

First report of beet curly top Iran virus infecting cantaloupe in Iran

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The family *Geminiviridae* comprises a large group of plant-infecting viruses with twined particles and one or two molecules of circular single-stranded DNA genome (Navas-Castillo & Fiallo-Olivé, 2021). During a survey for identification of geminivirus-infecting crops in 2017, diseased cantaloupe plants (*Cucumis melo* L. subsp. *melo*) (n=10) showing cup-shaped and crinkling leaves symptoms (Fig. 1) were sampled from Sabzevar farms in the west of Khorasan Razavi Province, Iran. Total DNA were extracted from diseased samples using a CTAB method followed by enrichment of circular DNA molecules of the samples using rolling circle amplification (RCA) method and phi29 DNA polymerase enzyme (TempliPhi, GE Healthcare, USA) as previously described by Shepherd et al. (2008). Subsequently, restriction pattern of the samples was analyzed using different enzymes. Due to identical restriction pattern of the resulted digested RCA product, the sample Ta-109 was chosen and *Hind*III restricted RCA product (~2.9 kb in size) was cloned into the *Hind*III digested pGreen0029 plasmid followed by

Sanger sequencing of a part (976 bp) of the recombinant plasmid. The resulted sequence of the isolate Ta-109 was used to search the database using basic local alignment search tool (BLASTn) (Altschul et al., 1990). Results indicated that beet curly top Iran virus (*Becurtovirus betae*, family *Geminiviridae*) is associated with the cantaloupe sample. The 976 bp sequence comprises the large intergenic region as well as the 5' end of the C1 ORF which encodes the N-terminal of the rep protein. Accordingly, the isolate Ta-109 shared maximum nucleotide identity (>97%) with two Iranian GenBank isolates of BCTIV previously reported from sugar beet and cowpea. In phylogenetic tree, Ta-109 isolate was grouped with these isolates from Khorasan Razavi Province, Iran (Fig. 2). This virus has a broad host range and widely distributed in Iran (Gharouni Kardani et al., 2013). Results of this study, confirm the importance of BCTIV in crop growing farms in Iran. To the best of our knowledge, this is the first report of BCTIV infecting cantaloupe in Iran.



Fig. 1. Symptoms of BCTIV infected cantaloupe showing crinkling (A) and cup-shape leaves (B) collected from cantaloupe growing farms (Sabzevar, Khorasan Razavi Province).

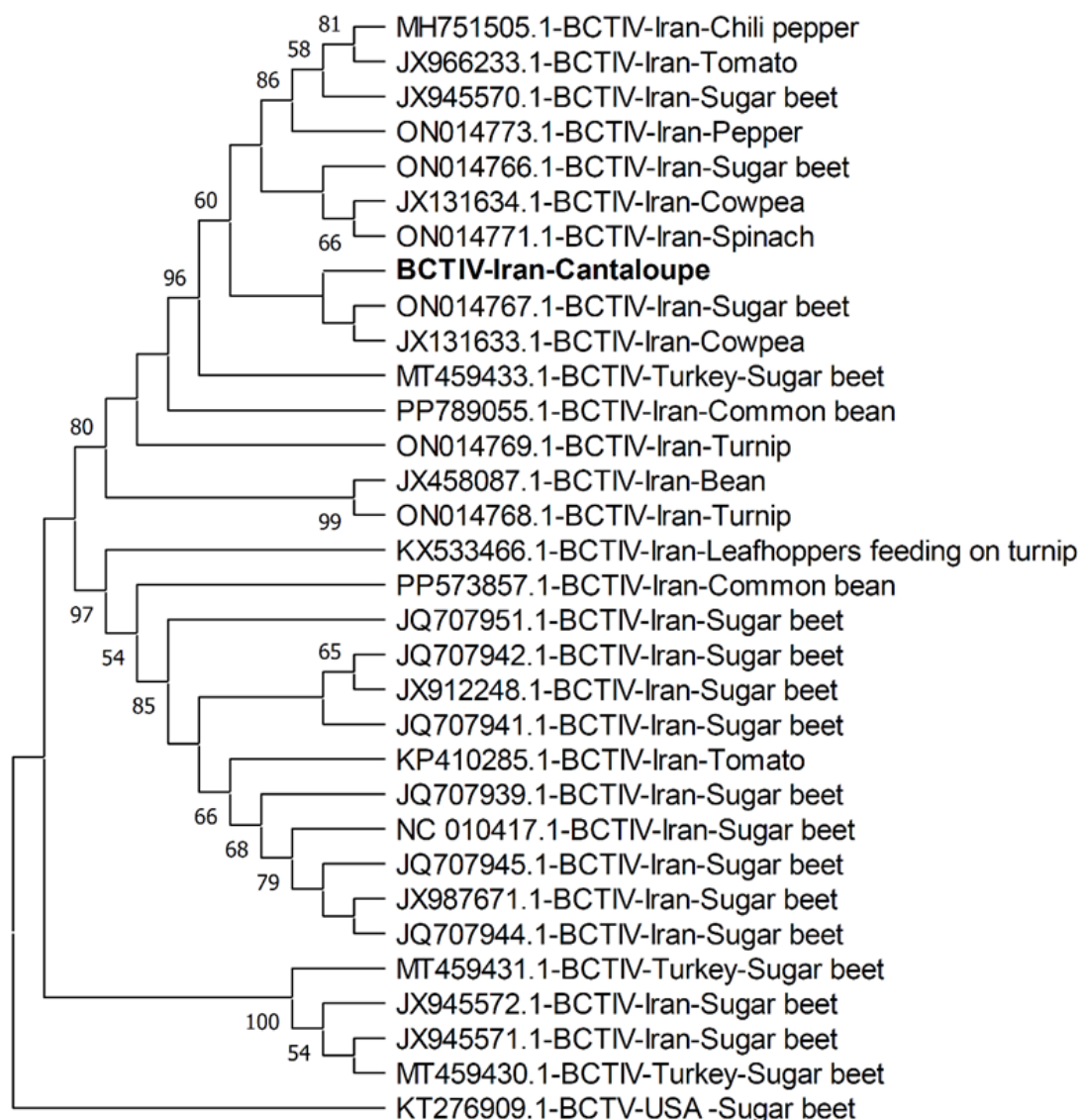


Fig. 2. Neighbor-Joining phylogenetic tree based on the nucleotide sequences of a 976 bp segment of the cantaloupe isolate of beet curly top Iran virus (BCTIV) genome from Sabzevar, Khorasan Razavi Province (bold letters) and 30 isolates from different hosts and regions. The tree was constructed using Maximum Composite Likelihood model in MEGA11 (Tamura et al., 2021). Bootstrap support (1000 replicates) above 50 % are shown at the nodes. The counterpart sequence of beet curly top virus (BCTV, accession number KT276909.1) was used as the outgroup.

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