

Draft Genome Sequence of *Rhodococcus* sp. Strain P14, a Biodegrader of High-Molecular-Weight Polycyclic Aromatic Hydrocarbons

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The genus *Rhodococcus* is known for its ability to degrade various xenobiotic compounds. *Rhodococcus* sp. strain P14 isolated from crude oil-contaminated sediments can degrade mineral oil and polycyclic aromatic hydrocarbons (PAHs). The draft genome sequence of *Rhodococcus* sp. P14 was obtained using Solexa technology, which provided an invaluable genetic background for further investigation of the ability of P14 to degrade xenobiotic compounds.

Rhodococci are widely distributed in the ecological environment (4). Members of the *Rhodococcus* genus have a remarkable ability to degrade a wide variety of xenobiotic compounds: nitriles, nitroaromatics, heterocyclic compounds, polychlorinated biphenyls, aliphatic, aromatic hydrocarbons, etc. Many of these substrates are relatively stable and toxic (1, 7, 8, 11).

Rhodococcus sp. strain P14 was isolated from crude oil-contaminated sediments. This strain could mineralize polycyclic aromatic hydrocarbons (PAHs) with three to five rings, including phenanthrene, pyrene, and benzo[a]pyrene. After 30 days of incubation with an initial PAH concentration of 50 mg/liter, P14 degraded 43% phenanthrene, 34% pyrene, and 30% benzo[a]pyrene. It also could degrade mineral oil with *n*-alkanes of C17 to C21 carbon chain length. P14 tended to float when cultivated in mineral oil-supplemented liquid medium (10).

The genome sequencing of *Rhodococcus* sp. P14 was performed by the use of high-throughput Solexa technology (Illumina GA2x). The whole-genome shotgun (WGS) sequence volume was 860 Mb, giving approximately 10-fold genome coverage. The WGS sequence was assembled into 418 contigs with an N50 length of 23,966 bp by the use of SOAPdenovo (5), and the contigs were joined into 62 scaffolds. The genome size of P14 is 5.68 Mb, with a G+C percentage of 70.42. Annotation of open reading frames was performed by using Glimmer software, version 3.0, and by comparison with the corresponding data from the COG, KEGG (2), Swiss-Prot, TrEMBL, and NR databases. There were 5,501 coding domain sequences (CDSs), with an average length of 935 bp. Further, 49 tRNA genes and 3 rRNA genes were identified by tRNAscan 1.21 (6) and rRNAmmer 1.2 (3), respectively.

Over 980 genes were predicted to be involved in xenobiotics biodegradation and metabolism. There were three alkane hydroxylase genes (*alkB*) identified in the P14 genome sequence. Among them, *alkB3* exists in an *alkB* gene cluster. The *alkB3* gene might be a classical alkane hydroxylase. Also, a ring-hydroxylating dioxygenase gene cluster with at least 43 dioxygenase genes related to PAH degradation was found. The ring-hydroxylating dioxygenase gene cluster was similar to the phenanthrene degradation gene cluster in *Nocardioides* sp. strain KP7 (9).

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank un-

der accession number [AJFC0000000](https://doi.org/10.1093/jb/jbs000). The version described in this paper is the first version, AJFC01000000.

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