




Draft Genome Sequence of *Microbacterium* sp. Strain LEMMJ01, Isolated from Antarctic Ornithogenic Soil

Júnia Schultz,^a Yuri Alves Pinheiro de Souza,^a
Maria Cristina Pinheiro Pereira Reis Mansur,^b Alane Beatriz Vermelho,^b
Fábio Faria da Mota,^c  Alexandre Soares Rosado^a

Laboratory of Molecular Microbial Ecology, Microbiology Institute, Federal University of Rio de Janeiro, Rio de Janeiro, Brazil^a; Biolnovar Laboratory, Microbiology Institute, Federal University of Rio de Janeiro, Rio de Janeiro, Brazil^b; Oswaldo Cruz Institute, Fiocruz, Rio de Janeiro, Brazil^c

ABSTRACT We report here the 3,637,012-bp draft genome sequence of *Microbacterium* sp. strain LEMMJ01, isolated from ornithogenic soil from King George Island, Antarctica. The total number of genes presented in the draft genome sequence was 3,553, and the total number of coding sequences was 3,497. In addition, genes related to the production of terpene and carotenoids were revealed.

The genus *Microbacterium* is a member of the phylum *Actinobacteria*, a Gram-positive, aerobic, and heterotrophic bacterium (1, 2). It is found in different habitats, having been described in sponges, deep-sea sediments, humans, and polar environments (3–6). *Microbacterium* species have biotechnological importance, such as in biosurfactant production, bioremediation (7), and the application of their natural pigments, such as carotenoids, in the food, cosmetics, textiles, and pharmaceutical industries (8, 9).

We sequenced the draft genome sequence of *Microbacterium* sp. strain LEMMJ01, isolated from Antarctic ornithogenic soil collected close to the Arctowsky Polish Station near an Adelie penguin nest (62°09'790"S; 58°27'687"W) in Admiralty Bay, King George Island, Antarctica. The soil processing protocol was described in a previous work (10), and single colonies of the psychrophilic bacteria were isolated on LB medium after growing at 12°C for 48 h. The isolated colonies were then grown in liquid LB medium (12°C for 48 h), and their genomic DNA was extracted using the FastDNA SPIN kit for soil (MoBio) and quantified using a Qubit fluorometer (Thermo Fisher Scientific). The Nextera XT DNA library kit was used to build paired-end 250-bp libraries, which were sequenced on an Illumina MiSeq. Assembly was performed by MR DNA (Shallowater, TX) using NGen version 12 from DNASTar, and the coding DNA sequences (CDSs) were predicted and annotated using two tools, the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP) and the Rapid Annotations using Subsystems Technology (RAST) server (11).

The draft assembly of *Microbacterium* sp. LEMMJ01 resulted in 3,637,012 bp, with 300× coverage and 70.20% GC content, present in 44 contigs, with an N_{50} of 335,663 bp. The total number of genes presented in the draft genome sequences was 3,553, and the total number of coding sequences was 3,497. In addition, 46 tRNAs and 56 rRNAs were predicted in the complete genome.

The results revealed, by PGAAP, that carotenoid biosynthesis genes were localized as a cluster that included genes encoding C50 carotenoid epsilon cyclases. Genes related to the production of terpenes were detected with antiSMASH (12), highlighting the biotechnological interest in this strain. The presence of resistance genes was verified by ResFinder 2.1 (13), with no positive results. Further analyses will be carried

Received 25 May 2017 Accepted 30 May 2017 Published 20 July 2017

Citation Schultz J, de Souza YAP, Mansur MCPPR, Vermelho AB, da Mota FF, Rosado AS. 2017. Draft genome sequence of *Microbacterium* sp. strain LEMMJ01, isolated from Antarctic ornithogenic soil. *Genome Announc* 5:e00672-17. <https://doi.org/10.1128/genomeA.00672-17>.

Copyright © 2017 Schultz 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 Alexandre Soares Rosado, asrosado@micro.ufrj.br.

out with the genome sequences of the psychrophilic bacterium in order to better understand the biotechnological applications originating from the production of carotenoids at low temperatures by *Microbacterium* sp. LEMMJ01.

Accession number(s). This whole-genome sequence project has been deposited at DDBJ/ENA/GenBank under the accession no. [NCTV00000000](https://www.ncbi.nlm.nih.gov/nuccore/NCTV00000000). The version described in this paper is version NCTV01000000.

ACKNOWLEDGMENTS

This work received scientific and financial support from the National Council for Research and Development (CNPq) and the Carlos Chagas Research Support Foundation of the State of Rio de Janeiro (FAPERJ).

We thank the Brazilian Antarctic Program for logistical support during the Antarctica Operation.

REFERENCES

- Collins M, Bradbury J. 1992. The genera *Agromyces*, *Aureobacterium*, *Clavibacter*, *Curtobacterium*, and *Microbacterium*, p 1355–1368. In Balows A, Truper HG, Dworkin M, Harder W, Schleifer K-H (ed), *The prokaryotes*. Springer, New York, NY.
- Richert K, Brambilla E, Stackebrandt E. 2007. The phylogenetic significance of peptidoglycan types: molecular analysis of the genera *Microbacterium* and *Aureobacterium* based upon sequence comparison of *gyrB*, *rpoB*, *recA* and *ppk* and 16S rRNA genes. *Syst Appl Microbiol* 30:102–108. <https://doi.org/10.1016/j.syapm.2006.04.001>.
- Karimi E, Gonçalves JMS, Reis M, Costa R. 2017. Draft genome sequence of *Microbacterium* sp. strain Alg239_V18, an actinobacterium retrieved from the marine sponge *Spongia* sp. *Genome Announc* 5(3):e01457-16. <https://doi.org/10.1128/genomeA.01457-16>.
- Bernier AM, Bernard K. 2016. Draft genome sequences of *Microbacterium hominis* LCDC-84-0209^T isolated from a human lung aspirate and *Microbacterium laevaniformans* LCDC 91-0039 isolated from a human blood culture. *Genome Announc* 4(5):e00989-16. <https://doi.org/10.1128/genomeA.00989-16>.
- Wu YH, Zhou P, Cheng H, Wang CS, Wu M, Xu XW. 2015. Draft genome sequence of *Microbacterium profundum* Shh49^T, an actinobacterium isolated from deep-sea sediment of a polymetallic nodule environment. *Genome Announc* 3(3):e00642-15. <https://doi.org/10.1128/genomeA.00642-15>.
- Leiva S, Alvarado P, Huang Y, Wang J, Garrido I. 2015. Diversity of pigmented Gram-positive bacteria associated with marine macroalgae from Antarctica. *FEMS Microbiol Lett* 362:fnv206. <https://doi.org/10.1093/femsle/fnv206>.
- Lima JMS, Pereira JO, Batista IH, Neto PQC, dos Santos JC, de Araújo SP, Pantoja MC, da Mota AJ, de Azevedo JL. 2016. Potential biosurfactant producing endophytic and epiphytic fungi, isolated from macrophytes in the Negro River in Manaus, Amazonas, Brazil. *Afr J Biotechnol* 15: 1217–1223. <https://doi.org/10.5897/AJB2015.15131>.
- Jin J, Yao J, Liu W, Zhang Q, Liu J. 2017. Fluoranthene degradation and binding mechanism study based on the active-site structure of ring-hydroxylating dioxygenase in *Microbacterium paraoxydans* JPM1. *Environ Sci Pollut Res* 24:363–371. <https://doi.org/10.1007/s11356-016-7809-4>.
- Han SR, Kim KH, Ahn DH, Park H, Oh TJ. 2016. Complete genome sequence of carotenoid-producing *Microbacterium* sp. strain PAMC28756 isolated from an Antarctic lichen. *J Biotechnol* 226:18–19. <https://doi.org/10.1016/j.jbiotec.2016.03.034>.
- da Silva AC, Rachid CTCDC, de Jesus HE, Rosado AS, Peixoto RS. 2017. Predicting the biotechnological potential of bacteria isolated from Antarctic soils, including the rhizosphere of vascular plants. *Polar Biol*, in press. <https://doi.org/10.1007/s00300-016-2065-0>.
- Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: rapid annotations using subsystems technology. *BMC Genomics* 9:75. <https://doi.org/10.1186/1471-2164-9-75>.
- Weber T, Blin K, Duddela S, Krug D, Kim HU, Bruccoleri R, Lee SY, 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>.
- Zankari E, Hasman H, Cosentino S, Vestergaard M, Rasmussen S, Lund O, Aarestrup FM, Larsen MV. 2012. Identification of acquired antimicrobial resistance genes. *J Antimicrob Chemother* 67:2640–2644. <https://doi.org/10.1093/jac/dks261>.