De Novo Genome Project for the Aromatic Degrader Rhodococcus pyridinivorans Strain AK37

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Here, we present the complete genome sequence of Rhodococcus pyridinivorans strain NCAIM PB1376, which was isolated from an oil-polluted site in Hungary. R. pyridinivorans AK37 is an aerobic, nonsporulating, nonmotile, Gram-positive bacterium with remarkable aromatic-decomposing activity.

Members of the genus Rhodococcus are common in many environments, and a large number of them are known as toxic-material-decomposing strains (8, 10). Generally, rhodococi are regarded as masters of catabolic versatility, referring to their enzyme arsenal that enables them to thrive on unusual organic compounds (7). Based on these catabolic properties, rhodococi have great significance in environmental biotechnology (1), the pharmaceutical industry (15), and waste management (16).

Rhodococcus pyridinivorans was originally isolated as an extremely efficient pyridine-degrading coryneform bacterium from industrial wastewater in Korea (18). The species R. pyridinivorans comprises strains that are metabolically versatile (3, 12) and are able to degrade numerous aromatic compounds, such as pyridine, biphenyl, and styrene, as well as BTEX (benzene, toluene, ethylbenzene, and xylene) chemicals (4, 5, 13, 18).

The subject of our genome project, R. pyridinivorans strain AK37, was isolated from a crude oil-contaminated site in Hungary. It was identified by molecular taxonomy as R. pyridinivorans and deposited into the National Collection of Agricultural and Industrial Microorganisms (NCAIM PB1376), Hungary. Regarding its metabolic properties, it has been described as a good BTEX-degrading strain (14).

Genome sequencing of R. pyridinivorans strain AK37 was performed by combining the cycled ligation sequencing on the SOLiD 3Plus system (Life Technologies) with 454 FLX pyrosequencing (Roche). We generated 22,858,968 mate-paired (2×25-bp) and 8,577,169 50-bp fragment reads on SOLiD along with 201,647 ~400-bp reads on 454 FLX which, altogether, yielded >300-fold coverage. Assembly was performed using the Genomeworkbench 4.8. de novo plug-in and the Omixon Gapped SOLiD Alignment 1.3.2 plug-in (2), provided by CLCbio and Omixon, respectively, which generated 98 large (>200-bp) contigs. Automatic annotation of the genome was performed by using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html), which utilizes GeneMark, Glimmer, and tRNAscan-SE searches. The uncompleted draft genome of R. pyridinivorans strain AK37 consists of 5,244,611 bp, with a GC content of 67.8%. There are 4,822 putative coding sequences, 52 tRNAs, and 3 rRNA loci.

Until now, five Rhodococcus genome projects, for representa-

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ACKNOWLEDGMENTS

This study was supported by the NKTH TECH 08-A3/2-2008-0385 (OM-00234/2008) MYCOSSTOP grant, the KMOP 1.1.1.-07/1-2008-0002 project, the Hungarian-Japanese TET 10-1-2011-0071516 project, and by NKTH Teller Program grant OMFB-00441/2007.
We thank Marianna Nagymihály and Judit Cseklye for their valuable work in sequencing.

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