Genome Sequence of Uric Acid-Fermenting Eubacterium angustum DSM 1989T (MK-1)

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ABSTRACT Eubacterium angustum DSM 1989T (MK-1) is a strictly anaerobic and uric acid-, xanthine-, and guanine-fermenting organism isolated from sewage sludge. The draft genome consists of one circular chromosome (2.4 Mb) and harbors 2,397 predicted protein-encoding genes.

Only a few organisms are able to use purines as sole sources of carbon, nitrogen, and energy (1). Among these, anaerobic spore-forming bacteria Gottschalkia acidurici (formerly Clostridium acidurici) (2–4), Clostridium cylindrosporum (2, 3, 5), and Gottschalkia purinilytica (formerly Clostridium purinilyticum) (6) are obligately purinolytic, i.e., are nutritionally restricted to the degradation of purines (7). Eubacterium angustum is similar to these organisms in its nutritional properties but is unable to form spores, and it therefore has been classified into a different genus (8). E. angustum is a strictly anaerobic Gram-positive, non-spore-forming, and nonmotile bacterium, although flagella have been described (8). It is able to ferment uric acid, xanthine, and guanine. E. angustum has been isolated from sludge of the sewage plant in Göttingen, Germany (8). Here, we report the genome sequence of the type strain E. angustum DSM 1989 (MK-1).

Chromosomal DNA of E. angustum DSM 1989T (MK-1) was isolated using the MasterPure complete DNA purification kit (Epicentre, Madison, WI, USA). The extracted DNA was used to generate Illumina shotgun paired-end sequencing libraries, which were sequenced with a MiSeq instrument and the MiSeq reagent kit version 3, as recommended by the manufacturer (Illumina, San Diego, CA, USA). Quality filtering using Trimmomatic version 0.32 (9) resulted in 2,751,284 paired-end reads. The assembly was performed with the SPAdes genome assembler software version 3.9.0 (10). The assembly resulted in 93 contigs (>500 bp) and an average coverage of 225-fold. The assembly was validated and the read coverage determined with QualiMap version 2.1 (11). The draft genome of E. angustum DSM 1989T (MK-1) consists of a single chromosome (2,404,661 bp), with an overall G+C content of 43.67%. Automatic gene prediction and identification of rRNA and tRNA genes were performed using the software tool Prokka (12). The draft genome contained 9 rRNA genes, 73 tRNA genes, 1,764 protein-encoding genes with predicted functions, and 633 genes coding for hypothetical proteins.

In contrast to Gottschalkia acidurici 9a (13), the genome of E. angustum DSM 1989T harbors a gene cluster encoding the glycine reductase complex, which can be used for energy conservation. The gene arrangement in the cluster is very similar to that in other purinolytic bacteria, such as C. cylindrosporum DSM 605 (14) and G. purinilytica DSM 1384 (15), and in the amino acid-degrading Eubacterium acidaminophilum DSM 3953 (16) and Clostridium litorale DSM 5388 (17). Analysis of the genome also revealed the

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genes encoding electron-bifurcating formate dehydrogenase, which has been recently described in *G. acidurici* (18). This cluster shows an organization very similar to that found in *G. acidurici* (13) and *G. purinilytica* (15) but lacks the second copy of the formate dehydrogenase gene (*fdhF*). The cluster from *E. angustum* DSM 1989T also does not contain the second copy of the rubredoxin gene (*rbr*), which is present in the genome of *G. purinilytica* (15). The genome sequence of *E. angustum* will be used to clarify the phylogenetic position of this organism.

**Accession number(s).** The whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession no. MKIE00000000. The version described here is version MKIE01000000.

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**REFERENCES**

1. Andreesen JR. 2005. Degradation of heterocyclic compounds, p 221–238. In Dürre P (ed), Handbook on clostridia. CRC Press, Boca Raton, FL.

2. Barker HA, Beck JV. 1941. The fermentative decomposition of purines by *Clostridium acidi-urici* and *Clostridium cylindrosporum*. J Biol Chem 141:3–27.

3. Barker HA, Beck JV. 1942. *Clostridium acidi-urici* and *Clostridium cylindrosporum*, organisms fermenting uric acid and some other purines. J Bacteriol 43:291–304.

4. Andreesen JR, Zindel U, Dürre P. 1985. *Clostridium cylindrosporum* (ex Barker and Beck 1942) nom. rev. Int J Syst Bacteriol 35:206–208. https://doi.org/10.1111/j.1462-2920.1985.tb00997.x.

5. 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.

6. Dürre P, Andersch W, Andreesen JR. 1981. Isolation and characterization of an adenine-utilizing, anaerobic sporeformer, *Clostridium purinolyticum* sp. nov. Int J Syst Bacteriol 31:184–194. https://doi.org/10.1099/00207713-31-2-184.

7. Schiefer-Ullrich H, Wagner R, Dürre P, Andreesen JR. 1984. Comparative studies on physiology and taxonomy of obligately purinolytic clostridia. Arch Microbiol 138:345–353. https://doi.org/10.1007/BF00410902.

8. Beuscher HU, Andreesen JR. 1984. *Eubacterium angustum* sp. nov., a Gram-positive anaerobic, non-sporeforming, obligate purine fermenting organism. Arch Microbiol 140:2–8. https://doi.org/10.1007/BF00409763.

9. Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics 30:2114–2120. https://doi.org/10.1093/bioinformatics/btu170.

10. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Pyshkin AV, Pyshkin 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. https://doi.org/10.1089/cmb.2012.0021.

11. García-Alcalde F, Okonechnikov K, Carbonell J, Cruz LM, Götz S, Tarazona S, Dopazo J, Meyer TF, Conesa A. 2012. QualiMap: evaluating next-generation sequencing alignment data. Bioinformatics 28:2678–2679. https://doi.org/10.1093/bioinformatics/bts303.

12. Seemann T. 2014. Prokka: rapid prokaryotic genome annotation. Bioinformatics 30:2068–2069. https://doi.org/10.1093/bioinformatics/btu153.

13. Hartwich K, Poehlein A, Daniel R. 2012. The purine-utilizing bacterium *Clostridium acidurici* 9a: a genome-guided metabolic reconsideration. PLoS One 7:e51662. https://doi.org/10.1371/journal.pone.0051662.

14. Poehlein A, Montoya Solano JD, Bengelsdorf FR, Schiel-Bengelsdorf B, Daniel R, Dürre P. 2015. Draft genome sequence of purine-degrading *Clostridium cylindrosporum* HC-1 (DSM 605). Genome Announc 3(4):e00917-15. https://doi.org/10.1128/genomeA.00917-15.

15. Poehlein A, Bengelsdorf FR, Schiel-Bengelsdorf B, Daniel R, Dürre P. 2015. Draft genome sequence of purine-degrading *Gottschalkia purinilytica* (formerly *Clostridium purinilyticum*) WA1 (DSM 1384). Genome Announc 3(5):e01088-15. https://doi.org/10.1128/genomeA.01088-15.

16. Poehlein A, Andreesen JR, Daniel R. 2014. Complete genome sequence of the amino acid-utilizing *Eubacterium acidaminophilum* al-2 (DSM 3953). Genome Announc 2(3):e00573-14. https://doi.org/10.1128/genomeA.00573-14.

17. Poehlein A, Alghaithi HS, Chandran L, Chibani CM, Davyodova E, Dhamotharan K, Ge W, Gutierrez-Gutierrez DA, Jagirdar A, Khonsari B, Nair KP, Daniel R. 2014. First insights into the genome of the amino acid-metabolizing bacterium *Clostridium litoreum* DSM 5388. Genome Announc 2(4):e00754-14. https://doi.org/10.1128/genomeA.00754-14.

18. Wang S, Huang H, Kahnt J, Thauer RK. 2013. *Clostridium acidurici* electron-bifurcating formate dehydrogenase. Appl Environ Microbiol 79:6176–6179. https://doi.org/10.1128/AEM.02015-13.