

Ammonia-oxidizing Thaumarchaeota form a large fraction of the archaeal community in pristine limestone aquifers

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A considerable proportion of microbial communities in subsurface habitats is accounted for by Archaea, however knowledge of their role in biogeochemical cycles is limited. This study focuses on archaeal community diversity in two superimposed aquifers each characterized by different oxygen availability. Samples were obtained from eight groundwater wells ranging from 12 to 88 m depth in the Hainich region (Thuringia, Germany).

Quantitative PCR of archaeal 16S rRNA genes revealed that Archaea accounted for up to 9 % of the groundwater microbiota. In a DNA-based analysis, 66 to 99 % of the archaeal 16S rRNA gene sequence reads were related to the ammonia oxidizing thaumarchaeon Marine Group I (MG-I). Other gene sequence reads were related to uncultured archaeal clades typically detected in soil habitats, such as the Soil Crenarchaeotal Group, the Forest Soil Crenarchaeotal Group, or the Valkea Kotinen group III (VAL-III). However, analysis of the metabolically active archaeal communities on the RNA level showed equal fractions of the MG-I Thaumarchaeota and of the euryarchaeotal group VAL-III in the lower oxygen-rich aquifer. The upper oxygen-deficient aquifer was dominated by gene sequence reads affiliated to the uncultured clade of a possibly facultative autotrophic archaea, the Miscellaneous Crenarchaeotal Group. Our results suggested an input of soil Archaea to the groundwater community; and that ammonia oxidation could be an important metabolism of Archaea in deep limestone aquifers making a considerable contribution to autotrophic archaeal CO₂-fixation.