




Genome Sequence of *Bradyrhizobium mercantei* Strain SEMIA 6399^T, Isolated from Nodules of *Deguelia costata* in Brazil

Renan Augusto Ribeiro,^a Luisa Caroline Ferraz Helene,^{b,c,d}
Jakeline Renata Marçon Delamuta,^{b,d}  Mariangela Hungria^{a,b,c}

Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), Brasília, Brazil^a; Embrapa Soja, Londrina, Brazil^b; Universidade Estadual de Londrina (UEL), Department of Biochemistry and Biotechnology, Londrina, Brazil^c; Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES), Brasília, Brazil^d

ABSTRACT SEMIA 6399^T is the type strain of *Bradyrhizobium mercantei*, a nitrogen-fixing symbiont of *Deguelia costata*. Its draft genome contains 8,842,857 bp with 8,246 predicted coding sequences (CDS), several related to amino acids and derivatives and to stress tolerance, with an emphasis on oxidative stress, in addition to symbiotic genes.

Bacteria known as rhizobia are capable of establishing symbioses with a broad range of legumes, resulting in the nitrogen fixation process, with high impact on agriculture productivity and environmental sustainability. In the tropics, *Bradyrhizobium* bacteria are the predominant symbionts of legumes (1–3). The genus occupies a variety of ecosystems and is enriched in living styles (1–4), and in the past few years, our group has reported large genetic diversity among Brazilian *Bradyrhizobium* strains (2, 3), resulting in the description of new species within this genus (5–7).

Here, we report the draft genome of strain SEMIA 6399^T (=CNPSo 1165^T = BR 6010^T = U675^T = LMG 30031^T) of the recently described new species *Bradyrhizobium mercantei* (8). The strain is a symbiont of *Deguelia costata* (syn. *Lonchocarpus costatus*), an important legume native to eastern Brazil; SEMIA 6399^T has been used in commercial inoculants for this legume in Brazil since 1994 (8). The species is named after Fábio Martins Mercante (1963 to 2016), an extraordinary Brazilian microbiologist from Embrapa who dedicated his career to studies on biological nitrogen fixation (8).

To access the bacterial genome sequence, total DNA was extracted using the DNeasy blood and tissue kit (Qiagen) and processed on the MiSeq platform (Illumina) at Embrapa Soja, Londrina, Brazil. Shotgun sequencing allowed a genome coverage of approximately 29-fold. The FASTQ files were *de novo* assembled by the A5-MiSeq pipeline (9). The genome was estimated at 8,842,857 bp, assembled in 72 contigs, with a G+C content of 63.99 mol%. Average nucleotide identity (ANI) with the closest species, *B. tropiciagri* CNPSo 1112^T, was 91.5%.

Sequences were submitted to RAST (10), and annotation identified 8,243 coding sequences (CDS). The analysis at the SEED system (11) allowed the classification of 41% of the CDS in 502 subsystems. Nitrogen fixation genes (*nif*) showed similarity with *Bradyrhizobium diazoefficiens* USDA 110^T, and strain SEMIA 6399^T also possesses genes coding for the hydrogenase that may improve the efficiency of the nitrogen fixation process (12). Interestingly, the major category of putative genes was of the metabolism of amino acids and derivatives (15.3%), followed by the carbohydrates (14.5%). The genome is enriched with genes of resistance to antibiotics and toxic compounds (117 CDS) and genes of type I, II, III, and IV secretion systems, and it carries 214 CDS of stress response, the majority (55.1%) of which are related to the oxidative stress metabolism.

Received 27 July 2017 Accepted 31 July 2017 Published 7 September 2017

Citation Ribeiro RA, Helene LCF, Delamuta JRM, Hungria M. 2017. Genome sequence of *Bradyrhizobium mercantei* strain SEMIA 6399^T, isolated from nodules of *Deguelia costata* in Brazil. *Genome Announc* 5:e00943-17. <https://doi.org/10.1128/genomeA.00943-17>.

Copyright © 2017 Ribeiro et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Mariangela Hungria, mariangela.hungria@embrapa.br.

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under accession number [MKFI00000000](https://doi.org/10.1093/jis.0.009779-0). The version described in this paper is MKFI01000000.

ACKNOWLEDGMENTS

This work was funded by CNPq-Universal (400468/2016-6), Embrapa (02.13.08.001.00.00), and INCT-Plant-Growth Promoting Microorganisms for Agricultural Sustainability and Environmental Responsibility (CNPq 465133/2014-2; Fundação Araucária).

REFERENCES

- Menna P, Barcellos FG, Hungria M. 2009. Phylogeny and taxonomy of a diverse collection of *Bradyrhizobium* strains based on multilocus sequence analysis of the 16S rRNA gene, ITS region and *glnII*, *recA*, *atpD* and *dnaK* genes. *Int J Syst Evol Microbiol* 59:2934–2950. <https://doi.org/10.1099/ijs.0.009779-0>.
- Menna P, Hungria M. 2011. Phylogeny of nodulation and nitrogen-fixation genes in *Bradyrhizobium*: supporting evidence for the theory of monophyletic origin, and spread and maintenance by both horizontal and vertical transfer. *Int J Syst Evol Microbiol* 61:3052–3067. <https://doi.org/10.1099/ijs.0.028803-0>.
- Hungria M, Menna P, Delamuta JRM. 2015. *Bradyrhizobium*, the ancestor of all rhizobia: phylogeny of housekeeping and nitrogen-fixation genes, p 191–202. *In* de Bruijn FJ (ed.), *Biological nitrogen fixation*. John Wiley & Sons, Hoboken, NJ. <https://doi.org/10.1002/9781119053095.ch18>.
- Eaglesham ARJ, Ellis JM, Evans WR, Fleischman DE, Hungria M, Hardy RWF. 1990. The first photosynthetic N₂-fixing *Rhizobium*: characteristics, p 805–811. *In* Gresshoff PM, Roth LE, Stacey G, Newton WE (ed.), *Nitrogen fixation: achievements and objectives*. Chapman & Hall, New York. https://doi.org/10.1007/978-1-4684-6432-0_69.
- Delamuta JRM, Ribeiro RA, Ormeño-Orrillo E, Melo IS, Martínez-Romero E, Hungria M. 2013. Polyphasic evidence supporting the reclassification of *Bradyrhizobium japonicum* group Ia strains as *Bradyrhizobium diazoefficiens* sp. nov. *Int J Syst Evol Microbiol* 63:3342–3351. <https://doi.org/10.1099/ijs.0.049130-0>.
- Delamuta JRM, Ribeiro RA, Ormeño-Orrillo E, Parma MM, Melo IS, Martínez-Romero E, Hungria M. 2015. *Bradyrhizobium tropiciagri* sp. nov. and *Bradyrhizobium embrapense* sp. nov., nitrogen-fixing symbionts of tropical forage legumes. *Int J Syst Evol Microbiol* 65:4424–4433. <https://doi.org/10.1099/ijsem.0.000592>.
- Helene LCF, Delamuta JRM, Ribeiro RA, Ormeño-Orrillo E, Rogel MA, Martínez-Romero E, Hungria M. 2015. *Bradyrhizobium viridifuturi* sp. nov., encompassing nitrogen-fixing symbionts of legumes used for green manure and environmental services. *Int J Syst Evol Microbiol* 65:4441–4448. <https://doi.org/10.1099/ijsem.0.000591>.
- Helene LCF, Delamuta JRM, Ribeiro RA, Hungria M. 2017. *Bradyrhizobium mercantei* sp. nov., a nitrogen-fixing symbiont isolated from nodules of *Deguelia costata* (syn. *Lonchocarpus costatus*). *Int J Syst Evol Microbiol* 67:1827–1834. <https://doi.org/10.1099/ijsem.0.001870>.
- Coil D, Jospin G, Darling AE. 2015. A5-MiSeq: an updated pipeline to assemble microbial genomes from Illumina MiSeq data. *Bioinformatics* 31:587–589. <https://doi.org/10.1093/bioinformatics/btu661>.
- Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: Rapid Annotations using Subsystems Technology. *BMC Genomics* 9:75. <https://doi.org/10.1186/1471-2164-9-75>.
- Overbeek R, Olson R, Pusch GD, Olsen GJ, Davis JJ, Disz T, Edwards RA, Gerdes S, Parrello B, Shukla M, Vonstein V, Wattam AR, Xia F, Stevens R. 2014. The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). *Nucleic Acids Res* 42:D206–D214. <https://doi.org/10.1093/nar/gkt1226>.
- Neves MCP, Hungria M, Sprent JI. 1987. The physiology of nitrogen fixation in tropical grain legumes. *CRC Crit Rev Plant Sci* 6:267–321. <https://doi.org/10.1080/07352688709382252>.