

Draft Genome Sequence of *Pseudomonas frederiksbergensis* SI8, a Psychrotrophic Aromatic-Degrading Bacterium

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***Pseudomonas frederiksbergensis* strain SI8 is a psychrotrophic bacterium capable of efficient aerobic degradation of aromatic hydrocarbons. The draft genome of *P. frederiksbergensis* SI8 is 6.57 Mb in size, with 5,904 coding sequences and 60.5% G+C content. The isopropylbenzene (cumene) degradation pathway is predicted to be present in *P. frederiksbergensis* SI8.**

Received 12 June 2015 Accepted 15 June 2015 Published 16 July 2015

Citation Ruiz ON, Brown LM, Striebich RC, Mueller SS, Gunasekera TS. 2015. Draft genome sequence of *Pseudomonas frederiksbergensis* SI8, a psychrotrophic aromatic-degrading bacterium. *Genome Announc* 3(4):e00811-15. doi:10.1128/genomeA.00811-15.

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Pseudomonas frederiksbergensis strain SI8 was isolated from a desert soil sample from under a fuel storage bladder in Kuwait. This strain grows in temperatures ranging from 4°C to 30°C and metabolizes toluene, ethylbenzene, and propylbenzene, among other compounds. Based on the 16S rRNA gene sequence, *P. frederiksbergensis* SI8 is at least 99.0% similar to *P. frederiksbergensis* strains V1R0E2, JW-SD2, DSM13022, CB2B1. An alkane-degrading psychrophilic *P. frederiksbergensis* strain and a psychrotrophic strain from soil at a coal gasification plant have been reported (1, 2). Due to the importance of cold-tolerant microorganisms in the environment and their potential application in bioremediation, we have sequenced the genome of *P. frederiksbergensis* SI8, to understand the underlying aromatic-degradation mechanisms.

P. frederiksbergensis SI8 was sequenced on a Roche 454-GS Junior platform using a whole-genome shotgun (WGS) approach, resulting in 728,652 reads. The sequence reads were assembled with the Roche *de novo* Assembly software. More than 99% or 724,816 reads were assembled into 65 large (>500 bp) contigs, with an N_{50} of 320,712 bp. The longest contig was 684,101 bp. The draft genome sequence was 6,569,267 bases in length, with a G+C content of 60.5%. Rapid genome annotation using RAST annotation server (3) described 5,904 coding sequences (CDSs) and 64 RNAs. The coding sequences were classified into 546 subsystems of which amino acids and derivatives ($n = 671$ CDSs); carbohydrates ($n = 509$); membrane transport ($n = 282$); protein metabolism ($n = 235$); fatty acids, lipids, and isoprenoids ($n = 222$); RNA metabolism ($n = 210$); stress response ($n = 206$); cell wall and capsule ($n = 186$); virulence, disease, and defense ($n = 159$); respiration ($n = 155$); metabolism of aromatic compounds ($n = 146$); motility and chemotaxis ($n = 143$); regulation and cell signaling ($n = 127$); and DNA metabolism ($n = 144$) were the most abundant.

The NCBI Prokaryotic Genome Annotation Pipeline (http://www.ncbi.nlm.nih.gov/genome/annotation_prok/) predicted the benzene 1,2-dioxygenase, vanillate monooxygenase, catechol 1,2-dioxygenase (*catA*), homogentisate 1,2-dioxygenase, and 4-hydro-

xybenzoate 3-monooxygenase genes. The *cum* gene cluster (4) for isopropylbenzene (cumene) degradation was present. This cluster is 99% similar to that of *P. fluorescens*, accession number D37828. *P. frederiksbergensis* SI8 showed at least 71% homology with twenty of the twenty-one genes, with the exception of *ditE*, of the *dit* cluster for abietane diterpenoids catabolism of *P. abietaniphila*, accession number AF119621 (5). Additionally, the genes encoding protocatechuate 3,4-dioxygenase (*ligA* and *ligB*), 3-carboxymuconate cycloisomerase, and 4-carboxymuconolactone decarboxylase, of the central protocatechuate catabolic pathway for aromatic degradation were observed (6). The gentisate 1,2-dioxygenase (*gdo*) gene essential for the gentisate catabolic pathway of polycyclic aromatics was not detected (6). Important hydrocarbon degradation genes encoding 2,4-dichlorophenol 6-monooxygenase, alkanesulfonate monooxygenase, 2-polypropenyl-6-methoxyphenol hydroxylase, aminobenzoate oxygenase, and 2-nitropropane dioxygenase were observed. A gene cluster with at least 80% homology to the *ttg2* operon encoding an ABC-type transporter essential for toluene resistance in *P. Putida* and *P. aeruginosa*, was observed (7, 8). The *alkB* genes were not detected, explaining its inability to degrade *n*-alkanes. This genome will provide valuable insight into the genetics and metabolism of hydrocarbon-degrading psychrotrophic bacteria.

Nucleotide sequence accession number. This project has been deposited in DDBJ/EMBL/GenBank under the accession number JQGJ00000000.

ACKNOWLEDGMENTS

Research reported in this article was supported by funds from the United States Air Force Research Laboratory, Fuels and Energy Branch, and the U.S. Department of Energy in collaboration with Lawrence Livermore National Laboratory (IAA DE-NA0002320/0002) to O.N.R.

This material is based on research sponsored by Air Force Research Laboratory under agreement FA8650-10-2-2934. The views and conclusions contained herein are those of the authors and should not be interpreted as necessarily representing the official policies or endorsements, either expressed or implied, of Air Force Research Laboratory or the U.S. Government.

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