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, 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.

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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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