Genome Sequence of *Acinetobacter* sp. Strain P8-3-8, Isolated from *Fistularia commersonii* in Vietnam[▽]

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***Acinetobacter* sp. strain P8-3-8 is an aerobic, Gram-negative marine bacterium isolated from the intestine of the bluespotted cornetfish (*Fistularia commersonii*). Here, we present the draft genome sequence of *Acinetobacter* sp. P8-3-8 (3,905,565 bp, with a G+C content of 37.6%) containing 3,621 putative coding sequences. The genome data reveal a high density of genes encoding transcriptional regulators involved in anaerobic respiration.**

Acinetobacter spp. are strictly aerobic, Gram-negative coccobacilli that have a ubiquitous geographical distribution. The *Acinetobacter* genus is best known for its capacity to bioremediate alkanes and aromatic hydrocarbons and its ability to produce heteropolysaccharides, which act as powerful emulsifiers. The type strain of *Acinetobacter* sp. strain P8-3-8 was isolated from the intestine of a bluespotted cornetfish (*Fistularia commersonii*) caught in Vietnam and produces esterolytic enzymes (12, 13). *Acinetobacter* sp. strain P8-3-8 was cultured at 30°C in Luria-Bertani (LB) medium (14), and a cell pellet was obtained by centrifugation. This was washed after suspension in phosphate-buffered saline (PBS) (0.9% NaCl), and homogenized using TissueLyser (Restch, Qiagen) (1, 11). Genomic DNA was extracted from the cultured bacteria using the alkaline lysis method (5). We sequenced the genome of this species because it had not been sequenced at the time our sequencing project began, according to the Genomes On Line Database (GOLD) (9).

We report the genome sequence of *Acinetobacter* sp. strain P8-3-8, obtained using a whole-genome shotgun strategy (7) with a Roche 454 genome sequencer (GS FLX titanium) pyrosequencing system (320,142 reads, totaling ~104 Mb; ~28.9-fold coverage of the genome) (4). Pyrosequencing was processed using Roche's software according to the manufacturer's instructions. All of the paired reads were assembled using the Newbler Assembler 2.3 (454 Life Science), which generated 244 contigs (largest contig, 263 kb) of >100 bp in size. The predicted proteins were annotated using Basic Local Align-

ment Search Tool (BLAST) (2) and the Rapid Annotation using Subsystem Technology (RAST) server (3). In addition, the contigs were searched against the Glimmer 3.02 modeling software package (6), tRNAscan-SE 1.21 (10), RNAMmer 1.2 (8), and Clusters of Orthologous Groups (COG) (15) databases to annotate the gene descriptions.

The *Acinetobacter* sp. strain P8-3-8 draft genome includes 3,905,565 bp and is composed of 3,621 predicted coding sequences (CDSs), with a G+C content of 37.6%. There are single predicted copies of the large-subunit (LSU) and small-subunit (SSU) ribosomal proteins, a single predicted copy of the 5S rRNA gene, and 69 predicted tRNAs. There were 3,621 possible open reading frames (ORFs) in 146 contigs with a size range between 12 and 15,828 bp. There were only 207 ORFs with lengths of >2,000 bp, and the average ORF was 882.3 bp. The genome contained representatives of 255 subsystems, and we used this information to reconstruct the metabolic network (determined using the RAST server). A distinguishing subsystem feature was the absence of a gene corresponding to pyruvate kinase, the enzyme that catalyzes carbohydrates to form pyruvate for respiration in the citric acid cycle. The CDSs annotated by the COG database were classified into eight major categories (L, P, C, J, S, V, E, and R) from among the 89 COG groups. The enzymes identified included NADH ubiquinone oxidoreductase (EC 1.6.5.3), 3-oxoacyl-reductase (EC 1.1.1.100), and ATP synthase (EC 3.6.3.14). More detailed analysis of this genome and a comparative analysis with other *Acinetobacter* sp. genomes may well identify other genes upon finalization of the genome.

Nucleotide sequence accession number. The draft genome sequence of *Acinetobacter* sp. strain P8-3-8 is available in GenBank under the accession number AFIE00000000.

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