

农村发展—生态资源环境

沙漠中褐沙蒿根际细菌群落结构特征分析

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摘要:

基于16S rDNA基因的文库构建和分析,本文对比分析了浑善达克和毛乌素沙漠中褐沙蒿根际细菌群落结构特点。结果表明:褐沙蒿根际细菌类群主要有9类,即芽单胞菌(Gemmatimonadetes)(4.26%/2.08%,浑善达克样/毛乌素沙样,下同)、酸杆菌(Acidobacteria)(2.15%/2.08%)、放线菌(Actinobacteria)(10.64%/8.33%)、拟杆菌(Bacteroidetes)(2.13%/4.17%)、绿弯菌(Chloroflexi)(0/2.08%)和α-变形菌(α-proteobacteria)(65.96%/56.25%)、β-变形菌(β-proteobacteria)(0/6.25%)、δ-变形菌(δ-proteobacteria)(2.08%/2.13%)和γ-变形菌(γ-proteobacteria)(10.64%/2.08%)。来自两个采样地的褐沙蒿根际细菌群落结构总体相似,表明植物在此结构组成决定方面起了重要作用;两地根际细菌群落最主要差别之一是毛乌素褐沙蒿根际细菌比浑善达克沙漠多了三种光合细菌,即红螺菌(Rhodospirillales)、红细菌(Rhodobacter)和绿弯菌。

关键词: 16S rDNA

Characterization for Rhizobacterial Community Structure of Artemisia intramongolica in Deserts

Abstract:

Analysis and construction of library based on 16S rDNA gene, this study comparatively characterize the rhizobacterial community structure of Artemisia intramongolica sampled from Deserts of Hunsaderk and Mowosu. The results showed that rhizobacteria of Artemisia intramongolica composed of nine groups, i.e. Gemmatimonadetes (4.26%/2.08%, Hunsaderk/Mowos, the same with followings), Acidobacteria (2.15%/2.08%), Actinobacteria (10.64%/8.33%), Bacteroidetes (2.13%/4.17%), Chloroflexi (0/2.08%), α-proteobacteria (65.96%/56.25%), β-proteobacteria (0/6.25%), δ-proteobacteria (2.08%/2.13%) and γ-proteobacteria (10.64%/2.08%). Similar rhizobacterial community structure suggested that the associated plant was crucial for rhizobacteria composition, but some important difference between the plants from two deserts were observed, one of which was some photosynthetic bacteria existed in rhizosphere of Artemisia intramongolica from Mowosu while not in that from Hunsaderk.

Keywords: 16S rDNA

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