

Draft Genome Sequence of *Ochrobactrum anthropi* Strain W13P3, a Halotolerant Polycyclic Aromatic Hydrocarbon-Degrading Bacterium

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***Ochrobactrum anthropi* W13P3 was isolated from saline soil contaminated by polycyclic aromatic hydrocarbons (PAHs) and could degrade PAHs with 5% NaCl. We report the 5.3-Mb draft genome sequence of this strain, which is helpful for understanding the diversity of *Ochrobactrum* spp. and the mechanism of PAH degradation in saline environments.**

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Polycyclic aromatic hydrocarbons (PAHs) are widespread hazardous contaminants that can be degraded by a number of bacteria, such as members of the genus *Ochrobactrum* (1–3). However, genomic information about PAH-degrading *Ochrobactrum* is still limited. The draft genome sequence of halotolerant PAH-degrading *Ochrobactrum anthropi* W13P3 is reported for the first time, isolated from a PAH-contaminated saline site (4).

Genomic DNA was extracted and sequenced by Illumina HiSeq 2000, which produced 14,006,606 paired-end reads with about 260-fold coverage. Reads were filtered, assembled, scaffolded, gap filled, and validated by the NGS QC toolkit version 2.3 (5), SOAPdenovo version 2.04 (6), SSPACE version 2.0 (7), Gap-Filler version 1.10 (8), and the Burrows-Wheeler alignment tool version 0.7.4 (9). This assembly generated 48 contigs with an N_{50} length of 475,065 bp and an average length of 109,953 bp, which were assembled into 43 scaffolds with an N_{50} length of 475,065 bp and an average length of 122,740 bp. The genome sequence was annotated by the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP) (http://www.ncbi.nlm.nih.gov/genome/annotation_prok).

The draft genome comprised 5.3 Mb with a GC content of 56.3%. A total of 4,965 coding sequences (CDSs), 53 tRNA genes, 1 noncoding RNA (ncRNA), 1 rRNA operon, and 53 pseudogenes were identified. Of the CDSs, 50.1% can be assigned into 2,029 KEGG orthologous groups by KAAS (10), involving 182 metabolic pathways, and 72.1% can be assigned to COGs with amino acid transport and metabolism as the most abundant class. IS-Finder revealed that the IS3 family dominated the insertion sequence (IS) elements (11). A total of 62 tandem repeats were detected by Tandem repeats finder version 4.07 (12), and 451 potentially secreted proteins were identified by SignalP version 4.0 (13). The plasmid stabilization gene *ParB* was detected on contig 17, which suggests the occurrence of plasmid. One incomplete prophage sequence was identified by PHAST (14). A clustered regularly interspaced short palindromic repeat (CRISPR) element

was not detected by CRISPRFinder (15). Average nucleotide identity (ANI) analysis (16) revealed that *O. anthropi* W13P3 is phylogenetically related to *O. anthropi* ATCC 49188 (97.0%) (17), *O. anthropi* CTS325 (98.8%) (18), *O. anthropi* ML7 (98.9%) (19), and *O. anthropi* ATCC 49687 (97.1%) (20).

Two protocatechuate 3,4-dioxygenase genes and 3 alkane 1-monoxygenase genes were identified, which were responsible for the degradation of PAHs and alkanes. Moreover, 8 genes were identified as being involved in the uptake and synthesis of compatible solute, including 6 glycine/betaine ABC transporter genes, 1 ectoine synthase gene, and 1 betaine-aldehyde dehydrogenase gene. Nitrogen fixation genes were detected, which were responsible for the assimilation of gaseous nitrogen. These genes may be essential to survival in a saline oligotrophic environment. Information about the genome sequence of *O. anthropi* W13P3 offered an opportunity to understand the genetic diversity of *Ochrobactrum* spp. and the mechanism of PAH degradation in saline environments.

Nucleotide sequence accession number. The draft genome sequence of *O. anthropi* W13P3 was deposited in GenBank under the accession number [JENZ00000000](https://www.ncbi.nlm.nih.gov/nuccore/JENZ00000000). The version described in this paper is the first version.

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REFERENCES

1. Wu Y, He T, Zhong M, Zhang Y, Li E, Huang T, Hu Z. 2009. Isolation of marine benzo[a]pyrene-degrading *Ochrobactrum* sp. BAP5 and proteins characterization. *J Environ Sci* 21:1446–1451. [http://dx.doi.org/10.1016/S1001-0742\(08\)62438-9](http://dx.doi.org/10.1016/S1001-0742(08)62438-9).
2. Arulazhagan P, Vasudevan N. 2011. Biodegradation of polycyclic aro-

- matic hydrocarbons by a halotolerant bacterial strain *Ochrobactrum* sp. VA1. *Mar Pollut Bull* 62:388–394. <http://dx.doi.org/10.1016/j.marpolbul.2010.09.020>.
3. Ghosal D, Chakraborty J, Khara P, Dutta TK. 2010. Degradation of phenanthrene via meta-cleavage of 2-hydroxy-1-naphthoic acid by *Ochrobactrum* sp. strain PWTJD. *FEMS Microbiol Lett* 313:103–110. <http://dx.doi.org/10.1111/j.1574-6968.2010.02129.x>.
 4. Wang X, Zhang Z, Jin D, Zhou L, Wu L, Li C, Zhao L, An W, Chen Y. 2014. Draft genome sequence of *Brachybacterium phenoliresistens* strain w13a50, a halotolerant hydrocarbon-degrading bacterium. *Genome Announc* 2(5):e00899-14. <http://dx.doi.org/10.1128/genomeA.00899-14>.
 5. Patel RK, Jain M. 2012. NGS QC toolkit: a toolkit for quality control of next generation sequencing data. *PLoS One* 7:e30619. <http://dx.doi.org/10.1371/journal.pone.0030619>.
 6. 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. 2012. SOAPdenovo2: an empirically improved memory-efficient short-read *de novo* assembler. *GigaScience* 1:18. <http://dx.doi.org/10.1186/2047-217X-1-18>.
 7. Boetzer M, Henkel CV, Jansen HJ, Butler D, Pirovano W. 2011. Scaffolding pre-assembled contigs using SSPACE. *Bioinformatics* 27: 578–579. <http://dx.doi.org/10.1093/bioinformatics/btq683>.
 8. Boetzer M, Pirovano W. 2012. Toward almost closed genomes with Gap-Filler. *Genome Biol* 13:R56. <http://dx.doi.org/10.1186/gb-2012-13-6-r56>.
 9. Li H, Durbin R. 2009. Fast and accurate short read alignment with Burrows-Wheeler transform. *Bioinformatics* 25:1754–1760. <http://dx.doi.org/10.1093/bioinformatics/btp324>.
 10. Moriya Y, Itoh M, Okuda S, Yoshizawa AC, Kanehisa M. 2007. KAAS: an automatic genome annotation and pathway reconstruction server. *Nucleic Acids Res* 35:W182–W185. <http://dx.doi.org/10.1093/nar/gkm321>.
 11. Siguier P, Perochon J, Lestrade L, Mahillon J, Chandler M. 2006. ISfinder: the reference centre for bacterial insertion sequences. *Nucleic Acids Res* 34:D32–D36. <http://dx.doi.org/10.1093/nar/gkj014>.
 12. Benson G. 1999. Tandem repeats finder: a program to analyze DNA sequences. *Nucleic Acids Res* 27:573–580. <http://dx.doi.org/10.1093/nar/27.2.573>.
 13. Petersen TN, Brunak S, von Heijne G, Nielsen H. 2011. SignalP 4.0: discriminating signal peptides from transmembrane regions. *Nat Methods* 8:785–786. <http://dx.doi.org/10.1038/nmeth.1701>.
 14. Zhou Y, Liang Y, Lynch KH, Dennis JJ, Wishart DS. 2011. PHAST: a fast phage search tool. *Nucleic Acids Res* 39:W347–W352. <http://dx.doi.org/10.1093/nar/gkr485>.
 15. Grissa I, Vergnaud G, Pourcel C. 2007. CRISPRFinder: a Web tool to identify clustered regularly interspaced short palindromic repeats. *Nucleic Acids Res* 35:W52–W57. <http://dx.doi.org/10.1093/nar/gkm360>.
 16. Richter M, Rosselló-Móra R. 2009. Shifting the genomic gold standard for the prokaryotic species definition. *Proc Natl Acad Sci USA* 106: 19126–19131. <http://dx.doi.org/10.1073/pnas.0906412106>.
 17. Chain PS, Lang DM, Comerci DJ, Malfatti SA, Vergez LM, Shin M, Ugalde RA, Garcia E, Tolmasey ME. 2011. Genome of *Ochrobactrum anthropi* ATCC 49188T, a versatile opportunistic pathogen and symbiont of several eukaryotic hosts. *J Bacteriol* 193:4274–4275. <http://dx.doi.org/10.1128/JB.05335-11>.
 18. Cheng Y, Xie Y, Zheng J, Wu Z, Chen Z, Ma X, Li B, Lin Z. 2009. Identification and characterization of the chromium(VI) responding protein from a newly isolated *Ochrobactrum anthropi* CTS-325. *J Environ Sci (China)* 21:1673–1678. [http://dx.doi.org/10.1016/S1001-0742\(08\)62472-9](http://dx.doi.org/10.1016/S1001-0742(08)62472-9).
 19. Tobias NJ, Mishra B, Gupta DK, Ke LP, Thines M, Bode HB. 2015. Draft genome sequence of *Ochrobactrum anthropi* strain ml7 isolated from soil samples in Vinhphuc Province, Vietnam. *Genome Announc* 3(2): e00218-15. <http://dx.doi.org/10.1128/genomeA.00218-15>.
 20. Minogue TD, Daligault HA, Davenport KW, Bishop-Lilly KA, Bruce DC, Chain PS, Chertkov O, Coyne SR, Freitas T, Frey KG, Jaissle J, Koroleva GI, Ladner JT, Palacios GF, Redden CL, Xu Y, Johnson SL. 2014. Complete genome assembly of reference strain *Ochrobactrum anthropi* ATCC 49687. *Genome Announc* 2(5):e00962-14. <http://dx.doi.org/10.1128/genomeA.00962-14>.