



Genome Sequence of *Rhizobium jaguaris* CCGE525^T, a Strain Isolated from *Calliandra grandiflora* Nodules from a Rain Forest in Mexico

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ABSTRACT We present the genome sequence of *Rhizobium jaguaris* CCGE525^T, a nitrogen-fixing bacterium isolated from nodules of *Calliandra grandiflora*. CCGE525^T belongs to *Rhizobium tropici* group A, represents the symbiovar *calliandrae*, and forms nitrogen-fixing nodules in *Phaseolus vulgaris*. Genome-based metrics and phylogenomic approaches support *Rhizobium jaguaris* as a novel species.

Rhizobium jaguaris CCGE525^T was isolated from nodules of the medicinal legume *Calliandra grandiflora* growing in a rain forest in Chiapas, Mexico, and was described as related to *Rhizobium tropici* group A (1). *R. tropici* group A was defined by 16S rRNA gene sequences and distinctive phenotypic characteristics (2). We report the genome sequence of strain CCGE525, the type strain of *Rhizobium jaguaris*.

A single colony from a freeze-dried culture sample of *R. jaguaris* CCGE525^T was incubated on peptone yeast (PY) medium (5 g/liter peptone, 3 g/liter yeast extract, and 0.6 g/liter CaCl₂) for 3 days at 30°C. DNA was extracted from 3 ml of culture using a kit for cells and tissues (Roche Applied Science, Germany). A SMRTbell library of 15- to 20-kb insert size was constructed using standard protocols. The library was sequenced on a PacBio RS II sequencer (3) using P6-C4 chemistry, which yielded 3.4 Gb of data. Reads were filtered and assembled *de novo* using Canu v.1.5 (4). Annotation was performed using the NCBI Prokaryotic Genome Annotation Pipeline (https://www.ncbi.nlm.nih.gov/genome/annotation_prok/) (5). Amino acid sequences served as input to PhyloPhlAn (6) to predict evolutionary relationships. The progressive Mauve tool was used for genome alignments (7). DNA-DNA hybridization (DDH) values were computed using the Genome-to-Genome Distance Calculator v.2.1 (8). Average nucleotide identity (ANI) values were calculated as previously proposed (9) using the ANI calculator from the Konstantinidis Lab (<http://enve-omics.ce.gatech.edu/ani/>) (10). Default parameters were used for all programs.

The genome of *R. jaguaris* CCGE525^T (8,025,568 bp, 58.95% G+C content, and ~278-fold coverage) consisted of a chromosome (4,575,315 bp), a chromid (2,584,926 bp), a symbiotic plasmid required for establishing interactions with legumes (550,563 bp), and an additional plasmid (314,764 bp). The genome coded for 8,400 predicted genes.

The *R. tropici* group A affiliation of *R. jaguaris* CCGE525^T was supported by its position in a genome tree (Fig. 1A). This phylogenomic approach increased resolution and confirmed the placement of *R. jaguaris* CCGE525^T as an isolated branch in the vicinity of *Rhizobium leucaenae* USDA 9039^T.

R. jaguaris CCGE525^T is classified within the symbiovar *calliandrae* and has the capacity to form nitrogen-fixing nodules with common bean (1). A multiple sequence alignment revealed that the symbiotic plasmid of *R. jaguaris* CCGE525^T was less

Citation Servín-Garcidueñas LE, Guerrero G, Rogel-Hernández MA, Martínez-Romero E. 2019. Genome sequence of *Rhizobium jaguaris* CCGE525^T, a strain isolated from *Calliandra grandiflora* nodules from a rain forest in Mexico. *Microbiol Resour Announc* 8:e01584-18. <https://doi.org/10.1128/MRA.01584-18>.

Editor Julia A. Maresca, University of Delaware

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Received 19 November 2018

Accepted 23 January 2019

Published 28 February 2019

ACKNOWLEDGMENTS

This research was supported by CONACyT 253116 and PAPIIT IN207718 from UNAM.

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