Draft Genome Sequence of *Rhodococcus ruber* Strain P25, an Active Polychlorinated Biphenyl Degrader

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We report the 5,728,255-bp draft genome sequence of *Rhodococcus ruber* P25, isolated from a soil polluted with halogenated aromatic compounds in the city of Perm, Russia. The strain degrades polychlorinated biphenyls and a broad range of aromatic compounds. It possesses genes that mediate the degradation of biphenyls/polychlorinated biphenyls, naphthalene, and monoaromatic compounds.

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Actinobacterium *Rhodococcus ruber* P25 ( = IEGM896) was isolated from soil polluted with the wastes of a chemical plant producing halogen-containing compounds in Perm (Russia) by enrichment in a liquid minimal medium containing biphenyl. Taxonomic assignment to *R. ruber* P25 was based on a 16S rRNA gene nucleotide sequence (100% similarity with *R. ruber* DSM 43338T [GenBank accession no. X80625]), physiological, and biochemical features analysis (1). Strain P25 was capable of utilizing a broad range of aromatic compounds (biphenyl, phenol, toluene, naphthalene, salicylate, gentisate, ortho- and para-dihydroxybiphenyl, 3-hydroxybenzoate, 4-hydroxybenzoate, and 3,4-dihydroxybenzoate), as well as their substituted derivatives (chlorinated biphenyls and chlorobenzoates, paramethylbenzoate, and 2,4-dichlorophenoxyacetate) as a sole carbon and energy source (2–4). *R. ruber* P25 is an active degrader of polychlorinated biphenyls, which are toxic and persistent organic pollutants (5).

To better understand the metabolic versatility of the strain P25, in particular biphenyl and polychlorinated biphenyl destruction pathways, analysis of its genome sequence was carried out. Strain P25 was grown in minimal medium with biphenyl as a sole carbon and energy source. DNA was prepared following a standard genomic DNA purification protocol (6). The draft genome sequence of P25 was prepared using the GS Junior (Roche) system, largest contig measuring 483.3 kb. Its analysis showed a G+C content of 70.5%. Contigs constituting 95.6% of the total length (5,479,412 bp) could be ordered by mapping to the reference genome. The draft sequence contains 5,319 coding sequences (CDSs), four rRNAs (5S, 16S, and 23S), and 64 tRNAs genes. The coding regions constitute 91.1% of the total sequence and the average gene length is 964. A total of 3,677 genes (69.6%) were annotated with gene ontology (GO) terms.

Functional annotation showed that strain P25 possesses *bph* genes, benzoate, protocatehate-, gentisate-, and catechol-degrading genes, and genes of the phenol and naphthalene degradation pathways.

Organization of the *bph* gene cluster differed from other *bph* gene clusters known to date (12–15). It contained genes of the “upper” pathway, transcribed in the same direction: *bphAd-bphD-bphC-bphAa-bphAb-bphAc-bphB* (ferredoxin reductase, 2-hydroxy-6-oxo-6-phenylhexadienoate hydrolase and 2,3-dihydroxybiphenyl 1,2-dioxygenase, biphenyl 2,3-dioxygenase α- and β-subunits, ferredoxin, biphenyl 2,3-dihydropyridone dehydrogenase, respectively). This order is not typical. The genes of the “lower” pathway of biphenyl degradation, encoding 4-hydroxy-2-oxovalerat aldolase, acetaldehyde dehydrogenase, and 2-keto-4-pentenoate hydratase, are located downstream of *bphB* and are transcribed in the opposite direction.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. LDUF0000000. The version described in this paper is version LDUF01000000.

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