frontiers in Microbiology

ORIGINAL RESEARCH
published: 20 September 2019
doi: 10.3389/fmicb.2019.02103

16S rRNA Gene Amplicon Based Metagenomic Signatures of Rhizobiome Community in Rice Field During Various Growth Stages

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Specialty section:
This article was submitted to Plant Microbe Interactions, a section of the journal Frontiers in Microbiology

Received: *10 June 2019*
Accepted: *26 August 2019*
Published: *20 September 2019*

Citation:
Imchen M, Kumavath R, Vaz ABM, Góes-Neto A, Barh D, Ghosh P, Kozyrovska N, Podolich O and Azevedo V (2019) 16S rRNA Gene Amplicon Based Metagenomic Signatures of Rhizobiome Community in Rice Field During Various Growth Stages. Front. Microbiol. 10:2103. doi: 10.3389/fmicb.2019.02103

Rice is a major staple food across the globe. Its growth and productivity is highly dependent on the rhizobiome where crosstalk takes place between plant and the microbial community. Such interactions lead to selective enrichment of plant beneficial microbes which ultimately defines the crop health and productivity. In this study, rhizobiome modulation is documented throughout the development of rice plant. Based on 16S rRNA gene affiliation at genus level, abundance, and diversity of plant growth promoting bacteria increased during the growth stages. The observed α diversity and rhizobiome complexity increased significantly ($p < 0.05$) during plantation. PCoA indicates that different geographical locations shared similar rhizobiome diversity but exerted differential enrichment ($p < 0.001$). Diversity of enriched genera represented a sigmoid curve and subsequently declined after harvest. A major proportion of dominant enriched genera ($p < 0.05$, abundance $> 0.1\%$), based on 16S rRNA gene, were plant growth promoting bacteria that produces siderophore, indole-3-acetic acid, aminocyclopropane-1-carboxylic acid, and antimicrobials. Hydrogenotrophic methanogens dominated throughout cultivation. Type I methanotrophs ($n = 12$) had higher diversity than type II methanotrophs ($n = 6$). However, the later had significantly higher abundance ($p = 0.003$). Strong enrichment pattern was also observed in type I methanotrophs being enriched during water logged stages. Ammonia oxidizing Archaea were several folds more abundant than ammonia oxidizing bacteria. K-strategists *Nitrosospira* and *Nitrospira* dominated ammonia and nitrite oxidizing bacteria, respectively. The study clarifies the modulation of rhizobiome according to the rice developmental stages, thereby opening up the possibilities of bio-fertilizer treatment based on each cultivation stages.

Keywords: rhizobiome, *Oryza sativa*, environmental DNA, 16S rRNA gene amplicon metagenomics, next generation sequencing