

Metaproteomics Reveals the Metabolic Pathways of Active Chemoautotrophic Communities at Crab Spa, a Diffuse-Flow Deep-Sea Vent site at 9°N EPR

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Chemosynthetic microorganisms are at the nexus of deep-sea vent ecosystems by effectively transferring the energy from the geothermal source to higher trophic levels. We are using Crab Spa, a well-constrained diffuse-flow vent located on the East Pacific Rise at 9°N, as a model system to gain insights into the underlying microbial processes. Depletions of chemosynthetic substrates in vent fluids indicate microbial consumption in the subseafloor. Combining this information with results from 'omic' approaches and incubations reveals a highly active microbial community, that has remained stable from '07 to '14. Here, we used metaproteomics to identify the metabolically active community members and their utilized pathways. An actively growing community was indicated by a high abundance of growth related proteins. Further, the results highlight the importance of chemosynthesis, with limited evidence for heterotrophy. Enzymes for the utilization of nitrate and oxygen are well represented, while enzymes for the usage of electron donors are less represented, possibly reflecting electron acceptor limitation. There appears to be partitioning of labor among different community members, with different organisms expressing different parts of pathways. Our results further indicate that the microbial communities are characterized by functional redundancy, with a core set of metabolic repertoire despite a high microdiversity evidenced by 16S rRNA based surveys. This suggests that different taxa might perform similar functions using homologous pathways, but being optimally adapted along geochemical gradients. Overall, our data provide insights into the functioning of the subseafloor biosphere underlying this vent site and its biogeochemical significance for the surrounding deep ocean.