Complete Genomic Data of *Burkholderia glumae* Strain GX Associated with Bacterial Panicle Blight of Rice in China

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Abstract

Burkholderia glumae is a seedborne pathogen causing bacterial panicle blight of rice. Here, we report the complete genome of *B. glumae* strain GX, which represents the first whole-genome sequence of an isolate from China. The assembled genome consisted of five contigs, with two circular chromosomes of 3,712,850 and 2,750,046 bp and three plasmids of 201,571, 105,587, and 96,100 bp. This complete genome will provide a valuable resource for further studies on bacterial panicle blight worldwide.

Genome Announcement

Burkholderia glumae is a gram-negative, seedborne rice pathogen responsible for causing bacterial panicle blight (BPB), also known as bacterial grain rot. BPB was first described in Japan in the 1950s. It has caused significant reductions in the rice yield in many rice-growing countries (Cui et al. 2016). Considering the optimal temperature range for the growth of *B. glumae* (30 to 35°C), the environmental conditions prevalent during the rice-growing season, and global climate change, it is believed that this disease will occur more frequently (Ham et al. 2011). A growing body of evidence shows that phytotoxins and lipases are the major pathogenic determinants of *B. glumae*. Two polycistronic operons, *toxABCDE* and *toxFGHI*, are responsible for the toxoflavin biosynthesis pathway and toxoflavin transport, respectively (Kim et al. 2004; Suzuki et al. 2004). The expression of both of these operons requires a transcriptional activator, ToxJ, which is regulated by quorum sensing (QS). LipA is the most important lipase related to virulence, and it is also dependent on the QS system (Devescovi et al. 2007). In 2004, BPB was first reported in Heilongjiang Province, China. *B. glumae* was listed in the "Entry Plant Quarantine Pest List" of the People's Republic of China in 2007. However, the complete genome sequences of *B. glumae* strains isolated from China remain to be determined and the genomic difference between Chinese isolates and other strains are still unclear. Thus, in this study, we report the complete whole-genome sequence of the first Chinese *B. glumae* strain, GX.

B. glumae strain GX was isolated from diseased rice seed, obtained from Guangxi Province, China, in 2009. Genomic DNA of *B. glumae* was extracted using the AxyPrep Bacterial Genomic DNA Miniprep Kit (Axygen). A ligation sequencing kit (SQK-LSK109) was used, with 1 µg of DNA, to prepare the sequencing library for Nanopore sequencing. The library was loaded onto an R9.4 flow cell and sequenced using a MinION device, with the default basecalling integrated in MinKNOW v3.1.13 software. In total, 53,338 reads were

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Keywords

Burkholderia glumae, Pacbio, toxoflavin

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*The *e-Xtra* logo stands for "electronic extra" and indicates that one supplementary figure is published online.

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Table 1. Genome comparison between *Burkholderia glumae* GX and BGR1

Genomic status	Strain	Accession	Size (bp)	ANI (%)	GC (%)	Coding sequences (with protein)
Chromosome 1	GX	CP045087.1	3,712,850	99.63	68.1	3,210
	BGR1	CP001503.2	3,906,507	...	68.11	3,544
Chromosome 2	GX	CP045089.1	2,750,046	99.63	68.99	2,117
	BGR1	CP001504.2	2,827,333	...	68.77	2,202
Plasmid 1	GX	CP045090.1	201,571	99.59	61.42	152
	BGR1	CP001505.1	133,591	...	60.59	114
Plasmid 2	GX	CP045091.1	105,587	96.92	62.12	96
	BGR1	CP001506.1	282,889	...	62.94	106
Plasmid 3	GX	CP045092.1	96,100	97.25	64.28	75
	BGR1	CP001507.1	141,067	...	62.68	119
Plasmid 4	BGR1	CP001508.1	134,346	...	62.71	117
	GX	...	6,866,154	99.62	68.12	5,650
Sum	BGR1	...	7,284,636	...	67.93	6,202

obtained after sequencing, with an N_{50} value of 25,729 bp and average read length of 20,410 bp, consisting of 1,088,656,593 bases in total. After quality control, an assembly of contigs from the subreads was generated using Canu 1.8 (Koren et al. 2017), and Pilon was used for improving the genome assembly (Walker et al. 2014). Finally, chromosomes and plasmids were circularized using Circlator 1.5.5 (Hunt et al. 2015). Annotation of each contig was performed using the NCBI Prokaryotic Genome Annotation Pipeline (Tatusova et al. 2016). Toxoflavin genes were detected and annotated using antiSMASH 5.0 (Blin et al. 2019), while the average nucleotide identity (ANI) between the GX and BGR1 strains was calculated using Pyani (Pritchard et al. 2016).

The genome of *B. glumae* strain GX was found to be composed of two unique circular chromosomes and three unique circular plasmids (Table 1). This is similar to the genome of *B. glumae* strain BGR1, which is composed of two circular chromosomes and four circular plasmids (Lim et al. 2009). All ANI scores were greater than 95%, suggesting that GX and BGR1 belong to the same species. Chromosome 1 was 3,712,850 bp long, with 68.10% GC content, and was predicted to include 3,210 protein-encoding genes. The sequencing coverage of chromosome 1 was 137. Chromosome 2 was 2,750,046 bp long, with 68.99% GC content, predicted to include 2,117 protein-encoding genes. The sequencing coverage of chromosome 2 was 144. Plasmids 1, 2, and 3 consisted of 201,571, 105,587, and 96,100 bp, respectively (Table 1). These plasmids were predicted to include 152, 96, and 75 protein-encoding genes, respectively. The total genome size of *B. glumae* strain GX was 6,866,154 bp, including 5,650 protein-encoding genes. The circular representation of the complete genome of *B. glumae* strain GX is shown in Supplementary Figure S1. Overall, This complete genome will provide a valuable resource for further studies on bacterial panicle blight in China and worldwide.

Data availability. The whole-genome sequences reported here have been deposited in DNA Data Bank of Japan/European Nucleotide Archive/GenBank, under the accession numbers CP045087 for chromosome 1, CP045088 for chromosome 2, CP045089 for plasmid 1, CP045090 for plasmid 2, and CP045091 for plasmid 3. The versions described in this article are the first versions.

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