Complete Genome Sequence of Aneurinibacillus migulanus E1, a Gramicidin S- and D-Phenylalanyl-L-Propyl Diketopiperazine-Deficient Mutant

Lassaad Belbahri, a,b Faizah N. Alenezi, b,c Lenka Luptakova, a,b,d Mostafa E. Rateb, e Steve Woodward b,c

Laboratory of Soil Biology, University of Neuchâtel, Neuchâtel, Switzerland; NexBiotech, Agareb, Tunisia; University of Aberdeen, Institute of Biological and Environmental Science, Aberdeen, Scotland, United Kingdom; University of Veterinary Med & Pharmacy, Institute of Biology, Zoology & Radiobiology, Department of Biology and Genetics, Košice, Slovakia; School of Science & Sport, University of West of Scotland, Paisley, United Kingdom

L.B. and F.N.A. contributed equally to this article.

We report here the complete genome sequence of the Aneurinibacillus migulanus E1 mutant deficient in gramicidin S (GS) and D-phenylalanyl-L-propyl diketopiperazine (DKP) formation. The genome consists of a circular chromosome (6,301,904 bp, 43.20% G+C content) without any plasmid. The complete genome sequence enables further investigation of the biosynthetic mechanism and the biological function of gramicidin S.

Gramicidin S (GS) is a cationic cyclic decapetide with the primary structure [cyclo-(Val-Orn-Leu-D-Phe-Pro)] 2 (1). GS is an extremely powerful antibiotic drug against a broad spectrum of both Gram-negative and Gram-positive bacteria and against several pathogenic fungi (2–5). GS-deficient mutants in Aneurinibacillus migulanus have been classified into five different categories. The mutant E1 belongs to the fifth group that contains both a phenylalanine-activating enzyme and a complex of proline-, valine-, ornithine-, and leucine-activating enzymes similar to those of the wild-type strain (6). E1 is unable to synthetize GS or D-phenylalanyl-L-propyl diketopiperazine (DKP).

The genome of the A. migulanus E1 mutant was sequenced by the Illumina HiSeq 2000 platform (2 × 125 bp), and the sequencing coverage was 100X. After sequencing, the reads were assembled using CLC Genomics Workbench 7.0.3 (CLC bio). Annotation was performed using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) version 2.9 (7). The whole genome is represented by a circular chromosome of 6,301,904 bp with no plasmid. The G+C content was around 43.20%, as reported for other SMASH 3.0, 12 gene clusters for secondary metabolites have been predicted in the genome of the E1 chromosome has been deposited in GenBank under accession the no. LIXL00000000. The version described in this paper is the first version.

ACKNOWLEDGMENTS

This work was supported by the European Union’s Seventh Framework Programme grant 245268 (ISEFOR; to L.B.). Further support came from the SwissBOL project (the Swiss Federal Office for the Environment, to L.B.) and the Sciex-Scientific Exchange Programme NMS.CH (to L.L. and L.B.).

REFERENCES

