New Disease Reports

First report of *Pepper vein yellows virus* infecting chilli pepper (*Capsicum* spp.) in Italy

L. Tomassoli [1]*, A. Manglli [1], A. Ahmad [2], A. Tiberini [3] and M. Barba [1]

[1] *Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria - CREA, Centro di ricerca per la patologia vegetale, Via C.G. Bertero 22, 00156 Rome, Italy*; [2] *Plant Virology Laboratory, Department of Plant Pathology, PMAS-Arid Agriculture University. Rawalpindi, Pakistan*; [3] *Università degli Studi "Mediterranea" di Reggio Calabria, Dipartimento di Agraria, 89122 Feo di Vito, Reggio Calabria, Italy*

*E-mail: laura.tomassoli@crea.gov.it

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During 2014 and 2015, commercial crops and germplasm collections of chilli (*Capsicum* spp.) in Italy were surveyed for the presence of viral diseases. In 2015, 2% of plants from two fields located in different provinces of the Lazio region (Viterbo and Roma) and used for germplasm maintenance and seed production of chilli varieties and species, were observed showing interveinal yellowing or yellow patches, and brittleness of leaves (Fig. 1). Such symptoms are commonly caused by either nutritional disorders or may result from infections with viruses belonging to the genus *Polerovirus* (family *Luteoviridae*) or *Crinivirus* (family *Closteroviridae*). Among the criniviruses, only *Tomato chlorosis virus* (ToCV) has been reported to infect *Capsicum* spp. in Italy (Lozano *et al*., 2004) and it is present in several Italian regions. Total RNA from samples of diseased leaf tissue (three from Viterbo and five from Rome), belonging to different *Capsicum* species, tested negative for ToCV by RT-PCR (Louro *et al*., 2000). The samples were tested by RT-PCR using the generic primers targeting the RdRp coding sequence conserved amongst poleroviruses (Lotos *et al*., 2013). All samples showed an amplification product of the expected size (560 bp). Two amplicons, one from a sample from each cultivation site, were purified, sequenced and analysed by BLASTn search. The sequence in this region showed 96% identity with isolates of *Pepper vein yellows virus* (PeVYV) and 94% and 93% respectively with Pepper yellows virus and Pepper yellow leaf curl virus which are considered to be isolates of PeVYV (Murukami *et al*., 2011).

To confirm the virus identification, the same samples were amplified using specific primers to a region including the partial ORF2 and ORF3-ORF4 (Zhang *et al*., 2015). The final sequences (1054 bp) of the two isolates were obtained by assembling the overlapping sequences from the RT-PCR assays, and deposited in GenBank (Accession Nos. KU886193 and KU886194). The sequences of the two isolates shared 97% nucleotide identity with each other. When compared to previously reported isolates on GenBank the two isolates showed the highest nucleotide identity, 96% (KU886193) and 95% (KU886194), with a PeVYV isolate from bell pepper (*Capsicum annuum*) from Japan (AB594828). Phylogenetic analysis showed that there is no clear demarcation between African and Asiatic isolates and that the Italian isolates have a different origin in comparison to other PeVYV isolates reported in Mediterranean countries (Fig. 2).

In Europe, PeVYV has only been reported on *Capsicum* spp. in Spain (Villanueva *et al.,* 2013). This is the first report of PeVYV in Italy where it has been detected in three of the major species of cultivated chilli: *C. annuum*, *C. chinense* and *C. frutescens*. With the simultaneous findings of PeVYV in two distinct areas, and in different varieties, it is possible that the virus has a wider distribution in Italy where the cultivation of chilli is increasing for its ornamental, food and nutritional value, as well as posing a threat to sweet pepper production in the region.

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Figure 1

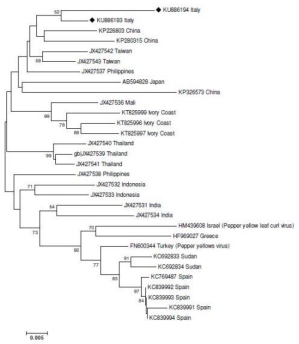

Figure 2

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