

Draft Genome Sequence of the Plant Growth-Promoting Bacterium *Bacillus siamensis* KCTC 13613^T

Haeyoung Jeong,^{a,b} Da-Eun Jeong,^a Sun Hong Kim,^a Geun Cheol Song,^{a,b} Soo-Young Park,^a Choong-Min Ryu,^{a,b} Seung-Hwan Park,^{a,b} and Soo-Keun Choi^{a,b}

Systems and Synthetic Biology Research Center, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Yuseong-gu, Daejeon, Republic of Korea,^a and Biosystems and Bioengineering Program, University of Science and Technology, Yuseong-gu, Daejeon, Republic of Korea^b

***Bacillus siamensis* KCTC 13613^T, a novel halophilic *Bacillus* species isolated from a salted Thai food, produced antimicrobial compounds against plant pathogens and promoted plant growth by volatile emission. We determined the 3.8-Mb genome sequence of *B. siamensis* KCTC 13613^T to reveal the plant-beneficial effect at the genomic level.**

The genus *Bacillus* includes ubiquitous Gram-positive endospore-forming bacteria that have a great impact on the environment, agriculture, biotechnology, and human health. Many *Bacillus* species have been used for their industrial enzymes (9) in the pharmaceutical (10) and food production (4, 7) industries. Another major application of *Bacillus* species is for enhancing growth of crop species (3, 5). Here, during a systematic approach to screen *Bacillus* species that produce novel antibiotic compounds, we found that *Bacillus siamensis* KCTC 13613^T significantly inhibited mycelial growth of the plant-pathogenic fungi *Rhizoctonia solani* and *Botrytis cinerea* (data not shown). The KCTC 13613^T strain also exhibited strong antibacterial activity against a Gram-positive bacterium, *Micrococcus luteus*. *B. siamensis* is a novel halophilic species that was isolated from a type of salted crab product (poo-khem) eaten in Thailand (11). Strain KCTC 13613^T significantly increased seedling growth of *Arabidopsis thaliana* without physical contact in the I Plate, indicating that bacterial volatiles promoted plant growth (data not shown). These observations led us to decipher its genome sequence to investigate the genomic basis for the plant growth-promoting effect and biocontrol potential.

The genome sequence of *B. siamensis* KCTC 13613^T was determined using a whole-genome shotgun strategy and an Illumina HiSeq 2000 instrument. Paired-end reads of 4.96 Gb (average read length of 96.1 bp) were produced from a 490-bp genomic library. Quality trimming and *de novo* assembly (word size, 64) were performed using CLC Genomics Workbench, version 4.8. The assembly contained 3,779,696 bp in 51 large contigs over 200 bp (N_{50} , 589,476 bp) with 46.3% G+C content. Maximum and average contig sizes were 965,626 bp and 74,112 bp, respectively. When Velvet, version 1.2.01, was used with various k-mers (55 to 75) (12), 38 scaffolds totaling 3,784,323 bp (N_{50} , maximum scaffold size of 1,991,923 bp) were obtained. Not only were the two assembly results consistent with each other by direct comparison using MUMmer (6), but they were also the largest aligned blocks between two 100% identical results (593,857 bp), suggesting that the assembled sequences were accurate regardless of the assembly software. Automatic gene prediction and functional annotation of CLC assemblies were carried out using the RAST server (2). Among the 3,892 putative protein-coding genes, 47% were assigned to 446 subsystem categories. Average nucleotide identity analysis using completely sequenced *Bacillus* species showed that *B. amyloliquefaciens* was closely related to *B. siamensis* (>94%

identity) (8). A polyketide synthase (PKS)/nonribosomal peptide synthetase (NRPS) gene analysis was performed using SBSPKS (1) and BLAST against known protein sequences from the NCBI nr database. We identified at least four gene clusters encoding biosynthetic enzymes for one NRPS, two PKs, and one PKS/NRPS hybrid. The sequence analysis revealed that they were all close to biosynthetic genes with known secondary metabolites such as fengycin, bacillaene, difficidin, and iturin, showing >90% identity at the amino acid level. In conclusion, this genome information may be useful for developing *B. siamensis* as a plant growth-promoting agent.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AJVF00000000. The version described in this paper is the first version, AJVF01000000.

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Address correspondence to Soo-Keun Choi, sookeun@kribb.re.kr.

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