



Functional compensation dominates the assembly of plant rhizospheric bacterial community

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ABSTRACT

Plant rhizosphere microbes play a key role in plant-soil feedbacks. However, the intrinsic principles governing the assembly of the rhizosphere microbial community remain unclear. To understand these principles, we studied the taxonomical and functional characteristics of the reassembled maize rhizosphere bacterial communities after transplanting between soils. The composition of the rhizosphere bacterial community was measured by high-throughput amplicon-based Illumina MiSeq sequencing of the V4 region of the 16S ribosomal RNA (rRNA) gene. The rhizosphere functional profile was assessed using 16S rRNA data in the PICRUSt (Phylogenetic Investigation of Communities by Reconstruction of Unobserved State) software. We found that the reassembled rhizosphere bacterial community was recruited from both soil and endosphere communities. The assembly and functional traits of the rhizosphere bacterial community were associated with the concentrations of soil available nutrients. The most important rhizospheric functions were to improve host stress tolerance, followed by nutrient cycling functions. The rhizosphere bacterial taxa that improved host stress tolerance were in low abundance and were primarily derived from the surrounding bulk soil. Moreover, the rhizosphere nutrient cycling functions were marginalized in nutrient-excessive soils. Plants may sacrifice stress tolerance functions and enhance compensatory colonization of nutrient cycling-related endophytes in the rhizosphere in nutrient-deficient soils. Our results demonstrate that the levels of soil available nutrients mediate the assembly of rhizosphere bacterial communities to satisfy plant-required functions. This assembly principle is useful for manipulating the bacterial communities of plant roots to improve agricultural sustainability.

1. Introduction

Rhizosphere microbes grow in association with plant roots and are crucial for plant productivity because of their irreplaceable roles in soil nutrient cycling (Zhang et al., 2019), abiotic stress tolerance (Yang et al., 2009) and soil-borne pathogen suppression (Kwak et al., 2018). Previous research provides comprehensive evidence that the plant rhizosphere bacterial community can be largely shaped by many properties, including soil physicochemical characteristics and nutrient availability (Castrillo et al., 2017; Lundberg et al., 2012), plant root exudates and other metabolites (Zhalnina et al., 2018), plant genotype (Bulgarelli

et al., 2015) and the developmental stage (Edwards et al., 2015). The rhizosphere bacterial community shows great variation in spatiotemporal distribution (Peiffer et al., 2013) and preserves a dynamic equilibrium state, integrating both ‘outside-in’ assembly by recruiting microbes from the surrounding soil (Bulgarelli et al., 2013) and ‘inside-out’ assembly through released endophytes (Berg and Raaijmakers, 2018). These features complicate the exploration of the general principles that govern the assembly of plant rhizosphere bacterial communities.

Functional traits might be key to clarifying the assembly pattern of plant rhizosphere bacterial communities because the functional

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