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GENOME ANNOUNCEMENTS

Complete Genome Sequence of *Burkholderia glumae* BGR1[▽]

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***Burkholderia glumae* is the causative agent of grain and seedling rot in rice and of bacterial wilt in many field crops. Here, we report the complete genome sequence of *B. glumae* BGR1 isolated from a diseased rice panicle in Korea.**

Burkholderia glumae BGR1 causes grain and seedling rot in rice and bacterial wilt in many field crops. The bacterium infects rice panicles at the flowering stage and causes serious yield losses when temperature and humidity are favorable for successful infection and in vivo proliferation (7). The bacterium produces yellow pigments, toxoflavin, reumycin, and fervenulin. Among these, toxoflavin is the most critical virulence factor of the bacterium (7). Genes involved in toxoflavin biosynthesis and transport are regulated by quorum sensing (7).

B. glumae was chosen for whole-genome sequencing for three major reasons. First, bacterial rice grain rot is becoming more prevalent in most rice-growing countries, including China, Japan, Vietnam, the Philippines, and India. Second, we feel that this is a good model pathosystem to understand how plant-pathogenic bacteria infect rice panicles and flowers. Finally, as *Burkholderia* species have broad ecological niches and are genetically very diverse, it is worthwhile to add more genome information to this genus. This is the first genome information reported about a plant-associated *Burkholderia* species.

The complete genome sequence of *B. glumae* BGR1 was determined at the Crop Functional Genomics Center, Seoul National University, Seoul, Korea, using a traditional whole-genome shotgun sequencing strategy. Total genomic DNA of strain BGR1 was purified by CsCl gradient centrifugation (10). Two genomic libraries (~2 kb and ~10 kb) were constructed with randomly sheared genomic DNA from strain BGR1. One cosmid library and one fosmid library were constructed and subjected to shotgun sequencing. Draft assemblies were compiled using the Phred/Phrap/Consed software package (3, 4) and Arachne (5), based on 102,798 reads, to give 10.6-fold coverage of the genome. Gaps among contigs were closed with a combination of primer walking on gap-spanning clones and direct sequencing of combinatorial PCR products. Protein-coding genes were first predicted using Glimmer (2) and GenMark.hmm (8) and annotated by comparison with the NCBI-NR (1), COG (11), and KEGG databases (6). The annotation results were verified using Artemis (9).

The genome of *B. glumae* BGR1 consists of two chromosomes and four plasmids. Chromosome 1 contains 3,906,529 bp (68.11% G+C content), 3,290 predicted coding sequences (CDS), 144 pseudogenes, three rRNA operons, and 56 tRNAs. Chromosome 2 contains 2,827,355 bp (68.76% G+C content), 2,079 CDS, 192 pseudogenes, two rRNA operons, and eight tRNAs. Plasmid bglu_1p contains 133,591 bp (60.59% G+C content, 102 CDS, and 42 pseudogenes), plasmid bglu_2p contains 141,792 bp (63.21% G+C content, 97 CDS, and 24 pseudogenes), plasmid bglu_3p contains 141,067 bp (62.68% G+C content, 106 CDS, 36 pseudogenes, and one tRNA), and plasmid bglu_4p contains 134,349 bp (62.71% G+C content, 102 CDS, 12 pseudogenes, and one tRNA).

The gene organization of the origin of replication of chromosome 2 is similar to that of a plasmid, which was also found in previously sequenced *Burkholderia* genomes. Three different plasmid replication initiation systems were found among the four plasmids, as follows: ParA-ParB-TrfA in bglu_1p and bglu_3p, ParA-ParB-putative plasmid replication protein in bglu_2p, and ParA-ParB-RepA in bglu_4p. Approximately 50% of the bglu_3p sequences show a high degree of similarity with those of bglu_4p, suggesting that these plasmids may share a common ancestor.

Pathogenicity-related genes (such as those involved in hypersensitive response and the pathogenicity type III protein secretion system), which are essential for many plant-pathogenic bacteria, are found in chromosome 2. Toxoflavin biosynthesis and transport genes are also present in chromosome 2. These results indicated that chromosome 2 possesses important genes for the pathogenicity or virulence of *B. glumae*. This is the first whole-genome information reported for a plant-pathogenic *Burkholderia* species and will facilitate comparative analysis with other human pathogenic or environmental strains belonging to this genus.

Nucleotide sequence accession numbers. The genome sequence was deposited in GenBank with accession numbers

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CP001503, CP001504, CP001505, CP001506, CP001507, and CP001508 for the chromosomes and plasmids bglu_1g, bglu_2g, bglu_1p, bglu_2p, bglu_3p, and bglu_4p, respectively.

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