DISEASE NOTE

OCCURRENCE OF ALTERNARIA SPECIES INVOLVED IN FRUIT BLIGHT OF PISTACHIO IN TUNISIA

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During summer 2007-2010, a new disease was observed on pistachio (Pistacia vera L.) cv. Mateur in several orchards of Tunisia. Symptoms on the nuts consisted of black lesions with red halos, resulting in yield losses often exceeding 20%. A fungus recovered on potato dextrose agar (PDA) from surface-disinfected symptomatic nuts, produced cottony colonies characterized by an abundant branched, brownish, septate mycelium which, with time, turned olive-green to dark olive-green due to abundant sporulation. Conidiophores were simple or branched, septate, straight or flexuous, pale olivaceous-brown, and bore several conidial scars. Conidia were 100-200 mm in size, obclavate to ellipsoid, multiseptate and formed in single or, more often, branched chains. Based on these morphological characters, the fungus was identified as Alternaria sp. (Fr.) Keissler (Ellis, 1971). Pathogenicity tests were carried out on detached fresh pistachio nuts inoculating the hull (Fr.) Keissler (Ellis, 1971). Pathogenicity tests were carried out on detached fresh pistachio nuts inoculating the hull (Fr.) Keissler (Ellis, 1971). Pathogenicity tests were carried out on detached fresh pistachio nuts inoculating the hull (Fr.) Keissler (Ellis, 1971).


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DISEASE NOTE

MIXED INFECTION OF PAPAYA LEAF CURL CHINA VIRUS AND SIEGESBECKIA YELLOW VEIN VIRUS IN SIEGESBECKIA ORIENTALIS IN CHINA

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Six samples (SO1-SO6) of Siegesbeckia orientalis showing yellow vein symptoms were collected in Fujian province of China in 2008. Total DNA was extracted to amplify begomoviral components according to Haible et al. (2006). Two virus isolates denoted Fz10 and Fz11, to which a betasatellite (Fz115) was associated, were detected in sample SO3, and were selected for further sequence analysis. The complete DNA-A sequence of Fz10 (JF682837) comprised 2,754 nucleotides (nts). The complete DNA-A (JF682838) and betasatellite (JF682839) sequences of Fz11 consisted of 2,770 nts and 1,331 nts, respectively. Sequence alignments using MegAlign (DNASTAR, USA) showed that the complete DNA-A of Fz10 has the highest levels of nucleotide sequence identity (99.2%) with Papaya leaf curl China virus (PaLCuCNVTom[VN:Hat:Ts:05], DQ641700). The complete DNA-A of Fz11 has the highest sequence identity (93.7%) with Siegesbeckia yellow vein virus (SbYVV-[CN:Gd13:04], AM183224) while the betasatellite had 61.7% sequence identity with SbYVV betasatellite (SbYVB-[CN:Gd24:04], AM230644). This indicates that Fz10 and Fz11 are isolates of PaLCuCNV and SbYVV, respectively, while, Fz115 appears to be a new satellite species, for which the Siegesbeckia yellow vein Fujian virus betasatellite (SYV) is proposed. The fact that PaLCuCNV infecting tomato in China. Journal of Zhejiang University-Science B 11: 109-114.
