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Draft Genome Sequence of *Lysinibacillus* sp. Strain A1, Isolated from Malaysian Tropical Soil

Kok-Gan Chan,[a] Jian Woon Chen,[a] Chien-Yi Chang,[b,c] Wai-Fong Yin,[a] Xin-Yue Chan[a]

Division of Genetics and Molecular Biology, Institute of Biological Sciences, Faculty of Science, University of Malaya, Kuala Lumpur, Malaysia[a]; Interdisciplinary Computing and Complex BioSystems (ICOS) Research Group, School of Computing Science, Newcastle University, Newcastle upon Tyne, United Kingdom[b]; Centre for Bacterial Cell Biology, Medical School, Newcastle University, Newcastle upon Tyne, United Kingdom[c]

In this work, we describe the genome of *Lysinibacillus* sp. strain A1, which was isolated from tropical soil. Analysis of its genome sequence shows the presence of a gene encoding for a putative peptidase responsible for nitrogen compounds.

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Address correspondence to Kok-Gan Chan, kokgan@um.edu.my.

Lysinibacillus spp. are Gram-positive rod bacteria that can survive in a wide range of extreme environments, including heavy metal-contaminated soil (1–5). Even though *Lysinibacillus* sp. is well known for its bioremediation potential, knowledge about its biodegradation ability is limited. In this study, we analyzed the bacterial genome of *Lysinibacillus* sp. strain A1. In addition, we determined the peptidase-coding gene from its whole-genome sequence.

Lysinibacillus sp. strain A1 was isolated from soil surface (Rimba Ilmu, Kuala Lumpur, Malaysia) using KGm medium and cultivated in Luria-Bertani medium (6, 7). The genomic DNA was isolated using a MasterPure DNA purification kit (Epicenter, USA) (8). The extracted DNA was quantified and qualified using Qubit version 2.0 (Invitrogen, USA) and Nanodrop (Thermo Scientific, USA) (9). The high-quality DNA was sent for next-generation sequencing (NGS) library preparation using a Nextera DNA sample preparation kit (Illumina, USA) and sequenced using a MiSeq 600-cycle sequencing kit (version 3) on a MiSeq platform (Illumina, USA) (9). The preliminary analysis was performed with CLC Genomic Workbench version 7.5, while the annotation are performed using the NCBI prokaryote genome annotation pipeline (version 2.9) and NCBI BLAST against the nr database (10, 11).

The NGS of the *Lysinibacillus* sp. strain A1 genome by MiSeq generated 1.2 million paired-end reads. These reads were trimmed and assembled into 57 contigs with average coverage of 42-fold and an N_{50} of 206,495 bp. The genome size is 4.75 Mbps with 37.45% G+C content. This genome carried 4,449 coding DNA sequences (CDS) and coded for 4,693 genes and 159 pseudogenes.

A peptidase-coding gene was detected in contig 1 in the draft genome of *Lysinibacillus* sp. strain A1. The length of this gene is 1,089 bp, and it is located at a position between 182,713 and 183,801 bp at contig 1. Based on the gene alignment and comparison, it is classified into peptidase M28. It has been reported that peptidase is used by both macro- and microorganisms to break down protein by hydrolyzing its peptide bond in order to acquire nutrients (12). The cocatalytic active site of peptidase M28 was formed by two zinc ions (13, 14). To our knowledge, the production of peptidase M28 by *Lysinibacillus* has not been reported. Thus, our work on the genome and peptidase gene of *Lysinibacillus* sp. strain A1 will lead to further understanding on the function of this protein hydrolysis enzyme.

Nucleotide sequence accession numbers. This draft genome was deposited into DDBJ/EMBL/GenBank under the accession number JSZM00000000. The version described in this paper is the first version, JSZM01000000.

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