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گزارش علمی کوتاه

Identification of Cotton leaf curl Multan virus, a new threating *Begomovirus* in Iran

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The genus *Begomovirus* (family *Geminiviridae*) comprises a group of plant viruses with circular single-stranded DNA genome which predominantly are transmitted by ubiquitous whitefly, *Bemisia tabaci*. Previous studies have revealed the widespread distribution and divers host range for a number of monopartite and bipartite begomoviruses in Iran (Yazdani-Khameneh *et al.* 2016). As the most destructive members, cotton leaf curl viruses (CLCuVs) are monopartite begomoviruses with widespread distribution in Central and South-East Asia where they carrying different recombination to breakdown transgenic resistance in cotton cultivars (Qadir *et al.* 2019). Despite the occurrence of begomovirus-like symptoms such as leaf curling in fields of cotton in south of Iran and detection of Cotton leaf curl Multan betasatellite from symptomatic plants, CLCuVs genome has not detected from symptomatic cotton plants till now (Behjatnia *et al.* 2015). Betasatellites are begomovirus associated DNA molecules which may act as symptoms inducers in host plants (Behjatnia *et al.* 2015).

The Chinese hibiscus, *Hibiscus rosa-sinensis* L., is a common ornamental shrub in warm and humid regions of Iran *i., e.*, Khuzestan province, southwestern Iran. During 2019, several Chinese hibiscus plants showing begomovirus like symptoms including vein enation and cup-shaped leaves (Figure 1A) were observed in Ahvaz, Khuzestan province. New plants obtained from cuttings of symptomatic plants showed the same symptoms (Figure 1B). Leaf samples of parental and progeny plants were collected and total DNA was extracted by the CTAB method as described previously. Polymerase chain reaction (PCR) was employed to test the begomovirus infection of the samples using degenerate primer pairs B^C/PCR^V181, PCR^C $1/PBL1^V$ 2040 and β01/β02 for detection of a part of genomic components (DNA-A and DNA-B) and the associated betasatellites of begomoviruses, respectively. An expected 500 bp fragment corresponding to complete V2 and partial V1 ORFs of monopartite begomovirus genome was amplified from symptomatic *H. rosa-sinensis* plants while no amplicon was detected for DNA-B or betasatellite DNA.

PCR products were sequenced in both directions, edited and assembled using BioEdit Sequence Alignment Editor (7.0.5.3) and DNA Baser Assembler (version 5.15.0) programs. Multiple sequence alignment of Khuzestan and other known GenBank isolates was performed using the BLASTx program implemented in the NCBI server. Results indicated that the Iranian isolate shares 93 to 96% pairwise identities with different GenBank isolates of Cotton leaf curl Multan virus (CLCuMuV). Phylogenetic tree was constructed based on complete V2 ORF sequence of a number of monopartite begomoviruses using the Neighbor joining algorithm of the MEGA X software. Results revealed that all cotton leaf curl viruses isolated from *H. rosa-sinensis i., e.*, the Khuzestan isolate of CLCuMuV form a separated cluster (Figure 1C).

To our knowledge, this is the first report of the CLCuMuV incidence in Iran. Considering the widespread

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presence of the whitefly vector in the country, this virus can be potentially a serious threat to other economically important crops in Iran.

Figure 1. A. *H. rosa-sinensis* plants showing leaf curling and enation on the vein of leaves. B. Progeny scions from symptomatic parental plants showing the vein swelling at the first stage of growth. C. Constructed phylogenetic tree based on V2 ORF sequence of selected GenBank begomovirus and Khuzestan (Acc. No. MN956838) isolates using Neighbor joining algorithm by Mega X. Sequence of V2 ORF from Beet curly top Iran virus (Acc. No. MH751505) was used as outgroup OTU in the phylogenetic tree.

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