中国农学通报 2011, 27(第11期5月) 271-275 DOI: ISSN: 1000-6850 CN: 11-1984/S

本期目录 | 下期目录 | 过刊浏览 | 高级检索 [打印本页] [关闭]

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

冯福应[1],**刘发来**[2],[2],**孙丽鹏**[2],[2],**孟建宇**[2],[2],**秦玉英**[2],[2],

1. 内蒙古农业大学生命科学学院
2.

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菌群结构总体相似，表明植物在此结构组成决定方面起了重要作用；两地根际细菌菌群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

收稿日期 2011-01-17 **修回日期** 2011-03-07 **网络版发布日期** 2011-05-15

DOI:

基金项目:

国家自然科学基金;内蒙古自治区重大自然科学基金项目;内蒙古自然科学基金;内蒙古自治区高等学校科学研究项目

通讯作者: 冯福应

作者简介:

作者Email: forefeng@hotmail.com

参考文献:

1 胡江春,薛德林,马成新,王书锦.植物根际促生菌(PGPR)的研究与应用前景[J].应用生态学报, 2004, 15: 1963?

扩展功能
本文信息
Supporting info
PDF(582KB)
[HTML全文]
参考文献[PDF]
参考文献
服务与反馈
把本文推荐给朋友
加入我的书架
加入引用管理器
引用本文
Email Alert
文章反馈
浏览反馈信息
本文关键词相关文章
16S rDNA
本文作者相关文章
冯福应
刘发来
孙丽鹏
孟建宇
秦玉英
PubMed
Article by Feng,F.Y
Article by Liu,F.L
Article by Xun,L.P
Article by Meng,J.Y
Article by Qin,Y.Y

1966.

2 刘发来.内蒙古荒漠主要植物根际细菌菌群组成结构特征分析[D].内蒙古农业大学学位论文, 2010.

3 陆雅海,张福锁.根际微生物研究进展. 土壤[J], 2006, 38: 113?121.

4 申建波,张福锁.根分泌物的生态效应[J].中国农业科技导报, 1999, 1: 21?27.

5 吴建峰,林先贵.土壤微生物在促进植物生长方面的作用[J].土壤, 2003, (1): 18?23.

6 Acinas S.G., Sarma-Rupavtarm R., Klepac-Ceraj V., Polz M.F. PCR-induced sequence artifacts and bias: insights from comparision of two 16S rRNA clone libraries constructed from the same sample. Applied and Environmental Microbiology, 2005, 71: 8966–8969.

7 Bodelier P.L.E., Wijlhuizen A.G., Blom C.W.P.M., Laanbroek H.J. Effects of photoperiod on growth of and denitrification by Pesudomonas chlororaphis in the root zone of Glyceria maxima, studied in a gnotobiotic microcosm[J]. Plant Soil, 1997, 190: 91 ?103.

8 Buée M., Boer W.D., Martin F., van Overbeek L., Jurkevitch E. The rhizosheere zoo: an overview of plant-associated communities of microorganisms, including phages, bacteria, archaea, and fungi, and of some of their structuring factors [J]. Plant Soil, 2009, 321: 189?212.

9 Cole J.R., Wang Q., Cardenas E., Fish J., Chai B., Farris R.J., Kulam-Syed-Mohideen A.S., MacGarrell D.M., Garrity G.M., Tiedje J.M. The ribosomal database project: improved alignments and new tools for rRNA analysis. Nucleic Acids Research, 2009, 37: D141?D145.

10 Cruz-Martínez K., Suttle K.B., Brodie E.L., Power M.E., Andersen G. L., Banfield J.F. Despite strong seasonal reponses, soil microbial consortia are more resilient to long-term changes in rainfall than overlying grassland[J]. International Society for Microbial Ecology, 2009, 3: 378?744.

11 Dakora F.D., Phillips D.A. Root exudates as mediators of mineral acquisition in low-nutrient environments. Plant Soil, 2002, 245: 35?47.

12 Fierer N., Breitbart M., Nulton J., Salamon P., Lozupone C., Jones R., Robeson M., Edwards R.A., Felts B., Rayhawk S., Knight R., Rohwer F., Jackson R.B. Metagenomic and small-subunit rRNA analyses reveal the genetic diversity of bacteria, archaea, fungi, and viruses in soil[J]. Applied and Environmental Microbiology, 2007, 73: 7059?7066.

13 Gunatilaka A.A.L. Natural products from plant-associated microorganisms: distribution, structure diversity, bioactivity, and implications of their occurrence[J]. Journal Natural Products, 2006, 69: 509?526.

14 Kent A.D., Triplett E.W. Microbial communities and their interactions in soil and rhizosphere ecosystems[J]. Annual Reviews of Microbiology, 2002, 56: 211?236.

15 Kuske C.R., Ticknor L.O., Miller M.E., Dunbar J.M., Davis J.A., Barns S.M., Belnap J. Comparision of soil bacterial communities in rhizospheres of three plant species and the interspaces in an arid grassland.

16 Marchesi J.R. Design and evaluation of useful bacterium-specific PCR primers that amplify genes coding for bacterial 16S rRNA[J]. Applied and Environmental Microbiology, 1998, 2: 795?799.

17 Nautiyal C.S., Rehman A., Chauhan P.S. Environmental Escherichia coli as natural plant growth-promoting soil bacterium[J]. Archive Microbiology, 2010, 192: 185?193.

18 Porteous L.A., Seidler R.J., Watrud L.S. An improved method for purifying DNA from soil for polymerase chain reaction amplification and molecular ecology applications[J]. Molecular Ecology, 1997, 6: 787?791.

19 Prosser J.L., Bohannan B.J.M., Curtis T.P., Ellis R.J., Firestone M.K., Freckleton R.P. The role of ecological theory in microbial ecology[J]. Nature Review of Microbiology, 2007, 5: 384?392.

20 Ranjard L., Lejon D.P., Mougel C., Schehrer L., Merdinoglu D., Chaussod R. Sampling strategy in molecular ecology: influence of soil sample size on DNA fingerprinting analysis of fungal and bacterial communities[J]. Environmental Microbiology, 2003, 5: 1111?1120.

21 Sipos R., Székely A.J., Palatinszky M., Révész S., Márialigeti K., Nikolausz M. Effect of primer mismatch, annealing temperature and PCR cycle number on 16S rRNA gene-targeting bacterial community analysis. FEMS Microbiology Ecology, 2007, 60: 341–350.

22 Spain A.M., Krumholz L.R., Elshahed M.S. Abundance, composition, diversity, and novelty of soil Proteobacteria[J]. International Society for Microbial Ecology, 2009, 3: 992?1000.

23 Basil A.J., Strap J.L. Studies on the microbial populations of the rhizosphere of big sagebrush (Artemisia tridentata)[J]. Journal of Indian Microbiology and Biotechnology, 2004, 31: 278?288.

24 van der Heijden M. G.A., Bardgett R.D., van Straalen N.M. The unseen majority: soil microbes as drivers of plant diversity and productivity in terrestrial ecosystems[J]. Ecology Letter, 2008, 11: 296?310.

25 Yang J., Kloepper J.W., Ryu C-M. Rhizoshpere bacteria help plants tolerate abiotic stress [J]. Trends in Plant Science, 2010, 14: 1?4.

26 Youssef N.H., Elshahed M.S. Diversity rankings among bacterial lineages in soil[J]. International Society for Microbial Ecology, 2009, 3: 305?313.

本刊中的类似文章

1．雷娟利 寿伟松 董文其 张成浩 徐志豪 周艳虹 喻景权.不同磷钙元素水平番茄营养液中细菌多样性[J]. 中国农学通报, 2010,26(22): 213-217

2．邓崇岭 娄兵海 白先进 宋雅琴 陈国平 赵小龙 陈传武 邓光宙.广西黄皮、不同柑桔品种黄龙病检测及16S

rDNA序列分析[J]. 中国农学通报, 2010,26(20): 283-286
3. 杨杨 霞，陈 陆，常洪涛，刘红英，杨影影，符 峰，王川庆.乳酸粪肠球菌的分离鉴定与系统进化分析[J]. 中国农学通报, 2009,25(10): 1-5
4. 余贤美 单公华 吕菲菲 沈广宁 周广芳.枣疯病植原体的快速检测[J]. 中国农学通报, 2011,27(第4期2月): 76-80
5. 王兴强，曹 梅，阎斌伦，等.缢蛏致病菌气单胞菌的分子生物学鉴定[J]. 中国农学通报, 2009,25(04): 270-273
6. 盖丽娜.兔源抗动物腹泻益生菌Tu-1的分离、鉴定及耐受性研究[J]. 中国农学通报, 2009,25(23): 1-6