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PROKARYOTES

Draft Genome Sequence of *Pseudomonas* sp. Strain LLC-1 (NBRC 111237), Capable of Metabolizing Lignin-Derived Low-Molecular-Weight Compounds

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ABSTRACT *Pseudomonas* sp. strain LLC-1 (NBRC 111237), isolated from soil, metabolizes lignin-derived low-molecular-weight compounds and utilizes vanillin and vanillic acid as its sole sources of carbon. Here, we report the draft genome sequence of *Pseudomonas* sp. strain LLC-1.

Due to a recalcitrant nature, only limited groups of organisms, such as white-rot fungi, can degrade lignin. However, microorganisms capable of metabolizing lignin-derived low-molecular-weight compounds (LLCs) are ubiquitous in the natural environment, and their primary metabolism can be used to generate useful bioproducts from lignin (1). Vanillin, vanillic acid, and syringaldehyde are major components of LLCs. We isolated a Gram-negative aerobic bacterial strain, *Pseudomonas* sp. strain LLC-1, by using an enrichment culture in a medium containing LLCs and inorganic salts (2). This bacterial strain can utilize vanillin and vanillic acid as its sole sources of carbon and cometabolizes syringaldehyde, *o*-vanillin, and isovanillin. Here, we present the draft genome sequence of *Pseudomonas* sp. strain LLC-1.

The draft genome sequence of strain LLC-1 was determined by a combined method using the MiSeq system (Illumina) with paired-end runs and the 454 GS FLX+ system (Roche). A hybrid assembly of the reads obtained by the two sequencing methods was performed using Newbler version 2.6 (Roche). The assembled genome is composed of 42 contigs (>537 bp) totaling 5,946,122 bp, with a G+C content of 62.4%. The N_{50} contig size and the largest contig size are 322,774 bp and 480,886 bp, respectively.

The genome annotations were performed using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (3) and the Rapid Annotations using Subsystems Technology (RAST) server version 2.0 (4). PGAP predicted 5,208 coding DNA sequences (CDSs) and 66 tRNA sequences. RAST predicted 5,275 CDSs and 64 tRNA sequences. The coding sequences were classified by RAST into 4,334 subsystems, of which the systems for the metabolism of amino acid derivatives ($n = 752$ CDSs), carbohydrates ($n = 475$), cofactors, vitamins, prosthetic groups, and pigments ($n = 344$), and protein metabolism ($n = 287$) were the most abundant. Comparison of the genome sequences available in the RAST data sets revealed that *P. putida* GB-1 (5), with a score of 513, is the closest neighbor of strain LLC-1, followed by *P. putida* F-1 (6), with a score of 504. We are identifying the genes coding for vanillin metabolism from the draft genome sequence of strain LLC-1. An interesting feature of strain LLC-1 (2) is that it can metabolize vanillin and vanillic acid without reported inducer compounds, such as eugenol (7) or feruloyl-coenzyme A (CoA) (8). The whole-genome sequence of strain LLC-1 will enable the identification of genes coding enzymes metabolizing LLCs and will help advance our understanding of its unique vanillin metabolism.

Received 13 March 2018 **Accepted** 20 March 2018 **Published** 19 April 2018

Citation Hirose J, Tsuda N, Miyatake M, Yokoi H, Shimodaira J. 2018. Draft genome sequence of *Pseudomonas* sp. strain LLC-1 (NBRC 111237), capable of metabolizing lignin-derived low-molecular-weight compounds. Genome Announc 6:e00308-18. https://doi.org/10.1128/genomeA.00308-18.

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Accession number(s). The draft genome sequence of *Pseudomonas* sp. strain LLC-1 has been deposited in GenBank/ENA/DDBJ under the accession number LUVY00000000.

ACKNOWLEDGMENTS

We are grateful to Atsushi Yamazoe and Akira Hosoyama for their helpful technical advice regarding the genome assembly and analysis.

REFERENCES

1. Bugg TDH, Rahmanpour R. 2015. Enzymatic conversion of lignin into renewable chemicals. Curr Opin Chem Biol 29:10–17. https://doi.org/10.1016/j.cbpa.2015.06.009.
2. Hirose J, Nagayoshi A, Yamanaka N, Araki Y, Yokoi H. 2013. Isolation and characterization of bacteria capable of metabolizing lignin-derived low molecular weight compounds. Biotechnol Bioprocess Eng 18:736–741. https://doi.org/10.1007/s12257-012-0807-6.
3. 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.
4. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: Rapid Annotations using Subsystems Technology. BMC Genomics 9:75. https://doi.org/10.1186/1471-2164-9-75.
5. Geszvain K, Tebo BM. 2010. Identification of a two-component regulatory pathway essential for Mn(II) oxidation in *Pseudomonas putida* GB-1. Appl Environ Microbiol 76:1224–1231. https://doi.org/10.1128/AEM.02473-09.
6. Zylstra GJ, Gibson DT. 1989. Toluene degradation by *Pseudomonas putida* F1: nucleotide sequence of the *todC1C2BADE* genes and their expression in *Escherichia coli*. J Biol Chem 264:14940–14946.
7. Ryu J, Seo J, Unno T, Ahn J, Yan T, Sadowsky MJ, Hur H. 2010. Isoeugenol monooxygenase and its putative regulatory gene are located in the eugenol metabolic gene cluster in *Pseudomonas nitroreducens* Jin1. Arch Microbiol 192:201–209. https://doi.org/10.1007/s00203-010-0547-y.
8. Calisti C, Ficca AG, Barghini P, Ruzzi M. 2008. Regulation of ferulic catabolic genes in *Pseudomonas fluorescens* BF13: involvement of a MarR family regulator. Appl Microbiol Biotechnol 80:475–483. https://doi.org/10.1007/s00253-008-1557-4.