



## 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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Despite of great biodiversity present in the Amazon forest, ex. more than 3000 leguminous species, the knowledge about rhizobium diversity is scarce. Some studies have indicated *Bradyrhizobium* as an important nodulating-bacteria to different leguminous hosts.<sup>1–4</sup> *B. manausense* strain BR 3351<sup>T</sup> was isolated from a *Vigna unguiculata* root nodule growing as trap plant in a soil sample collected from the Brazilian Amazon rainforest.<sup>2,5</sup> This strain exhibited high capacity to fix nitrogen in symbiosis with *V. unguiculata* and the Phasoleae tribe seems to be the preferred host.<sup>2</sup> Here, we report the draft genome of

strain BR 3351<sup>T</sup>, a type strain of *B. manausense*, a member of the Alphaproteobacteria isolated from Amazon rainforest.

*B. manausense* (BR 3351<sup>T</sup>) was grown on YMA medium<sup>6</sup> for 5 days at 28 °C. A single colony was inoculated in 5 mL of YM medium and incubated at same condition to obtain cell biomass. After, 2 mL of the culture was centrifuged (16,000 × g; 4 min) and the pellet was submitted to DNA extraction with the kit Wizard miniprep. A sample of DNA, approximately 3 µg, was sent to Macrogen Inc. (Korea) for genome sequencing using the 100 bp pair-end Illumina MiSeq system. A total of 1,845,481,494 bp (aprox. 1.8 Gb) was generated, corresponding to 108 X genome coverage.

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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<sup>7</sup> was used to *de novo* assemble and contigs shorter than 200bp were eliminated. The genome annotation and metabolic pathways identification was carried out by RAST version 2.0 server.<sup>8</sup> 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 3351<sup>T</sup>) draft genome consists of 127 contigs with 9,145,311bp 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.<sup>9,10</sup> 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<sub>2</sub> fixation (photorespiration oxidative 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 3351<sup>T</sup>.

This whole genome sequence has been deposited in DDBJ/ENA/GenBank under the accession number LJYG000000000, the version described in this paper is the first version.

### Conflict of statement

The authors declare no conflict of interest.

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