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Passiflora edulis: new natural host of *Melochia yellow mosaic virus* in Brazil

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Abstract
Begomovirus infections in *Passiflora* plants in Brazil have increased in recent years. This contribution reports natural infection of *Passiflora* plants by Melochia yellow mosaic virus (MelYMV) in the state of Mato Grosso do Sul. MelYMV was transmitted to *Passiflora* plants by biolistics but not by *Bemisia tabaci* MEAM1 and MED. To our knowledge this is the first report of MelYMV infecting *Passiflora* plants.

Keywords Passifloraceae · Begomovirus · *Bemisia tabaci* · Diagnosis

Brazil is the world's largest producer of yellow passion fruit (*Passiflora edulis*). *Passiflora* plants are affected by the potyvirus Cowpea aphid-borne mosaic virus (CABMV) in all producing regions in the country. Recent years have seen frequent reports of *Passiflora* plants infected by begomoviruses, transmitted by the whitefly *Bemisia tabaci* (Novaes et al. 2003; Ferreira et al. 2010; Mituti et al. 2019). In 2016, eight samples of *Passiflora* plants, variety Sol do Cerrado, exhibiting symptoms of begomovirus infection including mosaic, yellow spots, leaf curling and malformation were collected in an orchard in the state of Mato Grosso do Sul. Total DNA was extracted from each sample according to the protocol described by Doyle and Doyle (1990) and analysed by PCR using the universal pair of degenerate primers PAR1c496/PAL1v1978 (Rojas 1993), which amplify part of the ORF AC1 (Rep), the common region and part of the ORF AV1 (CP) of DNA-A of begomoviruses. Two randomly chosen amplicons of 1100 bp were directly sequenced at Macrogen, Seoul, South Korea. Comparison of nucleotide sequences of different begomoviruses available from GenBank revealed 94–95% identity with the corresponding sequence of Melochia yellow mosaic virus (MelYMV) (GenBank accession no. KT201153), previously reported to infect plants of *Melochia* sp. (Fiallo-Olivé et al. 2015). To obtain the complete nucleotide sequence of the DNA-A, three pairs of primers were synthesised based on the nucleotide sequence of MelYMV (749F- 5'-CCGTGATCGTTTCAAGTCA-3′ and 2123R - 5′-GCAATAAACGCCTCCTCAAA-3′; 247F - 5'-ATAATGCCTAAGCGGGAAGC-3′ and 630R - 5′-AGGCACTAAACGCCTTCTCA-3′; 889F - 5′-GGRTTHGARGCATGSGTACATG-3′ and 325R - 5′-GCCYATRTAYAGRAAGCCMAG-3′). The amplicons obtained by PCR were directly sequenced and the DNA-A sequence was assembled with Geneious 8.1.9 (Biomatters Ltd.). The DNA-A is 2595 nt long (GenBank accession no. MG461177) and showed 95% identity with MelYMV DNA-A (KT201153). The DNA-A amplicon obtained from total DNA of field-infected *Passiflora* leaves by rolling-circle amplification (RCA) was inoculated using the PDS1000/He biolistics system

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Fig. 1 Symptoms of *Melochia yellow mosaic virus* in leaves of *Passiflora edulis* Sims. **a** plant of variety FB-200 inoculated by biolistics. **b** field-infected plant of variety Sol do Cerrado

(Bio30 Rad) into nine *Passiflora* plants of variety FB-200 and five plants of *Sida rhombifolia*. After 30 days, three *Passiflora* plants developed symptoms similar to those exhibited by field-infected plants (Fig. 1), and MelYMV infection was confirmed by PCR. Plants of *S. rhombifolia* were not infected. Transmission assays were performed with the whiteflies *B. tabaci* MEAM1 and MED, to *Passiflora*, cotton, tomato, pepper and *S. rhombifolia* plants, using experimentally infected *Passiflora* leaves as sources of inoculum. None of the inoculated test-plants exhibited symptoms of viral infection, nor was MelYMV detected by PCR 30 days after inoculation. Absence of experimental transmission of a different begomovirus by *B. tabaci* MEAM1 was previously reported by Novaes et al. (2003). To the best of our knowledge, this is the first report of natural infection of *Passiflora* plants by MelYMV. Studies are needed to evaluate the incidence of this begomovirus in *Passiflora* orchards in Mato Grosso do Sul and the potential to reduce the production of passion fruit.

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