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Complete Genome Sequence of the Polycyclic Aromatic Hydrocarbon-Degrading Bacterium *Alteromonas* sp. Strain SN2▽

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***Alteromonas* sp. strain SN2, able to metabolize polycyclic aromatic hydrocarbons, was isolated from a crude oil-contaminated sea-tidal flat. Here we report the complete 4.97-Mb genome sequence and annotation of strain SN2. These will advance the understanding of strain SN2's adaptation to the sea-tidal flat ecosystem and its pollutant metabolic versatility.**

Members of the genus *Alteromonas* are increasingly recognized as globally distributed heterotrophic marine bacteria, having a copiotrophic way of life as an *r*-strategist, i.e., they can grow rapidly when a new carbon source, such as crude oil, is released into marine habitats (6, 10). Thus, it may be anticipated that *Alteromonas* species are functionally important in the recovery of marine habitats from pollution. *Alteromonas* sp. strain SN2 was isolated from a sea-tidal flat, and it was shown to be responsible for the *in situ* degradation of polycyclic aromatic hydrocarbons (PAHs) in crude oil-contaminated marine sediment (H. M. Jin, J. M. Kim, S. H. Lee, E. L. Madsen, and C. O. Jeon, submitted for publication). Here we report the complete genome sequence and annotation of strain SN2.

This genomic sequence was determined using the Roche/454 technology. The total sequence (642 Mb [130-fold coverage] with 1,536,491 paired-end reads containing 5- to 8-kb inserts) was generated from the GS FLX Titanium system, and the resulting reads were assembled initially into 12 large scaffolds, including 72 contigs, using the Newbler program. All the intrascaffold and interscaffold gaps were closed by sequencing PCR products. The Phred/Phrap/Consed software (1, 2, 4) was used for sequence assembly and quality assessment. Illumina sequencing data were used to correct potential homopolymeric errors, and the final whole-genome sequence was further validated by Sanger sequencing of uncertain regions such as mononucleotide runs and low-quality/depth segments. The complete sequence was submitted to the NCBI's Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) for annotation. Genes encoding tRNAs and rRNA operons were determined by tRNAscan-SE (9) and RNAmmer 1.2 (8), respectively.

Alteromonas sp. strain SN2 has a circular chromosomal genome of 4,972,148 bp with a G+C content of 43.5% and no plasmids. The genome contains 4,355 predicted protein-coding sequences, 64 tRNA genes, 5 complete rRNA loci, and 8 noncoding RNAs. The coding density was 87.99%, with an average gene length of 976 bp. Fifteen putative genomic islands (GIs) were identified from the genome sequence using IslandViewer (5); the largest genomic island (with 60 protein-coding genes) harbored a PAH-degrading gene cluster, which was expressed during PAH biodegradation (Jin et al., submitted). The presence of phage remnant-like transcription regulator AlpA (AMBT_20760) in GI-2, GI-9, and GI-12 suggested active phage invasion into the genome of strain SN2. The presence of 66 transposases and 13 phage integrases, scattered throughout the genome, also supported the likelihood of active genetic rearrangement of strain SN2's genome. Twenty-one dioxygenase genes, known to be essential for metabolizing recalcitrant organic compounds (3, 7), were present in the genome. This dioxygenase frequency was significantly higher than those found in the genomes of other sequenced *Alteromonas* strains (AltDE [11 dioxygenase genes] and ATCC 27126 [8 dioxygenase genes] [6]) and likely indicates strain SN2's high versatility in pollutant metabolism.

Nucleotide sequence accession number. The complete genome sequence of strain SN2 has been deposited in GenBank under accession no. CP002339.

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