The Draft Genome Sequence of *Burkholderia* sp. Strain Nafp2/4-1b Confirms Its Ability To Produce the Plant Growth-Promoting Traits Pyoverdine Siderophores, 1-Aminocyclopropane-1-Carboxylate Deaminase, and the Phytohormone Auxin

Ahmed Idris Hassen,a L. S. Khambani,a Z. H. Swanevelderb

a Agricultural Research Council, Plant Health and Protection, Queenswood, Pretoria, South Africa
b Agricultural Research Council, Biotechnology Platform, Onderstpoort, South Africa

**ABSTRACT** *Burkholderia* sp. strain Nafp2/4-1b is a rhizobacterium isolated from the rhizosphere of grassland in South Africa. This draft genome report confirms the presence of genes related to iron acquisition, alleviation of abiotic stress in plants, and other essential traits of plant growth-promoting rhizobacteria (PGPR) that signify the potential of this strain as a plant growth-promoting agent.

Members of the genus *Burkholderia* are Gram-negative bacteria belonging to the beta subclass of *Proteobacteria* and are part of a larger group of rhizobacteria that can establish a positive interaction within plant roots. Several strains within the genus are known to colonize the rhizosphere and play key roles in crop yield, plant health, and soil fertility (1, 2). They are therefore often referred to as plant growth-promoting rhizobacteria (PGPR) due to their ability to improve the growth and health of several economically important crops (3, 4).

The *Burkholderia* sp. strain presented here, Nafp2/4-1b, was initially isolated from the rhizosphere of grassland in South Africa. For isolation, a 100-μl aliquot of serially diluted rhizosphere soil suspension was plated on solid nutrient agar (NA) medium and was incubated at 28°C for 24 h. Selected pure colonies of the bacteria were evaluated for their growth-promoting activity in maize (*Zea mays* L.) and *in vitro* detection of major PGPR traits.

Based on the growth-promoting traits exhibited in both the gnotobiotic test and the *in vitro* characterization, the genome of this strain was sequenced to confirm and increase our understanding of its PGPR properties for possible use as a biofertilizer inoculant in crop production. For DNA extraction, a single pure colony of the bacterium was grown in Luria Bertani (LB) broth for 24 h on a rotary shaker at 28°C. One milliliter of the culture suspension was used to extract total DNA using the Wizard genomic DNA purification kit and protocol (Promega, Madison, WI, USA). Paired-end DNA libraries were prepared using the Nextera protocol (Illumina, USA) at the Agricultural Research Council’s Biotechnology Platform in Onderstpoort, South Africa. About 13,542,806 paired-end sequences (125 bp each) were obtained prior to adaptor quality trimming and the merging of overlapped reads. CLC Genomics Workbench 8.5.1 was used for the trimming and genome assembly, with the default setting of 20 bp used. This resulted in a final number of merged and unmerged reads of 8,610,493 being used to produce the final assembly. The draft genome consists of 92 scaffolds (i.e., 110 contigs), with an N50 value of 322,407 bp and a maximum scaffold size of 1,302,675 bp. The total draft genome size is estimated at 7,786,570 bp (i.e., 123 × coverage), with a GC content of 66.2%. The NCBI

Received 12 October 2018 Accepted 14 November 2018 Published 13 December 2018

Citation Hassen AI, Khambani LS, Swanevelder ZH. 2018. The draft genome sequence of *Burkholderia* sp. strain Nafp2/4-1b confirms its ability to produce the plant growth-promoting traits pyoverdine siderophores, 1-aminocyclopropane-1-carboxylate deaminase, and the phytohormone auxin. Microbiol Resour Announc 7:e01383-18. https://doi.org/10.1128/MRA.01383-18.

Editor John J. Dennehy, Queens College

Copyright © 2018 Hassen et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International license.

Address correspondence to Ahmed Idris Hassen, hassena@arc.agric.za.
Prokaryotic Genome Annotation Pipeline (PGAP) was used for genome annotation (5, 6), which identified 7,223 putative coding regions.

This draft genome sequence of *Burkholderia* sp. Nafp2/4-1b revealed the presence of the genes that code for the following PGPR traits: 1-aminocyclopropane-1-carboxylate (ACC) deaminase (contig 3), iron-binding pyoverdine siderophore biosynthesis (contig 28), tryptophan synthase beta and alpha chains involved in auxin biosynthesis (contig 5), ferric (Fe$^{3+}$) hydroxamate siderophore iron transporter (*FhuB* gene) (contig 28), and ATP binding cassette (ABC) transporters that mediate the uptake of the heavy metal-complexing peptides iron, siderophores, and phytochelatin (contig 1).

**Data availability.** This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number **PXXL00000000**. The version described in this paper is version PXXL01000000. The SRA accession number for the raw data is **PRJNA438206**.

**ACKNOWLEDGMENTS**

Due acknowledgment goes to the National Research Foundation (NRF) of South Africa for the financial support to A. I. Hassen under the project for development of microbial inoculants for enhanced legume production.

Opinions expressed, and conclusions arrived at, are those of the authors and are not necessarily to be attributed to the NRF.

**REFERENCES**

1. Onfre-Lemus J, Hernandez-Lucas I, Girard L, Caballero-Mellado J. 2009. ACC (1-aminocyclopropane-1-carboxylate) deaminase activity, widespread trait in *Burkholderia* species, and its growth-promoting effect on tomato plants. Appl Environ Microbiol 75:6581–6590. https://doi.org/10.1128/AEM.01240-09.
2. Wong-Villarreal A, Caballero-Mellado J. 2010. Rapid identification of nitrogen-fixing and legume-nodulating *Burkholderia* species based on PCR 16S rRNA species-specific oligonucleotides. Syst Appl Microbiol 33:35–43. https://doi.org/10.1016/j.syapm.2009.10.004.
3. Klopper JW, Leong J, Teintze M, Schrot MN. 1980. Enhanced plant growth by siderophores produced by plant growth promoting rhizobacteria. Nature 286:885–886. https://doi.org/10.1038/286885a0.
4. Cellio DF, Bevivino A, Chiarini L, Fani R, Paffetti D, Tabacchioni S, Dalmastri C. 1997. Biodiversity of *Burkholderia cepacia* population isolated from the maize rhizosphere at different stages. Appl Environ Microbiol 63:4485–4493.
5. 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:D851–D860. https://doi.org/10.1093/nar/gkw569.
6. Haft DH, DiCuccio M, Badretdin A, Brover V, Chetvernin V, O’Neill K, Li W, Chitsaz F, Derbyshire MK, Gonzales NR, Gwadz M, Lu F, Marchler GH, Song JS, Thanki N, Yamashita RA, Zheng C, Thibaud-Nissen F, Geer LY, Marchler-Bauer A, Pruitt KD. 2018. RefSeq: an update on prokaryotic genome annotation and curation. Nucleic Acids Res 46:D851–D860. https://doi.org/10.1093/nar/gkx1068.