





## Draft Genome Sequence of *Gordonia lacunae* BS2<sup>T</sup>

Biocatalysis and Technical Biology Research Group, Institute of Biomedical and Microbial Biotechnology, Cape Peninsula University of Technology, Bellville, South Africa<sup>a</sup>; Department of Microbiology, Faculty of Science, Stellenbosch University, Stellenbosch, South Africa<sup>b</sup>; Department of Biotechnology, Faculty of Natural Sciences, Institute of Microbial Biotechnology and Metagenomics, University of the Western Cape, Bellville, South Africa<sup>c</sup>

**ABSTRACT** We report here the draft genome sequence of the soil bacterium *Gordonia lacunae* BS2<sup>T</sup> (= DSM 45085<sup>T</sup> = JCM 14873<sup>T</sup> = NRRL B-24551<sup>T</sup>), isolated from an estuary in Plettenberg Bay, South Africa. Analysis of the draft genome revealed that more than 40% of the secondary metabolite biosynthetic genes encode new compounds.

ctinobacteria are an excellent source of novel biologically active secondary metabolites (1). This group of bacteria account for the production of over two-thirds of known secondary metabolites (2). A new species—Gordonia lacunae, with strain BS2 as the type strain—was described by Le Roes et al. in 2008 (3). The genome was sequenced using the Illumina MiSeq platform. A sequencing library was constructed with 1 ng of input DNA using the Nextera XT (Illumina) kit according to the manufacturer's instructions, with the exception of the bead-based normalization step, which was omitted. Library quantification was performed using the Qubit HS assay (Invitrogen), diluted with Tris-HCl (pH 7.8), and pooled at 8 pM. The library was sequenced on an Illumina MiSeq sequencer using an Illumina MiSeq 600-cycle (2 × 300-bp) sequencing cartridge (V3). A 10% PhiX spike was included in the run to account for the high G+C content of actinobacterial DNA. The genome was assembled using the A5-miseq pipeline (4). Functional annotation of the predicted protein sequences was performed with the Rapid Annotations using Subsystems Technology (RAST) (5) and NCBI (6) servers. Secondary metabolite biosynthetic gene clusters (smBGCs) were predicted using antiSMASH (7). The draft genome sequence of G. lacunae BS2<sup>T</sup> is 5,756,417 bp in length, with an average G+C content of 68.08%. The assembled genome has a coverage of 100 $\times$  and an  $N_{50}$  size of 152.68 kb, consisting of 90 contigs with 5,102 coding sequences. Sixty-one RNA genes are found in the BS2<sup>T</sup> genome, comprising 12 rRNAs, 46 tRNAs and 3 other RNAs. Strain BS2<sup>T</sup> contains genes involved in processing and posttranslational modifications (apolipoprotein N-acyltransferase, lipoprotein signal peptidase, and prolipoprotein diacylglyceryl transferase) of bacterial lipoprotein precursors. The antiSMASH bioinformatics tool predicted 18 smBGCs, of which, there were 8 nonribosomal peptide synthetases (NRPSs), 1 NRPS-siderophore hybrid, 1 type I polyketide synthase, 1 bacteriocin, 2 terpene clusters, 1 aryl polyene cluster, 1 ectoine cluster, and 3 gene clusters labeled as "other." Eight of the 18 smBGCs showed no homology to the biosynthetic pathways of known compounds curated in the antiS-MASH database, one of which is the aryl polyene cluster. Bacterial pigments, such as the orange pigments produced by Gordonia spp., are a result of the expression of aryl polyene biosynthetic gene clusters. These pigments function as carotenoids that protect the bacterium from reactive oxygen species, thereby reducing potential oxidative stress-related cell damage (8). These results highlight the genetic potential of strain BS2<sup>T</sup> for natural product discovery.

**Received** 31 July 2017 **Accepted** 7 August 2017 **Published** 5 October 2017

Citation Durrell K, Prins A, Le Roes-Hill M. 2017. Draft genome sequence of *Gordonia lacunae* BS2<sup>T</sup>. Genome Announc 5:e00959-17. https://doi.org/10.1128/genomeA.00959-17.

Copyright © 2017 Durrell et al. This is an openaccess article distributed under the terms of the Creative Commons Attribution 4.0 International license.

Address correspondence to Marilize Le Roes-Hill, leroesm@cput.ac.za.

All authors contributed equally to this work.

**Accession number(s).** This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession number NGF000000000. The version described in this paper is the first version, NGF001000000.

## **ACKNOWLEDGMENTS**

This research was funded by the National Research Foundation (NRF) of South Africa (Marilize Le Roes-Hill was the recipient of NRF grant no. 90304).

We acknowledge Kirby-McCullough (Department of Biotechnology, University of the Western Cape, South Africa) for sequencing of the genome.

Any opinions, findings, or conclusions or recommendations expressed in this material are those of the author(s), and therefore the NRF does not accept any liability in regard thereto.

## **REFERENCES**

- Bérdy J. 2012. Thoughts and facts about antibiotics: where we are now and where we are heading. J Antibiot 65:385–395. https://doi.org/10 .1038/ia.2012.27.
- Lam KS. 2006. Discovery of novel metabolites from marine actinomycetes. Curr Opin Microbiol 9:245–251. https://doi.org/10.1016/j.mib.2006.03.004.
- Le Roes M, Goodwin CM, Meyers PR. 2008. Gordonia lacunae sp. nov., isolated from an estuary. Syst Appl Microbiol 31:17–23. https://doi.org/ 10.1016/j.syapm.2007.10.001.
- Coil D, Jospin G, Darling AE. 2015. A5-miseq: an updated pipeline to assemble microbial genomes from Illumina MiSeq data. Bioinformatics 31:587–589. https://doi.org/10.1093/bioinformatics/btu661.
- 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.
- NCBI Resource Coordinators. 2017. Database resources of the National Center for Biotechnology Information. Nucleic Acids Res 45:D12–D17. https://doi.org/10.1093/nar/gkw1071.
- Blin K, Medema MH, Kottmann R, Lee SY, Weber T. 2017. The antiSMASH database, a comprehensive database of microbial secondary metabolite biosynthetic gene clusters. Nucleic Acids Res 45:D555–D559. https://doi. org/10.1093/nar/gkw960.
- Schöner TA, Gassel S, Osawa A, Tobias NJ, Okuno Y, Sakakibara Y, Shindo K, Sandmann G, Bode HB. 2016. Aryl polyenes, a highly abundant class of bacterial natural products, are functionally related to antioxidative carotenoids. ChemBioChem 17:247–253. https://doi.org/10.1002/cbic .201500474.