Diseases Caused by Viruses

First Report of Passiflora Latent Virus Infecting Persimmon (*Diospyros kaki*) in Korea

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Passiflora latent virus (Passiflora latent virus; PLV), a member of the genus *Carlavirus* in the family *Betaflexiviridae*, has been reported in *Passiflora* species in Australia, Germany, Israel, the United States, and New Zealand (Tang et al. 2008). In September 2019, leaves showing a virus-like disease with mosaic, curling, and necrosis were collected from 10 persimmon (*Diospyros kaki* Thunb.) orchards in Gyeongsang province, Korea. Total RNA from a pooled sample of leaves from 21 trees was extracted using an RNeasy Plant Mini Kit (Qiagen, Germany) and subjected to high-throughput sequencing. After preprocessing and RiboZero rRNA removal, a cDNA library was prepared using an Illumina TruSeq Stranded Total RNA kit and sequenced on an Illumina NovaSeq 6000 system (Macrogen, Korea). De novo assembly of the 74,862,810 reads was performed using Trinity software (r20140717); the initially assembled 213,476 contigs were screened against the NCBI viral genome

database using BLASTN. By these means, 12 contigs derived from PLV were identified. Contigs with lengths of 209 to 802 nt shared nucleotide identities of 90.70 to 94.82% with PLV isolates, covering a total of 5,169 nt (~61.6% of the full PLV genome). Two additional viruses were also detected from the pooled sample: persimmon cryptic virus (PeCV) and persimmon virus A (PeVA). To confirm PLV infection, reverse transcription polymerase chain reaction (RT-PCR) was performed using virus-specific primers, PLV-F (5'-ACACAAAACCTGCGTGTGGA-3') and PLV-R (5'-CAAGACCCACCTACCTCAGTGTG-3'), designed based on a 633-nt contig sequence in the polymerase gene. RT-PCR products of the expected 571 bp were obtained from two of 21 individual original samples; no asymptomatic plants were tested. Amplicons were cloned into the pGEM-T Easy vector, and two clones per sample were Sanger sequenced bidirectionally (BIONEER, Korea). The identical sequences (GenBank LC556232) showed 99.65% nt identity to the contig and 93.87% identity with the corresponding polymerase sequence of PLV-Rehovot isolate from passion fruit in Israel (MH379331). The two PLV-positive samples showing leaf necrosis were also coinfecting with PeVA, identified by RT-PCR using previously reported primers PeVAfor/PeVArev (Morelli et al. 2014), but not with PeCV (mixed with PeVA in only 1/21 plants; PeVA was found in 19/21 plants). None of the tested viruses were detected in two trees, displaying mosaic and leaf curling, respectively. The foliar symptoms of PLV infection on passionfruit have been reported to vary throughout the year (Spiegel et al. 2007). No such observations in persimmon were possible, as the infected persimmon trees were removed and destroyed because they might pose a threat to the cultivation of passionfruit in Korea. To our knowledge, this is the first report of persimmon as a host of PLV anywhere in the world, and the first report of PLV in Korea in any host. A further survey is needed to determine possible presence of PLV on persimmon and *Passiflora* species.

References:

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