

## **Microbial Biogeochemistry of the Guaymas Basin Hydrothermal Plume**

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Microorganisms catalyze many biogeochemical transformations in deep-sea hydrothermal plumes and are therefore important players in determining the fate of hydrothermal inputs into the world's oceans. However, little is known about the microbes or mechanisms that underpin these transformations. The hydrothermal plume in Guaymas Basin (GB) is unusually highly enriched in manganese, methane, and ammonium. Previous studies have suggested that Mn(II) removal rates at GB are extremely fast, and therefore must be the result of microbially mediated Mn oxidation and precipitation. The aim of the work presented here was to confirm that microbes drive Mn(II) oxidation in the GB hydrothermal plume, and to identify the microbes and molecular mechanisms responsible. Mn(II) removal rates measured at GB were among the fastest ever observed in a deep-sea hydrothermal plume, whereas they were much slower in an adjacent basin without hydrothermal influence. The involvement of microorganisms was confirmed and Mn(II) oxidation displayed a distinct temperature optimum, suggesting an enzymatic mechanism. Mn oxidation was heat tolerant but very sensitive to small additions of  $\text{CuCl}_2$ , consistent with properties of Mn(II)-oxidizing enzymes from cultured organisms. Overall, our results reveal a vigorous Mn biogeochemical cycle in the deep-sea hydrothermal plume of GB, where microorganisms enzymatically catalyze rapid Mn(II) oxidation. Despite the dramatic difference in Mn(II) oxidation rates between the plume and background deep-sea waters, the dominant members of the microbial communities in these environments are strikingly similar based on 16S rRNA gene analysis. We propose that this apparent discrepancy can be explained by either (1) distinct activities of microbes within the plume or (2) unique genomic content of plume microbes that is not detectable by 16S rRNA gene analysis.

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