

Draft Genome Sequence of a *Pseudomonas aeruginosa* Strain Able To Decompose *N,N*-Dimethyl Formamide

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***Pseudomonas aeruginosa* is a Gram-negative bacterium, which uses a variety of organic chemicals as carbon sources. Here, we report the genome sequence of the Cu1510 isolate from wastewater containing a high concentration of *N,N*-dimethyl formamide.**

Received 8 December 2015 Accepted 18 December 2015 Published 4 February 2016

Citation Yan L, Yan M, Xu L, Wei L, Zhang L. 2016. Draft genome sequence of a *Pseudomonas aeruginosa* strain able to decompose *N,N*-dimethyl formamide. *Genome Announc* 4(1):e01609-15. doi:10.1128/genomeA.01609-15.

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Pseudomonas aeruginosa, which is infectious to plants (1, 2) and animals (3, 4), including human beings (5–7), is widely studied for its multidrug resistance (8–11). It is also used to degrade organic chemicals in wastewater because it can utilize a large range of organic chemicals as carbon sources (12–14) and survive in the presence of multiple metal ions (15–18). *N,N*-dimethyl formamide, an industrial organic solvent, possesses hepatotoxicity, embryotoxicity, teratogenicity, and possible carcinogenicity (19), but it is difficult to degrade. Here, we present the draft genome sequence of a wild-type strain of *P. aeruginosa* capable of degrading *N,N*-dimethyl formamide.

The Cu1510 isolate was selected from wastewater with M9-*N,N*-dimethyl formamide (DMF) medium containing 10% *N,N*-dimethyl formamide (the only carbon source) and then cultivated in the LB medium at 37°C overnight. Genomic DNA of Cu1510 was extracted according to the instructions of a Biomiga bacterial genomic DNA (gDNA) kit (product no. GD2411-01). The quality and quantity of DNA were assayed using a K5500 microspectrophotometer (Kaiao) and agarose gel electrophoresis. Genome sequencing was performed at CapitalBio Technology using Illumina technology with a DNA sequencing (DNA-seq) paired-end protocol. A library was prepared with the NEBNext Ultra DNA library prep kit for Illumina, and the instrument used for sequencing was HiSeq 2500. The resulted 15 million reads were assembled with Velvet 1.1 (20) and then refined with SEQuel version 1.0.2 (21). The remaining contigs were submitted to the ProDeGe website (22) for automatic decontamination. e-RGA (23) was applied for genome mapping. The resulting 6,122,906-bp draft genome containing 5,336 genes is rich in G+C content (66.65%). Finally, the assembled sequence was submitted to the National Center for Biotechnology Information (NCBI) Prokaryotic Genome Annotation Pipeline (PGAP) (24) for annotation. A detailed analysis on the *P. aeruginosa* pathway of DMF biodegradation will be presented in a later essay.

Nucleotide sequence accession numbers. The genome project was submitted to DDBJ/EMBL/GenBank under the accession no. CP013144. The version described in this paper is the first version, CP013144.1.

ACKNOWLEDGMENTS

The project was supported by 863 program 2012AA022101 released by the Ministry of Science and Technology of China.

We thank Liangliang Chen, Juan Xu, and Zhiling Zhang for their technical assistance.

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