

Functional microbial communities for As(III) oxidation coupled with nitrate reduction in paddy soil

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Arsenite (As(III)) oxidation coupled to nitrate (NO₃⁻) reduction is thermodynamically favored and experimentally tested. However, little is known about functional bacteria responsible for this coupling process in flooded paddy soil. In this study, three microcosms containing paddy soil amended with 1) As(III)+NO₃⁻, 2) As(III), and 3) NO₃⁻, respectively, were set up to investigate the rates of the coupled processes of As(III) oxidation and NO₃⁻ reduction and to characterize the associated functional bacteria. The results showed that As(III) was completely oxidized in As(III)+NO₃⁻ treatment after 6 days, while no As(III) oxidation was observed in the As(III) amendment. Meanwhile, NO₃⁻ reduction was observed in both As(III)+NO₃⁻ and NO₃⁻ amendments, where nitrite (NO₂⁻) and nitrous oxide (N₂O) were the major products. The real-time quantitative PCR showed that the abundance of 16S rRNA gene and functional genes affiliated with As(III)-oxidization (*aoxB*) and denitrification (*narG*, *nirS* and *nosZ*) increased over time in both As(III)+NO₃⁻ and NO₃⁻ amendments, suggesting that NO₃⁻ may play an important role in stimulating both As(III)-oxidizers and denitrifiers in paddy soil. In the As(III)+NO₃⁻ amendment, the 16S rRNA-based dominant genera were *Vogesella*, *Dechloromonas* and *Pseudogulbenkiania*; the *aoxB*-based dominant arsenite-oxidizers included *Acidovorax* and *Cupriavidus*; the *narG*-based nitrate reducers (NO₃⁻ → NO₂⁻) were *Dechloromonas* and *Pseudogulbenkiania*; the *nirS*-based dominant genera for NO₂⁻ reduction to nitric oxide (NO) were *Dechloromonas*, *Vogesella*, and *Pseudogulbenkiania*; the *nosZ*-based dominant genera for N₂O reduction to Nitrogen (N₂) were *Bradyrhizobium*, *Thauera* and *Azoarcus*. The study provided better understanding of the functional microbial communities involved in As(III) oxidation coupled with denitrification in anoxic paddy soil.

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