

张威,章高森,刘光琇,王鹭,董小培,岳君,李新荣,安黎哲. 腾格里沙漠东南缘可培养微生物群落数量与结构特征. 生态学报, 2012, 32(2): 567-577

腾格里沙漠东南缘可培养微生物群落数量与结构特征

Characteristics of cultivable microbial community number and structure at the southeast edge of Tengger Desert

投稿时间: 2010-12-14 最后修改时间: 2011-9-14

DOI: 10.5846/stxb201012141779

中文关键词: 腾格里沙漠东南缘 可培养细菌 土壤理化性质 系统发育树

English Keywords: [southeast edge of Tengger Desert](#) [cultivable bacteria](#) [soil physic-chemical properties](#) [phylogenetic tree](#)

基金项目: 国家自然科学基金项目(31100365, 31170465, 30800154, 40971034); 中国博士后科学基金项目(20080430794); 甘肃省科技计划(1011FKCA114, 1010RJZA009)

作者	单位	E-mail
张威	中国科学院 寒区旱区环境与工程研究所, 兰州 730000	
章高森	中国科学院 寒区旱区环境与工程研究所, 兰州 730000	
刘光琇	中国科学院 寒区旱区环境与工程研究所, 兰州 730000	liugx@lzb.ac.cn
王鹭	兰州大学, 兰州 730000	
董小培	兰州大学, 兰州 730000	
岳君	兰州大学, 兰州 730000	
李新荣	中国科学院 寒区旱区环境与工程研究所, 兰州 730000	
安黎哲	兰州大学, 兰州 730000	

摘要点击次数: 146

全文下载次数: 58

中文摘要:

以腾格里沙漠东南缘沙漠化土壤为研究对象,研究了不同沙漠化修复程度土壤结皮及结皮下微生物分布特征及多样性。结果表明:研究区域可培养细菌数量随沙漠化生态修复进程呈升高趋势,随采样深度呈下降趋势。数量以节杆菌属和芽孢杆菌属为主,其含量随沙漠化修复程度分别呈降低与升高趋势。修复过程中可培养土壤微生物数量与土壤碳、氮含量呈极显著正相关关系,与pH值呈极显著负相关关系,说明微生物数量与沙漠化土壤改良程度密切相关。通过16S rDNA基因测序及构建系统发育树,研究区域可培养细菌归类为18个属,分属于6个系统发育组:高G+C革兰氏阳性类群、低G+C革兰氏阳性类群、 α -变形菌、 β -变形菌、 γ -变形菌和CFB类群,序列比对显示菌株功能多样。

English Summary:

Desertification is a common environmental challenge for humans, which restricts social and economic development. Biotechnologies have been used for the management of soils in areas of desertification and the use of microorganisms has shown potential benefits, but such research is still in the initial stages. Here, we have studied the microbial distribution and diversity in soil crust and in the soil under the crust along sand dunes of different fixed ages at the southeast edge of the Tengger Desert, China. The Shapotou and Yiwuanquan regions were selected as sampling sites, which represented an artificial restoration region and a natural restoration region, respectively. The results showed that the number of culturable bacteria varied between 3.7×10^3 to 2.8×10^6 CFU/g, which was similar with other deserts worldwide. The number of culturable bacteria increased with the degree of sand dune fixation, and decreased with depth, which was similar to the trend of soil improvement in areas of desertification. Such characteristics did not show any significant differences between the artificial restoration region and the natural restoration region ($P > 0.05$). The genera *Arthrobacter* and *Bacillus* were the dominant bacteria at the southeast edge of the Tengger Desert. The genus *Arthrobacter* comprised 12.8%-69.5% and the genus *Bacillus* comprised 4.7%-60.7% of the total culturable bacteria, and these percentages increased and decreased with the degree of sand dune fixation, respectively. This result implied that *Arthrobacter* may play a significant role during preliminary soil crust formation. The results also showed that the quantity of culturable bacteria was positively correlated with the concentration of total soil carbon and total soil nitrogen ($P < 0.05$), but negatively correlated with pH values ($P < 0.05$). These results showed that microorganism number was closely related with the improvement status of desertification. Such results are likely to be caused by the interaction between soil microorganisms and soil carbon, nitrogen and organic acid. Based on 16S rDNA gene sequences and the phylogenetic tree, the culturable bacteria in the study area belonged to 18 genera: *Acinetobacter*, *Afiplia*, *Arthrobacter*, *Bacillus*, *Balneimonas*, *Brevundimonas*, *Chitinophaga*, *Chryseobacterium*, *Flavobacterium*, *Herbaspirillum*, *Janthinobacterium*, *Lysobacter*, *Microbacterium*, *Paenibacillus*, *Paracoccus*, *Phyllobacterium*, *Sphingomonas* and *Variovorax*, and fell into six phylogenetic groups: high G+C Gram positive bacteria, low G+C Gram positive bacteria, α -Proteobacteria, β -Proteobacteria, γ -Proteobacteria and Cytophaga-Flavobacterium-Bacteroides (CFB) group bacteria. Such a culturable bacterial community structure was similar with previous studies of desert ecosystems. Similar results also showed that the high proportion of G+C Gram positive, low G+C Gram positive and Proteobacteria, and a low proportion of CFB group bacteria could be the main bacterial community structure in the desert ecosystem. Blast results also showed that these bacterial strains had a variety of functions. Some strains showed accelerated function for the restoration of desertified areas. For example, *Afiplia*, *Balneimonas*, and *Herbaspirillum* had close relationships with nodule formation in plants. In contrast, some isolates in our study could also inhibit the restoration of desertified areas; some bacteria were plant pathogens, and some were identified as aerobic denitrifying bacteria. Besides these, pathogenic microorganisms and bacterial strains with potential applications were also found in desertification soil. The results of this study add to our knowledge of microorganism usage during the management of desertification.

您是本站第 3577390 位访问者

Copyright © 2005-2009 京ICP备06018880号

地址:北京海淀区双清路18号 邮编:100085 电话:010-62941099 E-mail: shengtaixuebao@rcees.ac.cn

本系统由北京勤云科技发展有限公司提供技术支持