



Draft Genome Sequence of *Burkholderia reimsis* BE51, a Plant-Associated Bacterium Isolated from Agricultural Rhizosphere

Qassim Esmaeel,^a Alaa Issa,^a Lisa Sanchez,^a Christophe Clément,^a Cédric Jacquard,^a Essaid Ait Barka^a

^aUnité de Résistance Induite et Bioprotection des Plantes–EA 4707, UFR Sciences Exactes et Naturelles, University of Reims-Champagne-Ardenne, Reims, France

ABSTRACT *Burkholderia reimsis* BE51, isolated from maize rhizosphere, has a promising biocontrol activity against a set of phytopathogens. Here, we report its draft genome sequence with the aim of providing insight into the potentially produced secondary metabolites and genes related to plant growth-promoting and biocontrol properties.

The high demand for agricultural crops is increasing and is expected to keep growing in the upcoming decades. Under exposure to different stress conditions, plant growth and development are affected, leading to a significant loss in crop productivity and quality (1). Traditionally, plant diseases are treated by the application of chemical pesticides, which are not always economical or effective. Further, chemical control methods may have unwanted health, safety, and environmental risks leading to an ecological problem, such as the development of resistance in pathogenic races (2). Therefore, the use of plant-associated bacteria that are able to enhance plant performance and increase their tolerance to different stresses has been reported (3, 4). The genus *Burkholderia* contains different members that have been isolated from different ecological niches (5–9). Different members of *Burkholderia* have been reported as plant growth-promoting and biocontrol agents, especially those related to the genus *Paraburkholderia* (10, 11).

The bacterium strain BE51 described here was isolated from maize rhizosphere according to a protocol that was previously described (12). The strain was found to be Gram negative, motile, facultative aerobic, and oxidase positive. The optimum growth conditions are 30°C and pH 7.0 in the presence of 0.5% NaCl. Based on phylogenetic analysis, chemical characteristics, and genotypic data, strain BE51 is distinct from previously known species and represents a novel species of the genus *Burkholderia*, for which the name *Burkholderia reimsis* BE51 is proposed. BE51 possesses antifungal activities against *Fusarium oxysporum*, *Fusarium poae*, *Fusarium graminearum*, *Fusarium culmorum*, *Botrytis cinerea*, and *Rhizoctonia solani* and has friendly interactions with grapevine.

The BE51 genome was sequenced at MicrobesNG (<http://www.microbesng.uk>) using Illumina MiSeq and HiSeq 2500 technology platforms, with 2 to 250-bp paired-end reads, and the mean coverage was 140×. For all software, default settings were used. The nearest reference genome, for *Burkholderia lata*, was determined using Kraken (13), and to assess data quality, reads were mapped to this genome using the Burrows-Wheeler Aligner (BWA) MEM algorithm (<http://bio-bwa.sourceforge.net>). The reads were assembled by *de novo* assembly using SPAdes (<http://cab.spbu.ru/software/spades/>). The draft genome sequences, assembled into 182 contigs with an N_{50} contig size of 157,936 bp, was estimated at 8,934,495 bp with a G+C content of 66.40%. The gene function prediction was detected using the Rapid Annotations using Subsystems Technology (RAST) server (<http://rast.nmpdr.org>) (14), followed by an annotation using the SEED database (15), resulting in 89 RNAs and 7,961 coding sequences distributed

Received 20 July 2018 Accepted 6

September 2018 Published 4 October 2018

Citation Esmaeel Q, Issa A, Sanchez L, Clément C, Jacquard C, Barka EA. 2018. Draft genome sequence of *Burkholderia reimsis* BE51, a plant-associated bacterium isolated from agricultural rhizosphere. Microbiol Resour Announc 7:e00978-18. <https://doi.org/10.1128/MRA.00978-18>.

Editor Frank J. Stewart, Georgia Institute of Technology

Copyright © 2018 Esmaeel 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 Qassim Esmaeel, qassin.esmaeel@univ-reime.fr, or Essaid Ait Barka, ea.barka@univ-reims.fr.

in 563 subsystems. The draft genome sequence was mined with the aim of screening all potentially produced secondary metabolites (SMs) using antiSMASH (16). *In silico* analysis revealed the presence of 14 putative biosynthetic gene clusters potentially involved in the synthesis of many SMs, including bacteriocin, phenazines, pyrrolnitrin, siderophores, and nonribosomal peptides. In addition, the BE51 genome harbors genes involved in indole acetic acid production, motility, and biofilm production and one gene related to 1-aminocyclopropane-1-carboxylate deaminase. All these features may reflect the biocontrol and plant growth-promoting effects of this bacterium.

Data availability. This whole-genome shotgun project has been deposited at GenBank under the accession no. [QMFZ00000000](https://doi.org/10.1093/nar/gkv437). The version described in this paper is the first version, QMFZ01000000. The SRA accession no. is [SRP156928](https://doi.org/10.1093/nar/gkv437).

ACKNOWLEDGMENTS

This work was supported by the University of Reims Champagne-Ardenne. We thank the European Union for funding through the INTERREG V (France Wallonie Flandre), a SmartBioControl project (BioScreen project).

We are thankful for MicrobesNG (<http://www.microbesng.uk>), supported by the BBSRC (grant no. BB/L024209/1), for performing the genome sequencing.

REFERENCES

- Tilman D, Balzer C, Hill J, Belfort BL. 2011. Global food demand and the sustainable intensification of agriculture. *Proc Natl Acad Sci U S A* 108:20260–20264. <https://doi.org/10.1073/pnas.1116437108>.
- Couderchet M. 2003. Benefits and problems of fungicide control of *Botrytis cinerea* in vineyards of champagne. *Vitis* 42:165–172.
- Pieterse CM, Zamioudis C, Berendsen RL, Weller DM, Van Wees SC, Bakker PA. 2014. Induced systemic resistance by beneficial microbes. *Annu Rev Phytopathol* 52:347–375. <https://doi.org/10.1146/annurev-phyto-082712-102340>.
- Compant S, Duffy B, Nowak J, Clément C, Barka EA. 2005. Use of plant growth-promoting bacteria for biocontrol of plant diseases: principles, mechanisms of action, and future prospects. *Appl Environ Microbiol* 71:4951–4959. <https://doi.org/10.1128/AEM.71.9.4951-4959.2005>.
- Esmaeel Q, Sanchez L, Robineau M, Dorey S, Clément C, Jacquard C, Barka EA. 2018. Draft genome sequence of plant growth-promoting *Burkholderia* sp. strain BE12, isolated from the rhizosphere of maize. *Genome Announc* 6:e00299-18. <https://doi.org/10.1128/genomeA.00299-18>.
- Eberl L, Vandamme P. 2016. Members of the genus *Burkholderia*: good and bad guys. *F1000Res* 5:1007. <https://doi.org/10.12688/f1000research.8221.1>.
- Depoorter E, Bull MJ, Peeters C, Coenye T, Vandamme P, Mahenthiralingam E. 2016. *Burkholderia*: an update on taxonomy and biotechnological potential as antibiotic producers. *Appl Microbiol Biotechnol* 100:5215–5229. <https://doi.org/10.1007/s00253-016-7520-x>.
- Sawana A, Adeolu M, Gupta RS. 2014. Molecular signatures and phylogenomic analysis of the genus *Burkholderia*: proposal for division of this genus into the emended genus *Burkholderia* containing pathogenic organisms and a new genus *Paraburkholderia* gen. nov. harboring environmental species. *Front Genet* 5:429. <https://doi.org/10.3389/fgene.2014.00429>.
- Compant S, Nowak J, Coenye T, Clément C, Ait Barka E. 2008. Diversity and occurrence of *Burkholderia* spp. in the natural environment. *FEMS Microbiol Rev* 32:607–626. <https://doi.org/10.1111/j.1574-6976.2008.00113.x>.
- Esmaeel Q, Pupin M, Jacques P, Leclère V. 2017. Nonribosomal peptides and polyketides of *Burkholderia*: new compounds potentially implicated in biocontrol and pharmaceuticals. *Environ Sci Pollut Res* <https://doi.org/10.1007/s11356-017-9166-3>.
- Ait Barka E, Gognies S, Nowak J, Audran JC, Belarbi A. 2002. Inhibitory effect of endophyte bacteria on *Botrytis cinerea* and its influence to promote the grapevine growth. *Biol Control* 24:135–142. [https://doi.org/10.1016/S1049-9644\(02\)00034-8](https://doi.org/10.1016/S1049-9644(02)00034-8).
- Loqman S, Barka EA, Clément C, Ouhdouch Y. 2009. Antagonistic actinomycetes from Moroccan soil to control the grapevine gray mold. *World J Microbiol Biotechnol* 25:81–91. <https://doi.org/10.1007/s11274-008-9864-6>.
- Wood DE, Salzberg SL. 2014. Kraken: ultrafast metagenomic sequence classification using exact alignments. *Genome Biol* 15:R46. <https://doi.org/10.1186/gb-2014-15-3-r46>.
- 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>.
- Disz T, Akhter S, Cuevas D, Olson R, Overbeek R, Vonstein V, Stevens R, Edwards RA. 2010. Accessing the SEED genome databases via Web services API: tools for programmers. *BMC Bioinformatics* 11:319. <https://doi.org/10.1186/1471-2105-11-319>.
- 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>.