**Genome Sequence of the Symbiotic Type Strain Rhizobium tibeticum CCBAU85039T**

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**ABSTRACT** Rhizobium tibeticum was originally isolated from root nodules of Trigonella archiducis-nicolai grown in Tibet, China. This species is also able to nodulate Medicago sativa and Phaseolus vulgaris. The whole-genome sequence of the type strain, R. tibeticum CCBAU85039T, is reported in this study.

Availability of nitrogen in soils is one of the main concerns for crop cultivation in agriculture. Nitrogen is essential for the biosynthesis of proteins, amino acids, vitamins, and other compounds. Chemical fertilizers commonly ensure sufficient nitrogen availability for crop production. However, these compounds may also cause environmental problems (1, 2). Alternatively, certain bacteria and archaea are able to fix atmospheric dinitrogen via reduction to ammonia. Rhizobia belonging to the classes Alphaproteobacteria or Betaproteobacteria inhabit soils and are able to enter into nitrogen-fixing symbiosis with leguminous plants. They induce the development of root nodules, where, after colonization and differentiation, bacteroids are able to fix dinitrogen (3). Rhizobia are highly diverse regarding their genetic, metabolic, and taxonomic characteristics (4). Mesorhizobium loti MAF303099 (5) and Ensifer melloti 1021 (6) were the first rhizobia for which complete genome sequences became available. Recently, the genome sequences of 163 further root-nodule bacteria were published, extending our knowledge regarding this group of bacteria (7). However, particular and important species/groups were not covered by the study cited above. An important clade within the group of rhizobia comprises the strains Rhizobium mesoamericanum CCG502T (8), Rhizobium grahamii CCG501T (9), Rhizobium favelukesi LP183T (10), and Rhizobium tibeticum CCBAU85039T (11). While genome sequence information is available for the first three strains, the genome of R. tibeticum CCBAU85039T had not yet been sequenced. The latter strain is able to nodulate Phaseolus vulgaris, Medicago lupulina, Medicago sativa, Trigonella archidicus-nicolai, and Trigonella foenum-graecum. With the objective to uncover mechanisms of rhizobial diversification and to complement genome sequence information for rhizobial species, the R. tibeticum CCBAU85039T genome was sequenced.

Genomic DNA of R. tibeticum CCBAU85039T was isolated using the GENTRA PureGene kit (Qiagen). A sequencing library was constructed and sequenced on the MiSeq platform applying the Illumina paired-end protocol (Illumina, Inc.). In total, 4,090,570 sequence reads were obtained, yielding a total of 1,102,161,679 bp of sequence information. The Illumina reads were assembled by the GS de novo assembler software.
The version described in this paper is the first version, FNXB01000000. The genome was annotated applying the Prokka pipeline and GenDB (12, 13), which predicted 6,977 protein-coding sequences (CDSs) and 45 tRNA genes. The rRNA operon was found on a 4-fold overrepresented contig, suggesting the presence of four rrn copies within the genome. Genome comparisons were done within the EDGAR version 2.0 platform (14). More than 5,200 CDSs of \( R. \) tibeticum (75% of all CDSs) represent orthologs to corresponding \( R. \) favelukessii LPUB37 genes (15). Moreover, phylogenetic analysis of the concatenated core genomes confirmed a close relationship between both strains, as previously described (16). Further comparative studies will elucidate the similarities and differences among different groups of sequenced rhizobial strains and refine their taxonomic classification.

**Accession number(s).** This whole-genome shotgun project has been deposited in the EMBL database under the accession numbers FNXB01000001 to FNXB01000167.

**REFERENCES**


