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GENOME SEQUENCES

Genome Sequences of *Brevundimonas naejangsanensis* Strain FS1091 and *Bacillus amyloliquefaciens* Strain FS1092, Isolated from a Fresh-Cut-Produce-Processing Plant

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ABSTRACT The complete genome sequences of *Brevundimonas naejangsanensis* strain FS1091 and *Bacillus amyloliquefaciens* strain FS1092, which were isolated from a commercial fresh-cut-produce-processing facility, were determined. Both FS1091 and FS1092 have one circular chromosome of approximately 3.15 and 4.24 Mb, respectively.

Brevundimonas naejangsanensis is a Gram-negative, motile, and rod-shaped bacterium that was first classified in 2009 (1). Su et al. (2) reported that *B. naejangsanensis* strain B1 could degrade several antibiotics, gaining advantages in competition in microbial communities and escaping antagonistic effects caused by different antimicrobial products. *Bacillus amyloliquefaciens* is a Gram-positive bacterium producing a natural antibiotic protein (barnase) with RNase activity (3). It has been applied in agriculture, aquaculture, and hydroponics to mitigate the threat of plant pathogens such as *Ralstonia solanacearum*, *Pythium* spp., *Rhizoctonia solani*, *Alternaria tenuissima*, and *Fusarium* spp. and to improve root tolerance to salt stress (4–10).

B. naejangsanensis strain FS1091 and *B. amyloliquefaciens* strain FS1092 were isolated from environmental surfaces in a fresh-cut-produce-processing facility in the mid-Atlantic region for their strong biofilm formation (11). Strain identification was carried out by sequencing the 16S rRNA genes using the universal bacterial primers 27F and 1492R (12).

Whole-genome shotgun DNA sequencing of *B. naejangsanensis* FS1091 and *B. amyloliquefaciens* FS1092 was performed using both Illumina MiSeq and Oxford Nanopore MinION platforms. Bacterial genomic DNA was extracted using the MagAttract high-molecular-weight DNA kit (Qiagen) for MiSeq sequencing and the Wizard genomic DNA purification kit (Promega) for MinION sequencing, following the manufacturers' instructions. MiSeq sequencing was performed using the MiSeq reagent kit version 2 with paired-end chemistry (2 × 250 bp), after library preparation using the Nextera DNA Flex kit (Illumina). Sequence reads generated by the MiSeq system were quality trimmed to remove adapter sequences and low-quality ends, using CLC Genomics Workbench version 12.0 (Qiagen). The total numbers of MiSeq reads were 1,019,621 for FS1091 and 1,015,953 for FS1092. The average length of MiSeq sequence reads was 230 bp. The MinION library was prepared from 600 ng of DNA with the rapid barcoding sequencing kit (product number SQK-RBK004) and sequenced using a flow cell with R9.4.1 chemistry following the manufacturer's instructions (Oxford Nanopore). The MinION run was base called live using default settings (MinKNOW version 18.12 and Guppy version 2.1.3), with output as fastq files. The sequences were demultiplexed and barcodes were removed using Guppy version 2.1.3. About 1.58 million sequence reads were generated by MinION sequencing, with an average length of 5,675 bases. Com-

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plete genome sequences for each strain were obtained by *de novo* assembly using SPAdes version 3.12.0 (13) hybrid assembly (with default settings) based on both MiSeq and MinION data generated for each strain. The synteny and correctness of the assembly for each strain genome were confirmed by comparing the hybrid assembly with *de novo* assembly of the genomes using Nanopore MinION data alone, performed with Canu software version 1.7 (14), as described previously (15). Default parameters were used for all software unless otherwise noted.

The genome of *B. naejangsanensis* strain FS1091 (single replicon, 3,150,039 bp, GC content of 67.3%) contains 2,967 protein-coding sequences, 49 tRNAs, and 2 copies of the rRNA coding genes. The *B. amyloliquefaciens* strain FS1092 genome (single replicon, 4,240,930 bp, GC content of 45.9%) contains 4,057 protein-coding sequences, 87 tRNAs, and 9 copies of the rRNA coding genes.

These are the first complete genome sequences of *B. naejangsanensis* and *B. amyloliquefaciens* strains isolated from a fresh-produce-processing facility. Further analysis of these genomes will provide insights regarding environmental bacteria interacting with foodborne pathogens and affecting their colonization and persistence in produce-processing environments.

Data availability. The genome sequences of these two strains have been deposited in GenBank. Illumina MiSeq raw reads, Nanopore MinION raw reads, and the assembled sequences for *B. naejangsanensis* strain FS1091 can be accessed under accession numbers SRR8697623, SRR8697008, and CP038027, respectively. The corresponding accession numbers for *B. amyloliquefaciens* strain FS1092 are SRR8697624, SRR8697007, and CP038028, respectively.

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