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Genome Sequence of *Rhodococcus* sp. Strain R04, a Polychlorinated-Biphenyl Biodegrader▽

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The genus *Rhodococcus* has proved to be a promising option for the cleanup of polluted sites and application of a microbial biocatalyst. *Rhodococcus* sp. strain R04, isolated from oil-contaminated soil, can biodegrade polychlorinated biphenyls. Here we report the draft genome sequence of *Rhodococcus* sp. strain R04, which could be used to predict genes for xenobiotic biodegradation and provide important insights into the applications of this strain.

The genus *Rhodococcus* is a very diverse group of bacteria that possess the ability to degrade a large number of organic compounds, including some of the most difficult compounds with respect to recalcitrance and toxicity. Several strains belonging to the genus *Rhodococcus* have been isolated from various contaminated environments (1, 3, 10, 11, 12), which have proved to be ideal candidates for enhancing the bioremediation of contaminated sites and a wide range of biotransformations, such as steroid modifications, enantioselective synthesis, and the production of amides from nitriles (4, 14).

Rhodococcus sp. strain R04 was isolated from oil-contaminated soil in northern China. Strain R04 was able to biodegrade polychlorinated biphenyls (PCBs) not only via ring cleavage but also through dechlorination (15). In addition, it metabolized phenol, benzoate, and 2-nitropropane when provided as the sole source of carbon and energy and cometabolized pentachlorophenol, dibenzofuran, benzothiophene, and atrazine. It is suggested that strain R04 will potentially be useful in the biotreatment of wastewater and bioremediation of contaminated soils.

The genome sequence of R04 was determined by using the high-throughput Solexa sequencing technology (Illumina GA2x) in Shenzhen, China. Whole-genome shotgun (WGS) sequence data for 825 Mb, giving approximately 92-fold genome coverage, were generated and assembled into 2,548 contigs using SOAPdenovo v.1.04 (7). Furthermore, the contigs were joined into 110 scaffolds (>1 kb in size) using paired-end information. The genome sequence analysis of R04 showed a genome size of 9,125,386 bp, with a mean GC content of 69.62%. Annotation of the open reading frames was performed using Glimmer v.3.0 (2) and by comparison with the corresponding data from the COG, KEGG, Swiss-Prot, TrEMBL, and NR databases. tRNA and rRNA genes were identified by tRNAscan and RNAmmer, respectively (6, 8). There were 9,318 coding sequences (CDSs) with an average length of 826 bp, 99 tRNAs, and 20 rRNAs.

At least 82 genes were found to be potentially involved in xenobiotic metabolism. Among these genes, four extradiol dioxygenase genes (*bphC*) and two hydrolase genes (*bphD*) were involved in PCB degradation by R04. In addition, the R04 genome contains at least six ring-hydroxylating dioxygenase genes and 15 cytochrome P450 genes, which enables strain R04 to adapt to catabolize a large number of substrates. Differing from *Rhodococcus jostii* RHA1 (formerly named by *Rhodococcus* sp. strain RHA1), whose genome holds two set of polychlorinated biphenyl transformation systems (5), *Rhodococcus* sp. strain R04 contains only a *bph* gene cluster consisting of *bphA1A2A3A4*, *bphB*, *bphC*, and *bphD* (16). In stain R04, ketosteroid-9-α-hydrolase, 3-ketosteroid-δ-dehydrogenase, 3-ketosteroid-1-dehydrogenase, and steroid δ-isomerase are involved in the transformation and metabolism of steroid compounds, and they share 69 to 96% of identity with those of *Rhodococcus jostii* RHA1, *Rhodococcus rhodochrous*, and *Rhodococcus erythropolis* (9, 10, 13). It has been suggested that *Rhodococcus* sp. R04 is a potential candidate for the industrial production of bioactive steroid compounds.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited into DDBJ/EMBL/GenBank under accession number AFAQ00000000. The version described in this paper is the first version, accession number AFAQ01000000.

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