First Report of Sweet Potato Symptomless Virus 1 Infecting Ipomoea batatas in Brazil

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DISEASE NOTES

C. A.Souza, Dept. Fitopatologia, Universidade de Brasília (UnB), Brasília–DF, Brazil; M.Rossato, Dept. Fitopatologia, UnB, Brasília–DF, Brazil; F. L.Melo, Dept. Biologia Celular, UnB, Brasília–DF, Brazil; L. S.Boiteux, Embrapa Vegetable Crops (CNPH), Brasília–DF, Brazil; and R. C.Pereira-Carvalho,†Dept. Fitopatologia, UnB, Brasília–DF, Brazil.

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Sweet potato (*Ipomoea batatas* L. [Lam.]) is the seventh most consumed crop in the world (Vargas et al. 2017). Mixed infections of disease-inducing as well as latent viruses may intensify symptoms and result in severe yield and quality losses in this vegetatively propagated crop (Paprotka et al. 2010). Therefore, early detection of novel viruses is of great importance for preemptive management of these pathogens in sweet potatoes. Recently, the complete genome of sweet potato symptomless virus 1 (SpSV/1), a putative species of the genus *Mastrevirus* (family *Geminiviridae*) was characterized (Cao et al. 2017). To examine the occurrence of this virus in Brazil, we performed a nationwide survey using polymerase chain reaction (PCR) assays with SpSV/1-specific primers. A total of 100 leaf samples (with and without conspicuous virus-like symptoms) were collected in five Brazilian regions: North (1), Southeast (2), South (4), Central-East (19), and Northeast (74 samples). Genomic DNA was extracted using a modified cetyltrimethylammonium bromide method (Boiteux et al. 1999) and used as a template for an initial enrichment of circular molecules using a rolling circle amplification (RCA) method (Inoue-Nagata et al. 2004). RCA samples were used as templates in PCR assays with a pair of SpSV/1-specific primers (Detect-1F, 5'-CCTAAGTCGTCGTCCGATAG-3'; and Detect-1R, 5'-TTGAGTCCAGGTAAACTGAGC-3') designed to amplify a 417-nt fragment encompassing the V1 (CP) and V2 (MP) genes (Cao et al. 2017). Fifty samples out of 100 were positive for SpSV/1: one sample from the North, one from the Sou

theast, two from the South, six from the Central-East, and 40 from the Northeast. The gel-purified amplicons were sequenced and displayed 98% nucleotide identity with SpSV/1 sequences deposited in GenBank. Furthermore, the complete genome of one SpSV/1 isolate (cultivar Branquinha collected in the Northeast region) was amplified with the primers Full-4F (5'-TGGATATTAGTAAACCGGGTCA-3') and Full-4R (5'-CACCATTCGACGTCACAA-3') (Cao et al. 2017), cloned, and sequenced. The resulting sequence (MG680260) displayed 99% identity at the nucleotide level with SpSV/1 isolate (KY565231) reported in Taiwan (Cao et al. 2017). SpSV/1 could not be recovered after grafting stem segments of all 50 infected sweet potato accessions onto *I. setosa*. SpSV/1 was eliminated (as confirmed after PCR assays) from 2 out of 22 virus-infected plants by meristem tip culture. The economic importance of SpSV/1 infection is yet unknown, but the occurrence of this mastrevirus in the New World area is a novelty. The detection of SpSV/1 in 50% of the samples collected across all major Brazilian regions indicates a broad distribution of this virus in the country. Further studies should be carried out to understand the interaction of SpSV/1 with other economically important viruses infecting sweet potatoes in Brazil, because mixed infections with potyviruses and/or begomoviruses were observed in the majority of our samples.

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