A NEW BIPARTITE BEGOMOVIRUS INFECTING TOMATOES IN BRAZIL

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Abstract:

Brazil is a center of diversity of begomoviruses, presenting a large number of species infecting cultivated and non-cultivated plant hosts. Currently, members of seventeen species are known to infect tomato (*Solanum lycopersicum*) in Brazil. However, there is great variation in distribution and predominance, with only a few species being widely disseminated in the field. In this study we report a new begomovirus found in tomato samples collected in fields located near the city of Altamira, state of Pará. Total DNA was extracted from the samples and used as a template for rolling circle amplification (RCA). Amplification products were cleaved with *restriction enzymes* and transformed into *Escherichia coli* DH5α. Viral inserts were sequenced commercially by primer walking. Full-length genomes were assembled using Geneious v. 8.1. Sequences were initially analyzed using BLASTn, and identities with the closest begomoviruses were calculated with Species Demarcation Tool v.1.2 (SDT). Full-length sequences corresponding to DNA-A and DNA-B components of begomoviruses were aligned with MUSCLE implemented in MEGA v. 7.0. Phylogenetic trees based on DNA-A and DNA-B alignments were generated by Bayesian inference using MrBayes v. 3.2.6, with the nucleotide substitution model selected by MrModeltest v. 2.2. The DNA-A sequences from the two samples showed 99,62% sequence identity amongst themselves and a maximum sequence identity of 84% with the DNA-A sequence of *Abutilon mosaic Brazil virus* (AbMBV; FN434438). In phylogenetic analysis based on DNA-A and DNA-B alignments, the isolates clustered with AbMBV and corchorus mottle virus (JQ805781). Based on the International Committee on Taxonomy of Viruses (ICTV) species demarcation criterion for the genus *Begomovirus*, a new species was thus identified, for which the name *Tomato chlorotic leaf curl virus* (ToCLCV) is suggested. This is the first report of a begomovirus in tomatoes in the state of Pará. Strikingly, despite the large number of begomoviruses already reported in tomato in Brazil, news species can still be detected in this host. In reality, considering the small number of samples from the Northern region of Brazil that have been analyzed in this and in previous studies, it is possible that the true extent of the begomovirus species diversity in tomatoes in this vast region is actually much higher. **Financial Support:** CNPq, Fapemig, Norte Energia S.A.

Keywords: RCA, Solanum lycopersicum, ToCLCV