



Draft Genome Sequence of *Bacillus* sp. Strain UFRGS-B20, a Hydrocarbon Degradator

Patricia Dörr de Quadros,^{a,b} Roberta Fulthorpe,^b Rosemary Saati,^b Vanessa Cerqueira,^a Fátima Menezes Bento^a

^aDepartment of Environmental Microbiology, Federal University of Rio Grande do Sul, Porto Alegre, Rio Grande do Sul, Brazil

^bDepartment of Physical and Environmental Sciences, University of Toronto, Toronto, Ontario, Canada

ABSTRACT *Bacillus* sp. strain UFRGS-B20 was isolated in 2012 from Brazilian land-farming soil contaminated with petrochemical oily sludge. This strain was subjected to hydrocarbon biodegradation tests, showing degradation rates of up to 60%. Here, we present the 6.82-Mb draft genome sequence of the strain, which contains 2,178 proteins with functional assignments.

Bacillus sp. strain UFRGS-B20 was isolated from soil contaminated with petrochemical oily sludge (bioremediation land-farming site) in South Brazil and cultured in Luria-Bertani (LB) medium containing different concentrations of sterilized oily sludge. It increased biomass significantly (Tukey test, $\alpha < 0.01$) in the presence of 1% oily sludge compared to the no-oily-sludge treatment (just LB medium). This strain was also tested in oily sludge-contaminated soil microcosms, where it degraded up to 60% of polycyclic hydrocarbons (1). This strain was proven to degrade polycyclic aromatic hydrocarbons in liquid and solid environments, and it has the genetic potential to be used in the bioremediation of contaminated soils or water.

The genomic DNA of *Bacillus* sp. strain UFRGS-B20 was isolated using the QIAamp DNA minikit (Qiagen), and it was used to generate the PacBio whole-genome shotgun library of sheared long inserts. The sequencing was performed using Pacific Biosciences (PacBio) RS II sequencing technology at McGill University and the Génome Québec Innovation Centre (30× coverage). The sequences were treated and assembled using miniasm (2) in PATRIC version 3.5.2 (3), and the genome annotation was performed using PATRIC. The N_{50} and N_{75} values of the assembly were 278,944 and 126,449 bp, respectively. The largest contig was 1,546,980 bp. The draft genome showed 88.07% similarity with that of *Bacillus cereus* (NCBI accession number GCA_000007825, NCBI assembly number ASM782v1) and 87.47% similarity with that of *Bacillus thuringiensis* (GCA_002243685, ASM224368v1), so its classification falls into an undefined species. The sequences consisted of 6,827,566 bp, with a GC content of 35.78%, distributed within 59 contigs. No plasmid sequences were detected.

Bacillus sp. strain UFRGS-B20 contains genes encoding enzymes related to 17 pathways of xenobiotic biodegradation and metabolism, including hydrolase aldolase (Al-2) LsrF (bisphenol degradation), succinate dehydrogenase, 3-hydroxyacyl-coenzyme A (3-hydroxyacyl-CoA) dehydrogenase, methyltransferases, alcohol and aldehyde dehydrogenases, and hydrolases involved in naphthalene, anthracene, and 1- and 2-methylnaphthalene degradation; (S)-2-haloacid dehalogenase, cytochrome P450 102A3, monooxygenases, acid and alkaline phosphatases, acetamidases, nitric oxide synthase oxygenase, and oxygen-insensitive NAD(P)H nitroreductase; and 3-ketoacyl-CoA thiolase, N-acetyltransferase, ureases, allophanate hydrolase, gluconolactonase, and enoyl-CoA hydratases. Furthermore, we also detected 31 genes coding for methyltransferases, 8 genes coding for antibiotic resistance, and 13 genes coding for efflux pump genes. *Bacillus* sp. strain UFRGS-B20 also contains genes related to the biosyn-

Received 16 January 2018 Accepted 30 January 2018 Published 22 February 2018

Citation Dörr de Quadros P, Fulthorpe R, Saati R, Cerqueira V, Bento FM. 2018. Draft genome sequence of *Bacillus* sp. strain UFRGS-B20, a hydrocarbon degrader. *Genome Announcements* 6:e00052-18. <https://doi.org/10.1128/genomeA.00052-18>.

Copyright © 2018 Dörr de Quadros 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 Patricia Dörr de Quadros, patiquadros@icloud.com.

thesis of secondary metabolites of biotechnological importance, such as puromycin, tetracycline, novobiocin, streptomycin, terpenoid backbone, diterpenoids, carotenoids, zeatin, phenylpropanoids, flavonoids, anthocyanin, flavone, flavonol, stilbenoids, diarylheptanoids, gingerol, isoquinoline alkaloids, tropane, piperidine alkaloids, betalain, and insect hormone, as well as for biosynthesis of polyketides and nonribosomal peptides such as ansamycins, siderophores, and type II polyketide backbone and products. Finally, this strain is involved in the metabolism of C₂₁-steroid hormones, porphyrin, and chlorophyll.

Accession number(s). This whole-genome shotgun project has been deposited at GenBank under accession number [POCE00000000](https://www.ncbi.nlm.nih.gov/nuclseq/POCE00000000).

ACKNOWLEDGMENTS

We thank the Coordination of Improvement of Higher Education (CAPES), the Brazilian Council of Research and Technology/CNPq, and the LabBio laboratory at the Federal University of Rio Grande do Sul for funding the research about *Bacillus* sp. strain UFRGS-B20, as well as R. Fulthorpe's lab at the University of Toronto Scarborough (Department of Physical and Environmental Sciences) for funding the genome sequencing.

REFERENCES

1. Dörr de Quadros P, Cerqueira VS, Cazarolli JC, Peralba MDCR, Camargo FAO, Giongo A, Bento FM. 2016. Oily sludge stimulates microbial activity and changes microbial structure in a landfarming soil. *Int Biodeterior Biodegrad* 115:90–101. <https://doi.org/10.1016/j.ibiod.2016.07.018>.
2. Li H. 2016. Minimap and miniasm: fast mapping and *de novo* assembly for noisy long sequences. *Bioinformatics* 32:2103–2110. <https://doi.org/10.1093/bioinformatics/btw152>.
3. Wattam AR, Davis JJ, Assaf R, Boisvert S, Brettin T, Bun C, Conrad N, Dietrich EM, Disz T, Gabbard JL, Gerdes S, Henry CS, Kenyon RW, Machi D, Mao C, Nordberg EK, Olsen GJ, Murphy-Olson DE, Olson R, Overbeek R, Parrello P, Pusch GD, Shukla M, Vonstein V, Warren A, Xia F, Yoo H, Stevens RL. 2017. Improvements to PATRIC, the all-bacterial bioinformatics database and analysis resource center. *Nucleic Acids Res* 45: D535–D542. <https://doi.org/10.1093/nar/gkw1017>.