

不同生境沙氏鹿茸草根际土壤细菌群落结构和多样性分析

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摘要:【目的】研究江西省内野生和人工栽培沙氏鹿茸草 (*Monochasma savatieri*) 根际土壤细菌群落结构与多样性及其与土壤理化性质间的关系, 旨在构建沙氏鹿茸草健康的根际微环境, 为进一步探究沙氏鹿茸草仿生栽培模式提供理论依据。【方法】应用高通量测序技术, 比较油茶 (*Camellia oleifera*)、栀子 (*Gardenia jasminoides*)、马尾松 (*Pinus massoniana*) 林下野生以及人工栽培 2 种生境下沙氏鹿茸草根际土壤细菌群落结构及多样性, 并结合根际土壤理化性质进行相关性分析。【结果】在 2 种生境下, 沙氏鹿茸草根际土壤理化性质差异显著, 人工仿生栽培的 Alpha 多样性最高, 但在各林分类型间差异未达显著水平; 各生境类型下优势菌门均为变形菌门、酸杆菌门、绿弯菌门、放线菌门, 共有优势属包括卡氏伯克霍尔德菌属、慢生根瘤菌属、*Candidatus Solibacter*、*Occallatibacter*、苔藓杆菌属和 uncultured_bacterium 等有益菌; 野生生境和人工栽培土壤细菌群落结构存在明显差异, 人工栽培生境下变形菌门丰度最高; 野生生境特有优势菌属嗜酸栖热菌属、FCPS473、丛毛单胞菌属、酸杆菌属、未培养酸杆菌属、uncultured_forest_soil_bacterium 等在人工栽培生境下显著降低, 而较之野生生境, 人工栽培生境特有优势细菌属鞘脂单胞菌属、粒状胞菌属、嗜盐囊菌属、*Mucilaginibacter* 却增加明显。冗余分析 (redundancy analysis, RDA) 表明, 根际细菌群落与土壤全氮、速效钾、碱解氮、有机质含量密切相关。【结论】不同生境下, 鹿茸草根际土壤理化性质、细菌群落结构具有显著差异, 但野生生境沙氏鹿茸草根际细菌群落之间的相似性较高。土壤全氮、速效钾、碱解氮和有机质是影响细菌群落结构的主要环境因子。研究结果为探明沙氏鹿茸草根际微生物资源和利用提供了参考依据。

关键词: 沙氏鹿茸草; 土壤细菌; 群落结构; 生境

Analysis of Bacterial Community Structure and Diversity in Rhizosphere Soil of *Monochasma savatieri* in Different Habitats

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Abstract: 【Objective】This study is devoted to the relationship between bacterial community structure and diversity and soil physical and chemical properties in the rhizosphere soil of wild and artificially cultivated *Monochasma savatieri* Franch ex Maxim. in Jiangxi Province, the aim is to build a healthy rhizosphere microenvironment and provide theoretical basis for further exploring the bionic cultivation mode of *M. savatieri*.

【Method】The rhizosphere soil bacteria in two habitats, including the natural forest such as *Camellia oleifera*, *Gardenia jasminoides*, *Pinus massoniana* and artificial cultivation were selected as the research objects. The community structure characteristics in different habitats of soil bacteria were compared and analyzed by using field investigation, Illumina Miseq sequencing, and RDA analysis. 【Result】The results indicated that there were significant differences in the soil physio-chemical properties of the rhizosphere soil of *M. savatieri* in two habitats, and the alpha diversity of artificial bionic cultivation was highest, but did not reach a significant level among different stand types. In two habitats, Proteobacteria, Acidobacteriota, Chloroflexi and Actinobacteriota were the dominant bacteria phyla; At the genus level, the common dominant genera included *Burkholderia*-*Caballeronia*-*Paraburkholderia*, *Bradyrhizobium*, *Candidatus Solibacter*, *Occallatibacter*, *Bryobacter* and

uncultured_bacterium. The structure of the bacterial communities between wild and artificial bionic cultivation was significant differences, with the highest abundance of Proteobacteria in artificial bionic cultivated habitats. The unique dominant genera in wild habitats included *Acidothermus*, *FCPS473*, *Conexibacter*, *Acidibacter*, *uncultured_Acidobacteria_bacterium*, *uncultured_forest_soil_bacterium* significantly decreased in artificial bionic cultivation habitat, while compared to wild habitat, *Sphingomonas*, *Granulicella*, *Haliangium* and *Mucilaginibacter*, which only dominated in artificial bionic cultivated habitat, increased significantly. Redundancy analysis (RDA) suggested that total nitrogen, available potassium, alkali-hydrolyzable nitrogen, and organic matter were the dominant influencing factors on the composition of soil dominant bacterial communities. **【Conclusion】** Under different habitats, there were significant differences in the physicochemical properties of the rhizosphere soil of *M. savatieri*, as well as significant differences in the structure of bacterial communities. The similarity between the rhizosphere bacterial communities in the rhizosphere of *M. savatieri* under wild habitat conditions was relatively high. The main environmental factors affecting bacterial community structure were soil total nitrogen, available potassium, alkaline nitrogen, and organic matter. This study provides reference basis for the resources and utilization of rhizosphere microorganisms of *M. savatieri*.