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DISEASE NOTES

First Report of *Papaya ringspot virus*-Type W Infecting *Fevillea* Species (Cucurbitaceae) in South America

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ABSTRACT

Nhandirobas (*Fevillea cordifolia* L. and *F. trilobata* L.) are neotropical species that are currently being developed in breeding programs as candidate crops for seed-oil extraction and biodiesel production (Rech and Arber 2013). In 2013, field-grown *Fevillea* plants at two sites of the Federal District (DF), Central Brazil, were found exhibiting symptoms characterized by foliar mosaic with blister-like patches. Affected fields were cultivated with two distinct *Fevillea* species: *F. cordifolia* (in Planaltina–DF) and *F. trilobata* (in Gama–DF). All 20 samples obtained from symptomatic plants reacted with polyclonal antiserum against *Papaya ringspot virus*-type W (PRSV-W) in either PTA-ELISA or NCM-ELISA. No reactions were observed with antisera against *Zucchini yellow mosaic virus* (ZYMV), which was previously detected in *F. trilobata* in Brazil (Boiteux et al. 2013), *Cucumber mosaic virus*, *Watermelon mosaic virus*, or *Zucchini lethal chlorosis virus*. One PRSV-W isolate obtained from *F. trilobata* was mechanically transmitted to 10 healthy plants of *F. trilobata*, *Cucurbita pepo* 'Caserta,' and *Citrullus lanatus* 'Charleston Gray' and induced severe mosaic and blistering symptoms10 days after inoculation in all hosts. However, the isolate from *F. trilobata* did not infect *Carica papaya* 'Formosa' seedlings. *F. trilobata* infection by PRSV-W was also confirmed using total RNA preparations obtained from symptomatic field-grown plants and RT-PCR. Amplicons of 643 bp were obtained from five randomly selected samples using primers specific for the coat protein (CP) region of the PRSV genome (Ali et al. 2004). Nucleotide alignments of a 630 bp sequence obtained with the primer pair *2F* (5′-GTCTGATGGTTTGGTGTATCG-3′) and *Not I* (dT)18 (5′-AACTGGAAGAATTCGCGGCCGCACGAAT$_{18}$)-3′)] revealed a 97% identity of the *F. trilobata* isolate (GenBank accession KX196160) with the corresponding genomic

segments of a Brazilian PRSV-W isolate from *C. pepo* (DQ374152). Previously, the complete genome sequence of one PRSV-W haplotype from *F. cordifolia* (KP462721) derived from RNA seq libraries synthesized from the whole seed tissues indicated an identity of 96% with the same DQ374152 isolate (Inoue-Nagata et al. 2007). PRSV-W infection was quite severe in plants of both *Fevillea* species and might induce substantial yield losses in early-infected plants. To our knowledge, this is the first report of species from the genus *Fevillea* as natural hosts of PRSV-W. Our results also indicate that both *Fevillea* species might be sources of virus inoculum for infection of melon, cucumber, watermelon, and zucchini crops to which PRSV-W infection induces severe yield and quality losses in neotropical areas (Inoue-Nagata et al. 2007; Rezende and Pacheco 1998).

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