



# Draft Genome Sequences of Two Isolates of *Colletotrichum lindemuthianum*, the Causal Agent of Anthracnose in Common Beans

Casley Borges de Queiroz,<sup>a</sup> Hilbert L. Nunes Correia,<sup>a</sup>  
Renato Pedrozo Menicucci,<sup>a</sup>  Pedro M. Pereira Vidigal,<sup>b</sup>  
Marisa Vieira de Queiroz<sup>a</sup>

Departamento de Microbiologia, Instituto de Biotecnologia Aplicada a Agropecuária (BIOAGRO), Universidade Federal de Viçosa, Minas Gerais, Brazil<sup>a</sup>; Núcleo de Análise de Biomoléculas (NuBioMol), Centro de Ciências Biológicas, Universidade Federal de Viçosa, Minas Gerais, Brazil<sup>b</sup>

**ABSTRACT** *Colletotrichum lindemuthianum* is the causal agent of anthracnose in common beans, one of the main limiting factors of their culture. Here, we report for the first time, to our knowledge, a draft of the complete genome sequences of two isolates belonging to 83.501 and 89 A<sub>2</sub> 2-3 of *C. lindemuthianum*.

*Colletotrichum* is one of the most widespread and economically important genera among the various damaging plant pathogens (1). This is especially true in tropical and subtropical regions, where *Colletotrichum* spp. limit the production of important crops, causing severe social and economic impacts (2). *Colletotrichum lindemuthianum* is the causal agent of anthracnose in the common bean (*Phaseolus vulgaris* L.) and attacks its leaves, stems, branches, string beans, and seeds (3). Under favorable conditions of humidity and temperature, in extreme cases, anthracnose can cause death of the plant (4). *C. lindemuthianum* has a high genetic variability, manifested by the presence of many physiologically diverse races (5). This high genetic variability is one of the main limiting factors to combating this pathogen, because it prevents the long-term use of resistant cultivars (6). The genomes of two isolates, 83.501 and 89 A<sub>2</sub> 2-3, of *C. lindemuthianum* were sequenced using the HiSeq 2500 Illumina platform with paired-end reads of 100 bp and an average coverage of 89.3× for isolate 83.501 and 157.7× for isolate 89 A<sub>2</sub> 2-3 (Laboratório Central de Tecnologias de Alto Desempenho em Ciências de Vida [LaCTAD]). The genes were predicted using Augustus version 3.2.2 (7). For *de novo* assembly, we used CLC Genomics Workbench 6.5.1. The completeness of the genome was estimated using Benchmarking Universal Single-Copy Orthologs (BUSCO) (8).

The contig assembly of isolate 83.501 using the CLC Genomics Workbench software resulted in 1,857 contigs ( $N_{50}$ , 111.275 kbp), the smallest containing a 1.02-kbp band and the largest containing a 623.12-kbp band, for a total of 97.4 Mbp and a G+C content of 37.6%. The contig assembly of isolate 89 A<sub>2</sub> 2-3 resulted in 1,276 contigs ( $N_{50}$ , 158.217 kb), the smallest containing 1.03 kbp and the largest containing 1.11 Mbp, for a total of 99.16 Mbp, with a G+C content of 37.3%. Assessment of the completeness of the genome using 1,438 BUSCO groups for fungi resulted in 98% complete (C) (6.1% duplicated [D]), 1.0% fragmented (F), 0.2% missed (M), and 1,438 genes (*n*) for isolate 83.501 and 98% C (6.0% D), 1.1% F, 0.4% M, and 1,438 *n* for isolate 89 A<sub>2</sub> 2-3, indicating that the assembled genome covered most of the coding regions. There were 11,673 (isolate 83.501) and 11,627 (isolate 89 A<sub>2</sub> 2-3) predicted genes.

In this study, we present a draft of the genome sequences belonging to two isolates from different races of *C. lindemuthianum*. This information will provide a valuable

Received 13 March 2017 Accepted 15 March 2017 Published 4 May 2017

**Citation** de Queiroz CB, Correia HLN, Menicucci RP, Vidigal PMP, de Queiroz MV. 2017. Draft genome sequences of two isolates of *Colletotrichum lindemuthianum*, the causal agent of anthracnose in common beans. *Genome Announc* 5:e00214-17. <https://doi.org/10.1128/genomeA.00214-17>.

**Copyright** © 2017 de Queiroz 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 Marisa Vieira de Queiroz, [mvqueiro@hotmail.com](mailto:mvqueiro@hotmail.com).

resource for identifying the mechanisms of pathogenesis and the plant-pathogen interactions, as well as new pathogenicity factors. Our data will also allow for comparative genomic studies with other fungal plant pathogens.

**Accession number(s).** The sequences from this whole-genome shotgun project for the two strains have been deposited in the DDBJ/ENA/GenBank database under accession numbers [MASO00000000](#) and [MASP00000000](#). The versions described in this paper are the first versions.

## ACKNOWLEDGMENTS

This work was supported by Fundação de Amparo à Pesquisa do Estado de Minas Gerais (FAPEMIG) and Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq).

The research was conducted with the help of the Cluster UFV (Universidade Federal de Viçosa).

## REFERENCES

- O'Connell RJ, Thon MR, Hacquard S, Amyotte SG, Kleemann J, Torres MF, Damm U, Buiate EA, Epstein L, Alkan N, Altmüller J, Alvarado-Balderrama L, Bauser CA, Becker C, Birren BW, Chen Z, Choi J, Crouch JA, Duvick JP, Farman MA, Gan P, Heiman D, Henrissat B, Howard RJ, Kabbage M, Koch C, Kracher B, Kubo Y, Law AD, Lebrun MH, Lee YH, Miyara I, Moore N, Neumann U, Nordström K, Panaccione DG, Panstruga R, Place M, Proctor RH, Prusky D, Rech G, Reinhardt R, Rollins JA, Rounsley S, Schardl CL, Schwartz DC, Shenoy N, Shirasu K, Sikhakolli UR, Stüber K. 2012. Lifestyle transitions in plant pathogenic *Colletotrichum* fungi deciphered by genome and transcriptome analyses. *Nat Genet* 44:1060–1065. <https://doi.org/10.1038/ng.2372>.
- Cannon PF, Damm U, Johnston PR, Weir BS. 2012. *Colletotrichum*—current status and future directions. *Stud Mycol* 73:181–213. <https://doi.org/10.3114/sim0014>.
- Mahuku GS, Riascos JJ. 2004. Virulence and molecular diversity within *Colletotrichum lindemuthianum* isolates from Andean and Mesoamerican bean varieties and regions. *Eur J Plant Pathol* 110:253–263. <https://doi.org/10.1023/B:EJPP.0000019795.18984.74>.
- Campa A, Rodríguez-Suárez C, Giraldez R, Ferreira JJ. 2014. Genetic analysis of the response to eleven *Colletotrichum lindemuthianum* races in a RIL population of common bean (*Phaseolus vulgaris* L.). *BMC Plant Biol* 14:115. <https://doi.org/10.1186/1471-2229-14-115>.
- Dos Santos LV, de Queiroz MV, Santana MF, Soares MA, de Barros EG, de Araújo EF, Langin T. 2012. Development of new molecular markers for the *Colletotrichum* genus using RetroCl1 sequences. *World J Microbiol Biotechnol* 28:1087–1095. <https://doi.org/10.1007/s11274-011-0909-x>.
- Ansari KI, Palacios N, Araya C, Langin T, Egan D, Doohan FM. 2004. Pathogenic and genetic variability among *Colletotrichum lindemuthianum* isolates of different geographic origins. *Plant Pathol* 53:635–642. <https://doi.org/10.1111/j.0032-0862.2004.01057.x>.
- Stanke M, Steinkamp R, Waack S, Morgenstern B. 2004. AUGUSTUS: a Web server for gene finding in eukaryotes. *Nucleic Acids Res* 32:W309–W312. <https://doi.org/10.1093/nar/gkh379>.
- 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>.