

Genome Sequence of *Martelevella* sp. Strain AD-3, a Moderately Halophilic Polycyclic Aromatic Hydrocarbon-Degrading Bacterium

Changzheng Cui,^a Pengpeng Li,^b Gao Liu,^a Hongzhi Tang,^b Kuangfei Lin,^a Qishi Luo,^c Shanshan Liu,^d Ping Xu,^b Yongdi Liu^a

State Environmental Protection Key Laboratory of Environmental Risk Assessment and Control on Chemical Process, School of Resources and Environmental Engineering, East China University of Science and Technology, Shanghai, China^a; State Key Laboratory of Microbial Metabolism and School of Life Sciences & Biotechnology, Shanghai Jiao Tong University, Shanghai, China^b; State Environmental Protection Engineering Center for Urban Soil Contamination Control and Remediation, Institute of Wastes and Soil Environment, Shanghai Academy of Environmental Science, Shanghai, China^c; School of Environmental Science and Engineering, Shanghai Jiao Tong University, Shanghai, China^d

***Martelevella* sp. strain AD-3, enriched from a petroleum-contaminated site with high salinity, can efficiently degrade polycyclic aromatic hydrocarbons. Here, we report the 4.75-Mb genome sequence of strain AD-3 with its genetic feature of helping to remediate environmental organic pollutants.**

Received 10 December 2013 Accepted 13 December 2013 Published 16 January 2014

Citation Cui C, Li P, Liu G, Tang H, Lin K, Luo Q, Liu S, Xu P, Liu Y. 2014. Genome sequence of *Martelevella* sp. strain AD-3, a moderately halophilic polycyclic aromatic hydrocarbon-degrading bacterium. *Genome Announc.* 2(1):e01189-13. doi:10.1128/genomeA.01189-13.

Copyright © 2014 Cui et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/3.0/).

Address correspondence to Hongzhi Tang, tanghongzhi@sjtu.edu.cn, or Yongdi Liu, ydliu@ecust.edu.cn.

The petroleum industry generates a huge amount of oily and saline wastewater after separation of crude oil from the disposed reservoir. The main contaminants in this water are aromatic and polycyclic aromatic hydrocarbon (PAH) compounds (1, 2). Halophilic bacteria are helpful for removing organic pollutants from high-salinity industrial wastewaters without first reducing the levels of salts (3). *Martelevella* sp. strain AD-3 (CCTCC M2011218), a moderate halophilic bacterium, was isolated from a petroleum-contaminated soil with high salinity in China (4). It has high capabilities for degrading some PAHs, such as phenanthrene and anthracene, and it uses the toxicants as its sole carbon source (5). In addition, the strain can tolerate a broad range of salinities (0.1 to 15%) and a range of pHs (6.0 to 10.0) in the process of degrading PAHs (4, 5). To date, few genomes of *Martelevella* spp. have been sequenced; thus, this genome report of strain AD-3 may provide new genetic information regarding its remediation of environmental organic toxicants under high-salinity conditions.

Here, we present the draft genome sequence of *Martelevella* sp. strain AD-3, determined by using the Illumina HiSeq 2000 system, which was performed with a paired-end library at the Chinese National Human Genome Center, Shanghai, China. The reads of strain AD-3 were assembled into 197 contigs (longest contig size is 215,158 bp, median sequence size is 24,130 bp) using the Velvet software (version 1.2.10) (6). Gene prediction and genome annotation were carried out using RAST (7). The genome sequence of strain AD-3 is composed of 4,753,609 bases with a G+C content of 62.3%. There are 4,496 predicted coding sequences (CDSs), together with 50 RNAs. About 71 CDSs involved in the metabolism of aromatic compounds were predicted.

Genes related to degrading salicylic acid, gentisic acid, *p*-hydroxybenzoate, chloroaromatic compounds, and biphenyl have been annotated in the genome sequence of strain AD-3.

These genes or gene clusters will further explain its ability to degrade those organic toxicants. Moreover, there are 68 CDSs, which have been annotated as antibiotics and toxic compound resistance genes, and 242 CDSs annotated for membrane transport. These genes will contribute to the ability of strain AD-3 to remediate a petroleum-contaminated site with high salinity.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [AYGY000000000](https://www.ncbi.nlm.nih.gov/nuccore/AYGY000000000). The version described in this paper is version [AYGY020000000](https://www.ncbi.nlm.nih.gov/nuccore/AYGY020000000).

ACKNOWLEDGMENTS

This project was supported by the National Natural Science Foundation of China (no. 41301329 and 51378208), the Shanghai Municipal Natural Science Foundation (no. 13ZR1410900), the Specialized Research Fund for the Doctoral Program of Higher Education (no. 20110074130002), and the Fundamental Research Funds for the Central Universities (no. WB1114031).

REFERENCES

1. La Borgne S, Paniagua D, Vazquez-Duhalt R. 2008. Biodegradation of organic pollutants by halophilic bacteria and archaea. *J. Mol. Microbiol. Biotechnol.* 15:74–92. [http://dx.doi.org/10.1159/000121323](https://doi.org/10.1159/000121323).
2. Zhuang X, Han Z, Bai Z, Zhuang G, Shim H. 2010. Progress in decontamination by halophilic microorganisms in saline wastewater and soil. *Environ. Pollut.* 158:1119–1126. [http://dx.doi.org/10.1016/j.envpol.2010.01.007](https://doi.org/10.1016/j.envpol.2010.01.007).
3. Haddadi A, Shavandi M. 2013. Biodegradation of phenol in hypersaline conditions by *Halomonas* sp. strain PH2-2 isolated from saline soil. *Int. Biodeter. Biodegr.* 85:29–34. [http://dx.doi.org/10.1016/j.ibiod.2013.06.005](https://doi.org/10.1016/j.ibiod.2013.06.005).
4. Cui CZ, Feng TC, Yu YQ, Dong F, Yang XM, Feng YY, Liu YD, Lin HP. 2012. Isolation, characterization of an anthracene degrading bacterium *Martelevella* sp. AD-3 and cloning of dioxygenase gene. *Environ. Sci.* 33: 4062–4068. (Article in Chinese.)

5. Feng TC, Cui CZ, Dong F, Feng YY, Liu YD, Yang XM. 2012. Phenanthrene biodegradation by halophilic *Martelella* sp. AD-3. *J. Appl. Microbiol.* 113:779–789. <http://dx.doi.org/10.1111/j.1365-2672.2012.05386.x>.
6. Zerbino DR, Birney E. 2008. Velvet: algorithms for *de novo* short read assembly using de Bruijn graphs. *Genome Res.* 18:821–829. <http://dx.doi.org/10.1101/gr.074492.107>.
7. 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* 9:75–90. <http://dx.doi.org/10.1186/1471-2164-9-75>.