

Draft Genome Sequence of the Polyhydroxyalkanoate-Producing Bacterium *Burkholderia sacchari* LMG 19450 Isolated from Brazilian Sugarcane Plantation Soil

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***Burkholderia sacchari* LMG 19450, isolated from the soil of a sugarcane plantation in Brazil, accumulates large amounts of polyhydroxyalkanoates from sucrose, xylose, other carbohydrates, and organic acids. We present the draft genome sequence of this industrially relevant bacterium, which is 7.2 Mb in size and has a G+C content of 64%.**

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B*Burkholderia sacchari* LMG 19450 was isolated in the 1990s from the soil of a sugarcane plantation in Brazil (1) and was described as a new species (2). This bacterium has attracted interest from industry because of its capability to metabolize different carbon sources (sucrose, xylose, organic acids, etc.), reach high cell densities, and accumulate high levels of polyhydroxyalkanoates (PHA) (3–5) and also because it is sensitive to a large number of antibiotics (3). The aim of sequencing the genome was to identify genes involved in the catabolism of xylose and other sugars derived from biomass, as well as genes involved in PHA metabolism.

Genomic DNA was extracted using the DNeasy blood and tissue kit (Qiagen). The DNA was concentrated to 353.9 ng/μL, and the quality was assessed by agarose gel electrophoresis and on a NanoDrop spectrophotometer (Thermo Scientific). Whole-genome sequencing was performed by Macrogen (Seoul, South Korea) using the 454 GS FLX sequencing platform, which generated 785,669 reads. The sequencing reads were assembled with Newbler (Roche), and contigs annotation was carried out using the Rapid Annotation Server Subsystem Technology (RAST) (6).

The draft genome is composed of 121 contigs with a total length of 7,265,069 bp (depth of coverage, 49×) and a G+C content of 64.03%. The mean size of the contigs is 60,042 bp, and the N_{50} is 208,943 bp. RAST identified 6,741 coding regions, among which there were genes related to carbohydrate catabolism, e.g., xylose transporter ATP-binding subunit (*xylG*), xylose transporter substrate-binding protein (*xylF*), xylose isomerase (*xylA*), xylulokinase (*xylB*), and xylose operon regulatory protein (*xylR*) for xylose catabolism; to fatty acid catabolism, e.g., acyl-CoA synthetase (*fadD*), acyl-coenzyme A (CoA) dehydrogenase (*fadE*), enoil-CoA hydratase-S-specific (*fadB-fadJ*); and to PHA metabolism, e.g., polyhydroxyalkanoic acid synthase (*phaC*) and

3-ketoacyl-CoA thiolase (*phaA*). No pathogenesis-related gene was found in *B. sacchari* LMG 19450. Only one gene associated with resistance to antibiotics, encoding undecaprenyl diphosphatase, was found, and it has been associated with resistance to bacitracin (7).

Considering that this bacterium has the potential to convert a wide range of carbon sources, *B. sacchari* LMG 19450 represents a promising candidate for the production of PHA and other bio-based products.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [JTDB00000000](https://www.ncbi.nlm.nih.gov/nuclink/JTDB00000000). The version described in this paper is the first version, JTDB01000000.

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