

Distribution of ammonia-oxidizing archaea in Kamchatka hot springs

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Biological ammonia oxidation is a key component of the global nitrogen cycle. The aerobic oxidation of ammonia in low-temperature marine and terrestrial environments is characterized by a gene biomarker that encodes a subunit of the key enzyme ammonia monooxygenase (*amoA*), which is restricted to the β - and γ - *Proteobacteria*. However, recent molecular studies of the putative archaeal *amoA* gene suggest ammonia-oxidizing archaea (AOA) may also be ubiquitous in low temperature environments and perhaps even more abundant than their bacterial counterparts, although their role in nitrogen transformations in high temperature environments such as terrestrial hot springs remains largely unknown. We studied ammonia-oxidizing archaea in Kamchatka hot springs (42°C to 85°C and pH 5.5-7) by amplifying, cloning and sequencing the putative archaeal *amoA* genes from microbial mat and sediment samples. Phylogenetic analysis indicated that AOA in Kamchatka hot springs formed three distinct clusters, two of which corresponded to the Crenarchaeotal group 1.1a and 1.1b and represented the 49% and 7% of total obtained sequences. The third cluster counted 44% of total sequences but contained limited reference sequences from either estuary sediment or fertilized soils in the GenBank. The majority of hot spring sequences are distantly related to nonthermophilic Crenarchaeotal *amoA* genes and formed separate clades in each cluster. In addition, the richness and diversity of AOA in hot springs seemed to increase with a decrease in temperature. Our results suggest that Kamchatka hot springs harbor unique phylotypes of AOA, including potential thermophilic and hyperthermophilic members. Because terrestrial hot springs and deep sea hydrothermal vents are similar chemically, our results may shed light on the existence and potential role ammonia-oxidizing Archaea may play in the deep-sea mid-ocean ridges.

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