




Complete Genome Sequence of *Blautia producta* JCM 1471^T

Dieter M. Tourlousse,^a  Mitsuo Sakamoto,^b Takamasa Miura,^c Koji Narita,^d Akiko Ohashi,^a Yoshihito Uchino,^c Atsushi Yamazoe,^c Keishi Kameyama,^d Jun Terauchi,^d Moriya Ohkuma,^b Hiroko Kawasaki,^c Yuji Sekiguchi^a

^aBiomedical Research Institute, National Institute of Advanced Industrial Science and Technology (AIST), Tsukuba, Ibaraki, Japan

^bMicrobe Division/Japan Collection of Microorganisms, RIKEN BioResource Research Center, Tsukuba, Ibaraki, Japan

^cBiological Resource Center, National Institute of Technology and Evaluation (NITE), Kisarazu, Chiba, Japan

^dJapan Microbiome Consortium (JMBC), Osaka, Osaka, Japan

ABSTRACT We report a complete genome sequence of *Blautia producta* JCM 1471^T. The genome consists of a single circular chromosome of 6,197,116 bp with a G+C content of 45.7%. The genome was annotated as containing 5 complete sets of rRNA genes, 70 tRNA genes, and 5,516 protein-coding sequences.

The genus *Blautia* comprises some of the most abundant bacteria in the human gastrointestinal tract (1). *Blautia* spp. are thought to be important players in human health and disease based on the correlation between *Blautia* abundance and various health conditions, including diminished abundance in the elderly (2) and in patients with colorectal cancer (3). An abundance of *Blautia* was also associated with risk of death from acute graft-versus-host disease (4) and visceral fat accumulation (5). Within the genus, *Blautia producta* was identified as a key species responsible for restoration of colonization resistance against vancomycin-resistant enterococci (6), which was attributed to secretion of a lantibiotic (7). Here, we used Illumina and Oxford Nanopore Technologies (ONT) sequencing to generate a complete genome sequence of *B. producta* JCM 1471^T, the authentic type strain of *B. producta*, formerly known as *Ruminococcus productus* (8).

Cells were obtained from the Japan Collection of Microorganisms and cultured under an N₂ atmosphere in modified GAM broth with 1% glucose; DNA was purified using the EZ1 DNA tissue kit (Qiagen). Short-read Illumina libraries were constructed with the TruSeq Nano DNA kit and sequenced on a MiSeq instrument using V2 chemistry (2 × 251-bp reads) at a coverage of ~100×. For ONT sequencing, libraries were prepared with the ligation sequencing kit (SQK-LSK109) and native barcoding expansion pack (EXP-NBD104). Sequencing was run on an R9.4.1 flow cell (FLO-MIN106) using the MinION device. Default parameters were used for all software for read processing and assembly unless indicated otherwise. Illumina sequencing reads were processed with Trimmomatic v0.38 (9), yielding 2,676,800 reads for assembly. For ONT sequencing, bases were called with Guppy v3.1.5 in high-accuracy mode, along with library demultiplexing and trimming of barcodes. After additional trimming of remaining barcodes with Porechop v0.2.4 (<https://github.com/rrwick/Porechop>) and removal of reads with a length of <1,000 bp or a quality score of <9 with NanoFilt v2.5.0 (10), Filtlong v0.2.0 (<https://github.com/rrwick/Filtlong>) was employed to eliminate the poorest 10% of read bases using the Illumina reads as references. This resulted in a total of 61,232 ONT reads with an N₅₀ value of 7,955 bp and coverage of ~70×. Hybrid assembly of the Illumina and ONT reads was performed with Unicycler v0.4.7 (11) and run in bold mode using a long-read assembly generated using Flye v2.5 (12). The NCBI Prokaryotic Genome Annotation Pipeline v4.11 (13) was used for genome annotation.

The genome assembly of *B. producta* JCM 1471^T consists of a single circular chromosome with a length of 6,197,116 bp and a G+C content of 45.7%. Annotation

Citation Tourlousse DM, Sakamoto M, Miura T, Narita K, Ohashi A, Uchino Y, Yamazoe A, Kameyama K, Terauchi J, Ohkuma M, Kawasaki H, Sekiguchi Y. 2020. Complete genome sequence of *Blautia producta* JCM 1471^T. *Microbiol Resour Annot* 9:e00141-20. <https://doi.org/10.1128/MRA.00141-20>.

Editor David Rasko, University of Maryland School of Medicine

Copyright © 2020 Tourlousse 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 Yuji Sekiguchi, y.sekiguchi@aist.go.jp.

Received 17 February 2020

Accepted 6 April 2020

Published 23 April 2020

identified 5 complete sets of rRNA genes, along with 70 tRNA genes and 5,516 protein-coding sequences. The availability of a complete genome of *B. producta* JCM 1471^T will aid in advancing our understanding of the role of *B. producta* in the human gut by providing insights into its genomically encoded functional gene repertoire.

Data availability. The genome sequence described here has been deposited in DDBJ/EMBL/GenBank under the accession number [CP048626](https://doi.org/10.1101/2021.03.02.415862). The raw Illumina and ONT sequencing reads are available in the Sequence Read Archive (SRA) under the accession numbers [SRR10968453](https://doi.org/10.1101/2021.03.02.415845) and [SRR10968454](https://doi.org/10.1101/2021.03.02.415854), respectively.

ACKNOWLEDGMENT

This research was supported by the New Energy and Industrial Technology Development Organization (NEDO), Japan, as part of a research program for establishing standards in human microbiome community measurements.

REFERENCES

- Rajilić-Stojanović M, de Vos WM. 2014. The first 1000 cultured species of the human gastrointestinal microbiota. *FEMS Microbiol Rev* 38: 996–1047. <https://doi.org/10.1111/1574-6976.12075>.
- Odamaki T, Kato K, Sugahara H, Hashikura N, Takahashi S, Xiao JZ, Abe F, Osawa R. 2016. Age-related changes in gut microbiota composition from newborn to centenarian: a cross-sectional study. *BMC Microbiol* 16:90. <https://doi.org/10.1186/s12866-016-0708-5>.
- Chen W, Liu F, Ling Z, Tong X, Xiang C. 2012. Human intestinal lumen and mucosa-associated microbiota in patients with colorectal cancer. *PLoS One* 7:e39743. <https://doi.org/10.1371/journal.pone.0039743>.
- Jenq RR, Taur Y, Devlin SM, Ponce DM, Goldberg JD, Ahr KF, Littmann ER, Ling L, Gobourne AC, Miller LC, Docampo MD, Peled JU, Arpaia N, Cross JR, Peets TK, Lumish MA, Shono Y, Dudakov JA, Poeck H, Hanash AM, Barker JN, Perales MA, Giralt SA, Pamer EG, van den Brink MR. 2015. Intestinal *Blautia* is associated with reduced death from graft-versus-host disease. *Biol Blood Marrow Transplant* 21:1373–1383. <https://doi.org/10.1016/j.bbmt.2015.04.016>.
- Ozato N, Saito S, Yamaguchi T, Katashima M, Tokuda I, Sawada K, Katsuragi Y, Kakuta M, Imoto S, Ihara K, Nakaji S. 2019. *Blautia* genus associated with visceral fat accumulation in adults 20–76 years of age. *NPJ Biofilms Microbiomes* 5:28. <https://doi.org/10.1038/s41522-019-0101-x>.
- Caballero S, Kim S, Carter RA, Leiner IM, Sušac B, Miller L, Kim GJ, Ling L, Pamer EG. 2017. Cooperating commensals restore colonization resistance to vancomycin-resistant *Enterococcus faecium*. *Cell Host Microbe* 21:592–602. <https://doi.org/10.1016/j.chom.2017.04.002>.
- Kim SG, Becattini S, Moody TU, Shliha PV, Littmann ER, Seok R, Gjonbalaj M, Eaton V, Fontana E, Amoretti L, Wright R, Caballero S, Wang ZX, Jung HJ, Morjaria SM, Leiner IM, Qin W, Ramos RJF, Cross JR, Narushima S, Honda K, Peled JU, Hendrickson RC, Taur Y, van den Brink MRM, Pamer EG. 2019. Microbiota-derived lantibiotic restores resistance against vancomycin-resistant *Enterococcus*. *Nature* 572:665–669. <https://doi.org/10.1038/s41586-019-1501-z>.
- Liu C, Finegold SM, Song Y, Lawson PA. 2008. Reclassification of *Clostridium coccoides*, *Ruminococcus hansenii*, *Ruminococcus hydrogenotrophicus*, *Ruminococcus luti*, *Ruminococcus productus* and *Ruminococcus schinkii* as *Blautia coccoides* gen. nov., comb. nov., *Blautia hansenii* comb. nov., *Blautia hydrogenotrophica* comb. nov., *Blautia luti* comb. nov., *Blautia producta* comb. nov., *Blautia schinkii* comb. nov. and description of *Blautia wexlerae* sp. nov., isolated from human faeces. *Int J Syst Evol Microbiol* 58:1896–1902. <https://doi.org/10.1099/ijs.0.65208-0>.
- 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>.
- De Coster W, D'Hert S, Schultz DT, Cruts M, Van Broeckhoven C. 2018. NanoPack: visualizing and processing long-read sequencing data. *Bioinformatics* 34:2666–2669. <https://doi.org/10.1093/bioinformatics/bty149>.
- Wick RR, Judd LM, Gorrie CL, Holt KE. 2017. Unicycler: resolving bacterial genome assemblies from short and long sequencing reads. *PLoS Comput Biol* 13:e1005595. <https://doi.org/10.1371/journal.pcbi.1005595>.
- Kolmogorov M, Yuan J, Lin Y, Pevzner PA. 2019. Assembly of long, error-prone reads using repeat graphs. *Nat Biotechnol* 37:540–546. <https://doi.org/10.1038/s41587-019-0072-8>.
- 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>.