



First report of *Hibiscus chlorotic ringspot virus* in Turkey

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Hibiscus rosa-sinensis (rose of China) is an ornamental plant grown throughout the tropics and subtropics, and under glass in more temperate areas. It is commonly used in landscape design; however, pathogens causing diseases on *H. rosa-sinensis* are not well described, especially in Turkey. *Hibiscus chlorotic ringspot virus* (HCRSV) is one of the pathogens causing diseases on *H. rosa-sinensis*. The virus belongs to the genus *Betacarmovirus* in the family *Tombusviridae*. Symptoms of HCRSV vary from vein banding to chlorotic ringspots on leaves of *H. rosa-sinensis* (Waterworth *et al.*, 1976; Luria *et al.*, 2013). In September 2016, similar symptoms were observed on leaves of *H. rosa-sinensis* in the Mugla province of Turkey (Figs. 1-2).

Infected leaves were collected from eight different plants and stored at -80°C until further analyses. For RT-PCR, a pair of primers specific to parts of the coat protein (CP) gene of HCRSV were designed (AK-1 HCRSV-F 5'-AAGAGAGCAGCCAATAGA-3' and AK-2 HCRSV-R 5'-GAAGAAGAACAAGAAGCGA-3'), based on the complete genome sequence of HCRSV (GenBank Accession No. NC_003608; Huang *et al.*, 2000). Total RNA was isolated using the RNeasy Plant Mini Kit (Qiagen, Canada) and RT-PCR was done using the PrimeScript RT-PCR kit (Takara, Japan) according to the manufacturer's instructions. As expected, a 759 bp DNA fragment corresponding to the partial CP gene was amplified from all samples. Two PCR products, designated MGL1 and MGL2, were selected randomly, purified and sequenced bi-directionally using primers AK-1 HCRSV-F and AK-2 HCRSV-R. The sequences of isolates MGL1 and MGL2 were deposited in GenBank with the accession numbers KY420907 and KY420908, respectively BLAST analysis of these

sequences confirmed similarity to HCRSV sequences.

Different HCRSV sequences from various regions of the world were used for sequence analysis. The identities at nucleotide and amino acid level between Turkish and other HCRSV isolates were determined using a partial 517 bp sequence of the CP gene after alignment with ClustalW, and ranged from 94-98% and 86-97% identity, respectively. The phylogenetic relationship of different HCRSV isolates was determined by using the neighbor-joining-method and the Turkish isolates clustered closely with isolates from Iran and Israel (Fig. 3). To our knowledge, this is the first report of HCRSV in Turkey.

References

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Figure 1



Figure 2

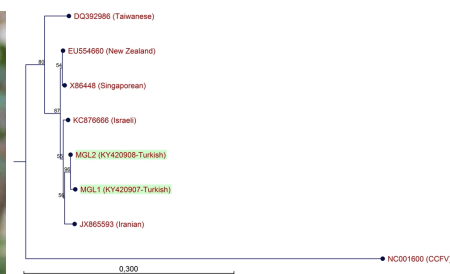


Figure 3

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