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Complete Genome Sequence of *Burkholderia phenoliruptrix* BR3459a (CLA1), a Heat-Tolerant, Nitrogen-Fixing Symbiont of *Mimosa flocculosa*

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The genome of *Burkholderia phenoliruptrix* strain BR3459a (CLA1), an effective diazotrophic symbiont of the leguminous tree *Mimosa flocculosa* Burkart, which is endemic to South America.

**Species definition within the genus Burkholderia** is still challenging and requires polyphasic approaches (2). The genus includes species with contrasting roles, from highly opportunistic pathogens to bacteria with biotechnological potential. Recently a new genus was suggested, encompassing plant-associated beneficial bacteria (4, 6); however, taxonomic problems within the genus continue and will probably be solved only when the genomes of several strains have been fully sequenced. Very few nonpathogenic strains, especially of diazotrophic symbiotic bacteria, have been sequenced. Here, we contribute with the complete genome sequence of *Burkholderia phenoliruptrix* strain BR3459a (CLA1), an effective diazotrophic symbiont of the leguminous tree *Mimosa flocculosa* Burkart, which is endemic to South America.

The complete genome sequence of *B. phenoliruptrix* BR3459a was obtained via Roche 454 pyrosequencing with a total of 1,336,569 reads (35-fold genome coverage). The genome was assembled using both the Newbler (version 2.6; 454 Life Sciences, Roche Diagnostics Corporation, Branford, CT) and Celera (WGS; version 7.0) assemblers (5). Annotation and analysis of the sequences were carried out using the System for Automated Bacterial Integrated Annotation—SABIA (1). Annotation and analysis of the sequences were carried out using the System for Automated Bacterial Integrated Annotation—SABIA (1). An automatic functional annotation was performed using the KEGG database, and a manual annotation by comparison with the UniProt/Swiss-Prot, KEGG, NCBI-NR, and InterPro databases was performed on the remaining open reading frames (ORFs).

The genome of *B. phenoliruptrix* BR3459a consists of two circular chromosomes of 1,452,217 and 2,713,495 bp and one plasmid of 785,419 bp with a total genome size of approximately 7.65 Mbp. The large chromosome (chromosome 1) and the small chromosome (chromosome 2) encode 3,561 and 2,313 predicted ORFs, respectively, and the plasmid contains 731 predicted ORFs. The GC content for the genome is 63.15%.

Complete Genome Sequence of *Burkholderia phenoliruptrix* BR3459a

**Nucleotide sequence accession numbers.** The complete genome sequence of *B. phenoliruptrix* BR3459a has been deposited at NCBI GenBank under accession numbers CP003863, CP003864, and CP003865.

**ACKNOWLEDGMENTS**

This work was supported by FAPERJ and CNPq. L.F.G.Z. was supported by grant 302674/2012-8 funded by CNPq.

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