

Soil microbial diversity of an artificial *Caragana korshinskii* plantation on the loess plateau of China

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Introduction Peashrub (*Caragana korshinskii*) is an important dune-fixation plant on the loess plateau of China and is valuable in ecological environment construction of North-western China. For determining relationships between peashrub and soil microbes, three clone libraries of 16S rDNA from rhizoplane, rhizosphere and bulk soil communities of peashrub were constructed with a culture-independent approach. The data obtained from three clone libraries were used to investigate the magnitude of vegetative changes in the microbial community, and to search for general ecological relationships.

Materials and methods Sampling from peashrub rhizoplane, rhizosphere, and bulk soil was done in October 2003 at Wuzhai, Shanxi Province (39°00'22.9"N, 111°45'39.7"E, with a ground water depth of 1362 m). Metagenomic DNA was prepared by the CTAB-SDS method. Three 16S rDNA clone libraries were constructed with pMD18-T, and every clone was sequenced through reverse and forward M13 primers. Phylogenetic tree construction was carried out by the nearest neighbour method. And the Shannon-Weaver index (H'), Simpson index (D) and the relative index were chosen to characterise the microbial communities.

Results One hundred seven positive clones were randomly selected and fully sequenced (about 900 bp) from 3 clone libraries of 16S rDNA genes. Based on sequence comparison, 3 phylogenetic trees were obtained and the closest relatives of most clones gave 13 distinct clusters except 7 sequences were closely associated with environmental clone sequences, i.e., uncultivated bacteria (Table 1). Bacteria were the dominant group in each of the 3 libraries, though their percentage decreased with the distance from peashrub roots. If rhizoplane, rhizosphere and bulk soil are figured as one line, the number of α -*Proteobacteria* and low-G+C gram positive bacteria decreased but high-G+C bacteria and archaea increased along the line. Otherwise, the *Acidobacterium* division was a major group in rhizosphere and bulk soil samples but was not detected in the peashrub rhizoplane.

Table 1 Summary of the phylogenetic assignments of 107 SSU rDNA clones made from a Loess Plateau *C. korshinskii* plantation soil within the major taxa

Major taxon and group	No. (%) of organisms identified			
	Rhizoplane	Rhizosphere	Bulk soil	Total
Archaea	2(5.0)	6(13.9)	6(25.0)	14(13.1)
<i>Crenarchaeota</i>	2(5.0)	6(13.9)	6(25.0)	14(13.1)
Eucarya	4(10.0)	0	0	4(3.7)
Plants	4(10.0)	0	0	4(3.7)
Bacteria	33(82.5)	34(79.1)	15(62.5)	82(76.6)
Green nonsulfur	0	1(2.3)	1(4.2)	2(1.9)
Low-G+C gram positive	2(5.0)	0	0	1(0.9)-
High-G+C gram positive	2(5.0)	3(6.9)	3(12.5)	8(7.5)
<i>Cytophaga-Flexibacter-Bacteroides</i>	2(5.0)	1(2.3)	0	3(2.8)
Planctomyces	1(2.5)	2(4.7)	1(4.2)	4(3.7)
<i>Verrucomicrobium</i>	1(2.5)	2(4.7)	1(4.2)	4(3.7)
Proteobacteria	26(65.0)	12(27.9)	5(20.8)	43(40.2)
α	6(15.0)	5(11.6)	2(8.3)	13(12.1)
β	2(5.0)	2(4.7)	0	4(3.7)
γ	18(45.0)	4(9.3)	3(12.5)	25(23.4)
δ	0	1(2.3)	0	1(0.9)-
Acidobacteria	0	13(30.2)	4(16.7)	17(15.9)
Unclassified	1(2.5)	3(6.9)	3(12.5)	7(6.5)
Total clones sequenced	40	43	24	107

Conclusions The microbial richness and diversity index was lower in bulk soil, which reflects the soil character and environmental condition at the loess plateau. But as a long-term planting of peashrub, many plant-associated bacteria appeared in the rhizoplane and rhizosphere of peashrub, which probably play a great role in peashrub growth and survival in an abominable environment.