

毛乌素沙地樟子松根内真菌对林龄和物候的响应

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摘 要:【目的】阐明不同物候期樟子松根内真菌群落组成及其功能群的时间动态变化特征及其对气候因子的响应。【方法】该研究以毛乌素沙地不同林龄(24、34 和 45 年)樟子松人工林为对象,采用野外调查取样、Illumina MiSeq 技术和生物信息学分析相结合的方法,比较分析不同物候期根内真菌群落结构和功能群,并探究环境因子对根内真菌群落多样性和功能群结构的影响。【结果】1) 毛乌素沙地樟子松根尖样品共获得 2828 个 OTUs,物候期对根内真菌 α 多样性和分布具有显著影响($P<0.05$)。2) 樟子松根内真菌隶属于 11 门 42 纲 114 目 241 科 487 属,优势菌门为子囊菌门(Ascomycota)和担子菌门(Basidiomycota),优势功能群为腐生-共生营养型、病理-腐生营养型和病理-腐生-共生营养型。3) 樟子松人工林根内真菌群落变化的主要驱动因子为年均空气湿度、年均降水量、土壤孔隙度、有效氮、年均日照时数、年均温和土壤含水量。【结论】环境变化塑造了毛乌素沙地樟子松根内真菌群落结构和功能的时间动态特征,而林龄对根内真菌群落的塑造贡献较小。研究结果可为樟子松人工林经营管理提供理论依据。

关键词: 樟子松; 根内真菌; 真菌功能; 环境因子; 林龄

Response of Root-associated Fungi to Stand Age and Phenology Associated with Mongolian Pine in Mu Us Sandy Land

Abstract: 【Objective】 This study aimed to illuminate the temporal dynamic variations of community composition and functional groups of root-associated fungi associated with Mongolian pine at different phenological periods, and investigated the environmental driving factors (climatic condition and soil property).

【Method】 Mongolian pine plantations with different stand ages (24, 34 and 45 a) in Mu Us Sandy Land were targeted. The community compositions, interaction and main drivers of ectomycorrhizal fungi at different phenological periods were identified by field investigation and sampling, illumina high-throughput sequencing and molecular ecological network analysis, respectively. 【Result】 1) A total of 2828 OTUs of fungi were obtained from root samples of Mongolian pine in Mu Us Sandy Land. Phenological period had significant influence on the α diversity and distribution of root-associated fungi. 2) The root-associated fungi were belonged to 11 phyla, 42 classes, 114 orders, 241 families and 487 genera. The dominant phyla were Ascomycota and Basidiomycota, and the dominant functional groups were saprotroph-symbiotroph, pathotroph-saprotroph and pathotroph-saprotroph-symbiotroph. 3) The main driving factors of the variations of root-associated fungal community were annual air humidity, annual precipitation, soil porosity, available nitrogen, annual sunshine hours and soil water content. 【Conclusion】 Our results demonstrated that the diversity and community composition of root-associated fungi associated with Mongolian pine were affected by the phenological periods in Mu Us Sandy Land. However, the

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stand age contributed less to the shaping of root-associated fungal community.

Key words: Mongolian pine; root-associated fungi; functional group; environmental factor; stand age.