

蓝莓根系微生物群落在不同根系空间生态位上的互作特征

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摘要:【目的】植物根系微生物群落在促进植物健康、提高植物生产力和耐受生物/非生物胁迫方面发挥着关键作用。蓝莓 (*Vaccinium* spp.) 适应酸性土壤, 探明特殊适应性生境下不同根系空间生态位微生物群落的相互作用尤为关键。【方法】以兔眼蓝莓、北高丛蓝莓和南高丛蓝莓为研究对象, 采集根际、非根际土壤样品以及根系样品, 利用 Illumina 高通量测序技术, 分析细菌和真菌的微生物多样性及群落结构特征。【结果】与宿主栽培品种相比, 蓝莓不同根系空间生态位显著影响根系微生物组的多样性和群落结构。在细菌和真菌群落中, 确定性过程沿着土壤-根际-根内的连续体逐渐增加。共现网络拓扑特征表明, 细菌和真菌群落的复杂性和紧密度沿着土壤-根际-根内的连续体逐渐降低。不同根系空间生态位显著影响了细菌和真菌的互作关系, 根际的互作关系明显较高。此外, 细菌和真菌的相互作用沿着土壤-根际-根内的连续体逐渐转变为以正向相互作用为主。功能预测表明, 根际细菌群落具有较高的纤维素分解能力, 根际真菌群落主要以腐食营养型为主。【结论】蓝莓不同根系空间生态位不仅影响蓝莓根系微生物组的多样性和群落结构, 还增强了土壤-根际-根内连续体中细菌和真菌群落间的积极正向相互作用, 这为利用人工合成微生物群落以实现可持续农业发展提供了重要基础。

关键词: 空间生态位; 根系微生物; 根际; 细菌和真菌群落; 共现网络

Root niches of blueberry imprint increase bacterial–fungal interkingdom interactions along the soil–rhizosphere–root continuum

Abstract: 【Objective】 Plant root-associated microbiomes play critical roles in promoting plant health, productivity, and tolerance to biotic/abiotic stresses. Blueberry (*Vaccinium* spp.) is adapted to acidic soils, while the interactions of the root-associated microbiomes in this specific habitat remain elusive under various root microenvironments. 【Method】 Here we investigated the diversity and community composition of bacterial and fungal communities in various blueberry root niches (bulk soil, rhizosphere soil, and root endosphere). 【Result】 The results showed that blueberry root niches significantly affected root-associated microbiome diversity and community composition compared to the host cultivars. Deterministic processes gradually increased along the soil–rhizosphere–root continuum in both bacterial and fungal communities. The co-occurrence network topological features showed that both bacterial and fungal community complexity and intensive interactions decreased along the soil–rhizosphere–root continuum. Different compartment niches clearly influenced bacterial–fungal interkingdom interactions, which were significantly higher in the rhizosphere, and positive interactions gradually dominated the co-occurrence networks from the bulk soil to the endosphere. The functional predictions showed that rhizosphere bacterial and fungal communiti

es may have higher cellulolysis and saprotrophy capacities, respectively. **【Conclusion】** Collectively, the root niches not only affected microbial diversity and community composition, but also enhanced the positive interkingdom interactions between bacterial and fungal communities along the soil–rhizosphere–root continuum. This provides an essential basis for manipulating synthetic microbial communities for sustainable agriculture.

Key words: Compartment niches, Root-associated microbiome, Rhizosphere, Bacterial and fungal community, Co-occurrence networks.