Genome Sequence of *Rhizobium grahamii* CCGE502, a Broad-Host-Range Symbiont with Low Nodulation Competitiveness in *Phaseolus vulgaris*

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Here we present the genome sequence of *Rhizobium grahamii* CCGE502. *R. grahamii* groups with other newly described broad-host-range species, which are not very efficient *Phaseolus vulgaris* symbionts, with a wide geographic distribution and which constitutes a novel *Rhizobium* clade.

*Rhizobium grahamii* CCGE502 was isolated from *Dalea leporina* (prairie clover) in Jalisco, Mexico (8). CCGE502 is the type strain of *R. grahamii* (6). It forms nodules on *Leucaena leucocephala* and *Phaseolus vulgaris* (common bean). In *P. vulgaris*, CCGE502 has a low capacity to fix nitrogen, and in interstrain nodulation assays, CCGE502 is outcompeted by common *Rhizobium* species that are *P. vulgaris* symbionts, such as *R. etli* CFN42 and *R. phaseoli* strains. *R. grahamii* is taxonomically related to *R. mesoamericanum* (6), *R. endophyticum* (7), and *R. tibeticum* (4). This novel clade, which also includes *Rhizobium* sp. strains Or191, STM3625, and LPU83 (2, 10, 14), is related to the tropici group of broad-host-range related *Rhizobium* species that contains very efficient *P. vulgaris* symbionts that are used as crop inoculants (5). The CCGE502 genome sequence was obtained by using Illumina GAIIx (36-bp paired-end reads of 300-bp fragments) and 8-kbp libraries. Reads obtained with Illumina were assembled into contigs by using Velvet (15) and combined with the Roche 454 data by using the gsAssembler implemented in the Newbler software (Roche). As a result, we obtained 87 large contigs (>500 bp), distributed in 11 scaffolds, with a total size of 7.10 Mbp. A 177-fold genome coverage was obtained. The genome was annotated using the RAST server (1). A total of 7,260 protein-coding genes distributed in 460 metabolic subsystems were predicted.

The CCGE502 genome comprises a 5.4-Mbp chromosome with a G + C content of 59.69% and two plasmids of 1.29 Mbp and 0.46 Mbp with G + C contents of 59.04% and 57.41%, respectively. The symbiotic plasmid (pSym; 0.46 Mbp) is most similar to that of *R. mesoamericanum* CCGE501, with similarity in some fragments to the *R. tropici* CIAT 899 symbiotic plasmid, and has repC as well as repABC replication systems. It also has a nodH gene that participates in sulfation of Nod factors and gibberellin biosynthesis genes, but it lacks teu (13) and nodS genes (11, 12), which are determinants of competitiveness in *R. tropici* and *R. etli*. pSym conjugal transfer is activated by quorin sensing (M. J. Althabegoiti, unpublished data). The megaplasmid has conserved regions with replications equivalent to pReCFN42e that have been designated chromids (3).

Genome analysis and comparison to other bean symbionts will contribute to a further understanding of bean-*Rhizobium* symbiosis (9).

Nucleotide sequence accession numbers. The results of this whole-genome shotgun project have been deposited at DDBJ/EMBL/GenBank under the accession number AEYE00000000. The version described in this paper is the first version, AEYE01000000.

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