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Genome Sequence of *Pseudomonas putida* Strain B6-2, a Superdegrader of Polycyclic Aromatic Hydrocarbons and Dioxin-Like Compounds

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***Pseudomonas putida* strain B6-2 can efficiently degrade environmental pollutants/toxicants, such as polycyclic aromatic hydrocarbons and dioxin-like compounds, and has unique tolerance to organic solvents. Here, we present a 6.24-Mb draft genome sequence of B6-2, which could provide further insights into the biodegradative mechanisms of a diverse range of chemical compounds.**

Polycyclic aromatic hydrocarbons (PAHs) and dioxin-like compounds, including sulfur, nitrogen, and oxygen heterocycles, are lipophilic organic pollutants/toxicants which have been identified widely in the environment and in industrial production waste (8, 12, 14). Many of these contaminated habitats are also characterized by high concentrations of organic solvents (10). Microbial remediation is one of the most effective ways to reduce these pollutants/toxicants from the environment (2, 3, 7, 9, 14). The versatile metabolic capacity of pseudomonads enables graceful degradation of these compounds (4, 6, 11).

Pseudomonas putida strain B6-2 was isolated and characterized (6). With its unique tolerance to organic solvents, this superstrain can efficiently and cometabolically degrade PAHs and dioxin-like compounds, such as (polychlorinated) biphenyls, (polychlorinated) dibenzofurans, (polychlorinated) dibenzo-*p*-dioxins, (polybrominated) diphenyl ethers, (methylated) carbazoles, (methylated) dibenzothiophenes, and (methylated) benzothiphenes (unpublished data). Biphenyl-grown B6-2 cells can transform dibenzofuran via a new 2-hydroxy-4-(3′-oxo-3′*H*-benzofuran-2′-yliden)but-2-enoic acid degradation pathway, which produces a series of benzofuran derivatives as metabolites (6). The excellent characteristics of strain B6-2 may play important roles in bioremediation of seriously polluted habitats. The genome sequencing of this species will provide great insights into its genetic variability and the biodegradation of a diverse range of chemical compounds.

Here, we report the draft genome sequence of *P. putida* B6-2, which was obtained using Solexa paired-end sequencing (total of 28,791,228 reads; 75 bp each read) and a 454 GS FLX (Roche) system (121,785 reads; 400 bp in average). The reads were assembled with the Velvet program to 227 large contigs (>500 bp) (16). The gaps were closed by specific PCR and Sanger sequencing. Contigs and PCR products were finally assembled by using the Phred/Phrap/Consed software package into 27 contigs. The genome sequence was annotated using the RAST server (1) and NCBI Prokaryotic Genomes Automatic Annotation Pipeline (http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html). The metabolic pathways were examined through the use of KEGG databases (5).

The draft genome sequence of *P. putida* B6-2 comprises 6,239,598 bases, which is bigger than the other six *P. putida* strains that have been fully sequenced (13, 15). The bigger genome capacity provides a genetic basis for metabolic diversity. The genome of strain B6-2 has a G+C content of 61.6%, 6 rRNA operons, an extra 5S rRNA gene, and 69 tRNA genes and contains 5,286 protein-coding sequences (CDSs) (986-bp average length, 82.6% coding density). Among these, 202 CDSs were not found in the other six fully sequenced *P. putida* strains compared by blast ($e < 10^{-5}$) (13, 15). There are 495 subsystems represented in the genome, and the metabolic network of B6-2 (determined by using the RAST server) was reconstructed (1). A gene cluster (*BphABCKHJID*) of the complete biphenyl degradation pathway was annotated, and the function of the *BphABC* subcluster was characterized (unpublished data). Additionally, strain B6-2 carries various gene clusters related to aromatic compounds biodegradations, such as benzoate, catechol, 4-hydroxybenzoate, and salicylate. Moreover, 30 CDSs encoding efflux pump systems were annotated, which may contribute to the organic solvent tolerance of strain B6-2.

Nucleotide sequence accession numbers. The data from the whole-genome shotgun project have been deposited in DDBJ/EMBL/GenBank under the accession number AGCS00000000. The version described in this paper is the first version, accession number AGCS01000000.

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