Genome Announcement

Draft genome sequence of *Bradyrhizobium manausense* strain BR 3351<sup>T</sup>, an effective symbiont isolated from Amazon rainforest

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**ABSTRACT**

The strain BR 3351<sup>T</sup> (*Bradyrhizobium manausense*) was obtained from nodules of cowpea (*Vigna unguiculata* L. Walp) growing in soil collected from Amazon rainforest. Furthermore, it was observed that the strain has high capacity to fix nitrogen symbiotically in symbioses with cowpea. We report here the draft genome sequence of strain BR 3351<sup>T</sup>. The information presented will be important for comparative analysis of nodulation and nitrogen fixation for diazotrophic bacteria. A draft genome with 9,145,311 bp and 62.9% of GC content was assembled in 127 scaffolds using 100 bp pair-end Illumina MiSeq system. The RAST annotation identified 8603 coding sequences, 51 RNAs genes, classified in 504 subsystems.

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The FASTX-Toolkit (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/) was used to trim the reads and only high quality bases (Q25) were used to assemble the genome. The ABySS software version 1.9.0 was used to de novo assemble and contigs shorter than 200 bp were eliminated. The genome annotation and metabolic pathways identification was carried out by RAST version 2.0 server. In addition, the contigs were also submitted to GenBank and annotated by NCBI Prokaryotic Genome Annotation Pipeline (released 2013; http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html).

The B. manausense (BR 3351T) draft genome consists of 127 contigs with 9,145,311 bp and 62.9% of GC content. This genome size and C+G content are compatible with other Bradyrhizobium. The RAST automatic annotation identified 51 copies of RNA genes and 8603 protein-coding gene sequences (CDSs), distributed in 504 subsystems. The nitrogen metabolism comprises 64 genes, including 8 genes for cyanate hydrolysis, 22 genes for nitrogen fixation, 14 genes for nitrate/nitrite/ammonification and 17 genes for ammonia assimilation. Furthermore, genes related to denitrification were not found, although the denitrification process has been described for some species on Bradyrhizobium genus.\(^9,10\) The carbohydrates metabolism seems to be quite complex, since a total of 698 genes related to this subsystem were annotated, including: 26 genes for CO\(_2\) fixation (photosynthesis oxidase C2 cycle), 17 and 114 genes related to polysaccharides and monosaccharides metabolism, respectively. These genomic data add information to clarify the B. manausense metabolic strategies to nodulate and fix nitrogen in association with legumes, especially from the Phaseoleae tribe. Additional comparative genomic and transcriptomic studies on this bacterium will help to understand the symbiotic efficiency and host range capacity of the strain BR 3351T.

This whole genome sequence has been deposited in DDBJ/ENA/GenBank under the accession number LJYG00000000, the version described in this paper is the first version.

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**References**


**Conflict of statement**

The authors declare no conflict of interest.