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Insights into Endophytic Bacterial Community Structures of Seeds Among Various *Oryza sativa* L. Rice Genotypes

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Abstract

This study aimed to investigate the endophytic bacterial communities among various rice seed genotypes, to define the core microbiome and to further explore the relationship between rice genotypes and their endophytic bacterial flora. Simple sequence repeats molecular marker technology was used to investigate the genetic polymorphism in five different genotypes of rice. Endophytic bacterial communities in rice seeds were investigated using the Illumina-based 16S rRNA gene. The results showed that rice genotype had little impact on the diversity and richness of endophytic bacteria in seeds. The various rice genotypes do not have significantly different communities of endophytic bacterial in seeds, but the endophyte abundance distributions are obviously different, especially the dominant endophytic genera. Some phyla, such as Acidobacteria, Fusobacteria, Chlamydiae and Gemmatimonadetes, were first detected in rice seeds using high-throughput sequencing technique. As expected, five different rice genotypes were found to have a shared microbiome. At the genus level, *Pantoea* (28.33–72.77%), *Acinetobacter* (0.16–34.23%) and *Xanthomonas* (3.20–13.51%), which are probably the core microflora in *indica* rice seeds, served as the dominant genera that coexisted in all rice seeds tested. However, the current studies cannot confirm the correlation of rice phylogeny and seed bacterial microbiome clearly, but provide some clues of technical possibility and valuable experiences for the future study.

Keywords Rice phylogeny · Seed endophytic bacteria · Correlation · High-throughput sequencing · Core microbiome

Introduction

Decades of research have demonstrated the importance of microorganisms for plant health. Deciphering the interaction between plants and their microbiomes is a hot topic for research in ecology, plant sciences and agronomy (Vandenkoornhuyse et al. 2015). Several studies have demonstrated that plant compartments (Wang et al. 2016a), genotypes and geographic locations (Edwards et al. 2015) have varying

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Electronic supplementary material The online version of this article (https://doi.org/10.1007/s00344-018-9812-0) contains supplementary material, which is available to authorized users.

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