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Draft Genome Sequence of *Rhizobium* sp. Strain PDO1-076, a Bacterium Isolated from *Populus deltoides*

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***Rhizobium* sp. strain PDO1-076 is a plant-associated bacterium isolated from *Populus deltoides*, and its draft genome sequence is reported.**

Plant-microbe interactions within the rhizosphere have been shown to have important roles in plant health and productivity (1, 5). The bacterium *Rhizobium* sp. strain PDO1-076 was isolated and characterized as part of an ongoing effort to characterize microbial rhizosphere communities of native *Populus deltoides* (4). It was isolated from surface-sterilized fine root material (<1 mm diameter) from a mature *P. deltoides* tree on the Oak Ridge Reservation, East Tennessee (35°55.325'N, 084°19.424'W) in March 2009. *Rhizobiaceae* taxonomy and systematics continue to evolve (8–11), and the ultimate placement of *Rhizobium* sp. strain PDO1-076 needs to be considered in greater detail elsewhere. A draft genome sequence was determined to provide insight into this organism's metabolic potential and the genetic basis of its rhizosphere competence.

Draft genome sequence data were generated using a combination of 454 (7) and Illumina (2) technologies essentially as described previously (3). The 454 FLX shotgun data consisted of 272,469 reads and generated 56,371,663 bp. A 500-bp Illumina HiSeq2000 paired-end library generated 3,290,528,086 bp of sequence data after trimming and filtering (CLC Genomics Workbench, version 4.7.1), which consisted of 32,491,358 reads with an average length of 82 bp.

Illumina data were assembled with Velvet (version 1.1.04) (12), and consensus sequences were distributed into 1.5-kbp overlapping fake reads using the fb_dice.pl script, which is part of FragBlast module (http://www.clarkfrancis.com/codes/fb_dice.pl). The Newbler application (version 2.6, 454; Life Sciences) was used to assemble the Illumina consensus and 454 reads into 441 large (≥500-bp) contiguous DNA elements of approximately 5.5 Mb. The average contig size was 12,482 bp, the N50 contig size was 29,829 bp, the largest contig was 119,564 bp, and the genome had an overall estimated G+C content of 60.2%.

The draft genome was annotated at Oak Ridge National Laboratory using an automated annotation pipeline based on the Prodigal gene prediction algorithm (6), which predicted 5,375 candidate protein-encoding gene models for *Rhizobium* sp. strain PDO1-076. Sequence data for DNA contigs, coding and translation models, annotations, and a metabolic reconstruction are available at http://genome.ornl.gov/microbial/PMI/PDO_076_Hybrid/. Predicted genes are organized by a number of different categories, and sequence data are searchable using BLAST tools.

Preliminary analysis indicates that many common metabolic pathways, such as the glycolysis pathway, have putative genes for each step, and this suggests that much of the coding potential of

this organism has been captured by the sequence. The *Rhizobium* sp. strain PDO1-076 genome encodes proteins important to rhizosphere processes such as motility and chemotaxis, myo-inositol catabolism, carbohydrate utilization, quorum sensing, salicylate degradation, and auxin synthesis and efflux. Genes for nitrogen fixation were not found in the genome, which is not uncommon among other plant-associated but free-living rhizobia (e.g., former *Agrobacterium* species). This *Rhizobium* PDO1-076 draft genome sequence will allow more comprehensive comparisons with other members of the genus and further characterization of the genes and gene regulatory networks involved in plant-microbe interactions.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under accession no. [AHZC000000000](https://www.ncbi.nlm.nih.gov/nuccore/AHZC000000000). The version described in this paper is the first version (accession no. [AHZC010000000](https://www.ncbi.nlm.nih.gov/nuccore/AHZC010000000)). The 454 GS FLX and Illumina HiSeq2000 data sets have been deposited in the National Center for Biotechnology Information Sequence Read Archive under accession numbers [SRX031570](https://www.ncbi.nlm.nih.gov/sra/SRX031570) and [SRX109672](https://www.ncbi.nlm.nih.gov/sra/SRX109672), respectively.

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