



## First report of Cucurbit yellow stunting disorder virus infecting cucurbits in Italy

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**Received:** 22 Sep 2016. **Published:** 14 Nov 2016. **Keywords:** crinivirus, *Cucumis melo*, *Cucurbita pepo*, yellowing disease

In June 2016, a survey was conducted in Sardinia, Italy to study the variability of cucurbit viral populations in melon (*Cucumis melo* var. *cantalupo* and *C. melo* var. *inodorus*) and zucchini (*Cucurbita pepo*). Two main cucurbit-growing provinces (Cagliari and Oristano) were investigated where, in the last decade, *Beet pseudo-yellows virus* (BPYV, genus *Crinivirus*) and *Cucurbit aphid-borne yellows virus* (CABYV, genus *Polevirus*) were found but not *Cucurbit yellow stunting disorder virus* (CYSDV, genus *Crinivirus*) despite having been tested for (Tomassoli *et al.*, 2003; Tomassoli & Meneghini, 2007). Leaf yellowing was widely observed on field-grown melon plants, often associated with thickening, brittleness or cracking and early browning of the lower leaves.

A total of 70 samples from 8 farms (covering an area of approximately 250,000 m<sup>2</sup>) were collected from melon and zucchini plants showing virus-like symptoms. In particular, 25 melon and two zucchini samples were selected for yellowing symptoms (Figs. 1-2) and total RNA was extracted for diagnosis. Molecular tests for CABYV and BPYV were performed as previously described (Tomassoli & Meneghini, 2007). Fourteen samples were positive for CABYV and two for BPYV. All samples were tested for the presence of CYSDV by single step RT-PCR using a specific primer set that amplifies the complete coat protein (CP) gene (Hourani & Abou-Jawdah, 2003). A product of the expected size (~770 bp) was amplified from four winter melon and one zucchini sample, all collected in the province of Cagliari. The DNA fragments were purified and directly sequenced in both directions. The sequence obtained from the five samples showed 100% identity when aligned. Therefore, the sequence of only one isolate was submitted to GenBank (Accession No. KX768875). BLAST analysis of the nucleotide sequence of this isolate revealed the highest identity (99%) in the CP gene with sequences published from USA (FJ492808) and Spain (AY242078 and AJ439690). Phylogenetic analysis of the CP gene sequence showed that the Italian isolate clustered with isolates from different countries in the Mediterranean basin and from the American continent within the "Western" group (Fig. 3) which is phylogenetically distant from the "Eastern" group including isolates from Iran, Saudi Arabia and Sudan (Rubio *et al.*, 2001; Keshevarz *et al.*, 2013).

Since its first identification in 1996 (Celix *et al.*, 1996), CYSDV has been

reported in different Mediterranean countries but CYSDV has not been found previously in Italy. The diagnostic results suggest a low incidence of CYSDV since the virus was found in only a few samples and in one surveyed area. For this reason, we presume a recent introduction of the virus and further investigation in Sardinia and other Italian regions is needed.

### Acknowledgements

The survey was supported by an ARIMNet2 project "EMERAMB".

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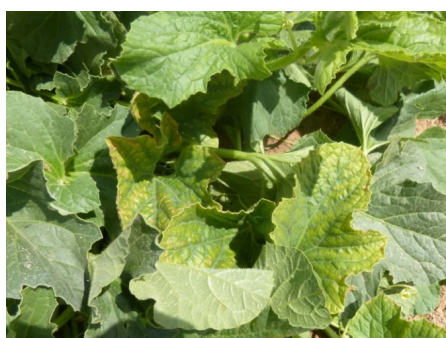


Figure 1



Figure 2

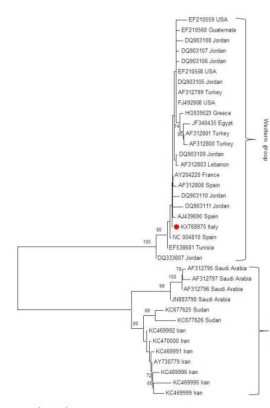


Figure 3

**To cite this report:** Manglli A, Murenu M, Sitzia M, Tomassoli L, 2016. First report of *Cucurbit yellow stunting disorder virus* infecting cucurbits in Italy. *New Disease Reports* **34**, 23. <http://dx.doi.org/10.5197/j.2044-0588.2016.034.023>

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