FIRST REPORT OF HOP STUNT VIROID INFECTING CITRUS ORCHARDS IN SYRIA

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Hop stunt viroid (HSVd), genus Hostuviroidae, family Pospiviroidae, has the broadest host-range known for any viroid. It infects a large number of herbaceous and woody hosts, including cucumber, grapevine, citrus, plum, peach, pear, apricot, almond, pomegranate, fig, and jujube. During a survey of citrus for HSVd in Syria, a total of 120 trees were sampled from four commercial orchards located in Lattakia and Tartous. Total RNA was extracted from leaves following the procedure described by Foissac et al. (2001) and used in RT-PCR using primers HSVd-R (5’-CCGGGGCTCCTTTCTCAGGTAAGT-3’) homologous to nucleotide (nt) positions 59 to 82 and HSVd-F (5’-GGCAACTCTTCTCAGAATCCAGC-3’) homologous to nt positions 83 to 105 of the HSVd reference sequence (Sano et al., 1988) (GenBank accession No. NC-001351). Results of RT-PCR showed that 39 samples contained HSVd, yielding the expected DNA amplification band of ca. 302 bp in agarose gels. There were 35 infected cvs Jaffa and Valencia sweet oranges in one orchard in Tartous. The remaining four infected cv. Valencia trees were in another grove in Lattakia. None of the infected trees exhibited conspicuous HSVd symptoms as they were all grafted onto sour orange rootstock. To the best of our knowledge, this is the first report of HSVd in citrus trees in Syria.


FIRST REPORT OF CASSAVA MOSAIC VIRUS INFECTING CHILLI (CAPSICUM ANNUUM) IN INDIA


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Chilli (Capsicum annuum L.) pepper is a major vegetable crop cultivated worldwide. In the past decade, there has been a considerable decrease in chilli production due to leaf curl disease caused by begomoviruses (Raj et al., 2010). A survey of chilli fields was conducted in Kerala in 2010 to assess the occurrence of begomoviruses. As cassava plants with mosaic symptoms were found nearby chilli fields, chilli plants were suspected to be infected with cassava mosaic virus disease. Therefore, chilli leaf samples were analyzed by PCR with a primer set designed in the coat protein gene of Sri Lankan cassava mosaic virus (SLCMV) [AV1 F (AJ579307; nts 297-313)/AV1 R (AJ579307; nts 1049-1067)]. A ca. 770 bp DNA amplicon was obtained from the 13 symptomatic chilli samples tested. The PCR products from three SLCMV isolates were randomly selected and sequenced. The nucleotide sequence of two SLCMV isolates was identical and deposited in GenBank under accession No. HQ113111; the sequence of the third isolate was submitted under accession No. HQ113112. A BLAST analysis indicated a 97-98% nucleotide sequence identity of the SLCMV isolates from chilli with various SLCMV and Indian cassava mosaic virus isolates from cassava (AJ579307, AF433180, AY312989, AY998122, AJ890225, AJ890224, DQ780004, AJ890228, AJ890227). The close relationship of SLCMV isolates from chilli and cassava was confirmed by phylogenetic analysis. Tomato leaf curl New Delhi virus (ToLCNDV) was not detected in symptomatic chilli plants by PCR using virus-specific primers. To our knowledge, this is the first report of SLCMV infecting chilli in India.


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Received December 24, 2010
Accepted January 21, 2011

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Received December 9, 2010
Accepted February 2nd, 2011