



Genome Sequence of *Bacillus velezensis* 5RB, an Overproducer of 2,3-Butanediol

Penka Petrova,^a Petya Velikova,^a Kaloyan Petrov^b

^aInstitute of Microbiology, Bulgarian Academy of Sciences, Sofia, Bulgaria

^bInstitute of Chemical Engineering, Bulgarian Academy of Sciences, Sofia, Bulgaria

ABSTRACT *Bacillus velezensis* 5RB is capable of producing large amounts of 2,3-butanediol. Whole-genome sequencing revealed that the strain contains one circular chromosome of 3.91 Mbp without plasmids. A large part of the genome is devoted to carbohydrate metabolism, encoding an abundance of enzymes participating in polysaccharide utilization pathways.

The organic chemical 2,3-butanediol (2,3-BD) is the starting reagent in chemical syntheses and an ingredient in foods and pharmaceuticals (1). Biotechnological approaches for 2,3-BD production have progressed over the past decade, turning 2,3-BD into a major product of mixed-acid fermentations (2, 3). Currently, the aims are to use nonpathogenic *Bacillus* strains (4) and convert renewable raw materials (5).

B. velezensis 5RB was isolated in the Veliko Tarnovo region of Bulgaria from lake sediment containing plant roots. Single colonies of the strain were grown in nutrient broth (Oxoid) at 30°C. Genomic DNA was extracted using a GeneJET genomic DNA purification kit (Thermo Fisher Scientific). The TruSeq DNA PCR-free kit was used for library construction; the sequencing was performed on an Illumina HiSeq 2500 instrument with FastQC quality control (Macrogen, Inc., South Korea). Quality-filtered data contained 43,639,513,900 total bases and 289,794,196 read counts. The assembly was done using SOAPdenovo2 software (6) yielding 26 contigs with a total length of 3,910,395 bp, 134.22× genome coverage, an N_{50} value of 394,584 bp, and a 46.5% G+C content. The NCBI Prokaryotic Genome Annotation Pipeline (7) detected 4,605 genes, 3,745 of them encoding proteins, 81 tRNAs, and 8 rRNAs.

Strain 5RB belongs to the *Bacillus amyloliquefaciens* operational group (8), with a 99% similarity with soy isolate *B. velezensis* YJ11-1-4 (GenBank accession number [NZ_CP020874](#)) (9). *In silico* DNA-DNA hybridization (DDH) (10) resulted in a DDH value of 90.20% with the *B. velezensis* FZB42 genome ([CP000560](#)) and a relatively lower DDH of 85.7% with that of the type strain NRRL B-41580 ([LLZC00000000](#)).

B. velezensis 5RB contains genes which are typical for plant-associated rhizobacterial genomes (11–13). The metabolic model of Rapid Annotations using Subsystems Technology (RAST) (default settings) (14) built by ModelSEED v2.3 predicted a 2,3-BD synthesis pathway engaging *ilvB*, *alsS*, and *ilvH* (encoding α -acetolactate synthase), *alsD* (α -acetolactate decarboxylase), and *bdhA* [(R,R)-2,3-butanediol dehydrogenase; EC 1.1.1.4]. The last enzyme was identical to the 2,3-butanediol dehydrogenase of *B. amyloliquefaciens* KHG19 (GenBank accession number [CP007242](#)) (15) but different from those of *B. velezensis* FZB42 and NRRL B-41580^T, which may explain the overproduction of 2,3-BD by *B. velezensis* 5RB.

A large portion of the genome of *B. velezensis* 5RB is devoted to carbohydrate metabolism (225 genes). The following genes encode glycoside hydrolases: *amyE*, *mall*, *sacA*, *xynA*, *xynB*, *xynD*, *xynC*, and *eglS*. This rich enzyme spectrum enables the conversion of cellulose, hemicellulose, starch, and inulin and is promising for the use of *B.*

Citation Petrova P, Velikova P, Petrov K. 2019. Genome sequence of *Bacillus velezensis* 5RB, an overproducer of 2,3-butanediol. Microbiol Resour Announc 8:e01475-18. <https://doi.org/10.1128/MRA.01475-18>.

Editor Julie C. Dunning Hotopp, University of Maryland School of Medicine

Copyright © 2019 Petrova et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](#).

Address correspondence to Penka Petrova, pepipetrova@yahoo.com.

Received 28 October 2018

Accepted 20 November 2018

Published 3 January 2019

velezensis 5RB to produce 2,3-BD in biotechnological processes for simultaneous saccharification and fermentation (SSF) of renewable plant substrates.

Secondary metabolite production was analyzed using the antiSMASH v4.2.0 tool (16). Seven complete genomic clusters encoding antimicrobials were observed. Three of them encode the synthesis of the polyketides macrolactin, bacillaene, and diffidin, and four of them encode the nonribosomal production of fengycin, bacillibactin, bacilysin, and the cyclic lipopeptide surfactin. The synthesis by *B. velezensis* 5RB of a number of substances with an antibiotic nature would allow its application in industrial microbial fermentations in nonsterile conditions.

Data availability. This whole-genome sequencing (WGS) project has been deposited at DDBJ/ENA/GenBank under the accession number [QXJL00000000](https://doi.org/10.1093/nar/gkx569) (raw data are available under SRA numbers [SRX5028064](https://doi.org/10.1093/nar/gkx569) and [SRR8208868](https://doi.org/10.1093/nar/gkx569)).

ACKNOWLEDGMENT

This study was supported by grant DH 17/1 from The National Science Fund, Ministry of Education and Science, Republic of Bulgaria.

REFERENCES

- Ji X-J, Huang H, Ouyang P-K. 2011. Microbial 2,3-butanediol production: a state-of-the-art review. *Biotechnol Adv* 29:351–364. <https://doi.org/10.1016/j.biotechadv.2011.01.007>.
- Petrov K, Petrova P. 2009. High production of 2,3-butanediol from glycerol by *Klebsiella pneumoniae* G31. *Appl Microbiol Biotechnol* 84: 659–665. <https://doi.org/10.1007/s00253-009-2004-x>.
- Petrov K, Petrova P. 2010. Enhanced production of 2,3-butanediol from glycerol by forced pH fluctuations. *Appl Microbiol Biotechnol* 87: 943–949. <https://doi.org/10.1007/s00253-010-2545-z>.
- Li L, Li K, Wang K, Chen C, Gao C, Ma C, Xu P. 2014. Efficient production of 2,3-butanediol from corn stover hydrolysate by using a thermophilic *Bacillus licheniformis* strain. *Bioresour Technol* 170:256–261. <https://doi.org/10.1016/j.biortech.2014.07.101>.
- Tsvetanova F, Petrova P, Petrov K. 2014. 2,3-Butanediol production from starch by engineered *Klebsiella pneumoniae* G31-A. *Appl Microbiol Biotechnol* 98:2441–2451. <https://doi.org/10.1007/s00253-013-5418-4>.
- Luo R, Liu B, Xie Y, Li Z, Huang W, Yuan J, He G, Chen Y, Pan Q, Liu Y, Tang J, Wu G, Zhang H, Shi Y, Liu Y, Yu C, Wang B, Lu Y, Han C, Cheung D-W, Yiu SM, Peng S, Xiaoqian Z, Liu G, Liao X, Li Y, Yang H, Wang J, Lam T-W, Wang J. 2012. SOAPdenovo2: an empirically improved memory-efficient short-read *de novo* assembler. *Gigascience* 1:18. <https://doi.org/10.1186/2047-217X-1-18>.
- Tatusova T, Di Cuccio 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>.
- Fan B, Blom J, Klenk H-P, Borriss R. 2017. *Bacillus amyloliquefaciens*, *Bacillus velezensis*, and *Bacillus siamensis* form an “operational group *B. amyloliquefaciens*” within the *B. subtilis* species complex. *Frontiers Microbiol* 8:22. <https://doi.org/10.3389/fmicb.2017.00022>.
- Lee HJ, Chun B-H, Jeon HH, Kim YB, Lee SH. 2017. Complete genome sequence of *Bacillus velezensis* YJ11-1-4, a strain with broad-spectrum antimicrobial activity, isolated from traditional Korean fermented soy-bean paste. *Genome Announc* 5:e01352-17. <https://doi.org/10.1128/genomeA.01352-17>.
- Meier-Kolthoff JP, Auch AF, Klenk HP, Göker M. 2013. Genome sequence-based species delimitation with confidence intervals and improved distance functions. *BMC Bioinformatics* 14:60. <https://doi.org/10.1186/1471-2105-14-60>.
- Dunlap CA, Kim SJ, Kwon SW, Rooney AP. 2016. *Bacillus velezensis* is not a later heterotypic synonym of *Bacillus amyloliquefaciens*; *Bacillus methylotrophicus*, *Bacillus amyloliquefaciens* subsp. *plantarum* and “*Bacillus oryzicola*” are later heterotypic synonyms of *Bacillus velezensis* based on phylogenomics. *Int J Syst Evol Microbiol* 66:1212–1217. <https://doi.org/10.1099/ijssem.0.000858>.
- He P, Hao K, Blom J, Rückert C, Vater J, Mao Z, Wu Y, Hou M, He P, He Y, Borriss R. 2013. Genome sequence of the plant growth promoting strain *Bacillus amyloliquefaciens* subsp. *plantarum* B9601-Y2 and expression of mersacidin and other secondary metabolites. *J Biotechnol* 164: 281–291. <https://doi.org/10.1016/j.jbiotec.2012.12.014>.
- 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>.
- Gao Y-H, Guo R-J, Li S-D. 2018. Draft genome sequence of *Bacillus velezensis* B6, a rhizobacterium that can control plant diseases. *Genome Announc* 6:e00182–e00118. <https://doi.org/10.1128/genomeA.00182-18>.
- Hong Y, Jung H-J, Han S-K, Kim H-Y. 2016. Potentiality of *Bacillus amyloliquefaciens* KFCC11574P isolated from Korean traditional doenjang as a starter in the production of functional soya bean paste. *Int J Food Sci Technol* 51:105–113. <https://doi.org/10.1111/ijfs.12973>.
- Weber T, Blin K, Duddela S, Krug D, Kim H-U, Brucoleri R, Lee S-Y, Fischbach MA, Müller R, Wohlleben W, Breitling R, Takano E, Medema MH. 2015. antiSMASH 3.0: a comprehensive resource for the genome mining of biosynthetic gene clusters. *Nucleic Acids Res* 43:W237–W243. <https://doi.org/10.1093/nar/gkv437>.