



Draft Genome Sequence of the Psychrotolerant Bacterium *Methylobacterium* sp. Strain BTF04, Isolated from Freshwater in Antarctica

Ahna Cho,^a Yong-Joon Cho,^{a,b} Soyeon Kim,^a Ok-Sun Kim^a

^aDivision of Polar Life Sciences, Korea Polar Research Institute, Incheon, Republic of Korea

^bDepartment of Biological Sciences and Research Institute of Basic Sciences, Seoul National University, Seoul, Republic of Korea

ABSTRACT *Methylobacterium* sp. strain BTF04, a pink-pigmented psychrotolerant bacterium, was isolated from freshwater on Barton Peninsula, King George Island, Antarctica. Here, we report the assembled draft genome sequence of *Methylobacterium* sp. strain BTF04.

Methylobacterium sp. strain BTF04, belonging to the class *Alphaproteobacteria*, was isolated from a freshwater (wetland) sample collected on Barton Peninsula, King George Island, Antarctica (62°14'17.0"S, 58°43'46.6"W) on 25 January 2015. This wetland is produced by melting snow and ice during the Antarctic summer period (December to February). The genus *Methylobacterium* has potential for ecological contributions to the promotion of plant growth, biotechnology, and biodegradation. In particular, this group can be used to remove environmental contamination due to its ability to biodegrade toxic substances and its resistance to heavy metal (1).

Interestingly, the growth temperature of the genus *Methylobacterium* ranges from 15°C to 35°C, and the species belonging to this genus have been found in various terrestrial habitats, such as leaf surfaces and nodules, soil, dust, freshwater, Antarctic subglacial lakes, drinking water, and oil-contaminated sites (2–5). However, unlike other strains, BTF04 was cultivated at 10°C on a 0.1% R2A agar plate. This strain was closely related to the *M. goeisingense* iE113 type strain and the *M. adhaesivum* AR27 type strain at 99.36% and 99.35%, respectively, by 16S ribosomal DNA typing using universal 27F-1492R primers and the EzTaxon-e database (6). Here, we report the genome sequence of the psychrotolerant bacterium *Methylobacterium* sp. strain BTF04.

Genomic DNA was extracted from *Methylobacterium* sp. strain BTF04 using a PowerSoil DNA isolation kit (Qiagen, USA). A DNA library for next-generation sequencing (NGS) was prepared using a Nextera DNA Flex library prep kit (catalog number 20018704; Illumina, USA) following the manufacturer's protocol. The sequencing was performed by Illumina MiSeq with 300-bp paired-end cycles. Raw data of 185,394 paired-end reads were obtained, and adapter removal and quality-trimming were performed using Trimmomatic v0.36 with default parameters (7). Assembly was performed using SPAdes v3.11.0 in multicell mode, along with read error and mismatch correction (8). As a result of the assembly, a 5,188,880-bp genome was obtained with 259 contigs, an N_{50} value of 103,303 bp, a GC content of 66.5%, and genome coverage of 21.44×. Gene prediction and annotation were performed using the NCBI Prokaryotic Genome Annotation Pipeline v4.11 (9), and functional annotation and KEGG pathway mapping were performed using BlastKOALA v2.2 against the "species_prokaryotes" database (10). The genome has a total of 4,921 genes, including 4,865 coding genes, 3 rRNAs, 49 tRNAs, 4 noncoding RNAs (ncRNAs), and 172 pseudogenes.

Many *Methylobacterium* species are known for their metal tolerance, and the genome of *Methylobacterium* sp. strain BTF04 also has genes involved in heavy metal

Citation Cho A, Cho Y-J, Kim S, Kim O-S. 2020. Draft genome sequence of the psychrotolerant bacterium *Methylobacterium* sp. strain BTF04, isolated from freshwater in Antarctica. *Microbiol Resour Announc* 9:e00171-20. <https://doi.org/10.1128/MRA.00171-20>.

Editor Catherine Putonti, Loyola University Chicago

Copyright © 2020 Cho et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Ok-Sun Kim, oskim@kopri.re.kr.

Received 25 February 2020

Accepted 26 April 2020

Published 21 May 2020

resistance, such as heavy metal translocating P-type ATPase (*G3T14_24095*), CusA/CzcA family heavy metal efflux RND transporter (*G3T14_19645*), nickel-responsive transcriptional regulator NikR (*G3T14_03080* and *G3T14_22525*), nickel transporter (*G3T14_00040* and *G3T14_10395*), cobalt transporter (*G3T14_12875*), nickel/cobalt efflux transporter RcnA (*G3T14_18340*), and cadmium-translocating P-type ATPase (*G3T14_20510*). There are three genes encoding cold shock protein (*G3T14_12600*, *G3T14_14945*, and *G3T14_16670*), which are supposed to help in adaptation to low-temperature environments, such as Antarctica. The genome information from strain BTF04, a *Methylobacterium* strain specialized in cold environments, gives insights into this microorganism's strategy for survival in its habitat and is useful for comparative genomics of this genus, which is found everywhere on our planet.

Data availability. The genome sequences and annotations were deposited in GenBank under the accession number [JAAHTB000000000](#) and can be found under BioProject accession number [PRJNA605674](#).

ACKNOWLEDGMENT

This work was supported by the Korea Polar Research Institute (grant numbers PE20170 and PE20130).

REFERENCES

1. Dourado MN, Camargo Neves AA, Santos DS, Araújo WL. 2015. Biotechnological and agronomic potential of endophytic pink-pigmented methylotrophic *Methylobacterium* spp. *Biomed Res Int* 2015:909016. <https://doi.org/10.1155/2015/909016>.
2. Gallego V, García MT, Ventosa A. 2006. *Methylobacterium adhaesivum* sp. nov., a methylotrophic bacterium isolated from drinking water. *Int J Syst Evol Microbiol* 56:339–342. <https://doi.org/10.1099/ijs.0.63966-0>.
3. Green PN, Bousfield IJ. 1981. The taxonomy of pink-pigmented facultatively methylotrophic bacteria, p 285–293. *In* Dalton H (ed), *Microbial growth on C1-compounds*. Heyden, London, United Kingdom.
4. Idris R, Kuffner M, Bodrossy L, Puschenreiter M, Monchy S, Wenzel WW, Sessitsch A. 2006. Characterization of Ni-tolerant methylotrophs associated with the hyperaccumulating plant *Thlaspi goesingense* and description of *Methylobacterium goesingense* sp. nov. *Syst Appl Microbiol* 29:634–644. <https://doi.org/10.1016/j.syapm.2006.01.011>.
5. Madhaiyan M, Poonguzhali S, Senthilkumar M, Lee J-S, Lee K-C. 2012. *Methylobacterium gossipiicola* sp. nov., a pink-pigmented, facultatively methylotrophic bacterium isolated from the cotton phyllosphere. *Int J Syst Evol Microbiol* 62:162–167. <https://doi.org/10.1099/ijs.0.030148-0>.
6. Kim O-S, Cho Y-J, Lee K, Yoon S-H, Kim M, Na H, Park S-C, Jeon YS, Lee J-H, Yi H, Won S, Chun J. 2012. Introducing EzTaxon-e: a prokaryotic 16S rRNA gene sequence database with phylotypes that represent uncultured species. *Int J Syst Evol Microbiol* 62:716–721. <https://doi.org/10.1099/ijs.0.038075-0>.
7. 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>.
8. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Pribelski 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. <https://doi.org/10.1089/cmb.2012.0021>.
9. Tatusova T, DiCuccio M, Badretdin A, Chetverin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI Prokaryotic Genome Annotation Pipeline. *Nucleic Acids Res* 44:6614–6624. <https://doi.org/10.1093/nar/gkw569>.
10. Kanehisa M, Sato Y, Morishima K. 2016. BlastKOALA and GhostKOALA: KEGG tools for functional characterization of genome and metagenome sequences. *J Mol Biol* 428:726–731. <https://doi.org/10.1016/j.jmb.2015.11.006>.