First report of *Hop stunt viroid* in *Hibiscus rosa-sinensis* in Italy

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*Hop stunt viroid* (HSVd), type member of the Hostaviroid genus in the Pospiviroidaceae family, has a very wide host range that includes trees, shrubs and herbaceous plants. In grapevine and almond, HSVd infection may be latent, whereas in other plants it causes various specific disorders; these include stunt on hop, dapple fruit on peach and plum, fruit deformation and ruggosity on apricot and plum, pale fruits on cucumber and cachexia on citrus. All these symptoms can lead to very high economic impact. In the past, *Hibiscus* spp. amongst ornamental plants were also reported as natural host of HSVd (Sänger, 1988), but further information on this has been lacking.

Recently, a survey of the phytosanitary status of ornamental hibiscus was conducted in wholesale nurseries in Central Italy (Mangilli et al., 2012). Plants of *Hibiscus rosa-sinensis* showing symptoms resembling virus infection were first examined for the presence of *Hibiscus chlorotic ringspot virus* (HCRSV), *Hibiscus latent Singapore virus* (HLSV) and *Hibiscus latent Fort Pierce virus* (HLFPV). However, several plants belonging to two different cultivars, showing severe symptoms of reduction in plant growth and upward curling and deformation of leaves (Fig. 1), tested negative for these viruses. Moreover, the observed symptoms did not resemble those of known viruses in hibiscus. Consequently, the same plants were tested for HSVd using a RT-PCR protocol by Faggioli et al. (2001) employing two primer pairs (VP-19 and VP-20; HSVF1 and HSFV2) designed respectively by Astruc et al. (1996) and Kofalvi et al. (1997). Out of 17 plants showing the aforementioned symptoms, four samples gave positive results. By contrast, HSVd was not detected in any of the 60 leaf samples showing only yellow spots and chlorotic mottle on leaves that tested positive for HCRSV, HLSV and/or HLFPV.

The four amplification products were cloned (pGem-T vector, Promega, WI, USA) and sequenced. Sequence analysis of different clones for each isolate (GenBank Accession Nos. KC137256 to KC137266) revealed that two isolates showed the same size (296 nt) and that both had a high homology amongst clones and between the two isolates. Furthermore, both isolates were closely related to a Turkish plum isolate (EF523829, Gazel et al., 2008) belonging to the Hop-group, as shown by the HSVd phylogenetic tree (Fig. 2; Kofalvi et al., 1997). The sequences of the other two isolates were 299 nt long and also showed a high homology amongst clones and between the two isolates. They were practically identical to an apricot isolate (Y08437, Kofalvi et al., 1997), thus grouping in the recombinant Plum–Citrus phylogenetic group (Fig. 2). These results suggest a different origin of infection in the vegetative propagation and cultivation of hibiscus plants. This study confirms that *Hibiscus rosa-sinensis* is a natural host of HSVd as reported by Sänger in 1988. However, to our knowledge, this is the first report of HSVd in *H. rosa-sinensis* in Italy.

**References**


