

Complete Genome Sequence of the Endophytic Bacterium *Burkholderia* sp. Strain KJ006

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Endophytes live inside plant tissues without causing any harm and may even benefit plants. Here, we provide the high-quality genome sequence of *Burkholderia* sp. strain KJ006, an endophytic bacterium of rice with antifungal activity. The 6.6-Mb genome, consisting of three chromosomes and a single plasmid, contains genes related to plant growth promotion or degradation of aromatic compounds.

An endophyte is an endosymbiont that resides within plants without any harmful effects to its hosts (10). Many of the endophytic bacteria are known to promote plant growth or exhibit antimicrobial activities to protect plants against pathogens (8). The genus *Burkholderia* is widespread in diverse environments, including animals and plants, as well as the rhizosphere, soil, and water. The genus *Burkholderia* has received attention from the agricultural industry and bioremediation field due to its abilities related to plant growth promotion and aromatic compound degradation. *Burkholderia* sp. strain KJ006 is an endophytic bacterium isolated from surface-sterilized rice root (3). Strain KJ006 is known to have a broad range of antifungal activities but does not exhibit any symptoms related to pathogenicity to rice. Strain KJ006 containing the homoserine lactonase gene of *Bacillus thuringiensis* repressed the seedling rot caused by *Burkholderia glumae* that occupies the same ecological niche (3).

Genome sequencing was performed using the Illumina and Solexa platforms (NICEM and Macrogen, Inc., South Korea). A total of 34.81 Gb of reads with 2,491-fold coverage of the genome were generated from a 400-bp paired-end library and 2-kb and 6-kb mate-pair libraries. Sequence trimming and assembly were performed with CLC Genomics Workbench, and scaffolds were constructed by SSAPCE (2). IMAGE (9) and perl scripts developed in-house were used to close the gaps. Primer walking was conducted to close gaps and to improve the assembly. Structural genes were predicted by Glimmer3 and GeneMarkS. RNAmmer and tRNAscan-SE were used to detect rRNAs and tRNAs. Functional assignment of the predicted genes was performed by BLAST or HMMER with COG, GenBank, Pfam, and TIGRFam databases. The RAST server was additionally used for annotation (1).

The 6,629,912-bp KJ006 genome (67.18% G+C content) is composed of three chromosomes (3,145,156 bp, 2,356,985 bp, 1,082,410 bp) and a single plasmid (pKJ006; 45,361 bp). Six thousand twenty-four protein-coding sequences, 65 transfer RNAs, and 6 rRNA operons were predicted. As calculated by JSpecies (7), the average nucleotide identity value between the genomes of KJ006 and *Burkholderia vietnamiensis* G4 was 98.52%, suggesting that the two strains are phylogenetically close. The genome contains several genes related to plant growth promotion. They include the *accD* gene encoding 1-aminocyclopropane-1-carboxy-

late deaminase, the *pqq* operon for pyrroloquinoline quinone biosynthesis, and the *nif* gene cluster. The genome also harbors genes related to several kinds of aromatic compound degradation (6). In the KJ006 genome, a type III secretion system was detected which is known to play an important role in the endophytic life (5). The genome sequence represents the usefulness of KJ006 as a biocontrol agent in agricultural industry, as an aromatic compound degrader in environmental biotechnology, or as a recipient of useful genes to transform it into a more potent plant biofertilizer or biocontrol agent. Further comparative and functional analyses may provide insights about the genomic features of endophytism among *Burkholderia* strains.

Nucleotide sequence accession numbers. The genome sequence of *Burkholderia* sp. KJ006 has been deposited in NCBI GenBank under accession numbers CP003514 (chromosome I), CP003515 (chromosome II), CP003516 (chromosome III), and CP003517 (pKJ006). The sequence and annotation are also available from the Genome Encyclopedia of Microbes (GEM; <http://www.gem.re.kr>) (4).

ACKNOWLEDGMENTS

This project was conducted in part as the Microbial Genome Sequencing and Analysis course at the University of Science and Technology in Fall 2011. We are grateful to students in the class for critical comments on the manuscript and to members of GEM and the KRIBB sequencing team for technical help.

This work was supported by the Next-Generation BioGreen 21 Program (grant PJ008201012011) and Cooperative Research Program for Agriculture Science & Technology Development (grant PJ006901) of the Rural Development Administration, the National Research Foundation of Korea (grant 2011-0017670), and the KRIBB Research Initiative Program.

Received 10 May 2012 Accepted 31 May 2012

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doi:10.1128/JB.00821-12

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