

Dynamics of ectomycorrhizal fungi and response of ectomycorrhizal-seedlings associated with Mongolian Pine to drought stress and re-watering

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Abstract: 【Objective】 This study aimed to illuminate the temporal dynamic variations of community composition ectomycorrhizal fungi (EMF) associated with Mongolian pine at different phenological periods and investigated the environmental driving factors (climatic condition and soil property), and to explore the response of mycorrhizalized seedlings todrought stress and re-watering. **【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. 2-year-old seedlings of Mongolian Pine and key fungi were used as experimental material for pot experiment. **【Result】** 1) The diversity and composition of EMF communities in the Mu Us Sandy Land have distinct temporal dynamic features. α diversity index of the EMF were significantly affected by sampling month rather than stand age. 2) The dominant phylum is Ascomycetes, and the dominant genera are *Geopora*, *Tomentella*, *Tuber*, and *Inocybe*. Soil pH and annual air humidity ware the key environmental factors that significantly affect the EMF diversity and composition of Mongolian Pine. 4) Drought stress had adverse effects on the growth and physiological characteristics of Mongolian Pine seedlings. Due to the different degrees of drought stress, the growth and physiological characteristics of seedlings showed different degrees after re-watering. The ectomycorrhizal-seedlings showed higher drought resistance, drought recovery and drought adaptation. **【Conclusion】**Our results demonstrated that 1) the temporal dynamic characteristics of EMF community structure and composition were shaped by environmental changes, the main environmental driving factor was the average annual air humidity, and the main soil driving factor was soil pH value. 2) The response mechanism of ectomycorrhizal-seedlings to drought and re-watering can be summarized as follows: EMF enhances ectomycorrhizal-seedling drought resistance by promoting seedling growth and photosynthetic physiological processes, increasing leaf water content, regulating mesophyll cell osmotic pressure and removing excessive reactive oxygen species.

樟子松外生菌根真菌动态特征及其菌根化幼苗对干旱-复水的响应*

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摘要: 【目的】 阐明外生菌根真菌群落时间动态特征及其主要环境驱动因子, 探究樟子松菌根化幼苗对干旱-复水的响应。**【方法】** 本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, 比较分析不同采样月份 (4 月-9 月) 与

不同林龄樟子松外生菌根真菌群落结构和物种组成, 探究环境因子对外生菌根真菌群落多样性和功能群落结构的影响。利用分子生态网络分析、指示菌种分析及相对丰度差异分析相结合的方法, 筛选樟子松外生菌根真菌群落的关键菌种为试验菌种; 通过室内控制实验, 深入探究不同干旱胁迫程度对樟子松菌根化幼苗生长和生理特征的影响。【结果】1) 毛乌素沙地外生菌根真菌群落多样性和组成具有明显的时间动态特征。采样月份对樟子松外生菌根真菌 Chao1 指数、ACE 指数和 Pielou 指数影响显著 ($P<0.01$), 而林龄对外生菌根真菌 α 多样性指数无显著影响 ($P>0.05$)。2) 毛乌素沙地樟子松根尖共鉴定到 191 个外生菌根真菌 OUT, 隶属于 2 门、4 纲、11 目、20 科和 32 属。外生菌根真菌优势门为子囊菌门 (Ascomycetes), 优势属为地星属 (*Geopora*)、棉革菌属 (*Tomentella*)、块菌属 (*Tuber*) 和丝盖伞属 (*Inocybe*)。3) 樟子松人工林外生菌根真菌群落变化的主要驱动因子为受年均空气湿度、年均温、土壤 pH 值、土壤含水量和年均降水量。4) 干旱胁迫对樟子松幼苗生长和生理特征造成不利影响, 复水后幼苗生长和生理特征因干旱胁迫程度不同而不同。在干旱-复水下, 樟子松幼苗接种须腹菌属真菌 (OTU485, *Rhizopogon* sp., 后续简称 R) 和棉革菌属真菌 (OTU788, *Tomentella* sp., 后续简称 T) 后表现出较高的抗旱能力、旱后恢复能力和干旱适应能力。【结论】环境变化塑造了毛乌素沙地樟子松外生菌根真菌群落结构和组成的时间动态特征, 主要环境驱动因子为年均空气湿度, 主要土壤驱动因子为土壤 pH 值。樟子松菌根化幼苗对干旱-复水的响应机制可总结为: 外生菌根真菌通过促进幼苗生长和光合生理过程、提高叶片水分、调节叶肉细胞渗透压和清除过量活性氧的伤害等过程增强樟子松幼苗抗旱性。

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