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GENOME ANNOUNCEMENT

Draft Genome Sequence of *Paenibacillus polymyxa* OSY-DF, Which Coproduces a Lantibiotic, Paenibacillin, and Polymyxin E1

En Huang[a] and Ahmed E. Yousef[a,b]

Department of Food Science and Technology, The Ohio State University, Columbus, Ohio, USA,[a] and Department of Microbiology, The Ohio State University, Columbus, Ohio, USA[b]

***Paenibacillus polymyxa* OSY-DF is a Gram-positive rod-shaped bacterium isolated from a fermented vegetable food. This bacterial strain displays potent antimicrobial activities against Gram-positive and Gram-negative pathogenic bacteria, attributed to the production of the lantibiotic paenibacillin and the colistin peptide polymyxin E1. Here we report the draft genome sequence of *Paenibacillus polymyxa* OSY-DF.**

There is a perpetual need to discover or develop new antimicrobial agents to combat emerging antibiotic-resistant bacterial pathogens (5). *Paenibacillus polymyxa* OSY-DF, an isolate from a fermented food, coproduces a lantibiotic (paenibacillin) and polymyxin E1 (7). Paenibacillin is a unique lantibiotic with an N-terminal acetyl group (8). Paenibacillin shows potency against Gram-positive bacteria, including methicillin-resistant *Staphylococcus aureus*, *Listeria monocytogenes*, and *Mycobacterium smegmatis*. Recently, there has been renewed interest in using polymyxin to treat infections caused by multidrug-resistant (MDR) Gram-negative bacteria (4, 12, 14, 19). Therefore, paenibacillin and polymyxin E1 from *P. polymyxa* OSY-DF have promising applications in treating bacterial infections or protecting foods as natural preservatives. To understand the biosynthesis of these antimicrobial agents, we determined the whole genome sequence of the producer strain, *P. polymyxa* OSY-DF.

Genomic DNA of *P. polymyxa* OSY-DF 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 instructions. The constructed library was sequenced (76 cycles, paired-end runs) in a flow cell lane using an Illumina genome analyzer II. *De novo* assembly of the short reads with a commercial software (CLC Genomics Workbench 4.7.2; CLCBio, Cambridge, MA) yielded 139 contigs (>200 bp), with a maximum contig size of 685,087 bp. The resulting draft genome of *P. polymyxa* OSY-DF consists of 5,695,430 bases; the overall GC content of the genome was calculated as 45.35% by the software Artemis (18). Automatic genome annotation was performed using RAST (Rapid Annotation using Subsystem Technology) (1). Among the 5,139 protein-coding sequences (CDSs), 72% have been assigned a putative function by RSAT. The chromosome has 1 rRNA operon and 42 tRNAs, as predicted by RNAmmer (11) and tRNAscan-SE (15), respectively.

In the draft genome of *P. polymyxa* OSY-DF, two complete lantibiotic gene clusters were identified. One of the lantibiotic gene clusters (11.7 kb) is responsible for paenibacillin biosynthesis, while the other may encode a new lantibiotic as predicted by the bacteriocin mining tool Bagel2 (3). Many nonribosomal peptide synthetase (NRPS) genes were identified in the draft genome. For instance, genes for polymyxin E1 production were found in four nonoverlapping contigs. The complete fusaricidin gene cluster was found in a large contig, whose predicted protein shows 93% identity to its homologues in *P. polymyxa* PKB1 and *P. polymyxa* E681 (2, 13).

The average nucleotide identity (ANI) between the draft genome of *P. polymyxa* OSY-DF and the four published *P. polymyxa* genomes of SC2 (16), M-1 (17), E681 (10), and ATCC 842^T (9) was determined using the *in silico* DNA-DNA hybridization (DDH) method implemented in the software JSpecies (6). The results indicated that *P. polymyxa* OSY-DF has the closest genetic relatedness to strain ATCC 842^T (97.50% ANI), followed by strains SC2 (94.52% ANI), M-1 (94.52% ANI), and E681 (91.78% ANI).

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under accession no. AIPP00000000. The version described in this article is the first version, AIPP01000000.

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 May 2012 **Accepted** 12 June 2012

Address correspondence to Ahmed E. Yousef, yousef.1@osu.edu.

doi:10.1128/JB.00846-12

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