Complete Genome Sequence of *Bacillus subtilis* BAB-1, a Biocontrol Agent for Suppression of Tomato Gray Mold

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*Bacillus subtilis* BAB-1, isolated from cotton rhizosphere soil, is an excellent biocontrol agent for tomato gray mold. The genome of *B. subtilis* strain BAB-1 was fully sequenced and annotated, genes encoding the antifungal active compound were identified, and multiple sets of regulatory systems were found in the genome.

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*Bacillus subtilis* has been widely studied and used for plant disease control. The contributing factors to the success of this bacterium include the production of various antimicrobial compounds (1), competition for nutrition and niche with plant pathogens (2), and induced systemic resistance to pathogens (3). *B. subtilis* strain BAB-1, isolated from cotton rhizosphere soil, showed strong inhibitory ability against the growth of phytopathogens *in vitro*. In addition, strain BAB-1 had been identified as an excellent biocontrol agent for tomato gray mold (4). Phylogenetic trees based on the gyrB and *phoR* gene sequences revealed that strain BAB-1 was closely related to *B. subtilis* 168 (5). To clarify the biocontrol mechanism and facilitate the detection of strain BAB-1, we sequenced and annotated the complete genome sequence of the strain.

Whole-genome sequencing of strain BAB-1 was performed with an Illumina GA IIx analyzer at the Beijing Genomics Institute (BGI) in China. Sequence reads were generated from a 500-bp paired-end library, giving 600-Mb sequences with approximately 120× genome sequence coverage. The paired reads were de novo assembled with SOAPdenovo v. 1.03 software (BGI) (http://soap.genomics.org.cn/soapdenovo.html) based on the genome sequence of type strain *B. subtilis* 168 (AL009126.3), and 98.6% of the reads were assembled into 23 large scaffolds. Most of the gaps within the scaffolds were filled by local assembly of Solexa reads. The remaining gaps between scaffolds were filled by sequencing of PCR amplification using an ABI 3730 sequencer. Protein-encoding genes, rRNA operons, and tRNAs were predicted by Glimmer v. 3.0 (6). Annotation was performed using the Rapid Annotation Using Subsystem Technology (RAST) server (7).

The complete genome sequence of strain BAB-1 is composed of a circular 4,021,944-bp chromosome with mean GC content of 43.89%. There are 4,104 coding genes, 376 rRNAs, and 48 tRNAs in the chromosome. Approximately 5.2% of the strain BAB-1 genome is devoted to synthesis of antimicrobial products, including nonribosomal peptide synthetase (NRPS) antibiotics, polyketide synthase (PKS) antibiotics, and lantibiotics, as well as bacillibac-tin. Among those products, the lipopeptides surfactin and fengy-cin were identified from strain BAB-1 by matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS). The fengycin was identified as a major antifungal active compound in inhibition against the growth of *Botrytis cinerea*, and when applied in combination with fengycin, the surfactin showed synergistic actions, which were confirmed by antifungal assay *in vivo* (8). The iturin lipopeptides have a strong antifungal ability, but gene clusters for iturin lipopeptides are absent from the genome of strain BAB-1. As in other prokaryotes, two-component signal transduction systems of *B. subtilis* are important elements of the adaptive response to a variety of external conditions (9). A total of 35 two-component systems (TCS) were identified from the genome of strain BAB-1, including the biocontrol function-related TCS *compI/compM* (10), *phoR/phoP* (11), and *degU/degS* (12). Finally, we identified 86 transposons, 25 phage-like elements, and type III restriction modification systems in strain BAB-1 genome.

**Nucleotide sequence accession number.** The complete genome sequence has been deposited in GenBank under accession no. CP004405.

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**REFERENCES**


