Complete Genome Sequence of the BTEX-Degrading Bacterium Pseudoxanthomonas spadix BD-a59

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Pseudoxanthomonas spadix BD-a59, able to metabolize all six BTEX (benzene, toluene, ethylbenzene, and o-, m-, and p-xylene) compounds, was isolated from gasoline-contaminated sediment. Here, we report the complete 3.45-Mb genome sequence and annotation of strain BD-a59. These advance the understanding of strain BD-a59’s genomic properties and pollutant metabolic versatility.

Bacteria that degrade BTEX (benzene, toluene, ethylbenzene, and o-, m-, and p-xylene) compounds are widely distributed, and many BTEX-degrading bacteria, including members of the genera Pseudomonas, Ralstonia, Burkholderia, Sphingomonas, Thaurea, Dechloromonas, Rhodococcus, and Acinetobacter, have been isolated. However, only a few bacteria, including Ralstonia pickettii PK01 and Dechloromonas sp. strain RCB, have been reported as degrading all six BTEX compounds (1, 9). Pseudoxanthomonas spadix BD-a59, which is able to degrade all six BTEX compounds, was isolated from gasoline-contaminated sediment and was shown to be responsible for the in situ degradation of BTEX compounds in gasoline-contaminated soil (6). Here, we report the whole genome sequence and annotation of strain BD-a59.

The whole genome of strain BD-a59 was sequenced using Roche 454 technology at Chunlab (Korea). A sequence of about 92 Mb (~27× coverage) with 408,469 paired-end reads containing 3-kb inserts and a sequence of 90 Mb (~26× coverage) with 212,173 single-end reads were generated using a 454 GS FLX Titanium system. Illumina (Solexa) sequencing data with 2,918 Mb (about 845× coverage) and with 34,036,718 single-end reads were also generated. The resulting sequences were assembled into two large scaffolds, including 60 contigs, by the use of the Newbler program (Roche) and CLC Workbench software (Denmark). For the genomic assembly, the complete genome of Xanthomonas campestris pv. campestris strain 8004 (NC_007086) was used as a reference sequence (10). All the intrascaffold and interscaffold gaps were closed by sequencing PCR products. Phred/Phrap/Consed software (2, 3, 5) was used for sequence assembly and quality assessment. The final whole-genome sequence was further validated by Sanger sequencing of uncertain regions such as mononucleotide runs and segments of low quality or depth. The whole-genome sequence was submitted to the Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) of the NCBI for annotation. Genes encoding tRNAs and rRNA operons were determined using the tRNAscan-SE (8) and RNAmmer (7) software programs, respectively.

Strain BD-a59 has a circular chromosomal genome of 3,452,554 bp with a G+C content of 67.65% and no plasmid. The genome contains 3,150 predicted protein-coding sequences, 50 tRNA genes coding 20 amino acids, and one complete rRNA locus. The coding density was 87.5%, with an average gene length of 959.04 bp. Twelve putative monoxygenase and 28 putative dioxygenase genes, known to be essential for metabolizing recalcitrant organic compounds, including BTEX (4), were identified from the genome. The monoxygenase and dioxygenase frequencies were significantly higher than those found in other sequenced Pseudoxanthomonas genome (P. suwonensis strain 11-1; four putative monoxygenase and 16 putative dioxygenase genes) (11), indicating strain BD-a59’s likely high versatility in pollutant metabolism.

Nucleotide sequence accession number. The genome information for the chromosome of Pseudoxanthomonas spadix strain BD-a59 has been deposited in NCBI under GenBank accession number CP003093.

ACKNOWLEDGMENTS

These efforts were supported by the Technology Development Program for Agriculture and Forestry (TDP AF) of the Ministry for Agriculture, Forestry and Fisheries and the Next-Generation BioGreen 21 Program (grant SSAC2011-PK008220), Rural Development Administration, Republic of Korea.

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Received 27 October 2011 Accepted 7 November 2011

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doi:10.1128/JB.06436-11