



Draft Genome Sequence of a Potential Commercial Biocellulose Producer, Strain *Komagataeibacter europaeus* GH1

Gulden Nagmetova,^{a,b} Kalysh Berdimuratova,^a Asylulan Amirgazin,^a Vladislav Shevtsov,^a Aisulu Ismailova,^c Yerlan Ramankulov,^{a,d} Alexandr Shevtsov,^a Askar Kurmanbayev^a

^aNational Center for Biotechnology, Nur-Sultan, Kazakhstan

^bL. N. Gumilyov Eurasian National University, Nur-Sultan, Kazakhstan

^cS. Seifullin Kazakh Agro Technical University, Nur-Sultan, Kazakhstan

^dSchool of Science and Technology, Nazarbayev University, Nur-Sultan, Kazakhstan

ABSTRACT In this work, we present the draft genome sequence of *Komagataeibacter europaeus* strain GH1, which is an extremely efficient biocellulose producer.

Acetic acid bacteria (AAB) belong to the *Alphaproteobacteria* family and have a unique metabolic system capable of producing a wide range of saccharides and vitamins and fermenting various biological substrates (1). *Komagataeibacter* spp. have applications in the industrial production of biocellulose for food, biomedicine, cosmetics, and engineering (2). Knowledge of the genomes of industrially valuable strains will increase the productivity of microorganisms and large-scale production.

A detailed description of the isolation of the *Komagataeibacter europaeus* GH1 strain was provided by Nagmetova et al. (3). Accumulated cultures have been identified to the level of the *K. europaeus* species by 16S rRNA gene sequencing using BigDye v3.1 (Applied Biosystems) with primers 8F and 806R (4, 5). The *K. europaeus* GH1 strain is capable of synthesizing a biocellulose film in Hestrin-Schramm (HS) broth with 1% ethanol (pH 4.8 at 30°C) with a peak performance after 7 days of cultivation (3). To determine strain performance, the biofilms were first washed according to the method of Stasiak-Róžańska and Ploska (6). The average productivity of biocellulose was 12 g/liter.

DNA was isolated using the DNA minikit (Qiagen). The preparation of libraries was carried out using the Nextera DNA Flex library prep kit (Illumina, USA). Sequencing was performed on a MiSeq system using MiSeq reagent kit v3 (600 cycles). The sequencing platform produced 1,893,358 paired-end reads. The reads were trimmed using Sickle v1.33 (7) up to value Q30 and *de novo* assembled using SPAdes v3.13.2 (8) with a 127 k-mer length in careful mode.

Genome annotation was performed using PGAP v4.11 (9). Determination of functional groups of genes was performed using RAST (10). The search for cellulose synthase operons was carried out using local BLAST+v2.9.0 (11). Identification of prophage sequences was carried out using the PHASTER Web service (12). All software was used with default parameters except when stated otherwise.

The draft genome assembly was obtained with a length of 3,809,040 bp and 105 contigs; the average coverage was 171×, the value of N_{50} was 64,110 bp, and the GC content was 61.5%. The annotation predicted 3,352 protein-coding genes and 58 RNA genes. The functional groups involved in carbohydrate and amino acid metabolism are the biggest and contain 187 and 248 genes, respectively. Both types of cellulose synthase operons were identified in the assembly. The *bcsI* and *bcsII* operon types are similar to those of the *K. europaeus* SRCM101446, *K. europaeus* 5P3, *K. europaeus* CECT8546, and *K. europaeus* LMG18890 strains but are in contrast to those of the *K. europaeus* LMG18494 and *K. europaeus* NBRC3261 strains, which are characterized by the absence of the *bcsII* type operon and have two major deletions in the *bcsC* gene

Citation Nagmetova G, Berdimuratova K, Amirgazin A, Shevtsov V, Ismailova A, Ramankulov Y, Shevtsov A, Kurmanbayev A. 2020. Draft genome sequence of a potential commercial biocellulose producer, strain *Komagataeibacter europaeus* GH1. *Microbiol Resour Annot* 9:e00963-20. <https://doi.org/10.1128/MRA.00963-20>.

Editor Kenneth M. Stedman, Portland State University

Copyright © 2020 Nagmetova 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 Askar Kurmanbayev, wberel@gmail.com.

Received 18 August 2020

Accepted 24 September 2020

Published 15 October 2020

(13). An intact prophage located in contig 8 was identified in the genome. This prophage has a length of 40.3 kbp and has 95.65% identity to the prophage in the genome of *K. europaeus* SRCM101446.

Data availability. This whole-genome shotgun project has been deposited in DDBJ/EMBL/GenBank under the accession no. [NZ_JACHUU000000000](https://doi.org/10.1093/nar/gkz569). The version described in this paper is the first version, [NZ_JACHUU000000000.1](https://doi.org/10.1093/nar/gkz569). The raw data from BioProject [PRJNA649655](https://doi.org/10.1093/nar/gkz569) were submitted to the NCBI SRA under experiment accession no. [SRR12349535](https://doi.org/10.1093/nar/gkz569).

ACKNOWLEDGMENT

This study was funded by the Ministry of Education and Science of Kazakhstan (grant no. AP05132472).

REFERENCES

- Gomes RJ, Borges MF, Rosa MF, Castro-Gómez RJH, Spinosa WA. 2018. Acetic acid bacteria in the food industry: systematics, characteristics and applications. *Food Technol Biotechnol* 56:139–151. <https://doi.org/10.17113/ftb.56.02.18.5593>.
- Gullo M, La China S, Falcone PM, Giudici P. 2018. Biotechnological production of cellulose by acetic acid bacteria: current state and perspectives. *Appl Microbiol Biotechnol* 102:6885–6898. <https://doi.org/10.1007/s00253-018-9164-5>.
- Nagmetova GZ, Kurmanbayev AA. 2019. Isolation and identification of bacterial cellulose producers with potential for medicine and biotechnology. *Eurasian J Appl Biotechnol* 2:114–120.
- Pearce MM, Theodoropoulos N, Mandel MJ, Brown E, Reed KD, Cianciotto NP. 2012. *Legionella cardiaca* sp. nov., isolated from a case of native valve endocarditis in a human heart. *Int J Syst Evol Microbiol* 62:2946–2954. <https://doi.org/10.1099/ijs.0.039248-0>.
- Kuibagarov M, Amirgazin A, Vergnaud G, Shustov A, Ryskeldina A, Ramankulov Y, Shevtsov A. 2020. Draft genome sequence of *Moraxella bovoculi* strain KZ-1, isolated from cattle in North Kazakhstan. *Microbiol Resour Announc* 9:e00670-20. <https://doi.org/10.1128/MRA.00670-20>.
- Stasiak-Różańska L, Płoska J. 2018. Study on the use of microbial cellulose as a biocarrier for 1,3-dihydroxy-2-propanone and its potential application in industry. *Polymers* 10:438. <https://doi.org/10.3390/polym10040438>.
- Joshi NA, Fass JN. 2011. Sickle: a sliding-window, adaptive, quality-based trimming tool for FastQ files (v1.33). <https://github.com/najoshi/sickle>.
- 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>.
- Tatusova T, DiCuccio M, Badretdin A, Chetvernin 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>.
- Brettin T, Davis JJ, Disz T, Edwards RA, Gerdes S, Olsen GJ, Olson R, Overbeek R, Parrello B, Pusch GD, Shukla M, Thomason JA, Stevens R, Vonstein V, Wattam AR, Xia F. 2015. RASTtk: a modular and extensible implementation of the RAST algorithm for building custom annotation pipelines and annotating batches of genomes. *Sci Rep* 5:8365. <https://doi.org/10.1038/srep08365>.
- Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. 1990. Basic local alignment search tool. *J Mol Biol* 215:403–410. [https://doi.org/10.1016/S0022-2836\(05\)80360-2](https://doi.org/10.1016/S0022-2836(05)80360-2).
- Arndt D, Grant JR, Marcu A, Sajed T, Pon A, Liang Y, Wishart DS. 2016. PHASTER: a better, faster version of the PHAST phage search tool. *Nucleic Acids Res* 44:W16–W21. <https://doi.org/10.1093/nar/gkw387>.
- Ryngajłto M, Kubiak K, Jędrzejczak-Krzepkowska M, Jacek P, Bielecki S. 2019. Comparative genomics of the *Komagataeibacter* strains—efficient bionanocellulose producers. *Microbiologyopen* 8:e00731. <https://doi.org/10.1002/mbo3.731>.