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GENOME ANNOUNCEMENT

Genome Sequence of *Pseudomonas aeruginosa* Strain SJTD-1, a Bacterium Capable of Degrading Long-Chain Alkanes and Crude Oil

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***Pseudomonas aeruginosa* strain SJTD-1 can utilize long-chain alkanes, diesel oil, and crude oil as sole carbon sources. We report the draft genome sequence of strain SJTD-1 (6,074,058 bp, with a GC content of 66.83%) and major findings from its annotation, which could provide insights into its petroleum biodegradation mechanism.**

Oil pollutants pose a serious threat to wildlife and humans with their ability to destroy the ecological balance, which may take years or decades to recover. Bioremediation is recognized as an efficient way to eliminate such environmental pollutants; many microorganisms capable of degrading the hydrocarbons in oil have been reported (1, 3, 5, 18). Among the compounds of petroleum, long-chain alkanes were considered to be slightly biodegradable due to their high hydrophobicity (8). Thus, exploiting more efficient petroleum-degrading organisms has become the key in petroleum pollution remediation.

Pseudomonas aeruginosa strain SJTD-1, isolated from oil-contaminated soil, is capable of utilizing long-chain alkanes (*n*-hexadecane, *n*-octadecane, *n*-docosane, *n*-tetracosane, and *n*-triacontane) as its sole carbon and energy source; it can also use diesel oil and crude oil efficiently (unpublished data). Therefore, strain SJTD-1 may play an important role in petroleum bioremediation; its genome sequencing will give useful information about its genetic variability and biodegradation mechanism.

The draft genome sequence of *P. aeruginosa* SJTD-1 has been obtained with a 454 GS-FLX (Roche) system (total of 64,121 reads averaging 400 bp) and Solexa paired-end sequencing (total of 6,307,058 reads, 151 bp each). The gaps were closed by specific PCR and Sanger sequencing. Genome sequences were assembled *in silico* using the AMOScmp program, resulting in 79 contigs (>500 bp in size) with an *N*50 length of 140,100 bp. The protein-coding genes were predicted using Glimmer 3.0 (6); tRNA and rRNA were identified with tRNAscan-SE (11) and RNAmmer (10). The genome sequence was annotated using the databases of RAST (2) and PGAAP (14). The functions of predicted protein-coding genes were annotated with the NCBI-NR (4), COG (16), and KEGG (9) databases.

The *P. aeruginosa* SJTD-1 draft genome sequence has a total of 6,074,058 bp with an average GC content of 66.83%. It contains 5,647 predicted coding sequences (CDSs), one 16S-23S-5S operon, and 50 tRNAs. Using COG functional assignment, the majority of predicted proteins (88.9%) could be classified into 22 COG categories. There are 557 subsystems represented in the genome, and the metabolic network of SJTD-1 was reconstructed (1). The five most abundant subsystems are related to amino acids (n = 672 CDSs), carbohydrates (n = 387), cofactors, vitamins, and pigments (n = 376), miscellaneous (n = 307), and protein metabolism (n = 276). In addition, many CDSs are involved in membrane transport (n = 203), cell wall and capsule (n = 195), fatty acids, lipids, and isoprenoids (n = 182), stress response (n = 178), iron acquisition and metabolism (n = 135), and virulence, disease, and defense (n = 134). These findings indicate that strain SJTD-1 has various catabolic abilities and unique adaptability to different environments.

According to the proposed alkane degradation mechanism (7, 12, 13, 15, 17), several putative enzymes were also found in the SJTD-1 genome, such as alkane hydroxylases, a rubredoxin reductase, an aldehyde dehydrogenase, and some regulatory proteins. Further studies will be performed to confirm their functions, and more detailed genome analysis will reveal the unique molecular characteristics of strain SJTD-1.

Nucleotide sequence accession numbers. The data from the whole-genome shotgun project have been deposited in DDBJ/EMBL/GenBank under the accession number AKCM00000000. The version described in this paper is the first version, with accession number AKCM01000000.

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