Draft Genome Sequence of Anaerobic Fermentative Bacterium
Anaeromicrobium sediminis DY2726D

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ABSTRACT Here, we report the draft genome sequence of Anaeromicrobium sediminis DY2726D, isolated from a west Pacific Ocean sediment sample. The genome comprises 4,710,590 bp in 56 contigs, with a G+C content of 31.2%. A total of 3,811 protein-coding sequences were predicted. The genome annotation revealed that DY2726D may represent a marine type of Clostridiaceae.

The Clostridiaceae family includes a large proportion of anaerobic fermentative microorganisms, and some species have been frequently isolated from marine environments, including Clostridium bryantii (1), Caloranaerobacter azorensis MV1087T (2), and Wukongibacter baidiensis DY30321T (3). Anaeromicrobium sediminis DY2726D was isolated in 2013 from a deep-sea sediment sample collected in the west Pacific Ocean. Anaeromicrobium sediminis DY2726D was found to be a member of the family Clostridiaceae and to be most closely related to species of the genera Clostridium and Alkaliphilus. The most closely related strain is Alkaliphilus transvaalensis SAGM1 (4), with which A. sediminis DY2726D has 90.0% 16S rRNA gene sequence similarity. DY2726D is the type strain of the new genus Anaeromicrobium (5). Here, we report the draft genome sequence of A. sediminis DY2726D, the first released Anaeromicrobium genome sequence.

The DY2726D genome was sequenced by using the Illumina HiSeq 2000 platform (Majorbio Co., Ltd., Shanghai, China). Paired-end reads with an average length of 500 bp and total read size of ~300 Mbp were assembled by using SOAPdenovo version 2.04 (6), and gap filling between contigs and the remaining gaps between scaffolds were closed by using GapCloser version 1.12 (7).

The assembled draft genome contained 4,710,590 bp in 56 contigs with an average of 20X coverage and 31.2% G+C content. The open reading frames (ORFs) were analyzed using Glimmer 3.02 (8), and all predicted ORFs were then searched by BLAST against all proteins from complete microbial genomes by using the NCBI Prokaryotic Genome Annotation Pipeline (9). tRNAscan-SE (version 1.3.1) was used to identify the tRNA genes (10), and rRNA identification was performed by Barrmap 0.4.2 (11). Classifications of some predicted genes and pathways were analyzed by using the COG database (12) and the KEGG database (13, 14). A total of 4,258 putative genes, of which 3,811 were protein-coding genes, and a total of 5 rRNAs (four 5S rRNA genes and one 16S rRNA gene) and 45 tRNAs were found in the genome. The 45 tRNAs may be involved in the transfer of 19 amino acids.

The draft genome sequence of DY2726D included a normal complement of genes for metabolic enzymes involved in glycolysis, carbohydrate utilization, and biosynthesis of amino acids and fatty acids, as well as essential genes for nucleotide metabolism, transcription, and replication. A. sediminis, which is a heterotrophic anaerobic bacterium, harbors genes that encode a large number of hydrolases, such as glucosidase,
β-galactosidase, chitinase, cellulose, protease, peptidase, and related substrate transporters. It is also able to grow heterotrophically on glucose, fructose, fumarate, or malate but may also use glycine or betaine as energy and carbon sources, as gene clusters coding for a glycine and betaine reductase are encoded. A. sediminis possesses a complete tricarboxylic acid (TCA) cycle, a modified Embden-Meyerhof pathway to glycolysis, and metabolism pathways for proteins and carbohydrates. Genome analysis also revealed the presence of genes encoding the Rnf complex and genes involved in quinone biosynthesis but the absence of cytochrome c synthesis genes. The respiration system is represented by membrane-bound iron-only hydrogenase and F1F0-type ATP synthase.

The genome of strain DY2726D will contribute to the increasing scope and depth of the *Clostridiaceae* genome database and may shed light on the marine environmental adaptation mechanisms and evolutionary history of *Clostridiaceae*.

**Accession number(s).** This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession no. NIBG00000000. The version described in this paper is the first version, NIBG01000000. Data also have been deposited under BioProject no. PRJNA387640 and RefSeq accession no. NZ_NIBG00000000.

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**REFERENCES**

1. Stieb M, Schink B. 1985. Anaerobic oxidation of fatty acids by *Clostridium bryanti* sp. nov. a sporeforming, obligately syntrophic bacterium. Arch Microbiol 140:387–390.  https://doi.org/10.1007/BF00446983.
2. Wery N, Moricet JM, Huff J, Pignet P, Lesongeur F, Cambon-Bonavita MA, Barbier G. 2001. *Caloranaerobacter azorenisis* gen. nov. sp. nov., an anaerobic thermophilic bacterium isolated from a deep-sea hydrothermal vent. Int J Syst Evol Microbiol 51:1789–1796.  https://doi.org/10.1099/00207713-51-5-1789.
3. Li G, Zeng X, Liu X, Zhang X, Shao Z. 2016. *Wukongibacter baidiensis* gen. nov., sp. nov., an anaerobic bacterium isolated from Indian Ocean, and proposal for the reclassification of the closely related members, *Clostridium halophilum* and *Clostridium caminithermale* into *Maledivibacter* gen. nov. and *Paramedivibacter* gen. nov. respectively. Int J Syst Evol Microbiol 66:4355–4361.  https://doi.org/10.1099/ijsem.0.001355.
4. Takai K, Moser DP, Onstott TC, Spoelstra N, Pfiffner SM, Dohnalkova A, Fredrickson JK. 2001. *Alkaliphilus transvaalensis* gen. nov., sp. nov., an extremely alkaliphilic bacterium isolated from a deep South African gold mine. Int J Syst Evol Microbiol 51:1245–1256.  https://doi.org/10.1099/00207713-51-4-1245.
5. Zhang X, Zeng X, Li X, Alain K, Jebar M, Shao Z. 2017. *Anaeromicrobiubium sediminis* gen. nov., sp., nov., a fermentative bacterium isolated from deep-sea sediment. Int J Syst Evol Microbiol 67:1462–1467.  https://doi.org/10.1099/ijsem.0.017739.
6. Luo R, Liu B, Xie Y, Li Z, Huang W, Yuan J, He G, Chen Y, Pan Q, Liu Y, Tang J, Wu G, Zhang H, Shi Y, Liu Y, Yu C, Wang B, Lu Y, Han C, Cheung DW, Yiu SM, Peng S, Xiaoqian Z, Liu G, Liao X, Li Y, Yang H, Wang J, Lam TW, Wang J. 2012. SOAPdenovo2: an empirically improved memory-efficient short-read de novo assembler. Gigascience 1:18–18.  https://doi.org/10.1186/2047-217X-1-18.
7. Delcher AL, Harmon D, Kasif S, White O, Salzberg SL. 1999. Improved microbial gene identification with Glimmer. Nucleic Acids Res 27: 4636–4641.  https://doi.org/10.1093/nar/27.23.4636.
8. Delcher AL, Bratke KA, Powers EC, Salzberg SL. 2007. Identifying bacterial genes and endosymbiont DNA with Glimmer. Bioinformatics 23: 673–679.  https://doi.org/10.1093/bioinformatics/btm009.
9. Angiuoli SV, Gussman A, Klimke W, Cochrane G, Field D, Garrity GM, Kodira CD, Kyripides 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.  https://doi.org/10.1089/omi.2008.0017.
10. Lowe TM, Eddy SR. 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Res 25:955–964.
11. Lagesen K, Hallin P, Redland EA, Stærfeldt HH, Rognes T, Ussery DW. 2007. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. Nucleic Acids Res 35:3100–3108.  https://doi.org/10.1093/nar/gkm160.
12. Tatusov RL, Natale DA, Garkavtsev IV, Tatusova TA, Shankavaram UT, Rao BS, Kyrutin B, Galperin MY, Federova ND, Koonin, Ev. 2001. The COG database: new developments in phylogenetic classification of proteins from complete genomes. Nucleic Acids Res 29:22–28.  https://doi.org/10.1093/nar/29.1.22.
13. Kanehisa M, Araki M, Goto S, Hattori M, Hirakawa M, Itoh M, Katayama T, Kawashima S, Okuda S, Tokimatsu T, Yamanishi Y. 2008. KEGG for linking genomes to life and the environment. Nucleic Acids Res 36:D480–D484.  https://doi.org/10.1093/nar/gkm882.
14. Moriya Y, Itoh M, Okuda S, Yamanishi A. 2007. KAAS: an automatic genome annotation and pathway reconstruction server. Nucleic Acids Res 35:W182–W185.  https://doi.org/10.1093/nar/gkm321.