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

Min-Jung Kwak,a,b Ju Yeon Song,a Seong-Young Kim,c,d Haeyoung Jeong,a,b Sung Gyun Kang,a,f Byung Kwon Kim,a
Soon-Kyeong Kwon,a,b Choong Hoon Lee,a Dong Su Yu,a Seung-Hwan Park,a,b and Jihyun F. Kim,a,g

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. RNAmer and tRNAscan-SE were used to detect tRNAs 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-carboxylate 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 lifestyle (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 endophytes such as Burkholderia strains.

Nucleotide sequence accession numbers. The genome sequence of Burkholderia sp. strain 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).

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Address correspondence to Jihyun F. Kim, jfk1@yonsei.ac.kr, or Seung-Hwan Park, shpark@kribb.re.kr.

M.-J. K and J.Y.S. are co-first authors.

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