AMERICAN SOCIETY FOR MICROBIOLOGY | genomeAnnouncements

Draft Genome Sequence of the Soil Isolate *Lysinibacillus fusiformis* M5, a Potential Hypoxanthine Producer

Ramses Gallegos-Monterrosa,[a] Gergely Maróti,[b] Balázs Bálint,[c] Ákos T. Kovács[a]

Terrestrial Biofilms Group, Institute of Microbiology, Friedrich Schiller University Jena, Jena, Germany[a]; Institute of Biochemistry, Biological Research Centre, Hungarian Academy of Sciences, Szeged, Hungary[b]; Seqomics Biotechnology Ltd., Mórahalom, Hungary[c]

***Lysinibacillus fusiformis* strain M5 is a potential hypoxanthine producer that was isolated from clay soil. Here, we present the draft genome sequence that was annotated in order to facilitate future studies of *L. fusiformis* M5.**

Received 16 September 2016 **Accepted** 21 September 2016 **Published** 10 November 2016

Citation Gallegos-Monterrosa R, Maróti G, Bálint B, Kovács ÁT. 2016. Draft genome sequence of the soil isolate *Lysinibacillus fusiformis* M5, a potential hypoxanthine producer. Genome Announc 4(6):e01272-16. doi:10.1128/genomeA.01272-16.

Address correspondence to Ákos T.Kovács, akos-tibor.kovacs@uni-jena.de.

Lysinibacillus fusiformis is a Gram-positive endospore-forming soil bacterium that was recently reclassified from the *Bacillus* genus due to differences in its cell wall components (1). Although *L. fusiformis* has been suspected for it pathogenicity (2–4), other studies reported the isolation of this species from diverse environmental samples, and it has been proposed as a potential producer of industrially attractive metabolites (5, 6).

Screening of a library of isolates obtained from a Mexican clay soil collected at the warm and humid region of Tepoztlán, Morelos, resulted in the identification of *L. fusiformis* M5. It was selected for further study due to its ability to produce hypoxanthine (R. Gallegos-Monterrosa and Á. T. Kovács, unpublished data). Hypoxanthine is a common metabolite produced by bacteria as part of the purine salvage pathway (7, 8). This nucleobase and its concomitant enzymes have been extensively studied due to their role in cell metabolism and signaling, and as potential drug targets (9, 10).

We performed whole-genome sequencing of *L. fusiformis* strain M5 in order to facilitate the identification of genes involved in hypoxanthine production. Genomic DNA of *L. fusiformis* M5 was isolated with GeneMATRIX bacterial and yeast genomic DNA purification kit, according to the manufacturer's instructions (EURx, Gdańsk, Poland). A mate-pair library was generated using the Illumina Nextera mate-pair kit (catalog no. FC-132-1001), with insert sizes ranging between 7 and 11 kb. DNA sequencing was carried out on an Illumina MiSeq machine using V2 sequencing chemistry, resulting in 2 × 250-bp reads. Raw data were preprocessed for *de novo* assembly according to the manufacturer's recommendations. Data processing of Nextera mate pair reads was performed using Illumina Sequencing Platforms (http://www.illumina.com/documents/products/technotes/technote_nextera_matepair_data_processing.pdf).

De novo assembly was performed with CLC Genomics Workbench 8.0.2 (CLC bio), with contigs being subsequently arranged into scaffolds using SSPACE 3.0 (11). Gaps in scaffolds were closed with SPAdes version 3.1.1 (12), together with an in-house R script (B. Bálint, unpublished data). The assembly produced 7 contigs and a circularized plasmid that comprise 4,744,577 and 134,678 bases, respectively, with G+C contents of 37 and 36%, respectively. Automated annotation was performed using the NCBI Prokaryotic Genome Annotation Pipeline (13); 4,753 genes were identified, including 74 tRNA and 22 rRNA regions. Around 96% of the identified genes corresponded to hypothetical proteins (4577 coding open reading frames [ORFs]).

Genes coding for proteins possibly involved in hypoxanthine production were identified among the annotated genes, namely, *pbuE*, a putative hypoxanthine transporter; and *adeC* and *yerA*, putative adenine deaminases involved in the purine salvage pathway. Genome comparison confirmed the presence of homologous genes (identity, ≥95%) in the genomes of *L. fusiformis* RB-21 (GenBank accession no. CP010820.1) and *L. fusiformis* SW-B9 (GenBank accession no. JRBA00000000.1) (14). Based on genomic BLAST, *L. fusiformis* M5 shows closest homology to *L. fusiformis* strain H1k (GenBank accession no. AYMK00000000.1).

Accession number(s). This whole-genome shotgun project has been deposited in GenBank under the accession no. MECQ00000000. The version described in this paper is the first version, MECQ00000000.1.

FUNDING INFORMATION

This work, including the efforts of Ákos T. Kovács, was funded by Marie Curie Career Integration Grant (PheHetBacBiofilm). This work, including the efforts of Ramses Gallegos-Monterrosa, was funded by Consejo Nacional de Ciencia y Tecnología, German Academic Exchange Service. This work, including the efforts of Ákos T. Kovács, was funded by Deutsche Forschungsgemeinschaft (DFG) (KO4741/2-1 and KO4741/3-1).

REFERENCES

1. **Ahmed I, Yokota A, Yamazoe A, Fujiwara T.** 2007. Proposal of *Lysinibacillus boronitolerans* gen. nov. sp. nov., and transfer of *Bacillus fusiformis* to *Lysinibacillus fusiformis* comb. nov. and *Bacillus sphaericus* to *Lysinibacillus sphaericus* comb. nov Int J Syst Evol Microbiol **57:**1117–1125. http://dx.doi.org/10.1099/ijs.0.63867-0.
2. **Smith EC.** 1933. Inoculation experiments with *Bacillus fusiformis* isolated from tropical ulcer with observations on the bacillus. J Hyg (Lond) **33:**95–102.

3. **Peters WH**. 1911. Hand infection apparently due to *Bacillus fusiformis*. J Infect Dis **8:**455–462. http://dx.doi.org/10.1093/infdis/8.4.455.
4. **Wenzler E, Kamboj K, Balada-Llasat JM**. 2015. Severe sepsis secondary to persistent *Lysinibacillus sphaericus*, *Lysinibacillus fusiformis* and *Paenibacillus amylolyticus* bacteremia. Int J Infect Dis **35:**93–95. http://dx.doi.org/10.1016/j.ijid.2015.04.016.
5. **He M, Li X, Liu H, Miller SJ, Wang G, Rensing C**. 2011. Characterization and genomic analysis of a highly chromate resistant and reducing bacterial strain *Lysinibacillus fusiformis* ZC1. J Hazard Mater **185:** 682–688. http://dx.doi.org/10.1016/j.jhazmat.2010.09.072.
6. **Zhao LQ, Sun ZH, Zheng P, Zhu LL**. 2005. Biotransformation of isoeugenol to vanillin by a novel strain of *Bacillus fusiformis*. Biotechnol Lett **27:**1505–1509. http://dx.doi.org/10.1007/s10529-005-1466-x.
7. **Hochstadt J**. 1978. Hypoxanthine phosphoribosyltransferase and guanine phosphoribosyltransferase from enteric bacteria. Methods Enzymol **51:** 549–558. http://dx.doi.org/10.1016/S0076-6879(78)51077-X.
8. **Dandanell G, Hove-Jensen B, Willemoës M, Jensen KF**. 2008. Nucleotides, nucleosides, and nucleobases. Ecosal Plus **3**. http://dx.doi.org/10.1128/ecosalplus.3.6.2.
9. **Nishino T, Okamoto K**. 2015. Mechanistic insights into xanthine oxidoreductase from development studies of candidate drugs to treat hyperuricemia and gout. J Biol Inorg Chem **20:**195–207. http://dx.doi.org/10.1007/s00775-014-1210-x.
10. **Wang C, Zhang C, Xing X**. 2016. Xanthine dehydrogenase: an old enzyme with new knowledge and prospects. Bioengineered **5979:**1–11. http://dx.doi.org/10.1080/21655979.2016.1206168.
11. **Boetzer M, Henkel CV, Jansen HJ, Butler D, Pirovano W**. 2011. Scaffolding pre-assembled contigs using SSPACE. Bioinformatics **27:** 578–579. http://dx.doi.org/10.1093/bioinformatics/btq683.
12. **Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA**. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol **19:**455–477.
13. **Angiuoli SV, Gussman A, Klimke W, Cochrane G, Field D, Garrity GM, Kodira CD, Kyrpides N, Madupu R, Markowitz V, Tatusova T, Thomson N, White O**. 2008. Toward an online repository of standard operating procedures (SOPs) for (Meta)genomic annotation. OMICS **12:**137–141.
14. **Zhang Z, Schwartz S, Wagner L, Miller W**. 2000. A greedy algorithm for aligning DNA sequences. J Comput Biol **7:**203–214. http://dx.doi.org/10.1089/10665270050081478.