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 its 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 Teotzolán, 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 T. Kovács, unpublished data).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 concomitants 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 sequencing 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/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 Gaps in scaffolds were closed with SPAdes version 3.1.1 (12), together with an in-house script (B. Bálint, unpublished data).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 yerÁ, 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. JRA00000000.1) (14). Based on genomic BLAST, L. fusiformis M5 shows closest homology to L. fusiformis strain H1k (GenBank accession no. AYMK0000000.1).

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 Deutsche Forschungsgemeinschaft (DFG) 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 Paeni- bacillus 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, Willemoes 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 5:979:1–11. http://dx.doi.org/10.1080/21655979.2016.1206168.
11. Boetzer M, Henkel CV, Jensen 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, Thompson 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.