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Draft Genome Sequence of *Pseudomonas veronii* Strain 1YdBTEX2

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***Pseudomonas veronii* strain 1YdBTEX2 was isolated from a benzene-contaminated site. Here we report the draft genome sequence of 1YdBTEX2 and its genes associated with aromatic metabolism. The broad catabolic potential of this strain is consistent with the environment from which it was isolated.**

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Environmental spills with recalcitrant pollutants are a common problem worldwide, threatening the environment and human health. The main mechanism for recovering these sites is through biodegradation by indigenous microorganisms. The reasons for some microorganisms persisting and successfully establishing under pollutant pressure are still to be elucidated.

Here we present the draft genome of *Pseudomonas veronii* strain 1YdBTEX2, isolated from soil highly contaminated with benzene (1). This strain harbors a unique catabolic pathway for the degradation of both benzene and toluene and has been purported to be a key player in the biodegradation of these pollutants at this site (1, 2). While the 16S rRNA gene of 1YdBTEX2 is 99.6% similar to that of *P. veronii* CIP104663^T and 98.7% similar to that of *Pseudomonas fluorescens* IAM12022^T, the housekeeping gene *gyrB* is 99.2% similar to that of *P. veronii* CIP104663^T and only 91.0% similar to that of *P. fluorescens* IAM12022^T (<http://www.uib.es/microbiologiaBD/Welcome.html>). Thus, 1YdBTEX2 is the first member of the *P. veronii* species to be sequenced.

The genome was sequenced using the Illumina GAI genome analyzer, which generated 110-bp paired-end reads. Approximately 9.5 million reads were obtained and the whole genome was assembled into 281 contigs using Velvet (3) and 344 contigs using Edena (4). Both datasets were then merged using Minimus2 (5), resulting in 119 contigs. In order to merge contigs, we constructed scaffolds using SSPACE (6). Comparisons between contigs and scaffolds were then made using Mauve (7), using the genome of *P. fluorescens* SBW25 (8) as a reference. Gaps between scaffolds were closed by PCR amplification followed by DNA Sanger sequencing. Annotation was performed with the RAST (Rapid Annotations using Subsystems Technology) server version 4.0 (9), generating 5,981 candidate protein-encoding genes. The resulting genome sequence consists of 63 contigs ($N_{50} = 229,690$; $L_{50} = 10$) of 6,680,724 bp with a GC content of 59%. Besides the peripheral aromatic degradation pathways for benzene/toluene, phenol, salicylate, tryptophan (via anthranilate), ferulate (via vanillate), p-coumarate (via 4-hydroxybenzoate), 3-hydroxyphenylpropionate, and phenylalanine (via 4-hydroxyphenylpyruvate), central aromatic degradation pathways for catechol (both via intra- and extradiol cleav-

age), protocatechuate (via intradiol cleavage), homogentisate, and 2,3-dihydroxyphenylpropionate and an *alkB* gene encoding alkane monooxygenase were also observed in strain 1YdBTEX2. Furthermore, while 1YdBTEX2 is versatile with respect to its use of a range of carbon sources, a cluster of genes comprising a complete denitrification pathway, including nitrate, nitrite, nitric oxide, and nitrous oxide reduction, was found, conferring flexibility in periods of anoxia. The presence of a (NiFe) hydrogenase with an entire operon similar to that found in *Ralstonia eutropha* H16 (10) was identified here, which indicates that hydrogen may be used as an electron donor, a feature unknown in *Pseudomonas* strains, with the exception of *P. extremaustralis* (11). The data are consistent with the environment from which 1YdBTEX2 was isolated and underline its broad catabolic potential.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [AOUH00000000](http://www.ncbi.nlm.nih.gov/nuccore/AOUH00000000). The version described in this paper is the first version, [AOUH01000000](http://www.ncbi.nlm.nih.gov/nuccore/AOUH01000000).

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