

Genome Sequence of the Polymyxin-Producing Plant-Probiotic *Rhizobacterium Paenibacillus polymyxa* E681[∇]

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***Paenibacillus polymyxa* E681, a spore-forming, low-G+C, Gram-positive bacterium isolated from the rhizosphere of winter barley grown in South Korea, has great potential for agricultural applications due to its ability to promote plant growth and suppress plant diseases. Here we present the complete genome sequence of *P. polymyxa* E681. Its 5.4-Mb genome encodes functions specialized to the plant-associated lifestyle and characteristics that are beneficial to plants, such as the production of a plant growth hormone, antibiotics, and hydrolytic enzymes.**

Among the plant-associated microbes, some are beneficial to plants, as they antagonize various plant pathogens, induce immunity, or even promote growth (2, 21, 29). These “plant-probiotic” bacteria (15, 16, 19, 22, 23, 28) have been isolated and commercially developed for use in the biological control of plant diseases or biofertilization (7, 10). Spore-forming bacteria, in particular, members of the phylum *Firmicutes* and streptomycetes, are considered advantageous in product formulation and stable maintenance in soil (9).

The genus *Paenibacillus* (1) has grown to encompass more than 110 species (<http://www.bacterio.cict.fr/p/paenibacillus.html>), but its genome information is severely underrepresented. *Paenibacillus* spp. are important members of soil- or plant-associated ecosystems (3, 8, 20), with *Paenibacillus polymyxa* as one of the most industrially significant bacteria (13, 17, 25, 31). *P. polymyxa* E681, an endospore former isolated from the rhizosphere of winter barley in South Korea (14, 27), suppresses plant diseases, produces antibiotics and a plant hormone, secretes a variety of hydrolytic enzymes, and has good root-colonizing ability (4, 26).

We determined the genome sequence of a rifampin-resistant clone of E681. About 62,000 chromatograms (~6.7-fold genome coverage) were produced from plasmid/fosmid/bacterial artificial chromosome libraries with an AB 3700/377 DNA analyzer. Base calling, fragment assembly, contig/scaffold edit-

ing, and finishing were performed with Phred/Phrap/Consed. Gaps were closed by primer walking. To improve the sequence quality, 2.4 Gb of 76-bp single-ended sequences were obtained from Illumina Genome Analyzer IIX. Errors were identified using Maq/MapView and rectified by confirmatory sequencing. Yacop-predicted coding sequences were translated and subjected to transitive annotation by searches against UniProt, COG, KEGG Genes, and TIGRFAMs.

The genome is composed of one circular chromosome of 5,394,884 bp (45.8% G+C). It has as many as 12 rRNA operons. No plasmid was found. Three-quarters of the 4,805 genes were assigned putative functions. Protein-coding genes are distributed preferentially on the leading strand. Apparently to cope with an ever-changing environment in the rhizosphere, the genome hosts at least 13 extracytoplasmic function sigma factors (12). There are 19 complete/disrupted insertion sequence elements but few phage-related genes.

Some antibiotic-biosynthetic genes have been characterized. Polymyxin, produced and transported by PmxA to -E (5), is a potent antimicrobial that recently attracted attention for the treatment of multidrug-resistant Gram-negative bacteria (11, 18, 30). Fusaricidin, an antifungal antibiotic consisting of six amino acids, is synthesized by a single-chain nonribosomal peptide synthetase (6). E681 may also synthesize a polyketide, a tridecaptin-like nonribosomal peptide, and a hybrid of polyketide and nonribosomal peptide. A gene cluster is responsible for the production of a novel lantibiotic.

Based on sequence investigation and biochemical analysis, auxin biosynthesis via the indole-3-pyruvic acid pathway was proposed as the only possible mechanism (24). The bacterium also produces volatile compounds that may promote growth and induce resistance of plants and one or more *N*-acyl-L-

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homoserine lactonases. Genome analysis revealed a rich set of secreted enzymes that degrade various plant-derived polysaccharides. They include xylanases, pectic enzymes, cellulases, and amylases. Genes involved in nitrogen fixation were not identified.

Nucleotide sequence accession number. The genome sequence of *P. polymyxa* E681 is available in GenBank under accession number CP000154, as well as in the Genome Encyclopedia of Microbes (GEM; <http://www.gem.re.kr/>).

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