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Genome Sequence of the 1,4-Dioxane-Degrading *Pseudonocardia dioxanivorans* Strain CB1190[▽]

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***Pseudonocardia dioxanivorans* CB1190 is the first bacterium reported to be capable of growth on the environmental contaminant 1,4-dioxane and the first member of the genus *Pseudonocardia* for which there is an annotated genome sequence. Preliminary analysis of the genome (chromosome and three plasmids) indicates that strain CB1190 possesses several multicomponent monooxygenases that could be involved in the aerobic degradation of 1,4-dioxane and other environmental contaminants.**

Here we report the genome sequence of the Gram-positive actinomycete *Pseudonocardia dioxanivorans* strain CB1190. *P. dioxanivorans* strain CB1190 (NCBI taxonomy ID 675635) was isolated from 1,4-dioxane-contaminated sludge and displays the rare ability to use 1,4-dioxane, an emerging groundwater contaminant, as a sole carbon and energy source (9, 10, 11, 14). This strain can also grow on other ethers (e.g., 2-methyl-1,3-dioxolane and butyl methyl ether), alcohols, and benzene as the sole carbon and energy source, and it can grow autotrophically with CO_2 by using H_2 as the electron donor (9, 14).

Pseudonocardia represents a genus of bacteria with diverse niches, from free-living microorganisms capable of degrading xenobiotic compounds (5–8, 15, 17) to the antibiotic-producing symbionts of fungus-farming ants (1, 2, 13, 20). Strain CB1190 was chosen for sequencing by the U.S. Department of Energy Joint Genome Institute (JGI) to gain insight into 1,4-dioxane metabolism, as well as to learn about general carbon and nitrogen metabolism in the genus.

Sequencing of strain CB1190 genomic DNA was carried out by the 454 and Illumina techniques. All techniques for DNA isolation, library construction, and sequencing were performed according to JGI standards and protocols (http://www.jgi.doe.gov). 454 reads (67-fold coverage) were assembled with Newbler (12). Illumina reads (136-fold coverage) were assembled with Velvet 0.7.63 (19), and then contigs of >800 bp were shredded into 1.5-kb pseudoreads. The pseudoreads were combined with the 454 reads into a hybrid 454/Illumina data set with parallel phrap, version SPS-4.24 (High Performance Software, LLC). dup454Finisher was used to correct misassembled repeats (4), and gapResolution (http://www.jgi.doe.gov) was used to resolve gaps in the assembly. Gaps between contigs were closed by editing in Consed, by PCR, and by Bubble PCR primer walks (J.-F. Cheng, unpublished data). The genome consists of 4 replicons, including the chromosome (7.1 Mb), plasmid 1 (circular, 192 kb), plasmid 2 (circular, 137 kb with gaps), and plasmid 3 (linear, 15 kb), and has an average G+C content of 73.1%. Coding sequences were predicted with Prodigal (http://prodigal.ornl.gov) and were automatically annotated by comparisons to the Pfam, KEGG, and COG databases. A total of 6,799 candidate protein-encoding genes were predicted in this manner. The genome contains 46 tRNA genes and three copies of the rRNA genes.

An analysis of the strain CB1190 genome revealed the presence of eight putative gene clusters encoding bacterial multicomponent monooxygenases, including a cluster with high similarity to a gene cluster associated with tetrahydrofuran degradation in *Pseudonocardia tetrahydrofuranoxydans* strain K1 (16). Discovery of these monooxygenase genes may indicate that strain CB1190 is capable of using a diversity of organic compounds as sole carbon and energy sources. Genes encoding complete citric acid and pentose phosphate pathways are present, indicating a heterotrophic mode of metabolism, and genes encoding the complete biosynthesis pathways for all 20 amino acids have been identified. The autotrophic capability of strain CB1190 (14) is explained by the presence of the typical Calvin-Benson-Bassham cycle for CO_2 fixation.

Nucleotide sequence accession numbers. The chromosome and plasmid sequences of *Pseudonocardia dioxanivorans* strain CB1190 have been deposited in GenBank with accession numbers NC_015312-4 and CP002595-7.

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