

Bacteria and genes associated with arsenite oxidation and nitrate reduction in a paddy soil

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Recent studies demonstrated that microbial arsenite (As(III)) oxidation associated with nitrate (NO₃⁻) reduction might be an important process in diminishing arsenic bioavailability and toxicity to rice when paddy soils are contaminated by arsenic. However, the responses of bacterial communities and functional genes to As(III) under nitrate-reducing conditions are poorly understood in a non-contaminated soil. In this study, our results revealed that microbial oxidation of As(III) to As(V) was substantially accelerated by nitrate addition in a paddy soil with low arsenic background content, while nitrate reduction was not affected by As(III) addition. Metagenomic binning revealed that *Pseudogulbenkiania* sp. was the main nitrate-reducing bacteria with *narG*, *nirS* and *norBC* genes, and *Azoarcus* sp. was the predominant As(III)-oxidizing bacteria with As(III) oxidase genes *aioA* and *aioB*. The draft genome of *Azoarcus* sp. also had complete sets of denitrification genes (mainly, *napA*, *nirK*, and *nosZ*). Quantitative PCR analysis also confirmed that the abundance of *Azoarcus* spp., *aioA* and *nosZ* genes were enhanced in the presence of As(III) and nitrate. These findings suggest the importance of *Azoarcus*- and *Pseudogulbenkiania*-related spp., both of which showed various physio-ecological characteristics for arsenic and nitrogen biogeochemistry, in coupling As(III) oxidation and nitrate reduction in flooded paddy soil.

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