

Genome Sequence of *Pseudomonas azelaica* Strain Aramco J

Magdy El-Said Mohamed,^a José L. García,^b Igor Martínez,^b Carlos del Cerro,^b Juan Nogales,^b Eduardo Díaz^b

R&DC, Saudi Aramco, Dhahran, Saudi Arabia^a; Environmental Biology, Centro de Investigaciones Biológicas, Consejo Superior de Investigaciones Científicas, Madrid, Spain^b

We report here the draft genome sequence of *Pseudomonas azelaica* strain Aramco J (7.3 Mbp; GC content, 61.9%), one of the few bacteria that can completely mineralize different hydroxybiphenyls, e.g., 2-hydroxybiphenyl, 2,2'-dihydroxybiphenyl, and 3-hydroxybiphenyl. The findings obtained from its genome annotation suggest that this strain becomes a useful biocatalyst for aromatic bioconversions.

Received 12 January 2015 Accepted 16 January 2015 Published 5 March 2015

Citation El-Said Mohamed M, García JL, Martínez I, del Cerro C, Nogales J, Díaz E. 2015. Genome sequence of *Pseudomonas azelaica* strain Aramco J. *Genome Announc* 3(2): e00037-15. doi:10.1128/genomeA.00037-15.

Copyright © 2015 El-Said Mohamed 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 Eduardo Díaz, ediaz@cib.csic.es.

Hydroxybiphenyls, such as 2-hydroxybiphenyl (2-HBP), are of great importance in the metabolism of toxic biphenyls, such as polychlorinated biphenyls, and 2-HBP is also a main byproduct of oil biodesulfurization produced through microbial conversion of dibenzothiophene (1). Moreover, 2-HBP is a bulk chemical with biocidal properties that is primarily used as an agricultural fungicide and therefore can be found in persistent low quantities in sewage effluents (2). However, bacterial degradation of 2-HBP is an uncommon trait, and only a few bacteria are known to completely metabolize 2-HBP (3, 4). Here, we report the genome sequence of a bacterium, the *Pseudomonas azelaica* Aramco J strain, isolated from an oil-contaminated soil sample from Abu Ali Island, Saudi Arabia, that uses 2-HBP, as well as other hydroxybiphenyls such as 2,2'-dihydroxybiphenyl and 3-hydroxybiphenyl, as the only carbon source.

The genome of the Aramco J strain has been sequenced using the 316-chip and 400-bp chemistry Ion Torrent PGM platform per the manufacturer's instructions. Preliminary assembly of raw lectures (528 Mbp sequence) was performed using Newbler software from Roche. This assembly was manually revised and improved, obtaining a quality draft of 91 contigs. The genome was structurally and functionally annotated using RAST (5), an automated genome annotation system, and the functions, names, and general properties of the gene products were predicted using this method. The Aramco J genome (7.3 Mbp) is highly similar (99% nucleotide identity) to that of *P. azelaica* HBP1 (6), indicating that this strain is a new member of the *P. azelaica* species. However, *P. azelaica* strain Aramco J lacks a 75-kb DNA fragment that is present in strain HBP1 in a megaplasmid. The smaller megaplasmid of strain Aramco J shows significant similarity to the pOZ176 IncP-2 megaplasmid of *Pseudomonas aeruginosa* (7), and its average GC content (57%) is lower than that of the whole genome (61.9%).

The *hbp* genes involved in the conversion of 2-HBP (and 2,2'-dihydroxybiphenyl) to benzoate (salicylate) and 2-hydroxy-pentadienoate (4) are located within an integrative-conjugative element (ICEhbp) similar to that found in *P. azelaica* HBP1 (6). Next to the *hbp* genes are located the *sal* and *dmp* genes encoding

a salicylate monooxygenase and a catechol *meta*-cleavage pathway for the metabolism of salicylate and 2-hydroxy-pentadienoate, respectively. Other catabolic functions present in ICEhbp are the *pob-pca* genes for 4-hydroxybenzoate degradation via the β -keto adipate *ortho*-cleavage pathway, as well as genes likely involved in channeling aromatic alcohols with methoxy substituents, e.g., coniferyl alcohol, to the β -keto adipate pathway. At least two different *ben-cat* clusters for benzoate degradation, and the *paa* and *hmg* clusters for phenylacetate and homogentisate degradation, respectively, can be identified outside the ICEhbp element.

Given the catabolic potential of the *P. azelaica* strain Aramco J toward aromatic compounds, as revealed by the genome information reported here, and its unique tolerance to high 2-HBP concentrations (up to 15 g/liter), this strain becomes an interesting host for engineering recombinant biocatalysts to be used in biotechnological processes such as biodesulfurization (1).

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [JUEH00000000](https://www.ncbi.nlm.nih.gov/nuclink/JUEH00000000). The version described in this paper is version [JUEH01000000](https://www.ncbi.nlm.nih.gov/nuclink/JUEH01000000).

ACKNOWLEDGMENTS

We acknowledge the financial support provided by Saudi Aramco and by project DBR-001/08/WCOD.

REFERENCES

- Kilbane JJ, II. 2006. Microbial biocatalyst developments to upgrade fossil fuels. *Curr Opin Biotechnol* 17:305–314. <http://dx.doi.org/10.1016/j.copbio.2006.04.005>.
- Yu Y, Huang Q, Cui J, Zhang K, Tang C, Peng X. 2011. Determination of pharmaceuticals, steroid hormones, and endocrine-disrupting personal care products in sewage sludge by ultra-high-performance liquid chromatography-tandem mass spectrometry. *Anal Bioanal Chem* 399: 891–902. <http://dx.doi.org/10.1007/s00216-010-4295-2>.
- Kohler HP, Kohler-Staub D, Focht DD. 1988. Degradation of 2-hydroxybiphenyl and 2,2'-dihydroxybiphenyl by *Pseudomonas* sp. strain hbp1. *Appl Environ Microbiol* 54:2683–2688.
- Czechowska K, Reimann C, van der Meer JR. 2013. Characterization of a MexAB-OprM efflux system necessary for productive metabolism of *Pseudomonas azelaica* HBP1 on 2-hydroxybiphenyl. *Front Microbiol* 4:203. <http://dx.doi.org/10.3389/fmicb.2013.00203>.

5. 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>.
6. García JL, Rozas D, del Cerro C, Nogales J, El-Said Mohamed M, Díaz E. 2014. Genome sequence of *Pseudomonas azelaica* HBP1, which catabolizes 2-hydroxybiphenyl fungicide. *Genome Announc* 2(1):e01248–13. <http://dx.doi.org/10.1128/genomeA.01248-13>.
7. Xiong J, Alexander DC, Ma JH, Déraspe M, Low DE, Jamieson FB, Roy PH. 2013. Complete sequence of pOZ176, a 500-kilobase IncP⁻² plasmid encoding IMP-9-mediated carbapenem resistance, from outbreak isolate *Pseudomonas aeruginosa* 96. *Antimicrob Agents Chemother* 57:3775–3782. <http://dx.doi.org/10.1128/AAC.00423-13>.