

林学一调查报告

云南元江干热河谷区植被梯度下土壤真菌群落研究

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摘要:

为了探讨极端环境因素是否会干扰植被对真菌群落的影响,采用克隆文库和变性凝胶梯度电泳(DGGE)的方法对云南元江干热河谷区植被梯度下土壤真菌群落的组成进行了研究。研究发现,尽管植被梯度变化显著,从灌丛过渡到草地,但是地下真菌的群落的变化比较微弱。主要真菌群落由Ascomycota组成,占全部克隆的70%。比较显著的群落组成差异是在不同的土层之间。特别是Ascomycota和Basidiomycota这两大类真菌的比例在腐殖质土和矿质土层间呈现很大差异,Ascomycota主要集中在表层腐殖质土中,而Basidiomycota主要分布在矿质土层中。研究结果与其他一般研究发现的植被变化决定土壤微生物变化不同,元江地区极端干燥炎热的环境干扰了地表植被对地面土壤真菌的群落组成,并呈现出与其它地区不一样的群落组成。

关键词: 变性凝胶梯度电泳

Soil Fungal Communities Along the Vegetation Gradient in Hot-dry Valley of Yuanjiang, Yunnan Province

Abstract:

In order to investigate whether the extreme environmental factors could be important factors in determining the composition of soil fungal communities by interfering with vegetation, we studied the soil fungal communities along the vegetation gradient in Hot-dry Valley of Yuanjiang, Yunnan Province. PCR-DGGE (denaturing gradient gel electrophoresis) and clone library technology were performed in the study. The soil fungal communities showed a very small change from shrub to grass in spite of a significant vegetation gradient existed. Ascomycota was found as the dominant species in the soil fungal communities, accounting for 70% of all clones. There were relatively significant differences in the fungal communities between different soil layers, for example, Ascomycota mainly distributed in the surface humus soil, while Basidiomycota mainly in the mineral soil. Our results demonstrated the soil fungal communities were interfered by the extreme hot and dry environment, showed a quite different community from other general findings, which declared vegetation change decided the soil microorganism.

Keywords: DGGE

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参考文献:

- [1] Torsvik V, Ovreas L. Microbial diversity and function in soil: from genes to ecosystems [J]. Current Opinion Microbiology, 2002(5): 240-245.
- [2] N. Fierer. Microbial biogeography: patterns in microbial diversity across space and time. In: Zengler K(ed). Accessing uncultivated microorganisms: from the environment to organisms and genomes and

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[3] Artz RRE, Anderson IC, Chapman SJ, et al. Changes in fungal community composition in response to vegetational succession during the natural regeneration of cutover peatlands [J]. *Microbial Ecology*, 2007(54): 508-522.

[4] Chan OC, Casper P, Sha LQ et al. Vegetation cover of forest, shrub and pasture strongly influences soil bacterial community structure as revealed by 16S rRNA gene T-RFLP analysis [J]. *FEMS Microbiology Ecology*, 2008(64): 449-458.

[5] 高庭艳, 马培, 张丹等. 云南元谋干热河谷区土壤微生物数量特征 武汉大学学报(理学版) [J]. 2008(2): 183-187.

[6] 宋富强, 曹坤芳. 元江干热河谷植物叶片解剖和养分含量特征 [J]. *应用生态学报*, 2005(1): 33-38.

[7] Vainio EJ, Hantula J. Direct analysis of wood-inhabiting fungi using denaturing gradient gel electrophoresis of amplified ribosomal DNA [J]. *Mycological Research*, 2000(104): 927-936.

[8] Lozupone C, Knight R. UniFrac: a new phylogenetic method for comparing microbial communities [J]. *Applied and environmental microbiology*, 2005(71): 8228-8235.

[9] Blackwood CB, Waldrop MP, Zak DR, et al. Molecular analysis of fungal communities and laccase genes in decomposing litter reveals differences among forest types but no impact of nitrogen deposition [J]. *Environmental Microbiology*, 2007(9): 1306 - 1316.

[10] Dixon P. VEGAN, a package of R functions for community ecology [J]. *Journal of Vegetation Science*, 2003(14): 927-930.

[11] De Castro AP, Quirino BF, Pappas G, et al. Diversity of soil fungal communities of Cerrado and its closely surrounding agriculture fields [J]. *Archives of Microbiology*, 2008(190): 129-139.

[12] Barroso CB, Nahas E. The status of soil phosphate fractions and the ability of fungi to dissolve hardly soluble phosphates [J]. *Applied Soil Ecology*, 2005(29): 73-83.

[13] Li T, Li LF, Sha T, et al. Molecular diversity of arbuscular mycorrhizal fungi associated with two dominant xerophytes in a valley-type savanna, southwest China [J]. *Applied Soil Ecology*, 2010(44): 61-66.

[14] Suzuki C, Nagaoka K, Shimada A, Takenaka M. Bacterial communities are more dependent on soil type than fertilizer type, but the reverse is true for fungal communities. *Soil Science and Plant Nutrition*, 2009(55): 80-90.

[15] Lindahl BD, Ihrmark K, Boberg J, et al. Spatial separation of litter decomposition and mycorrhizal nitrogen uptake in a boreal forest. *New Phytologist*, 2007(173): 611-620.

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