(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.

Palavras-chaves: RCA, Solanum lycopersicum, ToCLCV

Papaya meleira virus (PMeV) can survive in undifferentiated papaya cells.

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Resumo

Carica papaya L. has been extensively cultivated in tropical and subtropical regions. However, several orchards are destroyed by papaya sticky disease 'PSD' in worldwide. PSD is associated with a complex formed between a toti-like virus, papaya meleira virus (PMeV) and an umbra-like virus, papaya meleira virus 2 (PMeV2). Multiple evidence has been suggesting that PMeV can adopt a persistent lifestyle in papaya, as this virus does not induce symptoms and is transmitted vertically through seeds in cv. Maradol. Also, PMeV lacks a movement protein which leads the hypothesis that like persistent viruses, PMeV may be found in every tissue, including undifferentiated meristematic cells and moves when cell division occurs. To prove this point we reprogrammed papaya cells to the undifferentiated state through the induction of callogenesis in PMeV-infected papaya tissues. After 3 months, papaya callus was removed from the induction media and submitted to PMeV detection through RT-PCR. Molecular diagnosis assay showed that 50% of the 3-month-old callus tissue were infected with PMeV. The absence of PMeV in 50% of the callus samples may be explained by the faster division in the callus compared to the ability of the virus to multiply, which results in a competition between virus and host by molecules of the host itself. On the other hand, the detection of PMeV in the other 50% samples shows this virus can survive and replicate in undifferentiated cells. Moreover, as vascular connections are disrupted in callus tissue, the detection of PMeV in callus samples reinforces the idea that this virus could move simultaneously with cell division. PMeV2 was not detected in callus samples. In conclusion, this work provides insights into PMeV survival and movement through cells and reinforces the persistent lifestyle of this virus in papaya plants.

Financial Support: FAPES, CAPES, CNPq.

Palavras-chaves: Persistent Plant virus, PMeV complex, Plant tissue culture, Carica papaya

A NEW BEGOMOVIRUS INFECTING Hibiscus sp. IN BRAZIL

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Resumo

A high diversity of begomoviruses can be found in non-cultivated plants in Brazil, particularly in plant species of the Malvaceae, Fabaceae and Solanaceae families. These plants may act as natural begomovirus reservoirs and as sources of genetic variability, fulfilling an important ecological role. In this study we identified a new begomovirus infecting a *Hibiscus* sp. (Malvaceae) plant collected in 2016 near the city of Igarapé Miri, state of Pará, in the Northern region of Brazil. Total DNA from the sample was extracted and used as a template for rolling circle amplification (RCA). Amplification products were cleaved with restriction enzymes and transformed into *Escherichia coli* DH5α. The viral inserts corresponding to DNA-A and DNA-B begomovirus components were completely sequenced by primer walking and the full-length sequences were assembled using Geneious v. 8.1. The 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 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 sequences showed of a maximum DNA-A nucleotide identity of 79% with *Sida yellow mosaic Yucatan virus* (SiYMYuV). In the DNA-A-based phylogenetic tree, the isolate clustered with *Tomato golden mosaic virus* (TGMV), *Sida mosaic Bolivia virus* 2 (SiMBoV 2) and *Cleome leaf crumple virus* (ClLCV). The DNA-B was most closely related to *Tomato chlorotic mottle virus* (ToCMoV), *Tomato common mosaic virus* (ToCmMV) and *Blainvillea yellow spot virus* (BlYSV). According to the current taxonomic criteria established for the genus *Begomovirus*, the virus corresponds to a new species, for which the name *Hibiscus golden mosaic virus* (HGMV) is proposed. Non-cultivated plants have an important ecological role, since they are reservoirs of viruses for cultivated plants, especially between growing seasons. In addition, the great biodiversity of begomoviruses in these plants may contribute to the emergence of new, better adapted viruses in cultivated plants (which is highlighted by the close relation between HGMV and viruses found in cultivated plants). This is the first report of a begomovirus in *Hibiscus sp.* in the Northern region of Brazil. **Financial Support:** CNPq, Fapemig.

Palavras-chaves: begomoviruses, non-cultivated plants, RCA

VIRUS INDUCED GENE SILENCE (VIGS) FOR VALIDATION OF GENES ASSOCIATED TO THE LOCUS OF RESISTANCE TO BLUE DISEASE IN COTTON USING TOBACCO RATTLE VIRUS (TRV)

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