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GENOME ANNOUNCEMENT

Complete Genome Sequence of *Alcanivorax dieselolei* Type Strain B5

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***Alcanivorax dieselolei* B5^T was isolated from oil-contaminated surface water of the Bohai Sea of China and characterized by the efficient degradation of alkane (C_5-C_{36}). Here we report the complete genome of B5^T and genes associated with alkane degradation.**

Alcanivorax dieselolei B5^T (= MCCC 1A00001^T = DSM 16502^T = CGMCC 1.3690^T) was first isolated from oil-contaminated surface water of the Bohai Sea at the Yellow River dock at the side of the Shengli oilfield in November 2001 (5). By now, there are more than 150 strains of this species, isolated from various marine environments, in our lab (http://www.mccc.org.cn). Strain B5^T can use alkane (C_5-C_{36}) as sole sources of carbon and energy, and it can produce a novel linear lipoaminobiosurfactant, characterized as a proline lipid (9). Four alkane hydroxylases in strain B5^T had been characterized, including two homologues of AlkB (AlkB1 and AlkB2) and a CYP153 homologue (P450), as well as an AlmA-like alkane hydroxylase (AlmA) (6). The complete genome sequence of *A. dieselolei* B5^T was first determined by the Chinese National Human Genome Center at Shanghai (CNHGC, Shanghai, China) using 454 technology (8) and then was resequenced by Shanghai Majorbio Bio-pharm Technology Co., Ltd. (SMBTC, Shanghai, China), using Solexa paired-end sequencing technology (1) to ensure high accuracy. In the case of 454 pyrosequencing, a total of 116,648,053 high-quality base pairs, giving 23.7-fold coverage of the genome, was assembled into 66 contigs using the Newbler software of the 454 suite package (454 Life Sciences). Gaps between contigs were closed by custom primer walks, or by PCR amplification followed by DNA sequencing at the CNHGC. A total of 3,076,343 reads (500-bp library) was generated to reach a 99-fold depth of coverage with an Illumina/Solexa IIx genome analyzer (Illumina, San Diego, CA) and mapped to the complete genome using the Burrows-Wheeler alignment (BWA) tool (4). Together, 87 indels and 25 single nucleotide polymorphism (SNPs) were corrected for the complete genome sequence of strain B5^T. The two sets of sequencing data were combined, and the genome sequence was analyzed by SMBTC.

The genome of *A. dieselolei* B5^T consists of a single circular chromosome of 4,928,223 bp and has an average G+C content of 61.63%. There are a total of 4,417 putative open reading frames (with an average size of 994 bp) according to Glimmer (2), giving a coding intensity of 89.13%. Forty-two tRNA genes for all 20 amino acids and two 16S-23S-5S rRNA operons were identified by tRNAscan-SE (7) and RNAmmer (3), respectively. Three integral-membrane alkane monooxygenases (AlkB) (B5T_00103, B5T_00721, and B5T_04393) and three cytochrome P450 enzymes (B5T_02075, B5T_02349, and B5T_02506) are found in the genome. Moreover, three flavin-binding family monooxygenases (AlmA) (B5T_00581, B5T_00657, and B5T_02052) for long-chain-length *n*-alkane hydroxylation were found in the genome sequence. The ability of *A. dieselolei* B5^T to degrade long-chain *n*-alkanes is dependent on the expression of *almA* (6). The B5^T genome sequence and its curated annotation are important assets to better understand the physiology and metabolic potential of *A. dieselolei* and will open up new opportunities in the functional genomics of this species.

Nucleotide sequence accession number. The nucleotide sequence comprising the *Alcanivorax dieselolei* B5^T genome was deposited in GenBank with the accession number CP003466 (chromosome).

ACKNOWLEDGMENTS

We acknowledge Huajun Zheng and his colleagues for genome sequencing performed at the Chinese National Human Genome Center at Shanghai. We acknowledge Qiang Li and his colleagues for genome sequencing and analysis at Shanghai Majorbio Bio-pharm Technology Co., Ltd.

This work was financially supported by the National Natural Science Foundation of China (41176154/41276005/40906083) and the Public Welfare Project of SOA (201005032).

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Received 24 September 2012 **Accepted** 28 September 2012

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doi:10.1128/JB.01813-12