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MICROBIAL AMMONIA OXIDATION IN DEEP-SEA HYDROTHERMAL PLUMES

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ABSTRACT

Autotrophic ammonia oxidation has been documented for the first time in deep-sea hydrothermal plumes – along the Endeavour Segment, Juan de Fuca Ridge, and in the Guaymas Basin, Gulf of California. Ammonium concentrations as high as 341 nM have been detected in the Endeavour plume, which supports autotrophic ammonia oxidation at ≤ 91 nM d^{-1}, and potentially produces *de novo* organic carbon at a rate (0.6-13 mg C m^{-2} d^{-1}) equivalent to 1300% particulate organic carbon flux from the surface ocean. The thick organic-rich sediment cover in the Guaymas Basin endows an even higher ammonium concentration (≤ 2.9 μM) to the overlying hydrothermal plume, which fuels potential ammonia oxidation at ≤ 517 nM d^{-1}, but its relative contribution to organic carbon is perhaps small compared to the large amounts of organic carbon coming from the surface ocean and hydrothermal fluid discharges. In fact, the abundance of organic matter and other reduced chemicals in the Guaymas Basin water might have stimulated more heterotrophic activities and associated ammonium assimilation, or acted as natural inhibitors, thus preventing higher ammonia oxidation rates or larger populations of ammonia-oxidizing bacteria (AOB). Assimilation of ammonium occurs at rates comparable to ammonia oxidation. Hence, assimilation is an equally important ammonium uptake pathway in both water columns.

AOB in both β- and γ-proteobacterial subgroups are present in the deep-sea hydrothermal plumes and background deep water at both locations, as well as in the hydrothermal fluids and sediments in the Guaymas Basin. They are often associated with

particles greater than 3 μm in diameter (32-95%). The total abundance of AOB in the Endeavour plume ($\leq 16 \pm 1.8 \times 10^3$ cells ml^{-1}) is up to ten-fold that in the above-plume background ($1.6 \pm 0.7 \times 10^3$ cells ml^{-1}). A less dramatic increase is observed in the Guaymas Basin plume ($8.0 \pm 0.9 \times 10^3$ cells ml^{-1}) relative to its overlying deep water ($1.5\text{-}3.5 \times 10^3$ cells ml^{-1}). Sequence analyses of amplified partial 16S rRNA genes and the genes encoding ammonia monooxygenase subunit A (*amoA*) suggest that a novel lineage of β-Proteobacterial AOB might be present in both water columns.