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GENOME ANNOUNCEMENTS

Complete Genome Sequence of the Diesel-Degrading *Acinetobacter* sp. Strain DR1▽

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The genus *Acinetobacter* is ubiquitous in soil, aquatic, and sediment environments and includes pathogenic strains, such as *A. baumannii*. Many *Acinetobacter* species isolated from various environments have biotechnological potential since they are capable of degrading a variety of pollutants. *Acinetobacter* sp. strain DR1 has been identified as a diesel degrader. Here we report the complete genome sequence of *Acinetobacter* sp. DR1 isolated from the soil of a rice paddy.

The genus *Acinetobacter* appears to be metabolically versatile and has the ability to degrade aliphatic hydrocarbon, thus making it an organism of interest for its possible bioremediational potential (9). Despite its biotechnological potential, the majority of genome projects conducted with *Acinetobacter* species have focused on pathogenic strains of *A. baumannii*. Currently, the only available whole-genome sequence of environmental isolates is that of *A. baylyi* ADP1 (2). *Acinetobacter* sp. strain DR1 was isolated from the soil of rice paddies, located in Deok-So (Korea University Agricultural Station), in the Kyonggi province of South Korea. Strain DR1 is capable of utilizing aliphatic hydrocarbons and diesel oil (5). Similarly to *A. baylyi* ADP1, this strain is also competent for natural transformation. We demonstrated previously that sodium chloride added to the medium induces the overproduction of exopolysaccharide (EPS), which evidences protective activity against diesel toxicity (4). Interestingly, DR1 possesses a quorum sensing (QS) system, which has been shown to play a significant role in biofilm formation and hexadecane biodegradation. The results of proteomic studies have demonstrated that the QS system regulates a broad variety of proteins (6). Collectively, our findings demonstrate that DR1 has profound potential for environmental applications and is an environmental isolate distinct from pathogenic strains, thus indicating that the whole-genome sequencing of DR1 is a worthwhile pursuit.

Initial pyrosequencing using a GS-FLX system (454 Life Science Corporation) generated 652,162 reads (264,482,836 nucleotides; 64.3-fold coverage), which were assembled into 56 contigs. To determine the order of the contigs, 1,248 fosmid clones were constructed with an average insert size of 35 kb (10.5-fold coverage). The fosmid-end sequencing of 936 clones generated 1,372,452 bp. These high-quality Sanger reads allowed the assembly of 41 large contigs into 2 scaffolds containing 38 gaps. The gaps were filled via primer walking. All procedures for genome sequencing and gap filling were conducted by Macrogen (Seoul, South Korea). Protein coding regions were predicted with the GLIMMER3 software program (3), and automatic genome annotation was conducted on a RAST server (1) and the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP). The tRNA and rRNA genes were annotated using the tRNAScan-SE (8) and RNAmmer software programs (7), respectively. The genome of *Acinetobacter* sp. DR1 consists of a circular 4,152,543-bp chromosome with a G+C content of 38%, 3,874 predicted coding sequences, and 71 tRNAs. There are 6 rRNA operons with a 16S, tRNA-Ile, tRNA-Ala, 23S, 5S organization. The genes studied previously were clearly identified via genome sequencing (4, 5, 6). The availability of the complete genome sequence of *Acinetobacter* sp. strain DR1 will contribute to an in-depth understanding of the genetic potentials of *Acinetobacter* species.

Nucleotide sequence accession number. The complete genome sequence of *Acinetobacter* sp. strain DR1 has been assigned GenBank accession number CP002080.

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