Postprint: Analysis of Rhizosphere Soil Bacterial Communities of the Desert Steppe Plant *Peganum harmala*

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Abstract

Peganum harmala L. possesses strong drought and cold tolerance, playing an important role in maintaining the ecological environment. To understand its ecological adaptation and interaction mechanisms with the environment, high-throughput sequencing and pure culture methods were employed to investigate the characteristics of bacterial communities in the rhizosphere soil of P. harmala in the desert steppe region of Baiyin, Gansu Province, and to compare them with surrounding soils. The results showed that: the dominant bacterial phyla in the rhizosphere soil of P. harmala were Actinobacteria (30.01%), Proteobacteria (23.98%), Bacteroidetes (11.53%), and Acidobacteria (10.19%). The dominant bacterial phyla in the surrounding desert steppe soil were Actinobacteria (55.05%), Proteobacteria (21.11%), and Acidobacteria (6.07%). The culturable bacterial groups included Firmicutes, Proteobacteria, and Actinobacteria, among which the dominant bacteria isolated from rhizosphere soil were Brevibacterium (23.53%), Bacillus (23.53%), and Pseudomonas (17.65%), while the dominant culturable bacterial populations in surrounding soil were Arthrobacter (37.50%), Bacillus (18.75%), and Pseudomonas (12.50%). The composition and structure of the rhizosphere microbial community of P. harmala showed significant differences from those of the surrounding soil, with the microbial quantity and diversity index in rhizosphere soil being significantly higher than those in non-rhizosphere soil. The research findings provide a scientific basis for understanding the interactions between desert plants and rhizosphere microorganisms, revealing the role of soil microorganisms in promoting material cycling and transformation in the plant rhizosphere, screening for plant growth-promoting beneficial microorganisms, and strengthening the ecological protection of desert steppe.

Full Text

Diversities of Bacterial Community in Rhizosphere Soil of *Peganum harmala* L. in the Desert Steppe of Northwestern China

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Abstract

Peganum harmala L. exhibits strong resistance against harsh environments such as drought and low temperature. The plant plays an important role in maintaining the local ecological environments. In order to understand the mechanism of ecological adaptation and interaction with the environments, the characteristics of bacterial communities of *Peganum harmala* L. rhizosphere soil in Gansu Baiyin desert steppe region were studied by high-throughput sequencing and culture-dependent methods, and compared with those of the surrounding soils. The results showed that the bacterial community in the rhizosphere soil mainly consisted of 30.01% Actinobacteria, 23.98% Proteobacteria, 11.53% Bacteroidetes, and 10.19% Acidobacteria. The dominant bacterial community in the surrounding desert steppe soil comprised 55.05% Actinobacteria, 21.11% Proteobacteria, and 6.07% Acidobacteria. The cultivable bacteria group included Firmicutes, Proteobacteria, and Actinobacteria. Among the rhizosphere soil, the dominant bacteria are 23.53% *Brevibacterium*, 23.53% *Bacillus*, 17.65% *Pseudomonas*, and 11.76% *Brevundimonas*. The dominant populations of bacteria in the surrounding soil are 37.50% *Arthrobacter*, 18.75% *Bacillus*, and 12.50% *Pseudomonas*. The bacterial communities between the *Peganum harmala* L. rhizosphere soil and its surrounding desert steppe soils showed significant differences. The bacterial numbers and diversity index in the rhizosphere soil were significantly higher than those of the surrounding desert steppe soil. The results provided the scientific basis for exploring the interaction between desert grassland plants and their rhizobacteria, and understanding the roles of the rhizobacteria in promoting plant growth and soil material transformation. They were also very useful for screening beneficial microorganisms and protecting desert steppe ecosystems.

Keywords: Desert steppe; *Peganum harmala* L.; Rhizosphere soil; Bacterial community; High-throughput sequencing; Soil microorganism

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Note: Figure translations are in progress. See original paper for figures.