geochemical environment over time and space is fragmentary.

This work focuses on determining the microbial diversity and genomic content of the seafloor microbial community at geographically and geochemically distinct deep-sea hydrothermal seamounts. The approach uses a combination of methods, including the application of 454 tag sequencing, metagenomics, culturing, and geochemical methods to diffuse fluids from deep-sea hydrothermal seamounts. Diffuse vent fluid samples are being collected from three locations: Axial Seamount, an active submarine volcano on the Juan de Fuca Ridge in the Northeast Pacific Ocean (45.92° N, 130° W); seamounts along the Mariana Arc (14-22° N, 143-146° E) in the Western Pacific; and Loihi Seamount (18.92° N 155.27° W), located 30km southeast of the big island of Hawaii. All three locations, Axial, Loihi, and the Mariana Arc, are recently eruptive seamounts located above 2000 m and host diffusely venting fluids with high concentrations of carbon dioxide. However, their geological and chemical setting differs greatly; Axial is a mid-ocean ridge seamount with fluids dominated by high concentrations of hydrogen sulfide, Loihi is a mid-plate hotspot seamount with extremely high concentrations of dissolved iron (FeII), and the Mariana seamounts are at a convergent plate boundary and host a variety of fluids, including those with very low pH and high concentrations of particulate sulfur.

Questions to be addressed include, what is the distribution and relative abundance of microbial lineages in the seafloor environment? Is there a core set of lineages or genes specific to the seafloor environment? How do genes and lineages compare in different environments and are there unique lineages or genes at individual sites? If so, how are they linked to distinct parameters at that site? Finally, what is the extent of horizontal gene flow in the seafloor and how does this gene flow shape microbial lineages and their adaptation to this unique environment? Pilot studies at Axial Seamount have begun with the construction of fosmid libraries and 454 sequencing of PCR amplicons that span the V6-hypervariable region of ribosomal RNAs from two diffuse flow vents. The collection of this suite of samples and application of a combination of methods will allow us for the first time to look at the distribution and abundance of seafloor microbial communities at geographically and geochemically distinct deep-sea hydrothermal seamounts across the Pacific Ocean.