Microbial communities and functional genes of nitrogen cycling in the rhizosphere of rice

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Abstract

Nitrogen-cycling microbial communities in seven different soil types and a tropical rice field were investigated by monitoring the abundances of *nifH*, *amoA*, *nasA*, *narG*, *nirK*, *nirS*, and *nosZ* gene copies. Additions of N (10 and 100 mM) in the soil microcosms led to typical changes in the abundances of *nifH* and *nasA*. In the rhizosphere of field-grown rice, the application of N fertilizer or microbial inoculants in combination, the cultivation methods, and the plant growth stages showed characteristic changes. Rapid detection of changes in nitrogen-cycling microbial communities provides a new option to identify the best management practices.

Keywords: N-cycling, microbial communities, Functional gene copies

1. Introduction

Nitrogen-cycling microbial communities are an essential competitior for the soil available nitrogen. They also contribute significantly, the different N forms for acquisition by plant roots. A better understanding of N transformation is critical to improving N use efficiency in rice cultivation (Lassaletta et al. 2014).

2. Materials and Methods

Flooded and non-flooded microcosms using samples from New Delhi, Kuttanad, Rajasthan, Aduthurai, Umiam and Karnal of different soil types were analyzed for microbial activities and their compositions. Soil samples collected from the rhizospheres of rice (cv. Pusa 1506), from the experimental field plots under conventional flooding (CF)- and direct-seeded rice (DSR) method with different fertilizer management practices at three stages of plant growth for two seasons (2017 & 2018) were also studied. The functional gene abundances (*nifH*, *amoA*, *nasA*, *narG*, *nirK*, *nirS* and *nosZ*) were enumerated by the qPCR method.

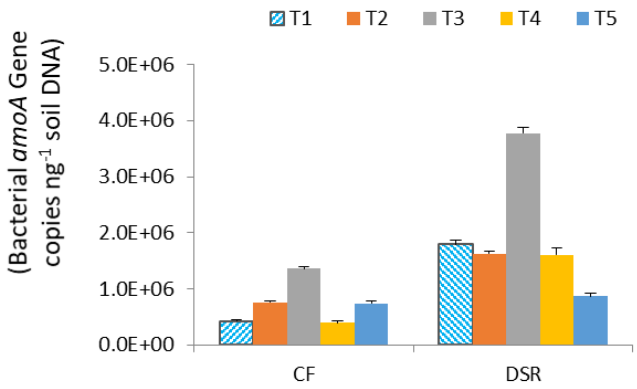

Fig. 1: Abundances of bacterial *amoA* gene copies in the rhizospheres of rice at vegetative stage under conventional flooding (CF) and direct-seeded rice (DSR) method using

different fertilizer management practices (T1:Recommended doses of NPK (110:60:50) kg ha^{-1}; T2: NPK (55:60:50) with N as urea (75%) and potassium nitrate (25%); T3: as in T2 with *Anabaena-Nostoc* consortium;T4: as in T2 with the biofilm of *Anabaena torulosa-Mesorhizobium ciceri*; T5: as in T2 with consortium of ammonium oxidizing microbial isolates.

3. Results

3.1 Effect of N additions in different soil types

The N-cycling microbial communities were characteristically different in microcosms with additions of N at 10 and 100 mM. The gene copies of both *nifH* and *nasA* were lesser, in the ranges of 10^2 to 10^4 g^{-1} soil.

3.2 Rhizosphere Influences

There were characteristic changes in the N-cycling microbial communities at different plant growth stages. The bacterial amoA gene copies under the DSR method were more than those under the CF method at vegetative growth stage. The functional gene copies related to denitrification were higher, influenced by fertilizer management practices.

4. Discussion

Rapid and simultaneous detection and quantification of N-cycling microbial communities in soils will be highly useful to select the timing and types of fertilizer management options.

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Reference

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