AMERICAN SOCIETY FOR MICROBIOLOGY | genomeAnnouncements™

PROKARYOTES

Draft Genome Sequence of *Rhodococcus opacus* Strain 04-OD7, Which Can Mobilize Phosphate

Bang-Xiao Zheng,[a,b,c,d] Huang-Kai Zhang,[e] Kai Ding[a]

[a]Key Laboratory of Urban Environment and Health, Institute of Urban Environment, Chinese Academy of Sciences, Xiamen, People's Republic of China

[b]University of Chinese Academy of Sciences, Beijing, People's Republic of China

[c]Consejo Superior de Investigaciones Científicas (CSIC), Global Ecology Unit, Centre for Ecological Research and Forestry Applications (CREAF)–CSIC–Universitat Autonoma de Barcelona (UAB), Barcelona, Catalonia, Spain

[d]CREAF, Cerdanyola del Vallès, Barcelona, Catalonia, Spain

[e]Xiamen Anjie Medical Data Technology Co. Ltd., Xiamen, People's Republic of China

ABSTRACT *Rhodococcus opacus* strain 04-OD7 (=CCTCC AB 2017148) is a Gram-positive bacterium showing inorganic phosphate solubilization capacity for the first time in the genus *Rhodococcus*. We present here the draft genome description of *R. opacus* 04-OD7 along with multiple phosphorus (P) mobilization-related genes, supporting its inorganic phosphate solubilization.

The actinomycete genus *Rhodococcus* belongs to the family *Nocardiaceae*, and its number of species has increased dramatically in the last decade (67 species and 57 type strains at the time of this writing, https://www.ezbiocloud.net/, February 2018). *R. opacus* was commonly seen with lipophilic accumulation ability (1, 2) and even with benzene tolerance (3); however, the phosphate (P) mobilization ability has not been reported before. *R. opacus* strain 04-OD7 was previously isolated from a fertilized soil sample from an agricultural field in Hailun, China (47°26′N, 126°38′E), and its calcium phosphate solubilization capacity reached 39.18 ± 6.08 μg liter^{-1} after 96 h of cultivation in Pikovskaya (PVK) medium (4) at 30°C with several organic acid exudations. This strain is a Gram-positive, rod-shaped, and pink-pigmented bacterium. In this study, the draft genome of *R. opacus* strain 04-OD was characterized.

R. opacus strain 04-OD7 was grown in PVK liquid medium, and the genomic DNA was extracted using a genomic DNA extraction kit for bacteria (BioTeke, Beijing, China) according to the manufacturer's instructions. Then, the genome was pair end sequenced using the Illumina HiSeq 2000 platform (Novogene, Tianjin, China). *De novo* assembly was performed by SOAP*denovo* version 2.01 (5), obtaining 217 contigs with an N_{50} contig length of 112,778 bp. Genome annotations were carried out using the NCBI Prokaryotic Genome Annotation Pipeline (6). The predicted coding DNA sequences (CDSs) were translated into amino acid sequences and submitted to the BLAST, GenBank, Swiss-Prot, Kyoto Encyclopedia of Genes and Genomes (KEGG), Cluster of Orthologous Groups of proteins (COG), and Gene Ontology (G) databases for further analysis.

The draft genome of *R. opacus* strain 04-OD7 comprises 9,322,710 nucleotides with an average G+C content of 64.47%. A total of 8,884 genes were predicted, of which, 8,407 (94.63%) protein-coding genes, 107 RNA genes (1.20%), and 6,484 functional genes (72.99%) were assigned. Based on COG database alignment, 633, 460, and 875 genes were assigned with amino acid, carbohydrate, and lipid transport and metabolism, respectively. The genome of *R. opacus* strain 04-OD7 contains genes for exopolyphosphatase (*ppx*), polyphosphate kinase (*ppk*), alkaline phosphatase synthesis re-

Received 1 May 2018 **Accepted** 1 May 2018 **Published** 7 June 2018

Citation Zheng B-X, Zhang H-K, Ding K. 2018. Draft genome sequence of *Rhodococcus opacus* strain 04-OD7, which can mobilize phosphate. Genome Announc 6:e00494-18. https://doi.org/10.1128/genomeA.00494-18.

Address correspondence to Kai Ding, kding@iue.ac.cn.

sponse regulator (*pho*P), alkaline phosphatase D (*pho*D), and pyrroloquinoline-quinone synthase (PQQ)-dependent glucose dehydrogenase (*pqq-gdh*, GenBank accession number PQP26070), which were all included in the P mobilization and cycles in the environment. By prediction using the alignment with the KEGG database, the coenzyme *pqqC* was also found. The secretion of gluconic acid and 2-keto-D-gluconic acid was considered an effective microbial pathway for enabling inorganic P solubilization (7). The genetic evidence shed light on the involvement of *pqq* operon genes (8, 9). The mutation of any one *pqq* gene would greatly reduce the P solubilizing capacity (10). Hence, *pqq-gdh* and *pqq*C would be promising candidates for inorganic P solubilization.

Accession number(s). The whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number PUIO00000000. The version described in this paper is version PUIO01000000. The raw sequences were deposited in the Sequence Read Archive (SRA) under the accession number SRR6785074.

ACKNOWLEDGMENTS

This study was financially supported by the Strategic Priority Research Program of the Chinese Academy of Sciences (grant XDB15020402), the Natural Science Foundation of China (grants 41771285, 41430858, and 41701299), and the National Key Research and Development Program of China (grant 2017YFD0200201).

We acknowledge Jian-Qiang Su (Institute of Urban Environment, Chinese Academy of Sciences) and Yu Yan (College of Chemical Engineering, Huaqiao University) for their helpful suggestions.

REFERENCES

1. Kurosawa K, Boccazzi P, de Almeida NM, Sinskey AJ. 2010. High-cell-density batch fermentation of *Rhodococcus opacus* PD630 using a high glucose concentration for triacylglycerol production. J Biotechnol 147:212–218. https://doi.org/10.1016/j.jbiotec.2010.04.003.
2. Kurosawa K, Wewetzer SJ, Sinskey AJ. 2013. Engineering xylose metabolism in triacylglycerol-producing *Rhodococcus opacus* for lignocellulosic fuel production. Biotechnol Biofuels 6:134. https://doi.org/10.1186/1754-6834-6-134.
3. Na K, Kuroda A, Takiguchi N, Ikeda T, Ohtake H, Kato J. 2005. Isolation and characterization of benzene-tolerant *Rhodococcus opacus* strains. J Biosci Bioeng 99:378–382. https://doi.org/10.1263/jbb.99.378.
4. Nautiyal CS. 1999. An efficient microbiological growth medium for screening phosphate solubilizing microorganisms. FEMS Microbiol Lett 170:265–270. https://doi.org/10.1111/j.1574-6968.1999.tb13383.x.
5. Luo R, Liu B, Xie Y, Li Z, Huang W, Yuan J, He G, Chen Y, Pan Q, Liu Y, Tang J, Wu G, Zhang H, Shi Y, Liu Y, Yu C, Wang B, Lu Y, Han C, Cheung DW, Yiu SM, Peng S, Xiaoqian Z, Liu G, Liao X, Li Y, Yang H, Wang J, Lam TW, Wang J. 2012. SOAPdenovo2: an empirically improved memory-efficient short-read *de novo* assembler. GigaSci 1:1–6. https://doi.org/10.1186/2047-217X-1-18.
6. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI Prokaryotic Genome Annotation Pipeline. Nucleic Acids Res 44:6614–6624. https://doi.org/10.1093/nar/gkw569.
7. Hwangbo H, Park RD, Kim YW, Rim YS, Park KH, Kim TH, Suh JS, Kim KY. 2003. 2-Ketogluconic acid production and phosphate solubilization by *Enterobacter intermedium*. Curr Microbiol 47:87–92. https://doi.org/10.1007/s00284-002-3951-y.
8. Babu-Khan S, Yeo TC, Martin WL, Duron MR, Rogers RD, Goldstein AH. 1995. Cloning of a mineral phosphate-solubilizing gene from *Pseudomonas* cepacia. Appl Environ Microbiol 61:972–978.
9. Rodríguez H, Fraga R, Gonzalez T, Bashan Y. 2006. Genetics of phosphate solubilization and its potential applications for improving plant growth-promoting bacteria. Plant Soil 287:15–21. https://doi.org/10.1007/s11104-006-9056-9.
10. Miller SH, Browne P, Prigent-Combaret C, Combes-Meynet E, Morrissey JP, O'Gara F. 2010. Biochemical and genomic comparison of inorganic phosphate solubilization in *Pseudomonas* species. Environ Microbiol Rep 2:403–411. https://doi.org/10.1111/j.1758-2229.2009.00105.x.