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Abundance and community structure of ammonium monooxygenase (*amoA*) genes in Liaohe estuary sediments

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Ammonia oxidation is an important part of the global nitrogen cycle. Ammonia-oxidizing archaea (AOA) and ammonia-oxidizing bacteria (AOB) are important players in the ammonia oxidation process. In this study, 13 sediment samples from the Liaohe

estuary were collected. The abundances of 16S rRNA and *amoA* genes were detected by real-time fluorescence quantitative PCR. The diversity and community structure of AOA and AOB were investigated by constructing clone libraries. Quantitative PCR results showed that the 16S rRNA gene abundances of archaea and bacteria were $1.05 \times 10^8 \sim 1.31 \times 10^9$ and $3.05 \times 10^{10} \sim 1.37 \times 10^{12}$ copies/g wet sediment, respectively. The AOA and AOB *amoA* gene abundances ranged from $3.10 \times 10^6 \sim 2.85 \times 10^7$ and 6.59×10^5 to 1.20×10^7 copies/g wet deposit, respectively. At all sites, AOA abundance

was greater than AOB. Phylogenetic analysis showed that the AOA *amoA* sequences were mainly Nitrososphaera and Nitrosopumilus, and the AOB *amoA* sequences were mainly located in estuarine sediments and wetland soils. In addition, canonical correspondence analysis showed that the environmental factors affecting AOA community distribution were salinity, pH, ammonia (NH_4^+), conductivity, total phosphorus, sand, and silt content, while the sand and silt content had a significant effect on AOB community structure.

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