

DISEASE NOTE

FIRST REPORT OF DAHLIA LATENT
VIROID IN TURKEYN. Önelge¹, B. Ertuğrul² and P. Güler³¹*Çukurova University, Agriculture Faculty,
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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 genetic variant from the Netherlands (GenBank accession No. JX263426). The occurrence of DLVd in dahlia was confirmed by viroid purification and sequential polyacrylamide gel electrophoresis (Semancik *et al.*, 1988). To our knowledge, this is the first report of DLVd on dahlia plants in Turkey.

Verhoeven J.Th.J., Meekes E.T.M., Roenhorst J.W., Flores R., Serra P., 2013. Dahlia latent viroid: a recombinant new species of the family *Pospiviroidae* posing intriguing questions about its origin and classification. *Journal of General Virology* **94**: 711-719.

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DISEASE NOTE

FIRST REPORT OF *COLLETOTRICHUM*
SIAMENSE AND *C. FRUCTICOLA*
CAUSING CLADODE BROWN SPOT IN
NOPALEA COCHENILLIFERA IN BRAZILC. Conforto¹, N.B. Lima², J.M. Garcete-Gómez³,
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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.

Prihastuti H., Cai L., Chen H., McKenzie E.H.C., Hyde K.D., 2009. *Fungal Diversity* **39**: 89-109.

Sharma G., Pinnaka A.K., Shenoy B.D., 2014. Resolving the *Colletotrichum siamense* species complex using ApMat marker. *Fungal Diversity* **71**: 247-264.

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