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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* EBRI 21 (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 Trimomatic 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 N_{50} 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

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This is scientific contribution number 2711.

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 *nif* and common *nod* 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. ecuadorensis*, 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. ecuadorensis* type strain (CNPSO 671) (18) suggesting that it is a subspecies of *R. ecuadorensis*.

Accession number(s). This whole-genome shotgun sequence has been deposited at DDBJ/EMBL/GenBank under the accession number [MAWZ00000000](https://www.ncbi.nlm.nih.gov/nuccore/MAWZ00000000). The version described in this paper is the first version, MAWZ01000000.

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