**DISEASE NOTE**

**FIRST REPORT OF DAHLIA LATENT VIROID IN TURKEY**

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Dahlia (Dahlia sp.) is a host of dahlia latent viroid (DLVd), but no information is available on the occurrence of this viroid in Turkey. Thirty asymptomatic dahlia plants were randomly selected in gardens of the cities of Gaziantep and Adana (Turkey) for this study. Total RNA was extracted from approximately 200 mg of leaf tissue of the sampled plants with AxyPrep Multisource Total RNA Midiprep Kit (Axygen Biosciences, USA) and screened by RT-PCR with primers DLVd-P1 (5’-GGGGCTCCTCAGAGAGTCTC-3’) and DLVd-P2 (5’-GGGGCAACTCCGAGAGTGCTG-3’) (Verhoeven et al., 2013). Twelve plants proved to be infected with DLVd. The amplified DNA bands of the expected size (ca. 340 nucleotides) were purified and directly sequenced. The sequence of five DLVd genetic variants from Turkey showed 98 to 100% maximum nucleotide identity with a viroid from the Netherlands (GenBank accession AJ962673). The sequence of five DLVd genetic variants from Turkey showed 98 to 100% maximum nucleotide identity with a viroid from the Netherlands (GenBank accession AJ962673). In 2015, cladodes of Nopalea cochenillifera showing brown and circular to elliptical spots were sampled from 12 fields of the State of Pernambuco, Brazil with a prevalence of 100%. Small pieces of symptomatic tissues were surface sterilized, plated onto potato dextrose agar, and kept at 28°C for 7 days. Four isolates (CMM 2118, CMM 2166, CMM 2207, CMM 2228), produced white colonies, reverse pale yellow, conidia, hyaline, fusiform, 10.4-18.4 × 2.8-4.3 μm (n = 50). One isolate (CMM 2159) presented white colonies, becoming grey at the centre, conidia hyaline, cylindrical, 11.13-17.3 × 3.9-5.4 μm (n = 50). These morphological characteristics are consistent with the descriptions of C. siamense and C. fructicola, respectively (Prihastuti et al., 2009). For molecular identification, the ITS, TUB-2 and ApMAT loci were amplified, sequenced and analyzed using Bayesian inference, including published ITS, TUB-2 and ApMAT data for Colletotrichum spp. (Sharma et al., 2014). The isolated fungi grouped with the C. siamense and C. fructicola clades. Sequences of the isolates were deposited in GenBank (ITS, KX129708 to KX129712; TUB-2, KX129713 to KX129717; and ApMAT, KX129718 to KX129722). Pathogenicity tests with all five isolates of Colletotrichum were conducted on 15 healthy superficially sterilized detached cladodes per isolate. Scalpel-wounded and unwounded cladodes were inoculated with 2 × 10⁵ conidial suspensions. Untreated controls were inoculated with sterile water. Cladodes were kept in a humid chamber for 72 h at 25°C in the dark. Fifteen days after inoculation all cladodes showed brown spots, with an average length of 1.1 cm and depth of 0.5 cm. Control cladodes remained symptomless. To our knowledge, this is the first report of C. fructicola and C. siamense causing cladode brown spot in Nopalea cochenillifera in Brazil and worldwide.

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