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## **Microbial Communities and Metabolisms From Basalt- and Ultramafic-hosted Vents**

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High-temperature vent fields along the Mid-Atlantic Ridge (MAR) are characterized by two different modes of hydrothermal circulation. In basalt-hosted systems fluids rise through gabbros or basaltic lavas, often over long distances along deep-reaching detachment structures. Similar detachments are likely responsible for the formation of hydrothermal fields several kilometres away from the neovolcanic zone in areas of mantle-derived rocks, where the fluids pass through the cooling ultramafic footwall. Consequently, fluid chemical signatures differ considerably according to the host rocks in the seafloor. The effluents from basalt-hosted settings are generally enriched in sulfide, whereas ultramafic regimes discharge H<sub>2</sub> and CH<sub>4</sub> enriched fluids. The dilution of the high-temperature endmember solutions with oxygenated ambient seawater also contributes to vent fluid chemistry by admixing oxygen, nitrate and sulfate to the reduced emissions. The fluid-rock interactions and the mixing processes likely denote geochemical constraints on the diversity and activity of local microorganisms.

The hydrothermal fluids of the basalt-hosted vent fields at 5°S and 9°S (Lilliput hydrothermal field) along the MAR are hallmarked by comparatively low H<sub>2</sub> concentrations. In contrast, those of the ultramafic-hosted vent fields at 15°N (Logatchev hydrothermal field) and at 8°S (Nibelungen field) along the MAR are considerably enriched in H<sub>2</sub>. Diffuse and hot hydrothermal effluents from two H<sub>2</sub>-poor sites in the basalt-hosted southern MAR fields and from four H<sub>2</sub>-rich localities within the ultramafic-hosted Logatchev field were used for comparing the diversity of H<sub>2</sub>-oxidizing microbes. To assess the microbial metabolic activities, hydrothermal fluids from seven basalt-hosted vents at 5°S and 9°S and from three ultramafic-hosted sites in the Logatchev and the Nibelungen fields were spiked with H<sub>2</sub> or sulfide and supplemented with radioactively labeled inorganic carbon. The fluids were incubated at moderate temperatures and microbial hydrogen or sulfide consumption as well as CO<sub>2</sub> fixation rates determined.

The enzyme catalyzing the microbial consumption of H<sub>2</sub> is the hydrogenase and its encoding gene is found in phylogenetically diverse microbial lineages. Only few phylogenetically diverging hydrogenase genes were identified in the two H<sub>2</sub>-poor effluents from the basalt-hosted sites and were associated with those of mesophiles only. On the contrary, a high hydrogenase diversity is illustrated in the four investigated H<sub>2</sub>-rich Logatchev habitats. Here the hydrogenase genes are affiliated with those of distinct mesophilic and (hyper)thermophilic microbes, reflecting the broad thermal range at which microbial H<sub>2</sub>-oxidation is putatively performed. The highest microbial H<sub>2</sub>-consumption rates were exhibited from a basalt-hosted venting sample characterized by extremely low H<sub>2</sub> concentrations in the natural

environment (<5 nM) and a very low hydrogenase diversity. In most of the ten fluid incubations H<sub>2</sub> could stimulate microbial CO<sub>2</sub> fixation, while only in one incubation CO<sub>2</sub> fixation could be significantly enhanced by spiking the fluids with sulfide. This indicates the importance of H<sub>2</sub> for stimulating microbial CO<sub>2</sub> fixation in H<sub>2</sub>-poor as well as H<sub>2</sub>-rich vent environments at moderate temperatures. The results also suggest that the availability of H<sub>2</sub> in the fluids is not the sole determinant for the diversity and activity of H<sub>2</sub>-oxidizing microorganisms. Other parameters such as mixing processes influencing the oxygen availability and temperatures of the effluents likely contribute to the metabolic diversity and activity of H<sub>2</sub>-oxidizing microorganisms in these vent regimes.

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