

DISEASE NOTE

FIRST REPORT OF *AGERATUM YELLOW VEIN VIRUS* AND *PAPAYA LEAF CURL GUANGDONG VIRUS* ON *EUPHORBIA PULCHERRIMA* IN CHINA

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Three *Euphorbia pulcherrima* (poinsettia, family *Euphorbia*) plants showing leaf curl and vein thickening symptoms were collected in Fujian Province, China, in 2006. Total DNA was extracted from each sample using a CTAB method. A fragment of approximately 500 bp was amplified by PCR in each sample, using the special degenerate primer pair PA/PB (Deng *et al.*, 1994). PCR products were gel-purified, ligated into pMD18-T vector (Takara Biotechnology, China), and sequenced. Six clones from each sample were sequenced. Phylogenetic analysis of the 500 bp fragments showed that these sequences formed three distinct branches, and sequence alignment among each branches (63.3% to 73.6%) in one sample indicated that each sample might be mixed infected by three distinct viruses. FE01, FE02 and FE03 isolates representing each virus were further studied. To amplify the full-length DNA-A of the three isolates, three pairs of abutting primers (FE01-F 5'-CCTTAGCAAGTAGTTCATTCCG-3'/FE01-R 5'-GACATGTCTTTGTCAGTTAGTGG-3', FE02-F 5'-CCACTCAGAACGCTCCCTCA-3'/FE02-R 5'-GTTCGTGGTAGGGACCACTT-3', and FE03-F 5'-TGCGCGCTCATCGCTTAGT-3'/FE03-R 5'-ATTATATTGGTCGAGGGCCCAC-3') were designed based on the obtained sequences, respectively. They were determined to be 2751 (FJ487911), 2754 (FJ495183) and 2733 (FJ495184) nucleotides, and had the typical genome organization of Old World monopartite begomoviruses, respectively. Sequence comparisons revealed that the three isolates were most closely related to those of *Euphorbia leaf curl virus* (ELCV, AJ558121), *Ageratum yellow vein virus* (AYVV, FJ869908) and *Papaya leaf curl Guangdong virus* (PaLCuGDV, FJ869907), with 92.8%, 99.8% and 99.1% sequence identity, respectively. The attempt to detect a DNA-B or a betasatellite component by using specific primers (Bridson *et al.*, 2002; Rojas *et al.*, 1993) was unsuccessful. To the best of our knowledge, this is the first report of AYVV and PaLCuGDV and mixed infection of three begomoviruses in poinsettia in China.

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Received September 17, 2014
Accepted December 3, 2014

DISEASE NOTE

FIRST REPORT OF *NEONECTRIA RADICICOLA* ASSOCIATED WITH ROOT ROT DISEASE OF OLIVE IN TUNISIA

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Olive (*Olea europaea*) is an economically important crop in Tunisia. During surveys of olive diseases conducted in 2013 in Tunisia, symptoms of leaf wilting and chlorosis, Brown-to-black discoloration of the wood in cross-sections of the stems and necrotic lesions in the roots were observed on young olive trees. Isolation of the pathogen was performed from 15 infected root and stem samples plated onto PDA medium amended with 50 µg ml⁻¹ of streptomycin sulfate. Fungal colonies were then cultured on synthetic nutrient-poor agar medium. All isolates were identified as *Cylindrocarpon* sp. based on colony morphology and conidial characteristics (Booth, 1966). The isolates developed abundant floccose mycelium, which varied in color from brown-yellow to sepia. All isolates produced only macroconidia, which were hyaline, straight, and predominantly three septate measuring 15.75 to 29.50 µm × 3.25 to 4.75 µm. Identity of these isolates was confirmed by sequencing the internal transcribed spacer region, which was amplified using primer pair ITS1 and ITS4 (White *et al.*, 1990). The ITS sequences were deposited in GenBank (KM503139). These sequences revealed 98% genetic identity with those of *Neonectria radiculicola* the anamorphic form of *Cylindrocarpon* species available in GenBank. Pathogenicity of *N. radiculicola* in olive cv. Chemlali was evaluated using three isolates. Three months after inoculation, the inoculated plants developed wilting and root symptoms similar to those observed in the field. *N. radiculicola* was recovered from all the symptomatic plants. This is the first report of *N. radiculicola* causing root rot of olive in Tunisia, which may potentially affect the sustainability of olive nurseries.

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Received September 19, 2014
Accepted September 29, 2014