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Rice genotype, parental lineage and physiological tolerance to soil salinity shapes the community structure of rice seed bacterial endophytes

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Abstract

Rice seeds are a home to endophytic bacterial communities which serve as a source of the plant's endophytes. As rice undergo physiological and adaptive modifications through cross breeding in the process of attaining salinity tolerance, this may also lead to changes in the endophytic bacterial community especially those residing in the seeds. This study explores the community structure of seed bacterial endophytes as influenced by rice parental lineage, genotype and physiological adaptation to salinity stress. Endophytic bacterial diversity was studied through culture dependent technique, cloning and Terminal-Restriction Fragment Length Polymorphism (T-RFLP) analysis. Results revealed considerably diverse communities of bacterial endophytes in the interior of rice seeds. The richness of ribotypes ranges from 5-14 T-RFs corresponding to major groups of bacterial endophytes in the seeds. Endophytic bacterial diversity of the salt-sensitive IR29 is significantly more diverse compared to those of salt-tolerant cultivars. Proteobacteria followed by Actinobacteria and Firmicutes dominated the overall endophytic bacterial communities of the indica rice seeds based on 16S rDNA analysis of clones and isolates. Community profiles show common ribotypes found in all cultivars of the indica subspecies representing potential core microbiota belonging to Curtobacterium, Flavobacterium, Enterobacter, Xanthomonas, Herbaspirillum, Microbacterium and Stenotrophomonas. Multivariate analysis showed that the bacterial endophytic community and diversity of rice seeds are mainly influenced by their host's genotype, physiological adaptation to salt stress and parental lineage.

Keywords: Rice seeds, Endophytic bacteria, T-RFLP analysis, Diversity

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