

内蒙古呼伦贝尔草原土壤氨氧化细菌多样性及群落结构

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Diversity and community structure of soil ammonia-oxidizing bacteria in Hulunbeier Grassland, Inner Mongolia.

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- 摘要
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摘要

采用聚合酶链式反应-变性梯度凝胶电泳技术及扩增产物序列分析方法,研究了呼伦贝尔5种草地类型(线叶菊草原、贝加尔针茅草原、羊草草原、大针茅草原、克氏针茅草原)土壤氨氧化细菌多样性及群落结构特征。研究表明:不同草地类型间土壤氨氧化细菌群落结构组成差异显著,相似性均低于50%。线叶菊草原土壤氨氧化细菌群落多样性最高,其次是贝加尔针茅草原、羊草草原和克氏针茅草原,大针茅草原最低。5种草地类型土壤氨氧化细菌均以 *Nitrosospira* cluster 3 为优势种群,此外还发现有 *Nitrosospira* cluster 1、2、4 和 *Nitrosomonas*。线叶菊草原土壤氨氧化细菌群落组成较其他草地类型复杂,而羊草草原和大针茅草原群落组成较简单。经相关性分析,土壤含水量、土壤全氮、有机碳、土壤C/N与土壤氨氧化细菌群落多样性显著正相关($P<0.05$)。

关键词: 呼伦贝尔草原 氨氧化细菌 多样性 系统发育分析

Abstract:

By the methods of polymerase chain reaction-denaturing gradient gel electrophoresis and sequence analysis, a comparative study was conducted on the diversity and community structure of soil ammonia-oxidizing bacteria in the *Filifolium sibiricum* steppe, *Stipa baicalensis* steppe, *Leymus chinensis* steppe, *Stipa grandis* steppe, and *Stipa kryrowi* steppe in Hulunbeier Grassland, Inner Mongolia. A significant difference was observed in the community structure of soil ammonia-oxidizing bacteria among the five steppes, with the similarity lower than 50%. The diversity of soil ammonia-oxidizing bacteria was the highest in *F. sibiricum* steppe, followed by in *S. baicalensis* steppe, *L. chinensis* steppe, *S. kryrowi* steppe, and *S. grandis* steppe. In the five steppes, *Nitrosospira* cluster 3 was the dominant group, and the *Nitrosospira* cluster 1, 2, and 4 as well as *Nitrosomonas* were also found. The community structure of soil ammonia oxidizing bacteria in *F. sibiricum* steppe was most complex, while that in *L. chinensis* steppe and *S. grandis* steppe was relatively simple. Correlation analysis indicated that there existed significant positive correlations between the diversity of soil ammonia-oxidizing bacteria and the soil moisture, total nitrogen, total organic carbon, and C/N ratio ($P<0.05$).

Key words: [Hulunbeier Grassland](#) [ammonia-oxidizing bacteria](#) [diversity](#) [phylogenetic analysis](#)

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