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GENOME ANNOUNCEMENT

Genome Sequence of the Alkane-Degrading Bacterium *Alcanivorax hongdengensis* Type Strain A-11-3

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***Alcanivorax hongdengensis* A-11-3^T was isolated from an oil-enriched consortium enriched from the surface seawater of Hong-Deng dock in the Straits of Malacca and Singapore. Strain A-11-3^T can degrade *n*-alkane and produce a lipopeptide biosurfactant. Here we report the genome of A-11-3^T and the genes associated with alkane degradation.**

Alcanivorax hongdengensis A-11-3^T (= CGMCC 1.7084^T = LMG 24624^T = MCCC 1A01496^T) was isolated from an oil-enriched consortium from the surface seawater of Hong-Deng dock in the Straits of Malacca and Singapore. It can degrade various kinds of alkanes and produce a lipopeptide biosurfactant (3). Up to now, only two strains of this species have been isolated from marine environments in our lab (http://www.mccc.org.cn): one is *A. hongdengensis* A-11-3^T, and the other is strain MCCC 1A03010 (identical in 16S rRNA gene sequence), isolated from sediment from Beibu Gulf in China (unpublished data). In addition, no other *A. hongdengensis* strains (with >97% 16S rRNA gene sequence similarity) can be retrieved in NCBI. Strain A-11-3^T grows well in artificial seawater medium (ASM) with *n*-alkane as the carbon source for chain lengths from C_8 to C_{36}. One member of the flavin-binding family of monooxygenases (AlmA), which is responsible for long-chain-length *n*-alkane hydroxylation, was previously identified in strain A-11-3^T by reverse transcription (RT)-PCR in 2009 (2), and six monooxygenase genes involved in alkane degradation were further characterized in strain A-11-3^T by heterogeneous expression, including two *alkB* genes encoding an integral-membrane alkane monooxygenase (AlkB), three cytochrome P450 genes, and one *almA* gene (1).

The genome sequence of *A. hongdengensis* A-11-3^T was determined by Shanghai Majorbio Bio-pharm Technology Co., Ltd. (Shanghai, China), using Solexa paired-end sequencing technology. A total of 5,855,964 paired-end reads (500-bp library) were generated to reach a 143-fold depth of coverage with an Illumina/Solexa Genome Analyzer IIx (Illumina, San Diego, CA), and the gaps among scaffolds were closed by custom primer walks or by PCR amplification followed by DNA sequencing. The resulting genome sequence of *A. hongdengensis* A-11-3^T consists of 93 contigs (N_{90} = 36) of 3,664,876 bp and had an average G+C content of 60.68%. Automatic gene annotation was carried out by the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html), which was followed by manual editing. The genome contains 3,416 candidate protein-coding genes (with an average size of 957 bp), giving a coding intensity of 89.1%. A total of 2,593 proteins could be assigned to clusters of orthologous groups (COG) families. Forty tRNA genes for 19 amino acids (lacking Ile) and one 16S-23S-5S rRNA operon were identified.

We particularly analyzed the genes possibly responsible for alkane degradation. Together, 10 alkane monooxygenase genes were found in the draft genome sequence, including four *alkB* genes, three cytochrome P450 genes, and three *almA* genes. Therefore, two new *alkB* genes and two new *almA* genes were found by genome sequencing in addition to those previously detected. The A-11-3^T genome sequence and its curated annotation are important assets to better understand the alkane degradation mechanism and its role in the bioattenuation of oil pollution in marine environments.

Nucleotide sequence accession number. The draft genome sequence of *Alcanivorax hongdengensis* A-11-3^T has been deposited in GenBank under accession no. AMRJ00000000 (chromosome).

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