



Genetic diversity and phylogeny of rhizobia isolated from *Caragana microphylla* growing in desert soil in Ningxia, China

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Genet. Mol. Res. 11 (3): 2683-2693 (2012)
Received January 10, 2012
Accepted May 25, 2012
Published June 25, 2012
DOI <http://dx.doi.org/10.4238/2012.June.25.5>

ABSTRACT. Rhizobia are soil bacteria with the capacity to induce nitrogen-fixing nodules on the roots or stems of legume plants. A total of 40 bacterial isolates from the root nodules of *Caragana microphylla* growing in desert soil in Ningxia, China, were analyzed for genetic diversity and phylogenetic position. These isolates were classified into 7 types of 16S ribosomal DNA (rDNA) using polymerase chain reaction-restriction fragment length polymorphism analysis. They were grouped into 4 clades, *Rhizobium-Agrobacterium*, *Sinorhizobium*, *Phyllobacterium*, and *Bradyrhizobium*, when the phylogenies of 16S rDNA, *recA*, and *atpD* genes were applied. Phylogenetic analysis showed that the tree generated from the 16S rDNA sequencing agreed with that produced from the *recA* and *atpD* genes. By analyzing phylogenetic relationship using the 3 loci, the isolates in the branches of *Phyllobacterium* and *Sinorhizobium* could be identified as *P. brassicacearum* and *S. meliloti*. The isolates in the branch of *Rhizobium-Agrobacterium* were the most abundant microsymbiont of *C. microphylla* and were designated *R. leguminosarum*, *R. galegae*, *R. alamii*, and *A. tumefaciens*. Two isolates with low sequence similarity

to the known species of *Bradyrhizobium* might be novel species in this genus.

Key words: Phylogeny; 16S ribosomal DNA; *recA*; *atpD*; Rhizobia; *Caragana microphylla*