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GENOME ANNOUNCEMENT

Genome Sequence of *Sphingomonas wittichii* DP58, the First Reported Phenazine-1-Carboxylic Acid-Degrading Strain

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***Sphingomonas wittichii* DP58 (CCTCC M 2012027), the first reported phenazine-1-carboxylic acid (PCA)-degrading strain, was isolated from pimiento rhizosphere soils. Here we present a 5.6-Mb assembly of its genome. This sequence would contribute to the elucidation of the molecular mechanism of PCA degradation to improve the antifungal's effectiveness or remove superfluous PCA.**

The members of the *Sphingomonas* genus have received increasing attention for their significant ability to degrade numerous recalcitrant compounds (6, 7, 18, 21). Phenazine-1-carboxylic acid (PCA), the synthetic precursor of phenazines produced by multiple strains of *Pseudomonas* and *Streptomyces*, is a broad-spectrum antifungal agent that protects crops from various fungal phytopathogens (8, 9, 11, 20). However, PCA has weaker antifungal activity in the field than in the laboratory, partly because of its degradation by microorganisms (22). Moreover, PCA is a biologically active factor that exhibits many effects on human airway epithelial cells, alters the immune and inflammatory responses, and thereby contributes to bacterial disease pathogenesis (5). Therefore, it is important to reveal the mechanism of its biodegradation so that we can improve the antifungal effectiveness of PCA by inhibiting its degradation (22) or remove superfluous PCA when it is a threat to the environment or health. *Sphingomonas wittichii* DP58 (CCTCC M 2012027), the first reported PCA-degrading bacterium, was isolated from pimiento rhizosphere soils (22).

Here we present the draft genome of strain DP58. The genome of strain DP58 was sequenced using the Illumina GAIIx instrument (250-fold coverage) and assembled with Velvet 1.1.07 (23), which generated more than 265 scaffolds (N_{50} length, 13,601 bp) including 739 contigs. Of these contigs, 28 (429,718 bases) were considered repeat sequences. The draft genome sequence of strain DP58 contains 5,628,887 bases with a mean GC content of 67.8%. The relatively high GC content would increase the number of contigs in the sequencing process (19). Putative open reading frames were predicted using Glimmer 3.02 (4). The tRNA and rRNA genes were predicted by tRNAscan-SE (12) and RNAmmer1.2 (10), respectively. The genome sequence was annotated by the RAST server (2) and the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (16). Metabolic pathways were analyzed by KAAS (15). Comparative genome analysis was performed using mGenomeSubtractor (17) and WebACT (1).

A total of 5,283 genes, including 3 rRNA genes and 45 tRNA genes, were predicted. Of these coding sequences, 3,449 were suggested as functional genes. A total of 91 genes encoding dioxygenases were predicted that may be related to the metabolisms of aromatic compounds such as PCA, biphenyl, salicylate, catechol, 4-hydroxyphenylacetic acid, and isoquinoline. A total of 16 transposase-related genes were also predicted in the sequence. Moreover, 39 ABC transporter-related genes and 107 TonB-dependent receptor genes probably involved in the transportation of aromatic compounds (13, 14) were predicted in the genome sequence. Strain DP58 could completely degrade 0.2 g/liter PCA in 40 h (22). Two kinds of metabolites have been identified by our group, 4-hydroxy-1-(2-carboxyphenyl)azacyclobut-2-ene-2-carbonitrile and 4-hydroxy-1-(2-carboxyphenyl)-2-azetidinecarbonitrile (3). Recently, a three-component dioxygenase (oxygenase, ferredoxin, and reductase) was supposed to be associated with PCA degradation (not demonstrated in detail). Sequencing and analysis of the strain DP58 genome will provide further insights into the molecular mechanism of PCA degradation to improve its effectiveness or remove superfluous PCA as needed.

Nucleotide sequence accession numbers. The draft genome sequence was deposited in the DDBJ/EMBL/GenBank database under accession no. AHKO00000000. The version described in this paper is the first version, AHKO01000000.

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