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## Data Article

Draft genome sequence data of *Lysinibacillus fusiformis* strain GM, isolated from potato phyllosphere as a potential probiotic

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## ARTICLE INFO

## Article history:

Received 18 October 2018

Accepted 20 November 2018

Available online 24 November 2018

## Keywords:

*Lysinibacillus fusiformis*

Probiotic

Cellulase

Illumina MiSeq

*In silico* DNA-DNA hybridization

## ABSTRACT

Here we present the morphological and physiological properties of isolated *Lysinibacillus fusiformis* strain GM, its draft genome sequence as well as annotation and analysis of its genome. Initial analysis of MALDI-TOF mass spectrometry, 16S rRNA gene analysis and *in silico* DNA-DNA hybridization revealed that the strain belongs to the species *Lysinibacillus fusiformis*. The 4,678,122 bp draft genome consist of 17 scaffolds encoding 4588 proteins and 137 RNAs. Annotation of the genome sequence revealed cellulase and protease encoding genes, genes of adhesion proteins and putative genes responsible for the biosynthesis of antimicrobial metabolites. The Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number NTMQ00000000.1 ([https://www.ncbi.nlm.nih.gov/nuccore/NZ\\_NTMQ00000000.1](https://www.ncbi.nlm.nih.gov/nuccore/NZ_NTMQ00000000.1)).

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<https://doi.org/10.1016/j.dib.2018.11.107>

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