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Draft Genome Sequence of *Flavobacterium johnsoniae* CI04, an Isolate from the Soybean Rhizosphere

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ABSTRACT *Flavobacterium johnsoniae* CI04 was coisolated with *Bacillus cereus* from a root of a field-grown soybean plant in Arlington, WI, and selected as a model for studying commensalism between members of the *Cytophaga-Flavobacterium-Bacteroides* group and *B. cereus*. Here we report the draft genome sequence of *F. johnsoniae* CI04 obtained by Illumina sequencing.

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Flavobacterium johnsoniae is a Gram-negative bacterium belonging to the *Cytophaga-Flavobacterium-Bacteroides* (CFB) group and is commonly found in soil and rhizospheres (1, 2). *F. johnsoniae* digests a wide array of complex polysaccharides, but is most recognized for its efficient degradation of insoluble chitin (1), the second most abundant biopolymer on Earth (3). *F. johnsoniae* has been used as a genetic and biochemical model to study CFB gliding motility, a form of translocation that does not appear to share underlying mechanisms of flagellar motility, type IV pilus-mediated twitching motility, or either myxobacterial or mycoplasma gliding motility (4). Moreover, *F. johnsoniae* may be useful for studying the ecological role of this type of motility, which is speculated to give CFBs a competitive advantage by enabling them to translocate to find new carbon and nutrient sources (5). Finally, *F. johnsoniae* is a prospective plant growth-promoting agent, as strain GSE09 produces a volatile compound 2,4-di-tert-butylphenol that inhibits development of the oomycete (protist) pathogen, *Phytophthora capsici*, and the fungal pathogen, *Colletotrichum acutatum*, and stimulates pepper fruit ripening (6, 7). Other *F. johnsoniae* strains produce monobactam and quinolone antibiotics (8–10).

F. johnsoniae CI04 was one among 66 bacteria coisolated with *B. cereus* from the roots of field-grown soybean plants (2). These coisolates were bacteria that, after at least 3 days of incubation, grew out of patches of a *B. cereus* culture that had been previously purified by repeated streaking for single colonies. Most of the coisolates were CFB bacteria whose growth was stimulated by *B. cereus in vitro* under conditions that mimic the rhizosphere. *F. johnsoniae* CI04 growth is stimulated by *B. cereus* peptidoglycan, which it appears to degrade with an as-yet-uncharacterized extracellular cell wall-hydrolyzing agent (2).

The *F. johnsoniae* CI04 genome was sequenced using a paired-end approach on the Illumina MiSeq platform. Low-quality sequences were trimmed using Trimmomatic (11) to obtain a total of 7,282,522 pair-reads, which were then assembled into 63 contigs, with a minimum length of 200 bp, using Velvet (12) and VelvetOptimiser (http://bioinformatics.net.au/software.velvetoptimiser). These contigs were ordered by Mauve (13) using the *F. johnsoniae* UW101 genome (14) as a reference. Contigs were assembled manually by joining neighboring sequences with a linker sequence of unknown nucleotide character "N." Gaps were then filled with GapFiller (15) using the trimmed reads to reduce the number of contigs to 13. The final assembly consisted of 5,492,177 bp in 13 contigs, with an N_{50} contig size of 422,475 bp.

We predict that the genome sequence will be useful in probing biocontrol and antibiotic activities of *F. johnsoniae* CI04 and in unraveling the genetic mechanisms driving its interactions with other rhizosphere microbes and plant hosts. These findings may then shed light on the larger ecological role played in the soil by members of the Bacteroidetes phylum, which is poorly understood.

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession no. MLFK00000000. The version described in this paper is the first version.

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