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ABSTRACT  Here, we report a draft genome sequence of the Sporomusaceae bacterial strain FL31, a novel lactate-fermenting bacterium of the family Sporomusaceae within the class Negativicutes. This genome furthers our understanding of the physiological functions of this taxonomic group in natural environments.

The class Negativicutes has recently been validated in the phylum Firmicutes and comprises 3 orders (1). The family Sporomusaceae of the order Selenomonadales has the largest number of genera, having 11 genera with 21 isolates (2). Members of this family have been found in various anoxic environments, including soils and subsurface sediments (3–5). However, little is known about the ecophysiological functions of this family. Genome information is important for the development of a thorough understanding regarding the metabolic potential of this taxonomic group. Here, we report a draft genome sequence of the lactate-fermenting Sporomusaceae bacterial strain FL31, isolated from an anoxic soil sample.

Strain FL31 was obtained from an anoxic soil sample (Matsudo City, Chiba, Japan [35°46’N, 139°53’E]) by using extinction dilution and a single-colony isolation technique. Strain FL31 was grown anaerobically in a minimum medium containing lactate (10 mM) as the sole carbon source. The medium contained the following ingredients (per liter): NH₄Cl (0.535 g), KH₂PO₄ (0.136 g), MgCl₂·6H₂O (0.204 g), CaCl₂·2H₂O (0.147 g), trace mineral element solution (1 ml), vitamin solution (1 ml), Se/W solution (1 ml), and NaHCO₃ (2.52 g). DNA was extracted by using a DNeasy blood and tissue kit (Qiagen, Germany). A paired-end DNA library (insert size, ~550 bp) was generated using a TruSeq DNA PCR-free LT sample prep kit (Illumina, CA, USA). The library was sequenced with an Illumina MiSeq platform. The paired-end library generated 3,507,417 reads (300 bp paired end). Low-quality sequences (Q < 10) were removed. Sequence assembly was performed by a de novo assembly using the CLC Genomic Workbench v. 11.0.1 (Qiagen) with default parameters, except for the minimum contig length (500 bp), and resulted in 118 scaffolds with 262.5× genome coverage from the library. The largest scaffold length was 821,961 bp. The N₅₀ value was 264,930 with 118 scaffolds. The draft genome sequence of strain FL31 was 4,000,006 bp with a G+C content of 42.2%.

The BLASTn analysis of the 16S rRNA gene suggests that this strain is a member of a novel genus within the family Sporomusaceae. The closest phylogenetic cultured relatives of strain FL31 were Propionispora hippei KST, Psychrosinus fermentans FCF9, and Pelosinus defluvii SH1-T, with gene sequence identities of 93.5%, 93.2%, and 93.2%, respectively, in the nearly full length (1,552 bp) of the analyzed 16S rRNA gene sequences.
Annotation was carried out by using the DDBJ Fast Annotation and Submission Tool v. 1.0.0 (6) with default parameters. The draft genome sequence comprises 89 tRNA genes and 9 rRNA genes. Of the 3,821 predicted protein-coding sequences, 73.4% were assigned to recognized functional genes. The draft genome of strain FL31 contained the functional genes encoding L-lactate dehydrogenase, pyruvate dehydrogenase, malate dehydrogenase, fumarate hydratase, succinate dehydrogenase, acetate kinase, NADP-dependent malic enzyme, 2-oxo acid dehydrogenase, phosphate acetyltransferase, 4-hydroxybutyrate coenzyme A (CoA)-transferase, methylmalonyl-CoA carboxyltransferase, methylmalonyl-CoA epimerase, and methylmalonyl-CoA mutase, all of which are associated with lactate fermentation to propionate and acetate via the Wood-Werkman pathway (7).

The draft genome sequence of the Sporomusaceae bacterial strain FL31 provides insights into physiological functions of this family in anoxic natural environments.

Data availability. The Sporomusaceae bacterial strain FL31 draft genome sequences have been deposited as 118 scaffolds in DDBJ/EMBL/GenBank under accession numbers BIFV01000001 to BIFV01000118. The version described in this paper is the first version. The raw sequencing data have been deposited in the same database under the accession number DRA007976.

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REFERENCES

1. Yutin N, Galperin MY. 2013. A genomic update on clostridial phylogeny: Gram-negative spore-formers and other misplaced clostridia. Environ Microbiol 15:2631–2641. https://doi.org/10.1111/1462-2920.12173.
2. Campbell C, Adeolu M, Gupta RS. 2015. Genome-based taxonomic framework for the class Negativicutes: division of the class Negativicutes into the orders Selenomonadales emend., Acidaminococcales ord. nov. and Veillonellales ord. nov. Int J Syst Evol Microbiol 65:3203–3215. https://doi.org/10.1099/ijs.0.000347.
3. Choi JK, Shah M, Yee N. 2016. Anaerosporomusa subterranea gen. nov., sp. nov., a spore-forming anaerobe belonging to the class Negativicutes isolated from saprolite. Int J Syst Evol Microbiol 66:3848–3854. https://doi.org/10.1099/ijsem.0.001275.
4. Ghihring TM, Zhang G, Brandt CC, Brooks SC, Campbell JH, Carroll S, Criddle CS, Green SJ, Jardine P, Kostka JE, Lowe K, Melhorn TL, Overholt W, Watson DB, Yang Z, Wu W-M, Schadt CW. 2011. A limited microbial consortium is responsible for extended bioreduction of uranium in a contaminated aquifer. Appl Environ Microbiol 77:5955–5965. https://doi.org/10.1128/AEM.00220-11.
5. Yamamura S, Sudo T, Watanabe M, Tsuboi S, Soda S, Ike M, Amachi S. 2018. Effect of extracellular electron shuttles on arsenic-mobilizing activities in soil microbial communities. J Hazard Mater 342:571–578. https://doi.org/10.1016/j.jhazmat.2017.08.071.
6. Tanizawa Y, Fujisawa T, Kaminuma E, Nakamura Y, Arita M. 2016. DFAST and DAGA: Web-based integrated genome annotation tools and resources. Biosci Microbiota Food Health 35:173–184. https://doi.org/10.12938/bmfh.16-003.
7. Gonzalez-Garcia R, McCubbin T, Navone L, Stowers C, Nielsen L, Marcellin E. 2017. Microbial propionic acid production. Fermentation 3:21. https://doi.org/10.3390/fermentation3020021.