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Permanent Draft Genome Sequence of the French Bean Symbiont Rhizobium sp. Strain RSm-3 Isolated from the Eastern Himalayan Region of India


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ABSTRACT The genus Rhizobium contains many species able to form nitrogen-fixing nodules on plants of the legume family. Here, we report the 6.9-Mbp draft genome sequence of Rhizobium sp. strain RSm-3, with a G+C content of 61.4% and 6,511 candidate protein-coding genes.

The genus Rhizobium, established in 1889, is a group of motile, aerobic, and Gram-negative bacteria in the alphaproteobacterial group with a moderate G+C percentage (60%) (1, 2). Members of the genus Rhizobium form a symbiotic association with various legume plants of the Fabaceae family (3–5) and form nodules on the root surface. These nodules are the sites of nitrogen fixation. The symbiosis between Rhizobium and legumes is of great importance (6). Compared to the use of chemical fertilizers, symbiosis offers cheaper and more effective agronomic practices by providing an adequate supply of N for legume-based crops (7, 8). The French bean, or common bean (Phaseolus vulgaris L.), is one of the most important plant hosts of Rhizobium spp., with the broadest genetic base (9, 10), and is one of the major cultivated crops containing large amounts of protein, minerals, and antioxidant compounds (11).

Rhizobium sp. strain RSm-3 was isolated from the root nodules of P. vulgaris collected from the Sonada region of Darjeeling district (26.9400°N, 88.250°E; altitude, 5,157 ft) of West Bengal, India. The strain showed antagonistic activity against the fungal pathogen Fusarium solani and resistance against most of the antibiotics tested against it. These interesting features led us to do 16S rRNA gene sequencing, which identified the strain as Rhizobium sp. and shared 99% identity with Rhizobium etli EBRI21 (accession no. AY221176.1). This strain was sequenced to provide a greater understanding of these physiological properties and its interaction with P. vulgaris.

Sequencing of the draft genome of Rhizobium sp. strain RSm-3 was performed at the Hubbard Center for Genome Studies (University of New Hampshire, Durham, NH) using Illumina techniques (12). A standard Illumina shotgun library was constructed and sequenced using the Illumina HiSeq 2500 platform, which generated 1,585,078 reads (260-bp insert size) totaling 341 Mbp. The Illumina sequence data were trimmed by Trimmomatic version 0.32 (13) and assembled using SPAdes version 3.5 (14), and ALLPaths-LG version r52488 (15). The final draft assembly for Rhizobium sp. strain RSm-3 consisted of 60 contigs, with an N50 contig size of 313.1 kb and 54.3× coverage of the genome. The final assembled genome contained a total sequence length of 6,912,093 bp, with a G+C content of 61.4%.

The assembled RSm-3 genome was annotated via the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) and resulted in 6,511 candidate protein-coding genes, 46
tRNAs, four rRNA (two 5S rRNA, one 16S rRNA, and one 23S rRNA) regions, and 111 (1.69%) pseudogenes. The genome of RSm-3 also revealed the presence of the nod and nodC operons involved in nitrogen fixation and host plant nodulation, respectively. A total of 590 signal peptide-coding genes and 1,563 enzyme-coding genes were assigned through the annotation program.

There are two major branches of common bean, Mesoamerican and Andean (16), and a third genetic diversification of the common bean is found in the Peru-Ecuador region (17). A new species of Rhizobium, R. ecuadorense, has been proposed for the microsymbiont of the Peru-Ecuador common bean. The average nucleotide identity (ANI) score for Rhizobium sp. strain RSm-3 was 98% similarity with the R. ecuadorense type strain (CNPSo 671) (18) suggesting that it is a subspecies of R. ecuadorense.

Accession number(s). This whole-genome shotgun sequence has been deposited at DDBJ/EMBL/GenBank under the accession number MAWZ00000000. The version described in this paper is the first version, MAWZ01000000.

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