





Complete Genome Sequence of *Xanthomonas citri* pv. *anacardii* Strain IBSBF2579 from Brazil

Wilson José Silva Junior,^a Antonio Roberto Gomes Farias,^a Nelson Bernardi Lima,^a Ana Maria Benko-Iseppon,^b
 Flávia Aburjaile,^b Valdir Queiroz Balbino,^b Raul Maia Falcão,^b Sérgio de Sa Leitão Paiva Júnior,^b
 Lucas Christian Sousa-Paula,^b Rosa Lima Ramos Mariano,^a Elineide Barbosa Souza,^c  Marco Aurélio Siqueira Gama^a

^aDepartment of Agronomy, Federal Rural University of Pernambuco, Recife, Brazil

^bDepartment of Genetics, Federal University of Pernambuco, Recife, Brazil

^cDepartment of Biology, Federal Rural University of Pernambuco, Recife, Brazil

ABSTRACT The bacterium *Xanthomonas citri* pv. *anacardii* is the agent of angular leaf spot of the cashew tree (*Anacardium occidentale* L.). The complete genome sequencing of the strain IBSBF2579 was done on an Illumina HiSeq 2500 platform. The *de novo* assembly of the *X. citri* pv. *anacardii* strain IBSBF2579 genome yielded 133 contigs, with a size of 5,329,247 bp and a G+C content of 64.03%. The prediction was performed by GeneMarkS and the automatic annotation by Rapid Annotations using Subsystems Technology (RAST), with 4,406 identified genes.

The cashew tree is native to Brazil (1) and grows in South America's tropical regions, mainly in the northeast of the country (2). Cashew nut production may be impaired by the occurrence of diseases, such as stand-out angular leaf spot caused by *Xanthomonas citri* pv. *anacardii* and *X. citri* pv. *mangiferaeindicae* (3, 4). These bacteria show pathological differences in cashew and mango trees, being able to multiply and survive in different hosts in the Anacardiaceae family (5, 6). However, until now, only *X. citri* pv. *mangiferaeindicae* (LMG 941) has been sequenced (7). Here, we report the whole-genome sequence of the type strain of *X. citri* pv. *anacardii* (IBSBF2579 = ICMP4088), which is nonpigmented and was isolated from a cashew tree in Brazil. The genome sequencing was performed by using the Illumina HiSeq 2500 platform at the Functional Genomics Center of the University of São Paulo. The libraries were prepared with the Illumina Nextera XT DNA library prep kit v 4, and sequencing was performed on a HiSeq flow cell v4, with the HiSeq SBS kit v4 and paired reads of 100 bp (2×). Initially, the quality reads were analyzed by FastQC (8), and read trimming to remove the adapters was performed by using FASTX-Toolkit (v. 0.0.13) (9). The genome *de novo* assembly was carried out using SPAdes (v. 1.10) (10), yielding 133 contigs of >500 bp (N_{50} , 150,594 bp), with the largest contig being 344,686 bp, for a total assembly size of 5,329,247 bp with a G+C content of 64.03%. The annotation using GeneMarkS (11) predicted 4,406 genes by Rapid Annotations using Subsystems Technology (RAST) (12). All assembly statistics were generated with QUAST (v.4.6) (13).

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number [PES10000000](https://doi.org/10.1128/genomeA.01574-17). The version described in this paper is version PES101000000.

ACKNOWLEDGMENTS

This study was supported by the Coordination for Improvement of Personnel with Higher Education (CAPES) Computational Biology Program and fellowships from the National Council for Scientific and Technological Development (CNPq) for the scholarships awarded to A.M.B.-I. (310871/2014-0), E.B.S. (305843-2016-8), and V.Q.B. (312002/2015-7).

Received 17 December 2017 Accepted 19 December 2017 Published 1 February 2018

Citation Silva Junior WJ, Farias ARG, Lima NB, Benko-Iseppon AM, Aburjaile F, Balbino VQ, Falcão RM, Paiva Júnior SDSL, Sousa-Paula LC, Mariano RL, Souza EB, Gama MAS. 2018. Complete genome sequence of *Xanthomonas citri* pv. *anacardii* strain IBSBF2579 from Brazil. Genome Announc 6:e01574-17. <https://doi.org/10.1128/genomeA.01574-17>.

Copyright © 2018 Silva Junior 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 Marco Aurélio Siqueira Gama, mas.gama@yahoo.com.br.

REFERENCES

1. Tim TK. 2012. Edible medicinal and non-medicinal plants. *In* Fruits edible medicinal and non-medicinal plants: Fruits, vol 4. Springer, New York, NY.
2. Viana FMP, Saraiva HAO, Freire FCO. 2006. Mancha-de-xanthomonas-do-cajueiro—sintomas e controle. *In* Empres bras pesqui e agropecuária, fortaleza comun técnico, no. 114 0–4. Embrapa Agroindústria Tropical, Fortaleza, Brazil. <http://www.infoteca.cnptia.embrapa.br/infoteca/handle/doc/427059>.
3. Ah-You N, Gagnevin L, Grimont PAD, Brisse S, Nesme X, Chiroleu F, Bui Thi Ngoc L, Jouen E, Lefeuvre P, Vernière C, Pruvost O. 2009. Polyphasic characterization of xanthomonads pathogenic to members of the Anacardiaceae and their relatedness to species of *Xanthomonas*. *Int J Syst Evol Microbiol* 59:306–318. <https://doi.org/10.1099/ijs.0.65453-0>.
4. Gama MAS, Mariano RLR, Viana FMP, Ferreira MASV, Souza EB. 2011. Polyphasic characterization of pigmented strains of *Xanthomonas* pathogenic to cashew trees. *Plant Dis* 95:793–802. <https://doi.org/10.1094/PDIS-05-10-0321>.
5. Ah-You N, Gagnevin L, Chiroleu F, Jouen E, Neto JR, Pruvost O. 2007. Pathological variations within *Xanthomonas campestris* pv. *mangiferaeindicae* support its separation into three distinct pathovars that can be distinguished by amplified fragment length polymorphism. *Phytopathology* 97:1568–1577. <https://doi.org/10.1094/PHYTO-97-12-1568>.
6. Zombre C, Sankara P, Ouédraogo SL, Wonne I, Boyer K, Boyer C, Terville M, Javegny S, Allibert A, Vernière C, Pruvost O. 2016. Natural infection of cashew (*Anacardium occidentale*) by *Xanthomonas citri* pv. *mangiferaeindicae* in Burkina Faso. *Plant Dis* 100:718–723. <https://doi.org/10.1094/PDIS-10-15-1137-RE>.
7. Midha S, Ranjan M, Sharma V, Pinnaka AK, Patil PB. 2012. Genome sequence of *Xanthomonas citri* pv. *mangiferaeindicae* strain LMG 941. *J Bacteriol* 194:3031. <https://doi.org/10.1128/JB.00433-12>.
8. Andrews S. 2010. FastQC: a quality control tool for high throughput sequence data. Babraham Bioinformatics. <http://www.bioinformatics.babraham.ac.uk/projects/fastqc>.
9. HannonLab. 2014. FASTX toolkit. Cold Spring Harbor Laboratory, Cold Spring Harbor, NY. http://hannonlab.cshl.edu/fastx_toolkit/.
10. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Pribelski AD, Pyshkin AV, Sirotkin 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>.
11. Besemer J, Lomsadze A, Borodovsky M. 2001. GeneMarkS: a self-training method for prediction of gene starts in microbial genomes. Implications for finding sequence motifs in regulatory regions. *Nucleic Acids Res* 29:2607–2618. <https://doi.org/10.1093/nar/29.12.2607>.
12. 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>.
13. Gurevich A, Saveliev V, Vyahhi N, Tesler G. 2013. QUASt: quality assessment tool for genome assemblies. *Bioinformatics* 29:1072–1075. <https://doi.org/10.1093/bioinformatics/btt086>.