

农业生态与环境科学

## 外来种互花米草盐沼土壤微生物16S rRNA特征分析——以江苏省潮间带为例\*

周虹霞<sup>1,2</sup>, 刘金娥<sup>1,3</sup>, 钦佩<sup>1\*\*</sup>

1. 南京大学生命科学院, 江苏 南京 210093;
2. 中国科学院昆明植物研究所, 云南 昆明 650204;
3. 南京师范大学地理科学学院, 江苏 南京 210093)

收稿日期 2006-2-18 修回日期

**摘要** 通过对互花米草盐沼和对应光滩的土壤微生物16S rRNA的特征检测, 分析了外来种互花米草的侵入对潮间带生态系统土壤微生物多样性的影响。试验中采集了江苏滨海不同季节光滩与互花米草(*Spartina alterniflora*)盐沼的土壤, 直接提取法分离得到其中的土壤微生物DNA, 并采用Sepharose 4B吸附柱对DNA进行纯化, 有效地去除了腐殖酸, 得到纯度较高的DNA样品模板。通过选取特异引物扩增16S rRNA基因序列, 得到了较清晰的结果: 有差异的16S rRNA扩增片断通过DGGE被分开, 形成可见条带; 不同的样品由于其中的微生物多样性的差异, 扩增出的条带数量及其在凝胶上的相对位置都有一定的差异。结果显示: 互花米草盐沼与光滩的土壤微生物群落多样性皆较低, 二者在互花米草生长初期其土壤微生物群落结构具有一定的相似性。但总体来说, 外来种互花米草的种植较明显地改变了滩涂的土壤微生物群落结构; 此外, 滩涂土壤微生物群落随着季节的变化而发生了较大的改变。

**关键词** [土壤微生物多样性](#) [16S rRNA](#) [DGGE](#) [外来种](#) [互花米草盐沼](#)

分类号 [S 154.32](#)

## Effects of an Alien Species (*Spartina alterniflora* Loisel) on 16S rRNA Profiles of Soil Microbial of Inter-tidal Ecosystem at Jiangsu Coastal Region, China

ZHOU Hong-xia<sup>1,2</sup>, LIU Jin-e<sup>1,3</sup>, QIN Pei<sup>1</sup>

1. Life Science School, Nanjing University, Nanjing 210093, China;
2. Kunming Institute of Botany, The Chinese Academy of Sciences, Kunming 650204, China;
3. Geography Science School, Nanjing Normal University, Nanjing 210093, China)

### Abstract

*Spartina alterniflora*, an introduced species vegetating on inter-tidal flats from the eastern coast of the United States, has become a hot topic focusing on its invasion to local species in the coastal zone of China. Impacts of *S. alterniflora* to soil microbial diversity in Jiangsu coastland was discussed by the result of denaturing gradient gel electrophoresis (DGGE) of polymerase chain reaction-amplified (PCR) 16S rDNA fragments in soil samples of *Spartina* salt marsh and mudflat. At each study site, fifteen plots were sampled to provide the sediment characteristics along the tidal flats in different seasons. The total bacterial DNA from the two studied soils was extracted directly, and the DNA was purified by Sepharose 4B absorbent column for wiping off the humus. 16S rDNA of bacteria from the two soils were amplified and were separated by DGGE. The samples got different DGGE bands because of the difference of microbial diversity in the two environments. DGGE profiles of the PCR productions were compared by similarity analysis. The results suggested that the soil microbial diversity in these two environments were not high. And, the two kind of soil samples got similar microbial community structure in spring time. As a whole, the microbial community components in inter-tidal zone differed with seasonal variety. And *S. alterniflora* has obviously changed the microbial community components when being introduced to Jiangsu coastal inter-tidal zone.

**Key words** [alien species](#) [Spartina salt marsh](#) [soil microbial diversity](#) [16S rRNA](#) [DGGE](#)

### 扩展功能

#### 本文信息

- ▶ [Supporting info](#)
- ▶ [PDF\(737KB\)](#)
- ▶ [\[HTML全文\]\(0KB\)](#)
- ▶ [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](#)
- ▶ [复制索引](#)

#### Email Alert

- ▶ [文章反馈](#)
- ▶ [浏览反馈信息](#)

#### 相关信息

- ▶ [本刊中 包含“土壤微生物多样性”的相关文章](#)
- ▶ [本文作者相关文章](#)

· [周虹霞](#)

· [刘金娥](#)

· [钦佩](#)

