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GENOME ANNOUNCEMENT

Complete Genome Sequence of the Fenitrothion-Degrading *Burkholderia* sp. Strain YI23

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***Burkholderia* species are ubiquitous in soil environments. Many *Burkholderia* species isolated from various environments have the potential to biodegrade man-made chemicals. *Burkholderia* sp. strain YI23 was isolated from a golf course soil and identified as a fenitrothion-degrading bacterium. In this study, we report the complete genome sequence of *Burkholderia* sp. strain YI23.**

Man-made organophosphorus insecticides inhibit the normal activity of the acetylcholine esterase in insects and mammals (8). Many bacterial strains capable of completely or partially degrading organophosphorus pesticides have been isolated from soils (4, 8, 11). Their insecticide-degradative genes, pathways, metabolites, and bioremediation potential have been researched (3, 9, 10). However, there have been no reports on genomic analyses of these insecticide-degrading bacteria. Therefore, we have analyzed the whole-genome sequence of *Burkholderia* sp. strain YI23, which was isolated as a fenitrothion (*O*,*O*-dimethyl-*O*-[*p*-nitro-*m*-tolyl]phosphorothioate)-degrading bacterium from a golf course soil and is able to quickly degrade diverse organophosphorus pesticides (4).

Whole-genome DNA sequencing was performed using the pyrosequencing method on an FLX Titanium genome sequencer system. In total, 271,089,161 and 177,899,085 bases were analyzed in single reads and paired-end reads, respectively. The sequence data were assembled with Newbler (version 2.5.3; 454 Life Sciences). In total, 138 contigs were produced in 14 scaffolds through *de novo* assembly. Gaps among the contigs were closed by primer walking on standard PCR products. Coding genes and pseudogenes across the genome were predicted using Glimmer (2) and annotated by comparison with the NCBI-NR database (1). Our annotation results were verified using Artemis (7).

The *Burkholderia* sp. strain YI23 genome is 8.89 Mb and consists of three chromosomes and three plasmids. Chromosome 1 (BYI23_A) contains 3,131,280 bp with a G+C content of 63.5% and 2,769 predicted coding sequences (CDS). Chromosome 2 (BYI23_B) contains 1,773,019 bp with a G+C content of 63.7% and 1,539 CDS. Chromosome 3 (BYI23_C) contains 1,569,570 bp with a G+C content of 63.7% and 1,364 CDS. Plasmid 1 (BYI23_D) contains 1,951,047 bp (63% G+C content and 1,651 CDS), plasmid 2 (BYI23_E) contains 356,263 bp (58.7% G+C content and 390 CDS), and plasmid 3 (BYI23_F) contains 115,232 bp (59.4% G+C content and 91 CDS). Four, one, and one rRNA operons were located on chromosome 1 (BYI23_A), chromosome 2 (BYI23_B), and chromosome 3 (BYI23_C), respectively (5). Chromosome 1 (BYI23_A), chromosome 2 (BYI23_B), chromosome 3 (BYI23_C), and plasmid 1 (BYI23_D) have 56, 4, 3, and 1 tRNA genes, respectively (6). The fenitrothion-degradative genes are located on plasmids BYI23_E and BYI23_F. The whole-genome sequences of *Burkholderia* sp. strain YI23 can provide valuable information on organophosphorus insecticide-degradative genes, including fenitrothion-degradative genes.

Nucleotide sequence accession numbers. The complete genome sequence of *Burkholderia* sp. YI23 has been assigned GenBank accession numbers CP003087, CP003088, CP003089, CP003090, CP003091, and CP003092.

ACKNOWLEDGMENTS

This study was supported by National Instrumentation Center for Environmental Management and the RDA GenBank Management Program from the Genetic Resources Division, National Institute of Agricultural Biotechnology.

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Received 7 November 2011 **Accepted** 29 November 2011

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doi:10.1128/JB.06479-11