

雌雄异株山桐子根际土壤微生物群落特征及功能预测分析³

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摘 要:【目的】明确雌雄异株山桐子根际土壤微生物群落多样性、结构及功能群的特征。【方法】以7年生雌雄株山桐子为材料,在山桐子花期(5月)、果实成熟期(10月)取样,分析根际养分含量特征同时采用Illumina高通量测序技术,对不同时期雌雄株根际多样性进行分析。【结果】(1)不同时期雌雄株山桐子根系中全氮及全钾含量存在差异。(2)根际真菌的 α 多样性指数在果实成熟期显著高于花期,花期雌雄株Shannon、Simpson和Chao1无显著差异,果实成熟期雄株土壤的Chao1和Shannon指数显著高于雌株。(3)山桐子土壤细菌优势菌门主要为变形菌门、酸杆菌门和放线菌门,果实成熟期土壤部分优势菌门的相对丰度显著减少,花期到果实成熟期,雌雄株土壤优势菌属从以放线菌门为主的菌群变为以变形菌门为主的菌群。(4)RDA冗余分析表示,pH与AK与山桐子根际细菌结构有显著相关($P<0.05$)。(5)PICRUSt功能预测表明,不同时期雌雄株共有6种一级子功能,47种二级子功能,显著差异的二级子功能有8种。【结论】山桐子土壤在花期优势菌门为放线菌门,在果实成熟期则为变形菌门。山桐子雌株土壤优势细菌属的数量多于雄株。功能预测表明雌雄株山桐子在不同时期的土壤细菌生态功能较为丰富,果实成熟期和花期的土壤代谢功能有明显差异。

关键词: 微生物; 木本油料; 雌雄异株; 功能群落; 土壤

中图分类号 S718.83

文献标识码: A

文章编号:

Characteristics and functional prediction of microbial community in the rhizosphere soil of dioecious *Idesia polycarpa* trees

Abstract: 【Objective】 The aim of this study was to investigate diversity, structure, and functional group characteristics of the rhizosphere soil microbial community of dioecious *Idesia polycarpa* trees. 【Method】 Seven year old male and female trees were taken as materials, and samples were taken at the flowering stage (May) and fruit maturity stage (October) of the fruit. The characteristics of nutrient content in the rhizosphere were analyzed. At the same time, Illumina high-throughput sequencing technology was used to analyze the diversity of the rhizosphere of male and female trees in different periods. 【Result】 (1) There are differences in the total nitrogen and total potassium contents in the roots of male and female trees in different periods of time. (2) The α diversity index was significantly higher during fruit ripening than during flowering, and there was no significant difference in Shannon, Simpson, and Chao1 between male and female plants during flowering. During fruit ripening, the soil Chao1 and Shannon indices of male plants were significantly higher than those of female plants. (3) The dominant bacterial phyla in the soil of *Idesia polycarpa* are mainly Proteobacteria, Acidobacteria and Actinomycetes. The relative abundance of some dominant bacterial phyla in the soil during the fruit ripening period is significantly reduced. From the flowering period to the fruit ripening period, the dominant bacterial genera in the soil of male and female plants change from actinomycetes to amomorpha. (4) RDA redundancy analysis showed that there was a significant correlation between pH and AK and the bacterial structure in the rhizosphere

基金项目: 河南省博士后科研项目(202002053); 中央财政林业科技推广示范项目(GTH[2023]02, GTH[2020]17)

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of *Idesia polycarpa* ($P < 0.05$). (5) PICRUST functional prediction shows that there are a total of 6 primary subfunctions and 47 secondary subfunctions in male and female plants at different stages, with 8 significantly different secondary subfunctions. **【Conclusion】** Our results demonstrated that during the flowering period, the dominant phylum in the soil of *Idesia polycarpa* is Actinobacteria, while during the fruit ripening period, it is Proteobacteria. The number of dominant bacterial genera in the soil of female plants of *Idesia polycarpa* is greater than that of male plants. The functional prediction indicates that the soil bacterial ecological functions of male and female trees of *Idesia polycarpa* are relatively rich at different stages, and there are significant differences in soil metabolic functions during fruit maturity and flowering stages.

Key words: microorganism; woody oil plants; dioecious plant; functional communities; soil.