DISEASE NOTES

OPEN

First Report of Tomato Apical Leaf Curl Virus Infecting Tomato in Brazil

J. G. Batista, F. L. Melo, R. C. Pereira-Carvalho, D. M. T. Alves-Freitas, and S. G. Ribeiro

Affiliations

Published Online: 7 May 2019 | https://doi.org/10.1094/PDIS-09-18-1636-PDN

Tomato (*Solanum lycopersicum*) is one of the most important vegetable crops in Brazil. The occurrence of begomovirus (genus *Begomovirus*, family *Geminiviridae*) infections is a predominant biotic constraint affecting the tomato production in the country and can cause up to 100% yield losses (**Inoue-Nagata et al. 2016**). Besides the plethora of tomato-infecting begomoviruses present in South America, new monopartite divergent geminiviruses were recently identified, tomato-associated geminivirus 1 (TaGV1) in Brazil (**Fontenele et al. 2017**) and tomato apical leaf curl virus (ToALCV) in Argentina (**Vaghi Medina et al. 2018**). In 2016, 15 tomato samples showing symptoms of mosaic, leaf curling, and necrosis were collected from an experimental field in Brasília, DF, Brazil. Total DNA was extracted from each sample using the cetyltrimethylammonium bromide method and was used in rolling circle amplification (RCA) reactions with phi-29 DNA polymerase (**Inoue-Nagata et al. 2004**). RCA-amplified samples were pooled and sequenced in an Illumina Hi-Seq2500 platform at Macrogen (South Korea) using a Nextera DNA Library Prep kit. The sequencing generated 21,128,652 (2 × 100 paired-end) reads, which were processed and assembled with CLC Genomic Workbench version 9.0 (Qiagen Bioinformatics). The resulting contigs (44,967 contigs) were compared with a local viral RefSeq database using BlastN and BlastX with Geneious R10.2. One circular contig (2,875 nucleotides) was identified exhibiting 96% identity to the ToALCV genome. Based in the contig sequence, primers Cap1PstIF (5'-CTGCAGAYTTGCGCGGATCGATTAAT-3') and Cap1PstIR (5'-CTGCAGAAATGCGTTGTAACTTCTCGGATAT-3') overlapping in a *Pst*I site were designed and used in polymerase chain reactions (PCRs) to detect individual infected plants and recover the complete viral genome. A fragment of ~2.9 kb was amplified only from one of the 15 initially collected samples (FAL-18). This fragment was cloned and was sequenced using Sanger methodology. The sequence from clone ToALCV:BR:Brasilia:Tom18 (MH539677) displayed 99% identity with the contig identified in the Illumina sequencing data and 96% identity with the Argentinian isolates of ToALCV (MG491195 to MG491197). To confirm the PCR diagnosis, Southern hybridization analysis was conducted with the total DNA from all plant samples using ^{32}P-labeled ToALCV:BR:Brasilia:Tom18 complete genome as a probe, and the typical geminivirus ssDNA and dsDNA replicative intermediate forms were observed only in the sample FAL-18. The complete genome of ToALCV:BR:Brasilia:Tom18 is 2,875 nt long with six open reading frames (ORFs). The nucleotide sequences of the ORFs and the deduced amino acid sequences of the proteins of ToALCV:BR:Brasilia:Tom18 share high identities with those of the Argentinian isolates. For V1, V3, C1, C1:C2, and C3 the identities are 96 to 97% and 94 to 98% for nucleotide and amino acid sequences, respectively. V2 shares 97% nucleotide and 92% amino acid identities with ToALCV-AR isolates. This is the first report of the occurrence of ToALCV in Brazil. Additional studies are needed to better understand the biology of ToALCV, its host range, and vector transmission and to evaluate the risk of ToALCV for the tomato crop in Brazil.

Funding: Financial support was provided by grants from Empresa Brasileira de Pesquisa Agropecuária, Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), and Fundação de Apoio à Pesquisa do Distrito Federal. J. G. Batista was supported by a scholarship from CAPES and D. M. T. Alves-Freitas by a fellowship from CNPq.

Vol. 103, No. 6
June 2019

ISSN: 0191-2917
e-ISSN: 1943-7692

Caption

Green mottle mosaic and leaf deformation symptoms on watermelon (Sui, Li, Shamimuzzaman, Wu, and Ling). Photo credit: K.-S. Ling. Postharvest rot on cucumber caused by *Ceratocystis fimbriata* (Li, Xu, Zhang, Song, Xie, Sun, and Huang). Photo credit: H. Song.

Metrics

Downloaded 486 times

Article History

Issue Date: 6 Jun 2019
Published: 7 May 2019
First Look: 25 Nov 2018
Accepted: 22 Nov 2018

Page: 1443

Information

Funding

Empresa Brasileira de Pesquisa Agropecuária
Conselho Nacional de Desenvolvimento Científico e Tecnológico
Fundação de Apoio à Pesquisa do Distrito Federal