

凋落物、根系和菌根输入对木荷恢复林地土壤微生物群落结构的影响

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摘要:【目的】阐明森林生态系统碳输入对土壤微生物群落结构的影响,为红壤退化地植被恢复过程中土壤肥力演变及生态系统恢复的微生物驱动机制提供理论依据。【方法】本文以亚热带红壤侵蚀退化地恢复形成的木荷纯林为研究对象,设置5种输入处理,即对照(CT)、菌根(M)、根系+菌根(RM)、凋落物+根系+菌根(LRM)和凋落物加倍+根系+菌根(DLRM),利用Illumina HiSeq 技术研究了不同有机碳输入对木荷纯林土壤微生物群落结构的影响。【结果】各有机碳输入处理均使土壤细菌总数降低了55~79%;M、RM和DLRM处理使土壤真菌OTUs数目提高了25-37%,使ACE指数提高了25-34%,Chao1指数提高了28-39%。木荷纯林土壤优势细菌门为Acidobacteria、Proteobacteria和Actinobacteria,LRM处理使Alphaproteobacteria的相对丰度降低了55%,M处理使Thermoleophilia的相对丰度提高了81%。优势真菌门为Basidiomycota和Ascomycota, RM、LRM和DLRM处理使sordariomycetes的相对丰度降低了46~64%,使mortierellomyetes的相对丰度提高了251~615%;不同有机碳输入对门水平细菌群落组成的影响顺序为LRM>RM>M>DLRM,对真菌群落组成的影响顺序为DLRM>LRM和RM>M。Alphaproteobacteria, Thermoleophilia, Sordariomycetes and Mortierellomycetes是有机碳输入变化影响的主要微生物类群。土壤有机碳、全氮是影响Mortierellomycetes变化的关键土壤因子。细菌群落主要影响了土壤酸性转化酶活性,而真菌群落影响了多种酶活性,且影响方向有正有负。【结论】有机碳输入改变了木荷森林土壤微生物的种类和数量,并且有机碳输入对真菌群落结构的影响大于细菌。

关键词:凋落物;根系;菌根;细菌群落;真菌群落;木荷林

Effects of litter, root and mycorrhiza input on soil microbial community structure in *Schima superba* restoration forest

Abstract: 【Objective】 The effects of different organic carbon inputs on soil microbial community structure were studied to provide a theoretical basis for soil fertility evolution and ecosystem restoration in the process of vegetation restoration in degraded red soil. 【Method】 The *Schima superba* pure forest recovered from eroded and degraded red soil in the subtropical region was taken as the research object. Five input treatments were set as follows: control treatment (CT), mycorrhiza (M), root + mycorrhiza (RM), litter + root + mycorrhiza (LRM), and double litter + root + mycorrhiza (DLRM). 【Result】 All organic carbon input treatments reduced the total quantity of soil bacteria by 55.02%~79.17%; M, RM and 2RM treatments increased the quantity of OTUs by 24.55%~36.93%, ACE index by 25.01%~33.97%, and Chao1 index by 28.10%~38.63%. The dominant bacteriophyta in *Schima superba* pure forest were Acidobacteria, Proteobacteria and Actinobacteria, and LRM treatment decreased the relative abundance of Proteobacteria by 43.2%; While the dominant fungal phyla were Basidiomycota and Ascomycota, and RM, LRM and DLRM treatments increased the relative abundance of Mortierellomycota by 250.73% to 614.67%; The order of effects of different organic carbon inputs on bacterial community composition at phylum level was LRM>RM>M>DLRM, and the order of effects on the fungal community composition was DLRM>LRM and RM>M. RDA analysis showed that soil pH, organic carbon, total nitrogen, available phosphorus and available content only accounted for 22.93% of the variation of soil bacterial community and 30.68% of the variation of soil fungal community, indicating that the variation of soil microbial community composition was also affected by other factors; There was a significant negative correlation between Chlorobacteria and soil total nitrogen, while there was a positive correlation between Chlorobacteria and soil organic carbon and total nitrogen. 【Conclusion】 Our results demonstrated that organic carbon input changed the species and quantity of soil microorganisms in *Schima superba* forest, and the effects of organic carbon input on the fungal community structure were greater than that of bacteria.

Key words: litter; roots; mycorrhiza; bacterial community; fungal community; *Schima superba*.

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