New Disease Reports

First report of *Tobacco streak ilarvirus* infecting jasmine and horse gram

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During the rainy season of 2012, symptoms resembling viral infection were observed on two crops - *Jasminum sambac* (jasmine) and *Macrotyloma uniflorum* (horse gram) at Cheruvu Belagal and Kadiri mandals of Kurnool and Anantapuram districts respectively of Andhra Pradesh (A.P) state, India. In jasmine, symptoms included severe leaf necrosis followed by wilting, together with necrotic streaking on petioles and branches and axillary shoot proliferation with small leaves (Fig. 1). In horse gram, leaves with necrotic spots with wrinkled margins, together with plant stunting and wilting were observed (Fig. 2). The symptoms observed in jasmine and horse gram were similar to those caused by *Tobacco streak virus* (TSV) infection in several hosts (Vemana & Jain, 2010). TSV belongs to the genus *Ilarvirus* in the family *Bromoviride* and virions are isometric particles (27-35 nm) containing a positive-sense RNA genome.

In DAS-ELISA, infected leaf samples of jasmine and horse gram gave positive reactions with a polyclonal TSV antiserum supplied by ICRISAT, India. RT-PCR amplification was carried out using oligonucleotide primers specific for the TSV coat protein (CP) gene following RNA extraction from infected and healthy leaf samples of jasmine and horse gram (Bhat *et al*., 2002). Amplicons of the anticipated size of ~700 bp were generated from extracts of diseased but not healthy plants (Fig. 3). Following gel extraction and purification of the amplicons, they were cloned into vector PTZ57R/T using the Ins TA clone PCR kit (Fermentas). Recombinant clones were sequenced and the sequences deposited in GenBank (Accession Nos. KC996725, jasmine; KC814177, horse gram). Later, two further CP gene sequences of jasmine TSV isolates were deposited (KC996726; KC996727) by sequencing infected samples collected from orchards of Anantapuram and Kadapa districts of A.P. A comparison of the CP gene sequences obtained in this study (BioEdit v 7.0.5 programme) was made with 17 TSV isolates from India and the prototype TSV isolate from white clover (X00435) (Fig. 4). This revealed close sequence identity with Indian TSV isolates irrespective of hosts and region (98-100%) and slightly more distant identity with TSV-WS type isolate (88-92%), observed at both the nucleotide and the amino acid levels. Phylogenetic analysis (Fig. 4) revealed that the jasmine and horse gram TSV isolates clustered together with Indian TSV in a corresponding manner while they slightly diverged from the prototype TSV isolate. This suggests that the virus infecting jasmine and horse gram is a strain of TSV. To our knowledge these are the first reports of TSV on jasmine and horse gram.

In India, TSV was first reported on sunflower (Bhat *et al*., 2002) and subsequently reported in several agricultural and horticultural crops (Prasada Rao *et al*., 2003; Vemana & Jain, 2010; Sivaprasad *et al*., 2010). TSV is pollen-borne and is easily spread by thrips under field conditions (Prasada Rao *et al*., 2003). TSV infection in jasmineis widespread in A.P. and its occurrence in other jasmine growing areas cannot be eliminated as it is propagated by cuttings. Wilting of jasmine branches results in severe yield loss. Similarly, incidence of TSV in horse gram ranged from 5 to 20% and yield loss depends on the stage of infection. Precautionary measures were advocated to contain the disease by destruction of infected plants.

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Figure 1

Figure 2

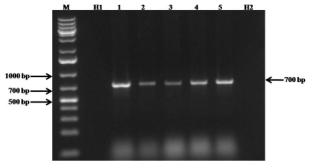

Figure 3

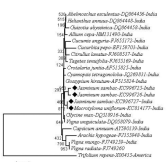

Figure 4

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