

First report of *Eggplant mottled crinkle virus* in geranium in Iran

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During a survey in a commercial greenhouse in Shiraz, Iran, in September 2006, ring spots and chlorotic spots were observed on the leaves of geranium (*Pelargonium hortorum*). Disease symptoms appeared as small chlorotic spots on young leaves, then expanded and changed into rings and necrotic spots as the leaves aged. Sap was extracted from affected leaf samples in 0.1 M potassium phosphate buffer, pH 7, and mechanically inoculated onto test plants. Geranium leaves with symptoms were also used for electron microscopy and total RNA extraction. RT-PCR amplification was carried out using a primer pair designed on sequences that flank the coat protein gene (CP) of *Pear latent virus* (PeLV) (Melgarejo *et al.*, 2003). The PCR product was ligated into pTZ57R/T vector (Fermentas), cloned in *E. coli* strain DH5 α and sequenced.

Among mechanically inoculated test plants, *Chenopodium amaranticolor*, *C. quinoa*, *Datura stramonium*, *Nicotiana tabacum* var. Turkish, *Osimum basilicum*, *Phaseolus vulgaris* and *Vigna unguiculata* reacted to the virus by producing local lesions on inoculated leaves. *Cucumis sativus*, *C. melo*, *Cucurbita pepo*, *Datura metel*, *Gossypium hirsutum*, *Lycopersicon esculentum*, *N. glutinosa*, *N. rustica* and *Solanum melongena* remained symptomless after inoculation. Electron microscopy of infected geranium leaves showed the presence of many isometric particles and RT-PCR amplification produced a fragment of approximately 1200 bp. These results were verified from mechanically inoculated cowpea leaves showing necrotic local lesions. A search of the GenBank database revealed 89, 88 and 87–88% amino acid sequence identity between the CP gene (388 aa) of the geranium virus (Acc. No. EF140907) and *Lisianthus necrosis virus*

(LNV), *Eggplant mottled crinkle virus* (EMCV) and PeLV, respectively. LNV (Chen *et al.*, 2006) and PeLV (Melgarejo *et al.*, 2003) share high amino acid sequence identity with EMCV and should be regarded as strains of this virus (Koenig *et al.*, 2004). These results indicate that the toombusvirus inducing ring spots and chlorotic spots in geranium plants in Shiraz is a strain of EMCV.

Since geranium has not previously been reported as natural host of EMCV, this is both the first report of EMCV naturally infecting geranium plants and of EMCV in Iran.

Acknowledgement

This work was supported in part by funds from Center of Excellence In Plant Virology and Iranian Chapter of TWAS.

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First report of an outbreak of *Rice stripe virus* on wheat in China

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During 2004 and 2005, a disease outbreak was observed on wheat in Jiangsu province, China, with plants showing yellow stripe symptoms. *Rice stripe virus* (RSV) was detected in leaf samples by an enzyme-linked immunosorbent assay (ELISA) using RSV-specific monoclonal antibodies. Using this assay, a survey found that 84% of wheat fields were infected by RSV in Funing county in 2005, with the incidence in fields ranging from 3.33 to 70%. In other counties, 3–6% of wheat plants were found to be infected by RSV. The virus was transmitted to healthy wheat plants by the small brown planthopper, *Laodelphax striatellus*, the known vector of RSV (Toriyama, 2000). Infected plants produced yellow stripe symptoms, which were identical to those observed in fields. A virus isolate JS-YM was obtained from a wheat field in Huaian, Jiangsu province in May 2005. Total RNA was extracted from the plant and RT-PCR was performed using RSV-specific primer pairs NS2-F (TCGGATCCATGGCATTACTCCTTTTCAATG) and NS2-R (GCGTCGACTCACATTAGAATAGGACACTCA), NS3-F (TCGGATCCATGAACGTGTT CACATCGTC) and NS3-R (CAGTCGACCTACAGCACAGCTGGAGAG), and CP-F (GAGGATCCATGGGTACCAACAAGCCAG) and CP-R (TCGTCGAC-

CTAGTCATCTGCA CCTTCTG) to amplify the NS2, NS3 and nucleoprotein genes of RSV respectively. Amplicons of the expected size were obtained from diseased but not from healthy leaf samples. The PCR products were cloned and sequenced, with all the sequences confirmed by comparing duplicate clones. Alignment of the sequences (GenBank Acc. Nos. AM397832-34) showed that they shared 97.3, 97.5 and 97% sequence identity at the nucleotide level and 99, 97.6 and 98.5% at amino acid level with the NS2, NS3 and nucleoprotein genes respectively of RSV isolate T (Acc. Nos. NC_003754 and NC_003776). These results indicate that the virus associated with yellow stripe disease of wheat in Jiangsu is an isolate of RSV. RSV is already known to be common in rice crops in China (Toriyama, 2000). However, this is the first record of RSV being widespread in wheat. This has major implications for the control of the disease.

Reference

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