

Complete Genome Sequence of *Bacillus pumilus* Strain WP8, an Efficient Plant Growth-Promoting Rhizobacterium

Yijun Kang,^{a,b} Min Shen,^a Huanli Wang,^a Qingxin Zhao^a

School of Life Science and Technology, Yancheng Teachers University, Yancheng, People's Republic of China^a; Jiangsu Key Laboratory for Bioresources of Saline Soils, Yancheng, People's Republic of China^b

***Bacillus pumilus* strain WP8 is an efficient plant growth-promoting rhizobacterium. Here, we present the complete genome of WP8 and its genes involved in plant growth promotion and biocontrol.**

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Address correspondence to Yijun Kang, chnyjkang@gmail.com.

Bacillus pumilus WP8, a plant growth-promoting rhizobacterium (PGPR), was isolated from the rhizosphere of wheat (*Triticum aestivum* L.) in Yangzhou City, China (1). Both the growth-promoting and biocontrol potentials of *B. pumilus* WP8 have been proven to be efficient and widely adapted to multiple plant species and environments (2–4). Some potential mechanisms of action of *B. pumilus* WP8, such as the attenuation of virulence in pathogenic bacteria, still need to be explored further.

After DNA shearing with a Covaris M220, clone library construction, and bridge amplification, the whole-genome sequencing of WP8 was performed using Illumina MiSeq and Pacific Biosciences platforms. A total of 0.95 Gb of sequence was generated from a 300-bp paired-end library after optimizing the raw sequence data, giving 260.65-fold coverage of the genome. Meanwhile, 0.72 Gb of sequence was obtained from a PacBio 8- to 10-kb library. The filtered reads generated by Illumina sequencing were assembled by SOAPdenovo version 2.04 (5), with which the sequence data from PacBio sequencing were adjusted. Gap filling between contigs and the remaining gaps between scaffolds were closed by using GapCloser version 1.12 and sequencing the PCR products. Annotation was performed using Glimmer 3.02 (6, 7), tRNAscan-SE version 1.3.1 (8), and Barrnap 0.4.2 (9). Putative proteins were searched against the Clusters of Orthologous Groups (COG) (10), nonredundant protein sequences (nr), string (11), and Gene Ontology (GO) (12) databases.

The complete genome sequence of WP8 is a circular 3,708,888-base chromosome with a G+C content of 41.57%. The number of putative genes totals 3,678, with an average G+C content 42.10% in the coding regions. Furthermore, 22 rRNA operons and 81 tRNAs were predicted. There are some genes associated with growth promotion and biocontrol, such as genes encoding capsular polysaccharides (QR42_15530) and sporulation transcription factors (QR42_00345) that are related to biofilm formation (13, 14), as well as genes encoding chemotaxis-related proteins (QR42_10155, QR42_15985, etc.) and cell wall degradation-related proteins (QR42_09230) that may be responsible for colonization. Relatively few genes are involved in antimicrobial biosynthesis in the genome besides a siderophore-synthetic gene

(QR42_05295). Genes encoding endoglucanase (QR42_07950), protease (QR42_17905), and β -1,3-glucanase (QR42_02755) are considered to play important roles in the biocontrol of some fungal pathogens and nematodes (15–18). Genes encoding nonribosomal peptide synthetase (QR42_01955–QR42_01980), putative pumilicidin, may be responsible for the attenuation of virulence in some pathogenic bacteria and need to be studied. In addition, genes encoding arsenical pump membrane protein (QR42_01870), monooxygenase (QR42_08825), UV damage repair endonuclease (QR42_16900), catalase (QR42_18570), and stress proteins (QR42_01610, QR42_02315, etc.) enable WP8 to adapt to a wide range of environments (19–21).

Nucleotide sequence accession number. The complete nucleotide genome sequence of *B. pumilus* WP8 has been deposited in GenBank with the accession number [CP010075](https://www.ncbi.nlm.nih.gov/nuccore/CP010075).

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