Complete Genome Sequence of *Burkholderia gladioli* BSR3

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We report the complete genome sequence of *Burkholderia gladioli* BSR3, isolated from a diseased rice sheath in South Korea.

Whole-genome shotgun DNA sequencing of *Burkholderia gladioli* BSR3, isolated from a diseased rice sheath in South Korea, was performed using the Roche/454 pyrosequencing method on a Genome Sequencer FLX system. In total, 359,799,231 and 209,679,192 bases were analyzed in single and paired-end reads, respectively. The genomic shotgun sequence data were assembled with Newbler (version 2.5.3; 454 Life Sciences). In total, 195 contigs were produced in 19 scaffolds through *de novo* assembly. Gaps among the contigs were closed by a combination of primer walking on gap-spanning clones and the direct sequencing of combinatorial PCR products. Coding genes and pseudogenes across the genome were predicted using Glimmer (2), GeneMarkHMM (4), and Prodigal (3) and annotated by comparison with the NCBI-NR (1). Our annotation results were verified using Artemis (5).

The *B. gladioli* genome is 9.05 Mb and consists of two chromosomes and four plasmids. Chromosome 1 contains 4,413,616 bp (67.5% G+C content) and 3,778 predicted coding sequences (CDS). Chromosome 2 contains 3,700,833 bp (68.6% G+C content) and 2,926 CDS. Plasmid bgla_1p contains 276,215 bp (63.3% G+C content and 189 CDS), plasmid bgla_2p contains 129,399 bp (62.8% G+C content and 104 CDS), plasmid bgla_3p contains 128,650 bp (59.6% G+C content and 94 CDS), and plasmid bgla_4p contains 403,586 bp (62.4% G+C content and 319 CDS).

Nucleotide sequence accession numbers. The sequences of the *B. gladioli* BSR3 chromosomes and plasmids (bgla_1g, bgla_2g, bgla_1p, bgla_2p, bgla_3p, and bgla_4p) have been deposited in GenBank under accession numbers CP002599, CP002600, CP002601, CP002602, CP002603, and CP002604, respectively.

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**REFERENCES**


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