



Ammonia oxidation driven by archaea rather than bacteria in the hot spring at Tengchong geothermal field, China.

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The occurrence of microbial mediated ammonia oxidation and these organisms are present in large numbers in natural environments indicated a potential biogeochemical role for them in the global nitrogen cycle. However, very little is understood about their role and contribution to nitrification in the high temperature extreme environments. Here we explore the ammonia oxidation rates and abundance of potential ammonia-oxidizing archaea (AOA) in upper and bottom sediments from Gongxiaoshe hot spring, Tengchong, Yunnan, China. The ^{15}N -incorporating AOA cells and cell aggregated were detected with Fluorescence in situ hybridization (FISH) and Nano secondary ion mass spectrometry (Nano-SIMS). Ammonia oxidation rates measured using $^{15}\text{N}\text{-NO}_3^-$ pool dilution in upper and bottom sediments (without NH_4^+ stimulated) were 4.8 and 5.3 $\text{nmol N g}^{-1}\text{h}^{-1}$, respectively. Close relatives of the autotrophic, ammonia-oxidizing archaeon 'Candidatus Nitrosocaldus yellowstonii' represented the most abundant OTU in both of the two spring sediments by 16S rRNA gene analysis. Furthermore, it should be noted that no ammonia-oxidizing bacterial clones detected in this study. Quantitative PCR (qPCR) indicated that AOA and 16S rRNA genes were present at $2.75\text{-}9.80 \times 10^5$ and $0.128\text{-}1.96 \times 10^8$ gene copies g^{-1} sediment. Based on the reaction rates and AOA abundance, we estimated the cell-specific nitrification rates were 0.41 to 0.79 $\text{fmol N archaeal cell}^{-1}\text{ h}^{-1}$, which are comparable to those observed in estuary environment. We suggest that AOA have the responsibility in nitrification in this hot spring, and these archaea rather than bacteria may be considered as a driver in nitrogen cycling in terrestrial hot ecosystems.

Key words: ammonia-oxidizing archaea (AOA); nitrification; ammonia-oxidizing rate; hot spring;