

# Draft Genome Sequence of *Pseudomonas abietaniphila* KF717 (NBRC 110669), Isolated from Biphenyl-Contaminated Soil in Japan

Nobutada Kimura,<sup>a</sup> Atsushi Yamazoe,<sup>b</sup> Akira Hosoyama,<sup>b</sup> Jun Hirose,<sup>c</sup> Takahito Watanabe,<sup>d</sup> Hikaru Suenaga,<sup>a</sup> Hidehiko Fujihara,<sup>e</sup> Taiki Futagami,<sup>f</sup> Masatoshi Goto,<sup>g</sup> Kensuke Furukawa<sup>e</sup>

Bioproduction Research Institute, National Institute of Advanced Industrial Science and Technology (AIST), Tsukuba, Japan<sup>a</sup>; Biological Resource Center, National Institute of Technology and Evaluation (NITE), Tokyo, Japan<sup>b</sup>; Faculty of Engineering, Department of Applied Chemistry, Faculty of Engineering, University of Miyazaki, Miyazaki, Japan<sup>c</sup>; Research Institute for Sustainable Humanosphere, Kyoto University, Kyoto, Japan<sup>d</sup>; Department of Food and Nutrition, Beppu University, Beppu, Japan<sup>e</sup>; Faculty of Agriculture, Education and Research Center for Fermentation Studies, Kagoshima University, Kagoshima, Japan<sup>f</sup>; Faculty of Agriculture, Laboratory of Future Creation Microbiology, Kyushu University, Fukuoka, Japan<sup>g</sup>

***Pseudomonas abietaniphila* KF717 utilizes biphenyl as a sole source of carbon and energy and degrades polychlorinated biphenyls (PCBs). We report here the 6,930,016-bp genome sequence of this strain, which contains 6,323 predicted coding sequences (CDSs), including the biphenyl-utilizing *bph* gene cluster.**

Received 4 February 2015 Accepted 10 February 2015 Published 19 March 2015

**Citation** Kimura N, Yamazoe A, Hosoyama A, Hirose J, Watanabe T, Suenaga H, Fujihara H, Futagami T, Goto M, Furukawa K. 2015. Draft genome sequence of *Pseudomonas abietaniphila* KF717 (NBRC 110669), isolated from biphenyl-contaminated soil in Japan. *Genome Announc* 3(2):e00059-15. doi:10.1128/genomeA.00059-15.

**Copyright** © 2015 Kimura 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/4.0/).

Address correspondence to Nobutada Kimura, n-kimura@aist.go.jp.

Polychlorinated biphenyls (PCBs) have been recognized worldwide as serious environmental pollutants. *Pseudomonas abietaniphila* strain KF717 was isolated from biphenyl-contaminated soil in Kitakyushu, Japan, as a PCB degrader that utilizes biphenyl as a sole source of carbon and energy (1, 2). Whole-genome shotgun sequencing on strain KF717 was performed by the National Institute of Technology and Evaluation (NITE) by using a combination of shotgun sequencing with a 454 GS FLX+ system (Roche) and paired-end sequencing using a MiSeq sequencing system (Illumina). The Newbler software package (version 2.6; Roche) was used for the genome assembly. The draft genome size is 6,930,016 bp and contains 97 contigs, with an average contig length of 71.4 kb, a median coverage depth of 92-fold, and an average G+C content of 59.4 mol%.

The genome sequence of strain KF717 was uploaded to the RAST server (<http://rast.nmpdr.org>) to predict the open reading frames (ORFs), tRNAs, and rRNAs (3). Rapid genome annotation using the RAST annotation server revealed 6,323 coding sequences (CDSs), 60 tRNA sequences, and 4 rRNA sequences. The coding sequences were classified into 4,026 subsystems, with the most abundant being systems involved in the metabolism of amino acid derivatives ( $n = 567$  CDSs) and carbohydrates ( $n = 509$ ), the production of cofactors, vitamins, prosthetic groups, and pigments ( $n = 301$ ), protein metabolism ( $n = 290$ ), the stress response ( $n = 227$ ), and the production of cell wall and capsule ( $n = 212$ ). A comparison of *P. abietaniphila* KF717 with other *Pseudomonas* strains within the RAST database identified *Pseudomonas syringae* pv. *actinidiae* CFBP 7286 (RAST server genome ID 1094176.3) as its closest neighbor, with a score of 494, followed by *P. syringae* pv. *phaseolicola* 1448A (genome ID 264730.3), with a score of 481. *Pseudomonas fluorescens* Q8r1-96 (genome ID 1038923.3) was the sixth closest neighbor, with a score of 459. *P. syringae* is known as a pathogen of many plant species (4), and *P. fluorescens* Q8r1-96 was identified as a plant growth-promoting rhizobacterium (PGPR) (5).

The comparison of the functional annotation was performed us-

ing the Kyoto Encyclopedia of Genes and Genomes (KEGG) (6). Strain KF717 was found to possess the ring-hydroxylating dioxygenase, the alpha and beta subunits of biphenyl degradation, wholebenzoate degradation via the hydroxylation pathway, and phenol hydroxylase components of the phenol degradation pathway.

**Nucleotide sequence accession numbers.** The whole-genome sequence of *P. abietaniphila* KF717 has been deposited in DDBJ/EMBL/GenBank under the accession numbers [BBQR01000001](https://www.ncbi.nlm.nih.gov/nuccore/BBQR01000001) to [BBQR01000097](https://www.ncbi.nlm.nih.gov/nuccore/BBQR01000097).

## ACKNOWLEDGMENT

This work was performed as part of a project supported by the Ministry of Economy, Trade, and Industry of Japan.

## REFERENCES

- Furukawa K, Hayase N, Taira K, Tomizuka N. 1989. Molecular relationship of chromosomal genes encoding biphenyl/polychlorinated biphenyl catabolism: some soil bacteria possess a highly conserved *bph* operon. *J Bacteriol* 171:5467–5472.
- Furukawa K, Miyazaki T. 1986. Cloning of a gene cluster encoding biphenyl and chlorobiphenyl degradation in *Pseudomonas pseudoalcaligenes*. *J Bacteriol* 166:392–398.
- Wijaya E, Frith MC, Suzuki Y, Horton P. 2009. Recount: expectation maximization based error correction tool for next generation sequencing data. *Genome Inform* 23:189–201. [http://www.worldscientific.com/doi/abs/10.1142/9781848165632\\_0018](http://www.worldscientific.com/doi/abs/10.1142/9781848165632_0018).
- Feil H, Feil WS, Chain P, Larimer F, DiBartolo G, Copeland A, Lykidis A, Trong S, Nolan M, Goltsman E, Thiel J, Malfatti S, Loper JE, Lapidus A, Detter JC, Land M, Richardson PM, Kyrpides NC, Ivanova N, Lindow SE. 2005. Comparison of the complete genome sequences of *Pseudomonas syringae* pv. *syringae* B728a and pv. *tomato* DC3000. *Proc Natl Acad Sci USA* 102:11064–11069. <http://dx.doi.org/10.1073/pnas.0504930102>.
- Raaijmakers JM, Weller DM. 2001. Exploiting genotypic diversity of 2,4-diacetylphloroglucinol-producing *Pseudomonas* spp.: characterization of superior root-colonizing *P. fluorescens* strain Q8r1-96. *Appl Environ Microbiol* 67:2545–2554. <http://dx.doi.org/10.1128/AEM.67.6.2545-2554.2001>.
- Ogata H, Goto S, Fujibuchi W, Kanehisa M. 1998. Computation with the KEGG pathway database. *Biosystems* 47:119–128. [http://dx.doi.org/10.1016/S0303-2647\(98\)00017-3](http://dx.doi.org/10.1016/S0303-2647(98)00017-3).