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Draft Genome Sequence of *Burkholderia cepacia* ATCC 17759, a Polyhydroxybutyrate-Co-Valerate Copolymer-Producing Bacterium

Casey Crooks,[a] Jonathan M. Palmer,[b] Daniel L. Lindner[b]

[a]Institute for Microbial and Biochemical Technology, Forest Products Laboratory, Madison, Wisconsin, USA
[b]Center for Forest Mycology Research, Northern Research Station, U.S. Forest Service, Madison, Wisconsin, USA

ABSTRACT *Burkholderia cepacia* ATCC 17759, isolated from forest soils in Trinidad, accumulates large amounts of polyhydroxyalkanoate copolymers when grown on xylose, mannose, arabinose, other carbohydrates, and organic acid cosubstrates. This 8.72-Mb draft genome sequence of *B. cepacia* ATCC 17759 will provide better insight into this organism's utility in lignocellulose bioconversion.

Burkholderia is a genus of Gram-negative *Betaproteobacteria* that is comprised of more than 100 species (http://www.bacterio.net/burkholderia.html). Members of the genus are characterized by large genomes, which are typically maintained on 2 to 4 replicons with average genome sizes of ~8 Mbp. These larger genomes allow *Burkholderia* spp. to utilize a variety of carbon sources and occupy diverse environmental niches, including the plant rhizosphere, while some species are opportunistic pathogens of both plants and animals (1–3). *Burkholderia cepacia* ATCC 17759 was isolated from forest soil in Trinidad in 1959 and has been shown to be able to accumulate high levels of polyhydroxybutyrate when grown on a variety of carbon sources, including xylose, mannose, and arabinose, and to produce polyhydroxybutyrate-co-valerate copolymers when supplemented with fatty acids such as levulinic acid (4, 5). *B. cepacia* ATCC 17759 has also been found to be comparatively resistant to various lignin-derived phenylpropanoid compounds, indicating the potential for this microbe to produce valuable polyhydroxyalkanoates (PHAs) from hydrolysates of forest biomass recovered from prepulping extracts, forest thinnings, and other unmerchantable material (6–8). To better determine the utility of this bacterium in PHA production, we performed whole-genome shotgun sequencing.

Genomic DNA was prepared from overnight cultures grown aerobically with shaking in nutrient broth (Gibco) at 30°C. DNA was extracted using a Wizard genomic DNA purification kit (Promega). DNA quality and concentration were determined by gel electrophoresis and spectrophotometry (Nanodrop, Thermo Scientific). A DNA library was prepared using the Ion Torrent Xpress Plus fragment library kit (400 bp), templated using the Ion Torrent OT2 400 template kit, and sequenced on the Ion Torrent PGM platform using the Ion Torrent PGM 400 sequencing kit (Thermo Scientific). The sequencing run generated 2,368,250 raw reads (50× depth of coverage).

An initial *de novo* assembly was generated using SPAdes 3.10.1 (9) and subsequently scaffolded using the closely related *B. cepacia* ATCC 25416 genome sequence as a template (10). The resulting draft genome sequence consists of 8,721,279 bp in 26 scaffolds containing 203 contigs, with an N_{50} value of 79,125 bp and a GC content of 66.7%. The majority of the sequence is in 3 large scaffolds (3.70, 3.43, and 1.31 Mbp) corresponding to the 3 chromosomes of the template organism. Gene prediction and annotation were performed using Prokka v2 (11). The genome is predicted to contain 8,319 protein-coding sequences, along with 61 tRNA and 7 rRNA genes.

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Address correspondence to Casey Crooks, ccrooks@fs.fed.us.

C.C. and J.M.P. contributed equally to this work.

B. cepacia ATCC 17759 is a member of the *Burkholderia cepacia* complex (Bcc), which has been phylogenetically categorized using the *recA* gene into at least 9 genomovars, of which *B. cepacia* ATCC 17759 is a member of genomovar I (12). More detailed analysis of individual Bcc species shows considerable variation in the presence or absence of loci contributing to virulence (13, 14). This draft genome sequence will allow more detailed consideration of carbon utilization, lignin-derived phenylpropanoid resistance, levulinic acid utilization, and virulence characterization, in order to better inform on the utility of *B. cepacia* ATCC 17759 in biorefinery applications.

Accession number(s). This *Burkholderia cepacia* ATCC 17759 whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number PEHY00000000. The version described in this paper is version PEHY01000000.

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