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<tr>
<td><strong>Citation</strong></td>
<td>Genome Announcements, 2014, v. 2 n. 1, p. e00047-14</td>
</tr>
<tr>
<td><strong>Issued Date</strong></td>
<td>2014</td>
</tr>
<tr>
<td><strong>URL</strong></td>
<td><a href="http://hdl.handle.net/10722/196403">http://hdl.handle.net/10722/196403</a></td>
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Draft Genome Sequence of the Haloacid-Degrading Burkholderia caribensis Strain MBA4

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Burkholderia caribensis MBA4 was isolated from soil for its ability to utilize 2-haloacid. An inducible haloacid operon, encoding a dehalogenase and a permease, is mainly responsible for the biotransformation. Here, we report the draft genome sequence of this strain.

Haloacetates such as monochloroacetate (MCA) are toxic and mutagenic and can be produced incidentally during disinfection of water. Burkholderia caribensis MBA4 is a Gram-negative bacterium that can utilize 2-haloacid as a growth substrate. This bacterium was characterized for its production of a dimeric hydrolytic dehalogenase (Deb4a) (1, 2) that removes the halogen from the carbon backbone. Here we describe the draft genome sequence of Burkholderia caribensis MBA4.

Analysis of B. caribensis MBA4 with pulsed-field gel electrophoresis showed that it has a genome size of more than 9 Mb with at least three replicons (data not shown). Whole-genomic sequencing was obtained with 454 GS FLX Titanium and Illumina HiSeq 2000. With low-quality short reads discarded, the 454 sequencing has 929,485 reads and 380,525,001 bp after trimming. Four sets of illumina paired-end libraries with insert sizes of 100, 300, 500, and 2,000 bp were constructed and sequenced. After trimming and filtering, the four libraries have sizes of 100, 300, 500, and 2,000 bp. Contig relationships were maintained in the shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AXDD00000000. The version described in this paper is version AXDD01000000.

ACKNOWLEDGMENTS

We thank S. Lok, A. Tong, N. Lin, J. Jiang, F. C. C. Leung, and the University Centre for Genomic Sciences for advice.

This work has been supported by grants from the University Small Project Funding 2010 and the General Research Fund (project number HKU 780511) of the Research Grants Council of the Hong Kong Special Administrative Region, China.

REFERENCES


