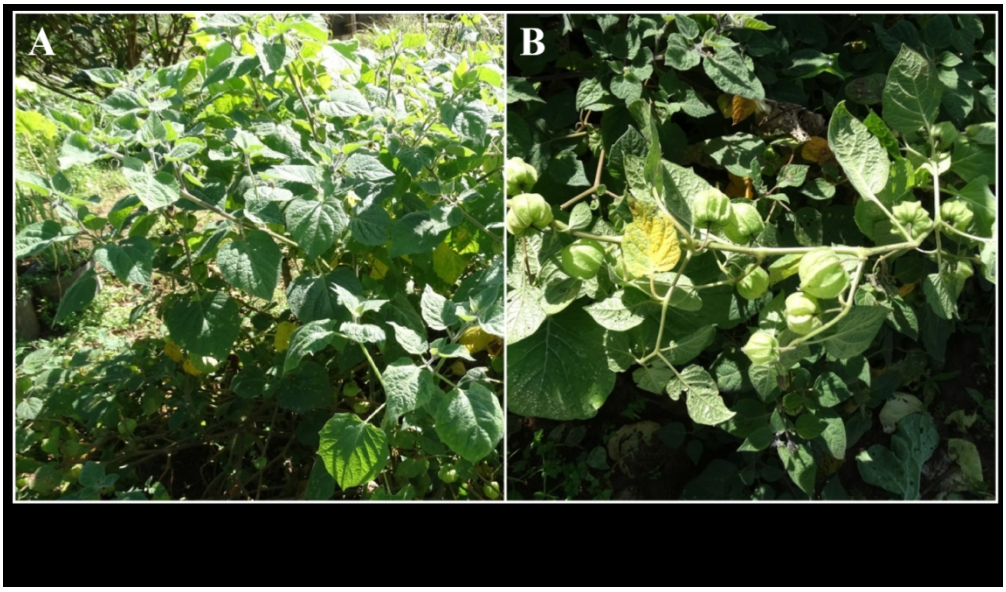

Figure 1: Physalis angulata (A) asymptomatics and (B) exhibiting typical begomovirus symptoms (apical chlorosis).

245x143mm (150 x 150 DPI)

Identification of *Physalis angulata* (Solanaceae) as a Natural Alternative Weed Host of Tomato Severe Rugose Virus in Brazil

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A diverse array of *Begomovirus* species (family *Geminiviridae*) can induce economically important diseases in all major tomato-producing areas in Brazil (Fernandes et al., 2008). Weeds of the Solanaceae family have been identified as important alternative hosts of the viral species reported infecting tomato crops in the country (Barreto et al., 2013). In 2016, about 10% of the plants of the weed *Physalis angulata* L. were observed with begomovirus-like symptoms (apical chlorosis and stunting; Supplementary Fig. 1) around and within tomato fields in Venda Nova do Imigrante–ES (Southeast Brazil). Leaf tissue was collected from ten symptomatic and five healthy-looking plants, respectively. Total DNA was extracted using the CTAB method in combination with organic solvents (Boiteux et al., 1999). PCR assays with the universal begomovirus primers for DNA-A and DNA-B detection (Rojas et al., 1993) were carried out using total genomic DNA samples (20 ng/μL) as templates. Amplicons of ≈ 1,100 bp and ≈ 550 bp were obtained only in the ten symptomatic samples, which are in agreement with the expected fragment sizes of DNA-A and DNA-B from begomoviruses (Rojas et al. 1993). These amplicons were directly Sanger sequenced at the Embrapa Vegetables Genomic Analysis Laboratory. BLASTn analyses of the amplicon sequences indicated high nucleotide identities (99%, 98%) with DNA-A and DNA-B of tomato severe rugose virus (ToSRV) isolates (accession numbers JX415196, MG837739) from Brazil, suggesting the infection of ToSRV in these plants. To fully prove the infection and to characterize the ToSRV isolate associated with *P. angulata*, the DNA samples were submitted to rolling circle amplification (RCA) method followed by Nanopore sequencing (Oxford Nanopore Technologies), as previously described (Naito et al., 2019). The full-length DNA-A component of one isolate obtained from *P. angulata* (MN059848) was 98% identical to the DNA-A genome of a Brazilian ToSRV isolate from tomato (JX415196). The complete DNA-B sequence from the *P. angulata* isolate (MN059849) was 96% identical

to the DNA-B genome of a tomato-infecting ToSRV isolate obtained in Southeast Brazil (MG837739). The complete DNA-A component (2,592 nts) displayed all genomic features of the New World species, with one virion-sense ORF (AV1) and four complementary sense ORFs (AC1, AC2, AC3, and AC4). The complete DNA-B component (2,571 nts) displayed two ORFs, virion-sense (BV1) and complementary sense (BC1). The common regions of DNA-A and DNA-B components were identified (183 nts in length) and the presence of iterons was confirmed. ToSRV is so far the most prevalent tomato-infecting begomovirus in Brazil (Fernandes et al., 2008). To our knowledge, this is the first report of natural infection of *P. angulata* by ToSRV, expanding the viral host range to this widespread tropical and subtropical weed. Considering that *P. angulata* may function as a relevant natural source of ToSRV inoculum to tomato crops across tropical and subtropical regions, control of the weed should be a part of the integrated management of ToSRV in tomato crops.

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