



Short communication

Turnip curly top virus, a highly divergent geminivirus infecting turnip in Iran

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ABSTRACT

From 2006 onwards turnip crops in Fars province, Iran, have been noted with unusual leaf curling and vein swelling symptoms which are characteristic of the leafhopper-transmitted viruses of the genus *Curtovirus* (family *Geminiviridae*). Rolling circle amplification was used to clone viruses from five turnip isolates exhibiting leaf curl symptoms. Analysis of the sequences showed them to have >93% sequence identity and to be distinct from all other geminiviruses previously characterised. Analysis of the sequence of this virus, for which we propose the name Turnip curly top virus (TCTV), showed it to have a genome arrangement in the complementary-sense similar to that of curtoviruses (consisting of four overlapping genes) but only two open reading frames in the virion-sense (the curtoviruses encode three). The complementary-sense genes are homologous to those of curtoviruses but show little sequence identity to their curtovirus homologs, with the exception of the product of the C4 open reading frame (ORF) which shows ~70.6% amino acid sequence identity to the C4 of the North American curtoviruses, Pepper curly top virus and Beet mild curly top virus. For curtoviruses the C4 protein is a symptom determinant, which likely explains the similarity of TCTV symptoms to those of curtoviruses. In the virion-sense the predicted product of the V2 ORF of TCTV shows no significant similarity with any proteins in the databases whereas the product of the V1 ORF (encoding the coat protein [CP] of geminiviruses) shows low levels of sequence identity to the CPs of curtoviruses. These findings show TCTV to be a highly divergent geminivirus with similarities to viruses of the genus *curtovirus*. The significance of these findings, particularly the taxonomic implications are discussed.

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Viruses of the family *Geminiviridae* are distinct in having genomes of circular, single-stranded (ss) DNA that are packaged within twinned quasi-isometric (“geminiate”) virions (Stanley et al., 2005). Geminiviruses are divided into four genera based on genome organisation and biological properties, most important of which are the type of insect vector (either whitefly, leafhopper or treehopper) and host range (either mono- or dicotyledonous hosts; Stanley et al., 2005). Whitefly (*Bemisia tabaci*)-transmitted geminiviruses, with either bipartite or monopartite genomes, are included in the genus *Begomovirus*. Those having monopartite genomes that are transmitted by leafhopper vectors, primarily to monocotyledonous plants, are included in the genus *Mastrevirus*. Viruses that have

monopartite genomes distinct from those of the mastreviruses and that are transmitted by leafhopper vectors to dicotyledonous plants are placed in the genus *Curtovirus*, with *Beet curly top virus* (BCTV) as the type species. The most recently established of the present four genera of the *Geminiviridae*, *Topocuvirus* holds just a single species: *Tomato pseudo-curly top virus* (TPCTV). TPCTV is a monopartite virus with a complementary-sense genome arrangement typical of, and homologous to, viruses of the *Begomo*- and *Curtovirus* genera, with four overlapping genes (Briddon et al., 1996). The main factor leading to the establishment of this fourth genus was the fact that TPCTV is the only known geminivirus transmitted by a treehopper (*Micrutalis malleifera*).

Over the past year two highly unusual geminiviruses have been identified in the Middle East and Africa. The first is Beet curly top Iran virus (BCTIV) isolated from sugar beet, tomato, spinach, and turnip originating from Iran (Yazdi et al., 2008). This virus has a virion-sense genome arrangement typical of curtoviruses (three overlapping genes) and the predicted amino acid sequences of each

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