



Complete Genome Sequence of *Methanobrevibacter smithii* Strain KB11, Isolated from a Korean Fecal Sample

Byoung-Chan Kim,^{a,c} Haeyoung Jeong^{b,d}

^aMetabolic Regulation Research Center, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Daejeon, Republic of Korea

^bInfectious Disease Research Center, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Daejeon, Republic of Korea

^cDepartment of Bioprocess Engineering, KRIBB School of Biotechnology, Korea University of Science and Technology (UST), Daejeon, Republic of Korea

^dDepartment of Biosystems and Bioengineering, KRIBB School of Biotechnology, Korea University of Science and Technology (UST), Daejeon, Republic of Korea

ABSTRACT The archaeon *Methanobrevibacter smithii* is a major colonizer of the human gut. *Methanobrevibacter smithii* strain KB11 was newly isolated from a Korean fecal sample. Here, we present the complete genome sequence of strain KB11 and a brief comparison with that of *M. smithii* type strain ATCC 35061^T.

Methanobrevibacter is a fastidious archaeal microorganism and obligate anaerobe. It can be cultivated in a pressurized anaerobic atmosphere of 80% hydrogen and 20% carbon dioxide (1, 2). Among *Methanobrevibacter* species, *M. smithii* is a near-ubiquitous resident of the human intestinal microbiome (3). The prevalence of methanogens in humans has been reported to be dependent on the age of the human host; populations increase gradually throughout childhood, reaching a maximum abundance level in adults (3, 4). *Methanobrevibacter smithii* may impact human health (5, 6), but its beneficial effect is still questionable. In the course of an investigation into the diversity of methanogens in the human gut, feces were collected with an anaerobic sampling system (7) and were maintained under strict anaerobic conditions, as previously described (8). A methanogenic strain, KB11, was purified from the feces of a healthy 43-year-old Korean male. This is the first human gut methanogen isolated from South Korea.

The genomic DNA of KB11 was extracted as previously described (2). Complete genome sequencing was carried out using Illumina MiSeq and PacBio RS II platforms, as recommended by the manufacturers, at ChunLab, Inc. (Seoul, Republic of Korea). A hybrid assembly was performed using SPAdes v3.9.0 (<http://cab.spbu.ru/software/spades/>) from a total of 1.98 Gb MiSeq reads (average length, 192.6 bp) and 850 Mb of PacBio RS II filtered subreads (mean length, 8,534 bp; N_{50} , 11,609 bp), generated by HGAP 2.0. The largest contig (1.81-Mb long) was cut into pieces and joined using the CLC Genomics Workbench v9.5.1 (Qiagen Bioinformatics, Aarhus, Denmark), allowing the finalized sequence to begin with the *dnaA* gene. Self-corrected PacBio long reads were used for fragment joining and confirmation of the circular structure of the chromosomal contig. Residual errors were corrected by three successive rounds of MiSeq read mapping and consensus sequence extraction. Genome sequences were annotated using the NCBI Prokaryotic Genome Annotation Pipeline (https://www.ncbi.nlm.nih.gov/genome/annotation_prok/) and the Rapid Annotations using Subsystems Technology (RAST) server (9). To the best of our knowledge, this is the first reported publicly available complete genome sequence of *Methanobrevibacter smithii* isolated from a human gut (*M. smithii* ATCC 35061^T was isolated from a sewage digester [10]).

Received 11 January 2018 Accepted 16 January 2018 Published 15 February 2018

Citation Kim B-C, Jeong H. 2018. Complete genome sequence of *Methanobrevibacter smithii* strain KB11, isolated from a Korean fecal sample. Genome Announcements 6:e00038-18. <https://doi.org/10.1128/genomeA.00038-18>.

Copyright © 2018 Kim and Jeong. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International license.

Address correspondence to Byoung-Chan Kim, bckim@kribb.re.kr, or Haeyoung Jeong, hyjeong@kribb.re.kr.

The KB11 genome has a 1,805,545-bp chromosome (31.2% G+C), which is 47,615 bp smaller than that of ATCC 35061^T. Despite the overall similarity, we found an inversion (699958 to 1484782) in the ATCC 35061^T chromosome that led to C-term truncation in the DNA helicase UvrD (Msm_0731). It is also noteworthy that an adhesin-like protein (Msm_0173, 2,879 amino acids [aa]) in ATCC 35061^T has 17 DUF11 domains (pfam01345), while the KB11 homolog is disrupted with a frameshift (BK798_03360). A KB11-specific region (500216 to 523396) was also found to accommodate genes encoding hypothetical proteins, a type I restriction-modification system, and transposases.

This additional genome information may be used to improve our understanding of the genetic diversity of human gut-associated *M. smithii* within individuals. This knowledge will enhance studies concerning the archaeal gut microbiota and human physiology, especially with respect to human health and disease.

Accession number(s). The complete genome sequences of *Methanobrevibacter smithii* KB11 have been deposited in DDBJ/ENA/GenBank under the accession number CP017803.

ACKNOWLEDGMENTS

This work was supported by the KRIBB Research Initiative Program, the Ministry of Science and ICT, Republic of Korea, and was partially supported by grants from the National Research Foundation of Korea (NRF) (2015M3C9A4053394) and from the Korea Health Technology R&D Project (HI14C0368).

REFERENCES

- Balch WE, Wolfe RS. 1976. New approach to the cultivation of methanogenic bacteria: 2-mercaptoethanesulfonic acid (HS-CoM)-dependent growth of *Methanobacterium ruminantium* in a pressurized atmosphere. *Appl Environ Microbiol* 32:781–791.
- Lee JH, Kumar S, Lee GH, Chang DH, Rhee MS, Yoon MH, Kim BC. 2013. *Methanobrevibacter boviskoreani* sp. nov., isolated from the rumen of Korean native cattle. *Int J Syst Evol Microbiol* 63:4196–4201. <https://doi.org/10.1099/ijs.0.054056-0>.
- Dridi B, Henry M, El Khéchine A, Raoult D, Drancourt M. 2009. High prevalence of *Methanobrevibacter smithii* and *Methanosphaera stadtmanae* detected in the human gut using an improved DNA detection protocol. *PLoS One* 4:e7063. <https://doi.org/10.1371/journal.pone.0007063>.
- Mihajlovski A, Doré J, Levenez F, Alric M, Brugère JF. 2010. Molecular evaluation of the human gut methanogenic archaeal microbiota reveals an age-associated increase of the diversity. *Environ Microbiol Rep* 2:272–280. <https://doi.org/10.1111/j.1758-2229.2009.00116.x>.
- Le Chatelier E, Nielsen T, Qin J, Prifti E, Hildebrand F, Falony G, Almeida M, Arumugam M, Batto J-M, Kennedy S, Leonard P, Li J, Burgdorf K, Grarup N, Jørgensen T, Brandslund I, Nielsen HB, Juncker AS, Bertalan M, Levenez F, Pons N, Rasmussen S, Sunagawa S, Tap J, Tims S, Zoetendal EG, Brunak S, Clément K, Doré J, Kleerebezem M, Kristiansen K, Renault P, Sicheritz-Ponten T, de Vos WM, Zucker J-D, Raes J, Hansen T; MetaHIT consortium, Bork P, Wang J, Ehrlich SD, Pedersen O. 2013. Richness of human gut microbiome correlates with metabolic markers. *Nature* 500:541–546. <https://doi.org/10.1038/nature12506>.
- Ghoshal U, Shukla R, Srivastava D, Ghoshal UC. 2016. Irritable bowel syndrome, particularly the constipation-predominant form, involves an increase in *Methanobrevibacter smithii*, which is associated with higher methane production. *Gut Liver* 10:932–938. <https://doi.org/10.5009/gnl15588>.
- Chang DH, Rhee MS, Kim BC. 2016. *Dermabacter vaginalis* sp. nov., isolated from human vaginal fluid. *Int J Syst Evol Microbiol* 66:1881–1886. <https://doi.org/10.1099/ijsem.0.000960>.
- Ahn S, Jin TE, Chang DH, Rhee MS, Kim HJ, Lee SJ, Park DS, Kim BC. 2016. *Agathobaculum butyriciproducens* gen. nov. & sp. nov., a strict anaerobic, butyrate-producing gut bacterium isolated from human faeces and reclassification of *Eubacterium desmolans* as *Agathobaculum desmolans* comb. nov. *Int J Syst Evol Microbiol* 66:3656–3661. <https://doi.org/10.1099/ijsem.0.001195>.
- Overbeek R, Olson R, Pusch GD, Olsen GJ, Davis JJ, Disz T, Edwards RA, Gerdes S, Parrello B, Shukla M, Vonstein V, Wattam AR, Xia F, Stevens R. 2014. The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). *Nucleic Acids Res* 42:D206–D214. <https://doi.org/10.1093/nar/gkt1226>.
- Bryant MP, Tzeng SF, Robinson IM, Joiner AEJ. 1971. Nutrient requirements of methanogenic bacteria, p 23–40. *In* Pohland FG (ed), *Anaerobic biological treatment processes*. American Chemical Society, Washington, DC.