

UNIVERSIDADE ESTADUAL DE CAMPINAS
SISTEMA DE BIBLIOTECAS DA UNICAMP
REPOSITÓRIO DA PRODUÇÃO CIENTÍFICA E INTELLECTUAL DA UNICAMP

Versão do arquivo anexado / Version of attached file:

Versão do Editor / Published Version

Mais informações no site da editora / Further information on publisher's website:

<https://journals.asm.org/doi/10.1128/genomeA.00455-15>

DOI: 10.1128/genomeA.00455-15

Direitos autorais / Publisher's copyright statement:

©2015 by American Society for Microbiology. All rights reserved.

DIRETORIA DE TRATAMENTO DA INFORMAÇÃO

Cidade Universitária Zeferino Vaz Barão Geraldo

CEP 13083-970 – Campinas SP

Fone: (19) 3521-6493

<http://www.repositorio.unicamp.br>

Draft Genome Sequence of *Burkholderia andropogonis* Type Strain ICMP2807, Isolated from *Sorghum bicolor*

Lucilene Lopes-Santos,^a Daniel Bedo Assumpção Castro,^b Laura Maria Mariscal Ottoboni,^b Duckchul Park,^c  Bevan Simon Weir,^c Suzete Aparecida Lanza Destéfano^a

Laboratório de Bacteriologia Vegetal, Instituto Biológico, Campinas, Brazil^a; Centro de Biologia Molecular e Engenharia Genética, Universidade Estadual de Campinas, Campinas, Brazil^b; Landcare Research, Auckland, New Zealand^c

Here, we report the draft genome sequence of *Burkholderia andropogonis* ICMP2807, a phytopathogenic bacterium isolated from *Sorghum bicolor* plants in the United States.

Received 6 April 2015 Accepted 14 April 2015 Published 14 May 2015

Citation Lopes-Santos L, Castro DBA, Ottoboni LMM, Park D, Weir BS, Destéfano SAL. 2015. Draft genome sequence of *Burkholderia andropogonis* type strain ICMP2807, isolated from *Sorghum bicolor*. *Genome Announc* 3(3):e00455-15. doi:10.1128/genomeA.00455-15.

Copyright © 2015 Lopes-Santos et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Suzete Aparecida Lanza Destéfano, suzete@biologico.sp.gov.br.

Burkholderia andropogonis was described as a causal agent of stripe disease in sorghum (*Sorghum bicolor*) by Smith in 1911 (1) and, subsequently, was classified as *Pseudomonas andropogonis* by Stevens in 1925 (2). Based on DNA-rRNA hybridizations, it was reclassified to the genus *Burkholderia* (3). This bacterial species has an extensive geographical distribution and can cause leaf spots, streaks, or stripes in a wide range of hosts (4–9). The *B. andropogonis* strains are highly similar in their morphological and physiological properties (10) and have unique features that are absent in most plant pathogenic bacteria, such as a single polar sheathed flagellum (11) and rhizobitoxine production (12–14).

Genomic DNA was isolated from culture of *B. andropogonis* ICMP2807 (IBSBF199; LGM 2129; ATCC 23061) using the DNeasy blood and tissue kit (Qiagen, USA) on the automated QIAcube instrument (Qiagen, USA) and sequenced with a 454 GS Junior system (Roche Diagnostics, USA) at Landcare Research (Auckland, New Zealand). The sequencing generated 162,643 reads with an average read length of 464 bp, totaling 75.4 Mbp. The reads were trimmed and assembled with Newbler version 2.9 (15). The draft genome comprises 6.29 Mbp in 272 contigs with a GC content of 58.92%, a mean contig length of 22,808 bp, and an N_{50} of 155,724 bp.

Functional annotation in SEED subsystems was performed on the RAST server (16, 17). The annotation presented 6,047 protein-coding genes (CDSs), 48 tRNAs, and 4 rRNAs (one 5S, one 23S, and two 16S). Genome analysis revealed 9 genes for the peptide antibiotic colicin V and 94 genes associated with resistance to antibiotic and toxic compounds. Several genes of the type VII, VI, IV, II, and III secretion systems were identified. The type III secretion system is a common infection mechanism found in phytopathogenic bacteria. In addition, the presence of the *catABCD* operon, the *pca* cluster, and other genes related to the degradation of aromatic compounds indicates a possible environmental relevance of this strain. Further analyses are in progress and will be published separately.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank un-

der the accession number [LAQU000000000](https://www.ncbi.nlm.nih.gov/nuclseq/laqu000000000). The version described in this paper is version LAQU01000000.

ACKNOWLEDGMENT

This work was supported by the São Paulo Research Foundation (FAPESP) grant 2011/12222-2.

REFERENCES

- Smith EF. 1911. Bacteria in relation to plant diseases. Carnegie Institute, Washington, DC.
- Stevens FL. 1925. Plant disease fungi. Macmillan, New York, NY.
- Gillis M, van Van T, Bardin R, Goor M, Hebbar P, Willenms A, Segers P, Kersters K, Heulin T, Fernandez MP. 1995. Polyphasic taxonomy in the genus *Burkholderia* leading to an emended description of the genus and proposition of *Burkholderia vietnamiensis* sp. nov. for N_2 -fixing isolates from rice in Vietnam. *Inter J Syst and Evol Microbiol* 45:274–289.
- Cother EJ, Noble D, Peters BJ, Albiston A, Ash GJ. 2004. A new bacterial disease of jojoba (*Simmondsia chinensis*) caused by *Burkholderia andropogonis*. *Plant Pathol* 53:129–135. <http://dx.doi.org/10.1111/j.0032-0862.2004.00982.x>.
- Duan YP, Sun X, Zhou LJ, Gabriel DW, Benyon LS, Gottwald T. 2009. Bacterial brown leaf spot of citrus, a new disease caused by *Burkholderia andropogonis*. *Plant Dis* 93:607–614. <http://dx.doi.org/10.1094/PDIS-93-6-0607>.
- European and Mediterranean Plant Protection Organization. 2014. PQR-EPPPO database on quarantine pests. European and Mediterranean Plant Protection Organization, Paris, France. <https://www.eppo.int/DATABASES/pqr/pqr.htm>.
- Gitaitis RD, Miller J, Wells HD. 1983. Bacterial leaf spot of white clover in Georgia. *Plant Dis* 67:913–914. <http://dx.doi.org/10.1094/PD-67-913>.
- Li X, De Boer SH. 2005. First report of *Burkholderia andropogonis* causing leaf spots of *Bougainvillea* sp. in Hong Kong and clover in Canada. *Plant Dis* 89:1132. <http://dx.doi.org/10.1094/PD-89-1132A>.
- Ullstrup AJ. 1960. Bacterial stripe of corn. *Phytopathology* 50:906–910.
- Moffett ML, Hayward AC, Fahy PC. 1986. Five new hosts of *Pseudomonas andropogonis* occurring in eastern Australia: host range and characterization of isolates. *Plant Pathol* 35:34–43. <http://dx.doi.org/10.1111/j.1365-3059.1986.tb01978.x>.
- Fuerst JA, Hayward AC. 1969. The sheathed flagellum of *Pseudomonas stizolobii*. *J Clin Microbiol* 58:239–245. <http://dx.doi.org/10.1099/00221287-58-2-239>.
- Mitchell RE. 1994. Dihydrorhizobitoxine, a minor product of *Pseudomonas andropogonis*. *Phytochemistry* 37:373–375. [http://dx.doi.org/10.1016/0031-9422\(94\)85062-3](http://dx.doi.org/10.1016/0031-9422(94)85062-3).

13. Okazaki S, Nukui N, Sugawara M, Minamisawa K. 2004. Rhizobial strategies to enhance symbiotic interaction: rhizobitoxine and 1-aminocyclopropane-1-carboxylate deaminase. *Microbes Environ* 19: 99–111. <http://dx.doi.org/10.1264/jsme2.19.99>.
14. Vial L, Groleau MC, Dekimpe V, Déziel E. 2007. *Burkholderia* diversity and versatility: an inventory of the extracellular products. *J Microbiol Biotechnol* 17:1407–1429.
15. Margulies M, Egholm M, Altman WE, Attiya S, Bader JS, Bemben LA, Berka J, Braverman MS, Chen YJ, Chen Z, Dewell SB, Du L, Fierro JM, Gomes XV, Godwin BC, He W, Helgesen S, Ho CH, Ho CH, Irzyk GP, Jando SC, Alenquer ML, Jarvie TP, Jirage KB, Kim JB, Knight JR, Lanza JR, Leamon JH, Lefkowitz SM, Lei M, Li J, Lohman KL, Lu H, Makhijani VB, McDade KE, McKenna MP, Myers EW, Nickerson E, Nobile JR, Plant R, Puc BP, Ronan MT, Roth GT, Sarkis GJ, Simons JF, Simpson JW, Srinivasan M, Tartaro KR, Tomasz A, Volkmer GA, Wang SH, Wang Y, Weiner MP, Yu P, Begley RF, Rothberg JM. 2005. Genome sequencing in microfabricated high-density picolitre reactors. *Nature* 437:376–380. <http://dx.doi.org/10.1038/nature03959>.
16. 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. <http://dx.doi.org/10.1186/1471-2164-9-75>.
17. Overbeek R, Olson R, Pusch GD, Olsen GJ, Davis JJ, Disz T, Edwards RA, Gerdes S, Parrello B, Shukla M, Vonstein V, Wattam AR, Xia F, Stevens R. 2014. The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). *Nucleic Acids Res* 42: D206–D214. <http://dx.doi.org/10.1093/nar/gkt1226>.