Draft Genome Sequence ofPseudomonassp. LAB-08 Isolated from Trichloroethene-Contaminated Aquifer Soil

著者	Suzuki Kenshi, Aziz Fatma A. A., Inuzuka Yuma, Tashiro Yosuke, Futamata Hiroyuki
journal or publication title	Genome Announcements
volume	4
number	5
page range	e00948-16
year	2016-09-22
出版者	American Society for Microbiology
権利	Copyright (C) 2016 Suzuki et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International license.
URL	http://hdl.handle.net/10297/9859

doi: 10.1128/genomeA.00948-16

AMERICAN SOCIETY FOR MICROBIOLOGY | genomeAnnouncements

Draft Genome Sequence of *Pseudomonas* sp. LAB-08 Isolated from Trichloroethene-Contaminated Aquifer Soil

Kenshi Suzuki,[a] Fatma A. A. Aziz,[b] Yuma Inuzuka,[c] Yosuke Tashiro,[c] Hiroyuki Futamata[a,c,d]

Graduate School of Science and Technology, Shizuoka University, Hamamatsu, Hamamatsu, Japan[a]; Laboratory of Food Crops, Institute of Tropical Agriculture, Universiti Putra Malaysia, Serdang, Malaysia[b]; Department of Applied Chemistry and Biochemical Engineering, Graduate School of Engineering, Shizuoka University, Hamamatsu, Japan[c]; Research Institute of Green Science and Technology, Shizuoka University, Suruga-ku, Shizuoka, Shizuoka, Japan[d]

***Pseudomonas* sp. LAB-08 was isolated from a phenol-fed bioreactor constructed with contaminated aquifer soil as the inoculum. Strain LAB-08 utilized phenol as a sole carbon and energy source. Here, we report the genome sequence and annotation of *Pseudomonas* sp. LAB-08.**

Received 13 July 2016 **Accepted** 1 August 2016 **Published** 22 September 2016

Citation Suzuki K, Aziz FAA, Inuzuka Y, Tashiro Y, Futamata H. 2016. Draft genome sequence of *Pseudomonas* sp. LAB-08 isolated from trichloroethene-contaminated aquifer soil. Genome Announc 4(5):e00948-16 doi:10.1128/genomeA.00948-16.

Address correspondence to Hiroyuki Futamata, futamata.hiroyuki@shizuoka.ac.jp, or Kenshi Suzuki, suzuki.kenshi.15@shizuoka.ac.jp.

Trichloroethene (TCE) is used for dry-cleaning and semiconductor manufacturing and its contamination of the subsurface environment is a serious problem for drinking-water sources. TCE is co-metabolically degraded by aliphatic, aromatic, and hydrocarbon-degrading bacteria (1, 2). In our previous work, a positive correlation between affinities for phenol and TCE was found (3). Thus, high-affinity (low K_S value) TCE-degrading bacteria were enriched in a phenol-fed chemostat (4–6). Here we present the genome sequence of *Pseudomonas* sp. LAB-08 which was isolated from such a chemostat to get insight into the metabolism of phenol.

The genome of strain LAB-08 was sequenced by whole-genome 400-bp shotgun and 300-bp paired-end strategies using 454 GS FLX Titanium (7) and gene walking methods. The 454 GS FLX Titanium data consisted of 700,462 reads and covering 212,407,357 bp. The Newbler GS De Novo Assembler (version 2.5) (7) was used for assembly, resulting in a scaffold (including 16,831 N). The genome was annotated by Rapid Annotation using Subsystem Technology (RAST) (8) and Microbial Genome Annotation Pipeline (MiGAP) (9). The draft genome sequence of strain LAB-08 has a total length of 6,733,957 bp, with an estimated G+C content of 59.2%. The annotated genome includes 6,063 coding sequences (CDSs), seven 5S-16S-23S rRNA clusters, and 73 tRNAs.

During phenol degradation in bacteria, phenol is converted to catechol by phenol hydroxylase (10). Two types of phenol hydroxylase are known, single and multicomponent enzymes (10); multicomponent type hydroxylases are considered predominant in the environment (10). The genome of strain LAB-08 contained one multicomponent phenol hydroxylase. Catechol is converted by either catechol 2,3-dioxygenase (C23O) or catechol 1,2-dioxygenase (C12O), and both products are then converted to acetyl-CoA via *meta*- or *ortho*-cleavage, respectively (11). There were a gene encoding C12O and also the downstream genes of the *ortho*-pathway in the genome of strain LAB-08 but no evidence of C23O. Instead, biphenyl 2,3-dioxygenase, which converts biphenyl-2,3-diol to 2-hydroxy-6-oxo-6-phenylhexa-2, 4-dienoate, and also converts catechol to 2-hydroxymuconic semialdehyde (12) was found. These results suggested that strain LAB-08 has two possible phenol-metabolic pathways and are presumably differentially regulated.

Accession number(s). The draft genome sequence of *Pseudomonas* sp. LAB-08 has been deposited at DDBL/GenBank under the accession no. AP017423.

ACKNOWLEDGMENTS

We thank Sean C. Booth for assistance in preparation of the manuscript.

This study was carried out as grant KAKENHI 15K12228 and KAKENHI (B) 26281038 from the Ministry of Education, Culture, Sports, Science and Technology of Japan.

FUNDING INFORMATION

This work, including the efforts of Hiroyuki Futamata, was funded by Japan Society for the Promotion of Science (JSPS) (15K12228 and 26281038).

REFERENCES

1. **Ensley BD.** 1991. Biochemical diversity of trichloroethylene metabolism. Annu Rev Microbiol **45:**283–299. http://dx.doi.org/10.1146/annurev.mi.45.100191.001435.
2. **Semprini L.** 1997. Strategies for the aerobic co-metabolism of chlorinated solvents. Curr Opin Biotechnol **8:**296–308. http://dx.doi.org/10.1016/S0958-1669(97)80007-9.
3. **Futamata H, Harayama S, Watanabe K.** 2001. Diversity in kinetics of trichloroethylene-degrading activities exhibited by phenol-degrading bacteria. Appl Microbiol Biotecnol **55:**248–253. http://dx.doi.org/10.1007/s002530000500.
4. **Haruta S, Yoshida T, Aoi Y, Kaneko K, Futamata H.** 2013. Challenges for complex microbial ecosystems: combination of experimental approaches with mathematical modeling. Microbes Environ **28:**285–294. http://dx.doi.org/10.1264/jsme2.ME13034.
5. **Futamata H, Harayama S, Watanabe K.** 2001. Group-specific monitoring of phenol hydroxylase genes for a functional assessment of phenol-stimulated trichloroethylene bioremediation. Appl Environ Microbiol **67:**4671–4677. http://dx.doi.org/10.1128/AEM.67.10.4671-4677.2001.
6. **Futamata H, Nagano Y, Watanabe K, Hiraishi A.** 2005. Unique kinetic properties of phenol-degrading *Variovorax* strains responsible for effi-

cient trichloroethylene degradation in a chemostat enrichment culture. Appl Environ Microbiol **71:**904–911. http://dx.doi.org/10.1128/AEM.71.2.904-911.2005.

7. **Margulies M, Egholm M, Altman WE, Attiya S, Bader JS, Bemben LA, Berka J, Braverman MS, Chen YJ, Chen Z, Dewell SB, Du L, Fierro JM, Gomes XV, Godwin BC, He W, Helgesen S, Ho CH, Ho CH, Irzyk GP, Jando SC, Alenquer ML, Jarvie TP, Jirage KB, Kim JB, Knight JR, Lanza JR, Leamon JH, Lefkowitz SM, Lei M, Li J, Lohman KL, Lu H, Makhijani VB, McDade KE, McKenna MP, Myers EW, Nickerson E, Nobile JR, Plant R, Puc BP, Ronan MT, Roth GT, Sarkis GJ, Simons JF, Simpson JW, Srinivasan M, Tartaro KR, Tomasz A, Vogt KA, Volkmer GA, Wang SH, Wang Y, Weiner MP, Yu P, Begley RF, Rothberg JM.** 2005. Genome sequencing in microfabricated high-density picolitre reactors. Nature **437:**376–380. http://dx.doi.org/10.1038/nature03959.
8. **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. http://dx.doi.org/10.1186/1471-2164-9-75.
9. **Sugawara H, Ohyama A, Mori H, Kurokawa K.** 2009. Microbial genome annotation pipeline (MiGAP) for diverse users, the 20th International Conference on Genome Informatics (GIW2009) poster and software Demonstrations (Yokohama), p S001-1-2.
10. **Powlowski J, Shingler V.** 1990. In vitro analysis of polypeptide requirements of multicomponent phenol hydroxylase from *Pseudomonas* sp. strain CF600. J Bacteriol **172:**6834–6840.
11. **Van Schie PM, Young LY.** 2000. Biodegradation of phenol: mechanisms and applications. Bioremediat J **4:**1–18. http://dx.doi.org/10.1080/10588330008951128.
12. **Ohtsubo Y, Nagata Y, Kimbara K, Takagi M, Ohta A.** 2000. Expression of the bph genes involved in biphenyl / PCB degradation in *Pseudomonas* sp. KKS102 induced by the biphenyl degradation intermediate, 2-hydroxy-6-oxo-6-phenylhexa-2, 4-dienoic acid. Gene **256:**223–228. http://dx.doi.org/10.1016/S0378-1119(00)00349-8.