DISEASE NOTE

A POTYVIRUS OF MALVA NEGLECTA IN IRAN

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During a spring 2012 survey, three malva (Malva neglecta Wallr.) leaf samples showing virus-like symptoms were collected in or around vegetable fields in the Khuzestan province of Iran. Leaf samples were tested for the presence of potyviruses by indirect (ELISA using the “poty group test” kit (Bioreba, Switzerland). One of the three samples, collected from an eggplant field, strongly reacted to the “poty group” antibodies. Mosaic and vein yellowing symptoms were associated with the infection. Viral infection was confirmed by RT-PCR using previously described universal primers to amplify a region in the N1b gene of potyviruses (Zheng et al., 2010). The RT-PCR resulted in the amplification of an expected fragment of ca. 0.4 kb in size. The nucleotide sequence of the amplified DNA fragment was determined and deposited in GenBank as accession No. KF017608. BLAST analysis showed the highest nucleotide sequence identity (88%) of isolate Kz-W331 to the corresponding region of the tomato isolate of Malva vein clearing virus (MVCV, accession No. FJ961293). Based on these results, the malva-infecting potyvirus could be a strain of MVCV, however, further studies are necessary to confirm this hypothesis. M. neglecta has been previously reported as a reservoir host for potyviruses (Massumi et al., 2010) but this is the first report of a potyvirus infection of M. neglecta in the mid-Eurasia of Iran.


DISEASE NOTE

CRYPTOCOCCUS ADELIENSIS A YEAST SPECIES INCITING STEM CANKER ON STONE FRUIT TREES

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Yeast isolates were consistently recovered from symptomatic branches of stone fruit trees showing twig and stem cankers indistinguishable from those caused by bacterial agents, especially Pseudomonas syringae pv. syringae, which have been prevalent throughout Khorasan province (northern Iran). Dark brown to black sunken lesions develop on twigs and branches, turning to typical stem cankers upon expansion. Yeast-like round, white to light cream-coloured, mucoid colonies were the predominant or the sole colony type recovered on sucrose nutrient agar from cankers. Yeast cells were circular and ca. 6.5 μm in diameter. The internal transcribed spacer (ITS) region of the rDNA and the D1/D2 domain of the large subunit (LSU) rDNA were amplified by PCR using primer pairs ITS4/ITS5 and NL1/NL4, (Kurtzman and Robnett, 1998; White et al., 1990), respectively. PCR products were sequenced, their sequences were aligned and compared with those deposited in GenBank. Sequences of the ITS (accession No. KC479045) and D1/D2 (accession No. KC196119) of a representative isolate showed 99-100% identity with those of Cryptococcus adeliensis isolates. The fatty acid composition of a representative isolate and of the type strain of C. adeliensis (CBS 8351) was determined by gas chromatography. Both isolates shared identical fatty acid profiles, with oleic acid (C18:1) and linoleic acid (C18:2) being the major fatty acids. Canker symptoms were reproduced on peach (Prunus persica) and nectarine (P. persica var. nucipersica) budlings inoculated with yeast suspensions (5 x 107 cells/ml). The same yeast was reisolated from cankers. Stem canker caused by C. adeliensis represents a hitherto undescribed disease of fruit trees. This yeast species has previously been isolated from decaying algae and from a human patient suffering from meningitis (Scorzetti et al., 2000; Rimek et al., 2004).


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