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Draft Genome Sequence of *Paenibacillus polymyxa* KF-1, an Excellent Producer of Microbicides

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We report here the draft genome sequence of *Paenibacillus polymyxa* KF-1, which exhibits excellent antimicrobial activity. It encodes the synthase of bacitracin, kalimantacin, bacillomycin, iturin, fusaricidin, tridecaptin, and pelgipeptin and biosynthetic pathways of antiviral curldan and levan polysaccharides. Also, a novel prophage is involved in this genome that contains endolysin-encoding genes.

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Paenibacillus polymyxa KF-1 was isolated from soil by our lab and was found to be able to produce many kinds of bioactive compounds and show a broad spectrum of antimicrobial activity (our unpublished data). Here, we report the draft genome sequence for further studies focusing on genes or gene clusters mining for the biosynthesis of these functional molecules.

Genomic DNA of *P. polymyxa* KF-1 was extracted and sequenced using an Illumina MiSeq platform. Shotgun sequencing produced 3,797,994 paired-end reads with approximately 154-fold coverage. Filtered reads were assembled by Newbler 2.8, and gaps were filled by GapCloser (http://soap.genomics.org.cn/about.html). This assembly generated 113 contigs with a total sequence length of 5,784,494 bp, which were assembled into 39 scaffolds with a total sequence length of 5,765,823 bp. The draft genome had an average G+C content of 45% and contained 5,229 open reading frames (ORFs) that were predicted by Glimmer 3.0 (1). The genome annotation was performed via search against the GenBank, UniProt, Pfam, KEGG, COG, and InterPro databases, which revealed rich sources of bioactive compounds. In addition, 107 tRNAs, 6 rRNA loci, and 68 other noncoding RNAs (ncRNAs) were identified via the tRNAsan-SE 1.3.1, RNAmmer 1.2 servers, and Rfam database, respectively.

antiSMASH (http://antismash.secondarymetabolites.org/) analysis showed that the genome contained 17 gene clusters encoding nonribosomal peptide synthases including bacitracin, kalimantacin, bacillomycin, iturin, fusaricidin, tridecaptin, pelgipeptin, and an additional two polyketide synthases. An NCBI conserved domains search revealed β-1,3-glycanases (curldan synthases) and levansucrases for biosynthesis of antiviral curldan and leven polysaccharides (2, 3). PHAge Search Tool (http://phast.wishartlab.com/index.html) scanning indicated that there was a 5.9-kb full-length prophage genome.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. LNZF00000000. The version described in this paper is the first version, LNZF00000000.1. The BioProject number is PRJNA304353. The Ref-Seq accession number is NZ_LNZF01000000.

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