

## **The Microbial Biogeography of Deep-Sea Hydrothermal Vents: Mapping the Landscape of Active Microbial Communities Across Space, Time, and Fluid Dynamics**

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The deep-sea hydrothermal vent biosphere is fed by reservoirs of geothermal energy, which are expelled as reduced fluids that interact with seawater to generate redox gradients, fueling microbial metabolism. This study executes a survey of diversity along thermal and redox gradients as a function of age, vent site, and biological regime. Microbial biomass was collected via sampling of fluids, young biofilms from experimental colonization devices, and mature biofilms from scrapings of invertebrates and substrate-seawater interfaces. Deep-sequencing of 16S rRNA transcripts generated from the samples revealed that fluids circulating in the shallow subsurface contain predominantly Epsilonproteobacteria of the genera *Sulfurovum* and *Sulfurimonas*, a subpopulation of which is found in the colonization devices, likely representing the portion of microbes flushed from the subsurface able to form biofilms at the seafloor. Epsilons on colonizers decreased as a function of temperature and H<sub>2</sub>S concentration, while Bacteroidetes (approx. 13-25% of population) were shown to correspond with age of the biofilm, and may likely represent part of the primary consumer community. Mature biofilms from scrapings showed an overall increase in diversity, with the presence of additional taxa including Gamma-, Deltaproteobacteria and Bacteroidetes. Community diversification in mature biofilms could reflect the settlement of successive species, including mixotrophic and heterotrophic microbes feeding on fixed carbon generated by the chemolithoautotrophic primary producers. Further analyses into the metabolic potential of each microbial order of succession will provide insight into the biogeochemical cycling at deep-sea vents from the birth of a vent site to the formation of a complex community.