



Complete Genome Sequence of the Facultative Methylophile *Methylobacterium extorquens* TK 0001 Isolated from Soil in Poland

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ABSTRACT *Methylobacterium extorquens* TK 0001 (DSM 1337, ATCC 43645) is an aerobic pink-pigmented facultative methylotrophic alphaproteobacterium isolated from soil in Poland. Here, we report the whole-genome sequence and annotation of this organism, which consists of a single 5.71-Mb chromosome.

The genus *Methylobacterium* contains rod-shaped Gram-negative bacteria and belongs to the family *Rhizobiales*. The members of this group of microorganisms are able to grow on reduced C₁ compounds such as methane, methanol, and methylamine as sole carbon and energy sources (1, 2). They have been isolated from diverse soil, air, and water environments (3). *Methylobacterium extorquens* TK 0001 was isolated from soil in Poland (4, 5).

M. extorquens TK 0001 was obtained from the DSMZ (Braunschweig, Germany) and was grown at 30°C in a minimal medium (DSMZ medium no. 1629) supplemented with 1% methanol. Genomic DNA was purified using the GenElute bacterial genomic DNA kit (Sigma). Genome sequencing was performed at Genoscope, using both Illumina and Nanopore technologies (6, 7). First, the long reads generated by the MinION device (Oxford Nanopore Technologies) were corrected using Canu software (8). The corrected reads were assembled using smartdenovo (<https://github.com/ruanjue/smartdenovo>), and the resulting assembly was then polished with the help of 2 × 150-bp paired-end reads generated by a MiSeq sequencer (Illumina) with a genome coverage of ~134×. The final assembly was composed of a single contig of 5.71 Mb with a GC content of 68.2%. Automatic functional annotation and comparative genome analysis were performed using the MicroScope platform (<http://www.genoscope.cns.fr/agc/microscope>) (9). In total, 6,251 genomic objects were identified comprising 6,160 coding sequences (CDSs), 17 miscellaneous RNAs, 59 tRNAs, and 15 rRNAs (5 5S, 5 16S, and 5 23S). The *M. extorquens* TK 0001 genome contains the *mx* gene clusters (*mx**ABCD* and *mx**FJGIR*) coding for methanol dehydrogenase and for enzymes involved in the synthesis of the periplasmic pyrroloquinoline quinone electron carrier. No methylamine dehydrogenase was found. The enzymes for the *N*-methylglutamate pathway, *mgsABC* and *gmaS*, are present, accounting for the growth on methylamine (10). Genes for the serine cycle and the ethylmalonyl-coenzyme A pathway implicated in C₁ assimilation are specified. *M. extorquens* TK 0001 is a facultative methylotroph growing also on complex carbon sources. Accordingly, the Entner-Doudoroff pathway and the pentose phosphate pathway are predicted, as well as the oxidative tricarboxylic acid cycle.

A comparative genome analysis was performed between TK 0001 and *M. extorquens* strains AM1, PA1, CM4, and DM4 showing that these strains are strongly related. A

Received 9 January 2018 Accepted 11 January 2018 Published 22 February 2018

Citation Belkhef S, Labadie K, Cruaud C, Aury J-M, Roche D, Bouzon M, Salanoubat M, Döring V. 2018. Complete genome sequence of the facultative methylotroph *Methylobacterium extorquens* TK 0001 isolated from soil in Poland. Genome Announc 6:e00018-18. <https://doi.org/10.1128/genomeA.00018-18>.

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fraction of 24.3% of the CDSs is specific to *M. extorquens* strain TK 0001, and 61.9% of the CDSs correspond to the core genome of this group of organisms.

Accession number(s). This whole-genome project has been deposited in DDBJ/EMBL/GenBank under the accession no. [LT962688](https://doi.org/10.1093/bib/bbx062).

ACKNOWLEDGMENTS

This work was financially supported by a CEA internal research project joining the Fundamental Research Division (DRF) and the Technological Research Division (DRT). The LABGeM (CEA/IG/Genoscope and CNRS UMR 8030) and the France Génomique national infrastructure (funded as part of Investissements d'Avenir program managed by the Agence Nationale pour la Recherche, contract ANR-10-INBS-09) are acknowledged for support within the MicroScope annotation platform and many other functionalities of the system.

REFERENCES

1. Anthony C. 1982. The biochemistry of methylotrophs. Academic Press, New York, NY.
2. Schrader J, Schilling M, Holtmann D, Sell D, Filho MV, Marx A, Vorholt JA. 2009. Methanol-based industrial biotechnology: current status and future perspectives of methylotrophic bacteria. *Trends Biotechnol* 27: 107–115. <https://doi.org/10.1016/j.tibtech.2008.10.009>.
3. Lidstrom ME. 2006. Aerobic methylotrophic prokaryotes. Springer, New York, NY.
4. Bousfield IJ, Green PN. 1985. Reclassification of bacteria of the genus *Protomonas* Urakami and Komagata 1984 in the genus *Methylobacterium* (Patt, Cole, and Hanson) emend. Green and Bousfield 1983. *Int J Syst Bacteriol* 35:209–209. <https://doi.org/10.1099/00207713-35-2-209>.
5. Urakami T, Komagata K. 1984. *Protomonas*, a new genus of facultatively methylotrophic bacteria. *Int J Syst Bacteriol* 34:188–201. <https://doi.org/10.1099/00207713-34-2-188>.
6. Magi A, Semeraro R, Mingrino A, Giusti B, D'Aurizio R. 2017. Nanopore sequencing data analysis: state of the art, applications and challenges. *Brief Bioinform* <https://doi.org/10.1093/bib/bbx062>.
7. Madoui MA, Engelen S, Cruaud C, Belser C, Bertrand L, Alberti A, Lemainque A, Wincker P, Aury JM. 2015. Genome assembly using nanopore-guided long and error-free DNA reads. *BMC Genomics* 16:327. <https://doi.org/10.1186/s12864-015-1519-z>.
8. Koren S, Walenz BP, Berlin K, Miller JR, Bergman NH, Phillippy AM. 2017. Canu: scalable and accurate long-read assembly via adaptive *k*-mer weighting and repeat separation. *Genome Res* 27:722–736. <https://doi.org/10.1101/gr.215087.116>.
9. Vallenet D, Calteau A, Cruveiller S, Gachet M, Lajus A, Josso A, Mercier J, Renaux A, Rollin J, Rouy Z, Roche D, Scarpelli C, Médigue C. 2017. MicroScope in 2017: an expanding and evolving integrated resource for community expertise of microbial genomes. *Nucleic Acids Res* 45: D517–D528. <https://doi.org/10.1093/nar/gkw1101>.
10. Nayak DD, Marx CJ. 2014. Methylamine utilization via the *N*-methylglutamate pathway in *Methylobacterium extorquens* PA1 involves a novel flow of carbon through C₁ assimilation and dissimilation pathways. *J Bacteriol* 196:4130–4139. <https://doi.org/10.1128/JB.02026-14>.