Functional microbial communities involved in nitrate reduction and Fe(II) oxidation commonly present in different paddy soils

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Nitrate (NO_3^-) reduction and ferrous (Fe(II)) oxidation during flooding season strongly influence the biogeochemistry transformation of iron and nitrogen (N) in paddy soil. Paddy soils in southern China are with high Fe contents and high inputs of organic C and N via fertilizers and atmospheric nitrogen deposition. However, little is known about the functional microbial communities responsible for NO_3^- reduction and Fe(II) oxidation in paddy soils. In this study, two paddy soils were collected from different areas (Taishan and Guangxi) in southern China and used as inocula in anaerobic microcosms to investigate the kinetics of Fe(II) oxidation and NO_3^- reduction as well as functional microbial communities during these processes. While the rates of NO_3^- reduction in the soil of Guangxi were similar in the presence and absence of Fe(II), the presence of Fe(II) decreased the NO_3^- reduction rate in the soil of Taishan. Fe(II) oxidation only occurred in the presence of NO_3^- in both tested soils. Metagenomic analyses of the microcosms for NO_3^- reduction and Fe(II) oxidation revealed that the presence of Fe(II) increased the relative abundance of *napA*, *nirB*, *norB*, and *nosZ* genes in both tested soils. During the Fe(II) oxidation and NO_3^- reduction in both soils, *Thauera* was the dominant genus for periplasmic nitrate reduction (*napA*-based), while Rhodocyclaceae was the most abundant family for the reduction of NO_2^- to NO (*nirB*-based). *Algoriphagus* and *Dechloromonas* were the dominant genera for the reduction of NO to N_2O (*norB*-based), while *Pseudogulbenkiania* was the most abundant genus for the reduction of N_2O to N_2 (*nosZ*-based). These results suggested that the presence of Fe(II) can strongly affect the functional microbial communities responsible for NO_3^- reduction, all of which commonly present in different paddy soils.

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