



First report of the natural occurrence of Chilli veinal mottle virus in *Solanum nigrum* and *Physalis floridana* in India

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3 **First report of the natural occurrence of *Chilli veinal mottle virus* in *Solanum nigrum* and**
4 ***Physalis floridana* in India**
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15 *Chilli veinal mottle virus* (ChiVMV; genus *Potyvirus*, family *Potyviridae*) is one of the nine
16 potyviruses so far reported in peppers (2). Although ChiVMV is known to infect different plant
17 species under experimental conditions (3, 4), no alternative hosts for the virus under field
18 conditions, other than *Capsicum* spp., has been reported. In disease surveys conducted during
19 rainy season (June-November) of 2008 and 2009 in Coimbatore area of Tamil Nadu State, India,
20 several plants of *Solanum nigrum* and *Physalis floridana* growing as weeds within and adjacent
21 to chilli pepper fields were observed with foliar symptoms consisting of vein clearing and
22 mottling. Symptomatic leaves from representative plants of both species as well as chilli peppers
23 were tested initially by one-tube, single-step reverse transcription-polymerase chain reaction
24 (RT-PCR) using potyvirus 'universal' degenerate primers [Upstream primer: 5'-
25 GGIVVIGTIGGIWSIGGIAARTCIAC-3'and Downstream primer: 5'-
26 ACICCRTTYTCDATDARTTTIGTIGC-3'] specific to the cylindrical inclusion (CI) gene (1). A
27 DNA fragment of approximately 630 base pairs was amplified from three representative samples
28 of *S. nigrum*, two of *P. floridana* and two of chilli peppers, indicating the presence of potyvirus.
29 No DNA fragment was amplified in RT-PCR with 'universal' primers specific to begomo- and
30 tospoviruses as well as *Cucumber mosaic virus*. RT-PCR positive samples from *S. nigrum* and
31 chilli pepper tested positive in antigen coated plate ELISA with potyvirus group-specific
32 monoclonal antibodies (Agdia Inc, Elkhart, IN) confirming the presence of potyvirus in these
33 samples. For further confirmation, DNA fragments were cloned separately into pCR 2.1-TOPO
34 vector (Invitrogen Corp, Carlsbad, CA, USA). Three independent clones for each amplicon were
35 sequenced in both orientations. In pairwise comparisons, the CI sequences of ChiVMV from *S.*
36 *nigrum* (GenBank accession no. GU294786, GU294787 and GU294788) and *P. floridana*
37 (GenBank accession no. GU294789 and GU294790) showed 79% and 83-92% nucleotide and
38 amino acid identities, respectively, with corresponding sequences of ChiVMV isolates from
39 India (AJ237843) and South Korea (AJ972878). Sequences of ChiVMV isolates from chilli
40 peppers (GenBank Accession No. GU294791 and GU294792) showed 80-81% and 93-94%
41 nucleotide and amino acid identities, respectively, with virus isolates from India (AJ237843) and
42 South Korea (AJ972878). The CI sequences of ChiVMV isolates from *S. nigrum* showed 80%
43 and 78-79% nucleotide sequence identities with corresponding sequences of virus isolates from
44 *P. floridana* and chilli peppers, respectively, while CI sequences of ChiVMV from *P. floridana*
45 showed 78-79% nucleotide sequence identities with corresponding sequences of virus isolates
46 from chilli peppers. Phylogenetic analysis of CI sequences from potyviruses available in
47 GenBank showed clustering of ChiVMV isolates from *P. floridana* and *S. nigrum* with ChiVMV
48 isolates from chilli peppers from India and South Korea to form a separate clade in the
49 phylogram. However, ChiVMV sequences from each plant species formed separate sub-clades
50 within the ChiVMV clade. To the best of our knowledge, this is the first report of the natural
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3 occurrence of ChiVMV in *S. nigrum* and *P. floridana*. The results extend our knowledge on the
4 natural host range of the virus and indicate presence of genetically diverse isolates of ChiVMV
5 in India. Considering that *S. nigrum* and *P. floridana* were found growing in proximity to chilli
6 pepper fields, these plant species could serve as potential reservoirs of ChiVMV and contribute
7 to off-season survival of the virus.
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