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GENOME ANNOUNCEMENT

Draft Genome Sequence of *Paenibacillus* sp. Strain OSY-SE, a Bacterium Producing the Novel Broad-Spectrum Lipopeptide Antibiotic Paenibacterin

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A strain of *Paenibacillus* sp., OSY-SE, was isolated from soil and found to produce a novel lipopeptide antibiotic. The antibiotic, paenibacterin, is active against Gram-negative and Gram-positive bacterial pathogens. Paenibacterin is biosynthesized by a nonribosomal peptide synthetase pathway. Here we report the draft genome sequence of *Paenibacillus* sp. OSY-SE.

Resistance of pathogens to antibiotics is a rapidly evolving phenomenon with serious public health implications. Methicillin-resistant *Staphylococcus aureus* (MRSA) exemplifies the emergence of multidrug resistance among Gram-positive bacterial pathogens. Similarly, some Gram-negative pathogens have become resistant to β-lactams, fluoroquinolones, and aminoglycosides, threatening the therapeutic choices for treating these pathogens (2). Antimicrobial lipopeptides may combat antibiotic-resistant pathogens, but some of these compounds have limitations. Polymyxin, for example, has strong activity against Gram-negative bacteria (5, 9), but concerns on nephrotoxicity and neurotoxicity have limited its broad use as a therapeutic agent. Therefore, new and effective antimicrobials are urgently needed to combat these emerging drug-resistant pathogens. Paenibacterin is a newly discovered cyclic lipopeptide produced by *Paenibacillus* sp. OSY-SE. The lipopeptide comprises 13 amino acids and a C_{15} fatty acyl moiety (3). Paenibacterin is active against Gram-negative and Gram-positive pathogens, including *Escherichia coli* O157:H7, *Salmonella enterica* serovar Typhimurium, *Listeria monocytogenes*, and methicillin-resistant *Staphylococcus aureus*. To understand the biosynthesis of paenibacterin, we determined the whole-genome sequence of the producer strain, *Paenibacillus* sp. OSY-SE.

Genomic DNA of *Paenibacillus* sp. OSY-SE was isolated using a DNA extraction kit (DNeasy blood and tissue kit; Qiagen, Valencia, CA). RNase-treated genomic DNA in Tris-Cl buffer (pH 8.5) was used for construction of a paired-end library with a TruSeq DNA sample preparation kit (Illumina, San Diego, CA) according to the manufacturer's instruction. The constructed library was sequenced (76-cycle paired-end runs) in a flow cell lane using Illumina Genome Analyzer II. *De novo* assembly of the short reads with commercial software (CLC Genomics Workbench 4.7.2; CLCBio, Cambridge, MA) yielded 205 contigs (>200 bp each), with a maximum contig size of 359,285 bp. The resulting draft genome of *Paenibacillus* sp. OSY-SE consists of 6,931,767 bases; the overall GC content of the genome was calculated as 48.66% by the software Artemis (8). Automatic genome annotation was performed using the rapid annotations using subsystems technology (RAST) server (1). Among the 6,475 protein-coding sequences (CDSs), 65.79% have been assigned a putative function by RAST. The chromosome has one rRNA operon and 38 tRNA genes, as predicted by RNAmmer (4) and tRNAscan-SE (6), respectively.

The average nucleotide identities (ANI) between *Paenibacillus* sp. OSY-SE and 20 genomes of *Paenibacillus* species that are available in GenBank were determined using the *in silico* DNA-DNA hybridization method implemented in the software JSpecies (7). The results indicated that *Paenibacillus* sp. OSY-SE has the closest genetic relatedness with *Paenibacillus lactis* strain 154 (ANI, 77.21%). The gene cluster responsible for paenibacterin biosynthesis was identified in a 52-kb region encoding three nonribosomal peptide synthetases and two ABC-like transporters.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number ALKF00000000. The version described in this paper is the first version, ALKF01000000.

ACKNOWLEDGMENT

This research was supported by the Virginia Hutchison Bazler and Frank E. Bazler Designated Professorship in Food Science.

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Received 17 August 2012 Accepted 29 August 2012

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doi:10.1128/JB.01506-12