Draft Genome Sequence of *Erwinia psidii*, Causal Agent of Bacterial Blight of Guava (*Psidium guava*) and Dieback of Eucalypt (*Eucalyptus* spp.)

Pollyane da Silva Hermenegildo,a Samuel A. Santos,b Lúcio M. S. Guimarães,b Isadora C. Pereira,d Pedro M. P. Vidigal,c Jorge L. Badel,d Poliane Alfenas-Zerbini,e Reginaldo G. Mafia,f Marisa A. S. V. Ferreira,a Acelino Couto Alfenasb

aLaboratory of Phytobacteriology, Department of Plant Pathology, Universidade de Brasília, Federal District, Brazil
bLaboratory of Forest Pathology, Department of Plant Pathology, Instituto de Biotecnologia Aplicada a Agropecuária (BIOAGRO), Universidade Federal de Viçosa, Minas Gerais State, Brazil
cLaboratory of Molecular Phytobacteriology, Department of Plant Pathology, Universidade Federal de Viçosa, Minas Gerais State, Brazil
dLaboratory of Molecular Phytobacteriology, Department of Plant Pathology, Universidade Federal de Viçosa, Minas Gerais State, Brazil
eDepartment of Microbiology, Instituto de Biotecnologia Aplicada a Agropecuária (BIOAGRO), Universidade Federal de Viçosa, Minas Gerais State, Brazil
fCentro de Tecnologia, Fibria Celulose S.A., Aracruz, Espírito Santo State, Brazil

**ABSTRACT**

Here, we present a draft genome sequence of the type strain IBSBF 435 of *Erwinia psidii* (*Enterobacteriaceae*), a phytopathogen that causes bacterial blight on guava (*Psidium guava*) and dieback and wilt on eucalypt (*Eucalyptus* spp.), both of which are important emerging diseases.

*Erwinia psidii* was first described in Brazil in 1983 as causing bacterial blight on guava plants in Pindamohangaba and Valinhos in the Brazilian state of São Paulo (1). The pathogen has spread to the Brazilian states of Minas Gerais (2), Espírito Santo (3), Distrito Federal (4), and Paraná (5). The disease has been shown to be of great importance since it causes significant losses in guava fruit production (6). Although the disease is currently restricted to Brazil, it is considered a potential risk for other guava-producing countries, such as India, Egypt, Mexico, and Pakistan (7). Recently, *E. psidii* was also reported to cause dieback and wilt in eucalypt plantations in Argentina, Uruguay, and Brazil, and polyphasic taxonomy in association with multilocus sequence analysis was used to confirm the taxonomy of this pathogen (8, 9). In Brazil, the disease on eucalypt has been observed in the states of Rio Grande do Sul, São Paulo, and Mato Grosso do Sul (9). Disease incidence may reach up to 100% in some areas and seasons, greatly reducing the productive capacity of the eucalypt crop (9).

In both hosts, the main symptoms caused by the pathogen consist of petiole necrosis and tanning of the central leaf vein. Macroscopic and microscopic ooze may emerge from the lesions. Necrosis and mummification of flowers and young fruits are often observed in guava, whereas wilt is observed in eucalypt trees, which may culminate with their death in the field (9, 10). In recent years, studies have been focused on pathogen detection (10, 11), host colonization (5, 12), and genetic variability in the pathogen populations (13). However, the genetic basis of *E. psidii* virulence remains unclear. Thus, the aims of this study were to sequence and annotate the whole genome of the type strain of *E. psidii* IBSBF 435 (also known as ATCC 49406, CFBP 3627, CIP 105200, DSM 17597, ICMP 8426, LMG 7039, NCPPB 3555, and PDDCC 8426), isolated from guava plants (1). The IBSBF 435 strain was obtained from the Phytobacteria Culture Collection of Instituto Biológico in Campinas, São Paulo State, Brazil. The strain was retrieved from a stock in 30% glycerol at −80°C and grown in petri plates containing solid 523 medium (14) at 28°C for 48 hours. Then, the bacterial cells were used for DNA...
were the first draft genome sequence of the plant-pathogenic bacterium deposited in GenBank under accession number Erwinia regions. The quality of our assembly is comparable to that of strains belonging to other single-copy, 2.5% missed, and no duplicated or fragmented gene groups specific for of 3,954 predicted genes. The assembly had an average coverage of 60-fold. The completeness of the assembled genome was estimated using Benchmarking Universal Single-Copy Orthologs (BUSCO) (17).

The size of the assembled E. psidii IBSBF 435 genome is 4.5 Mb, and its G+C content is 51.3%. The assembly contains 42 scaffolds with sizes ranging from 1,000 nucleotides (nt) to 628 kb, an average scaffold length of 107 kb, an N50 value of 268 kb, and a total of 3,954 predicted genes. The assembly had an average coverage of 60-fold. The completeness assessment of the genome by BUSCO identified 97.5% complete and single-copy, 2.5% missed, and no duplicated or fragmented gene groups specific for bacteria, which indicates that the assembled genome covers most of the coding regions. The quality of our assembly is comparable to that of strains belonging to other Erwinia species, such as E. mallophilovora (18), E. tracheiphila (19), and E. amylovora (20).

This is the first draft genome sequence of the plant-pathogenic bacterium E. psidii, which may be used as a reference for the species. This genome sequence will be an invaluable molecular tool for gaining a better understanding of the biology of the interaction of this important emerging pathogen with its host plants, by using diverse scientific approaches, including comparative genomics.

Data availability. The sequences from this whole-genome shotgun project were deposited in GenBank under accession number RHHM00000000. The raw data were also deposited in the Sequence Read Archive (BioProject number PRJNA498492).

ACKNOWLEDGMENTS

This work was funded by CNPq (Conselho Nacional de Desenvolvimento Científico e Tecnológico), CAPES, FAPEMIG (Fundação de Amparo a Pesquisa de Minas Gerais), and FAPDF (Fundação de Apoio a Pesquisa do Distrito Federal).

REFERENCES

1. Rodrigues Neto J, Robbs CF, Yamashiro T. 1987. A bacterial disease of guava (Psidium guajava) caused by Erwinia psidii sp. nov. Fitopatol Bras 12:345–350.
2. Romeiro RS, Moraes RMA, Oliveira JR, Couto FAA, Resende ST. 1993. Uma enfermidade da goiaba de etiologia bacteriana no estado de Minas Gerais, Brasil. Fitopatol Bras 18:238.
3. Oliveira JR, Ventura JA, Silva IT, Costa H. 2000. Ocorrência da bacteriose da goiaba, causada por Erwinia psidii, no estado do Espírito Santo. Fitopatol Bras 25:328.
4. Uesugi CH, Melo-Filho PA, Paz-Lima ML, Moraes CA, Tomita CK, Café-Filho AC, Ueno B. 2001. Ocorrência de Erwinia psidii em goiaba no Distrito Federal. Summa Phytopathol 27:118.
5. Teixeira AC, Ferreira MASV, Marques ASA. 2008. Detection of Erwinia psidii in guava plants in greenhouse and field conditions. Cienc Rural 46:1528–1534.
6. Macagnan D, Ferreira Mas V. 2018. Movement of the bacterial blight pathogen Erwinia psidii in guava varieties differing in susceptibility. Trop Plant Pathol 43:557–582. https://doi.org/10.1007/s40858-018-0236-y.
7. Janse JD. 2012. Bacterial diseases that may or do emerge, with (possible) economic damage for Europe and the Mediterranean basin: notes on epidemiology, risks, prevention and management on first occurrence. J Plant Pathol 94:54–54.29.
8. Coutinho TA, Brady CL, van der Vaart M, Venter SN, Telecha N, Roflo M, Perez C, Wingfield MJ. 2011. A new shoot and stem disease of Eucalyptus species caused by Erwinia psidii. Australas Plant Pathol 40:55–60. https://doi.org/10.1007/s13313-010-0013-y.
9. Arriel DAA, Fonseca NR, Guimarães LMS, Hermenegildo PS, Mafá RG, Borges Júnior N, de Souza HP, Alfenas AC. 2014. Wilt and die-back of Eucalyptus spp. caused by Erwinia psidii in Brazil. For Path 44:255–265. https://doi.org/10.1111/epf.12087.
10. da Silva CF, Uesugi CH, Blum LEB, Marques ASDA, Ferreira MÁDSV. 2016. Molecular detection of Erwinia psidii in guava plants under greenhouse and field conditions. Cienc Rural 46:1528–1534. https://doi.org/10.1590/0103-8478cr20151600.
11. Teixeira AC, Ferreira MASV, Marques ASA. 2008. Detection of Erwinia psidii through enrichment in guava leaf extract and double radial immunodiffusion. Trop Plant Pathol 33:212–218. https://doi.org/10.1590/S1982-567620080000300006.
12. Montoya-Estrada CN, Costa CR, Badel JL, Guimarães LMS, Alfenas AC. 7 November 2018. Root infection and aerial colonization of eucalypt host plants by Erwinia psidii. Trop Plant Pathol. https://doi.org/10.1007/s40858-018-0264-7.
13. Montoya-Estrada CN, Hermenegildo PS, Alvarez-Romo PI, Badel JL, Guimarães LMS, Alfenas AC. 2018. Genetic diversity and aggressiveness of Erwinia psidii on Eucalyptus spp. in Brazil. Plant Pathol 68:31–41. https://doi.org/10.1111/ppa.12927.
14. Kado CE, Heskett MG. 1970. Selective media for isolation of Agrobacterium, Corynebacterium, Erwinia, Pseudomonas and Xanthomonas. Phyto- pathology 60:969–976. https://doi.org/10.1094/Phyto-60-969.
15. Chen S, Huang T, Zhou Y, Han Y, Xu M, Gu J. 2017. AfterQC: automatic filtering, trimming, error removing and quality control for fastq data. BMC Bioinformatics 18:80. https://doi.org/10.1186/s12859-017-1469-3.

16. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sierotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol 19:455–477. https://doi.org/10.1089/cmb.2012.0021.

17. Simão FA, Waterhouse RM, Ioannidis P, Kriventseva EV, Zdobnov EM. 2015. BUSCO: assessing genome assembly and annotation completeness with single-copy orthologs. Bioinformatics 31:3210–3212. https://doi.org/10.1093/bioinformatics/btv351.

18. Redzuan RA, Abu Bakar N, Rozano L, Badrun R, Mat Amin N, Mohd Raih MF. 2014. Draft genome sequence of Erwinia mallotivora BT-MARDI, causative agent of papaya dieback disease. Genome Announc 2:e00375-14. https://doi.org/10.1128/genomeA.00375-14.

19. Shapiro LR, Scully ED, Roberts D, Straub TJ, Geib SM, Park J, Stephenson AG, Salaau Rojas E, Liu Q, Beattie G, Gleason M, De Moraes CM, Mescher MC, Fleischer SG, Kolter R, Pierce N, Zhaxybayeva O. 2015. Draft genome sequence of Erwinia tracheiphila, an economically important bacterial pathogen of cucurbits. Genome Announc 3:e00482-15. https://doi.org/10.1128/genomeA.00482-15.

20. Powney R, Smits THM, Savbridge T, Frey B, Blom J, Frey JE, Plummer KM, Beer SV, Luck J, Duffy B, Rodoni B. 2011. Genome sequence of an Erwinia amylovora strain with pathogenicity restricted to Rubus plants. J Bacteriol 193:785–786. https://doi.org/10.1128/JB.01352-10.