JOURNAL OF BACTERIOLOGY, Sept. 2011, p. 5026–5027 Vol. 193, No. 18
0021-9193/11/$12.00 doi:10.1128/JB.05447-11

Draft Genome Sequence of the *Paenibacillus polymyxa* Type Strain (ATCC 842^T), a Plant Growth-Promoting Bacterium$^\nabla$

Haeyoung Jeong,[1]* Soo-Young Park,[1] Won-Hyong Chung,[2] Sun Hong Kim,[1] Namshin Kim,[2] Seung-Hwan Park,[1,3] and Jihyun F. Kim[1,3]

Industrial Biotechnology and Bioenergy Research Center, Korea Research Institute of Bioscience and Biotechnology (KRIBB), 125 Gwahak-ro, Yuseong-gu, Daejeon 305-806, Republic of Korea[1]; Korean Bioinformation Center, KRIBB, 125 Gwahak-ro, Yuseong-gu, Daejeon 305-806, Republic of Korea[2]; and Biosystems and Bioengineering Program, University of Science and Technology (UST), 217 Gajung-ro, Yuseong-gu, Daejeon 305-350, Republic of Korea[3]

Received 3 June 2011/Accepted 29 June 2011

***Paenibacillus polymyxa* is an endospore-forming Gram-positive soil bacterium that is well-known for its ability to promote plant growth. Here we report the draft genome sequence of *P. polymyxa* ATCC 842^T, the type strain of the species *P. polymyxa*, and the family *Paenibacillaceae*. The *P. polymyxa* genome contains a repertoire of biosynthetic genes for antibiotics and hydrolytic enzymes that account for its beneficial effects in the rhizosphere to the host plants it associates with.**

Paenibacillus polymyxa is one of the well-characterized soil-dwelling bacterial species that are beneficial to crop plants. Its plant growth-promoting activity is often ascribed to nitrogen fixation, production of antimicrobial compounds against plant pathogens, and secretion of hydrolytic enzymes that can enhance the availability of nutrients to the plants (5, 15, 17). There is also evidence that certain *Paenibacillus* strains produce plant growth hormones, such as cytokinin and auxin (6, 11, 16, 20). It is one of the oldest species in the genus that was formerly grouped with the genus *Bacillus* (1, 19) and draws special interest due to its impact in sustainable agriculture and industrial potential (10).

Strain ATCC 842^T (= DSM 36^T = KCTC 3858^T) is the type strain of *P. polymyxa*, which originates from the culture collection of the eminent Dutch microbiologist A. J. Kluyver, as the original strain described by Prazmowski in 1880 has allegedly been lost (19). Despite the ecological and agricultural importance of this species, the genome sequence information was very limited until recently. There are only three complete genome sequences for the genus *Paenibacillus* that are publicly available, including two complete genomes of *P. polymyxa* strains (8, 14). Previously, we had reported the complete genome sequence of *P. polymyxa* E681 (8) and a genome survey of ATCC 842^T (7).

The genome of *P. polymyxa* ATCC 842^T was sequenced using an Illumina genome analyzer platform (~3,846.8 Mb; ~650-fold coverage). Pretreatment of the paired-end reads (a 500-bp library) and *de novo* assembly using CLC Genomics Workbench 4.6.1 produced 65 contigs totaling 5,896,780 bp (44.9% G+C) with N_{50} of 243,732 bp and the maximum contig size of 643,833 bp. The input reads were also subject to assembly using ABySS 1.2.7 (18) and SOAPdenovo 1.05 (http://soap.genomics.org.cn/) with an optimized *k*-mer size (66 and 69, respectively), but the result from the CLC Genomics Workbench was chosen for genome annotation because it was best in terms of contig number and N_{50}.

Genome annotation was performed using the RAST server (2) and the AutoFACT software (9). Among the predicted 5,433 protein-coding genes, 38% have been assigned putative function according to the subsystem categorization. 72 tRNA genes encompassing all 20 amino acids were identified using the tRNAscan-SE program (13). Complete gene clusters for the biosynthesis of lipopeptide antibiotics, such as tridecaptin (58.5 kb) and fusaricidin (4, 12), were predicted from the genome sequence. Genes for polymyxin production (3) were present in an overcollapsed contig due to its repetitive and modular structure. Genes for the biosynthesis of polyketides, a lantibiotic, a homoserine lactonase, and several extracellular carbohydrolases were also identified. Whole-genome comparison with the two completely sequenced *P. polymyxa* genomes revealed the close relatedness between ATCC 842^T and SC2 strains. Although large-scale chromosomal rearrangement was not identified, many strain-specific genomic regions were evident. The genome information provided here will allow further study of the plant growth-promoting activity of *P. polymyxa* species at the genomic level.

Nucleotide sequence accession number. The draft genome sequence was deposited in GenBank under accession number AFOX00000000. The version described in this paper is the first version, AFOX01000000.

We thank Jung-Hoon Yoon and Byung Kwon Kim for very helpful advice and Dong Su Yu for technical assistance.

This work was supported by the KRIBB Research Initiative Program, the 21C Frontier Microbial Genomics and Applications Center Program of the Ministry of Education, Science, and Technology, and the Next-Generation BioGreen 21 Program of the Rural Development Administration, Republic of Korea (to J.F.K.).

* Corresponding author. Mailing address: Industrial Biotechnology and Bioenergy Research Center, Korea Research Institute of Bioscience and Biotechnology (KRIBB), 125 Gwahak-ro, Yuseong-gu, Daejeon 305-806, Republic of Korea. Phone: 82 42 860 4237. Fax: 82 42 879 8595. E-mail: hyjeong@kribb.re.kr.

$^\nabla$ Published ahead of print on 8 July 2011.

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