First Report of Cucurbit Chlorotic Yellows Virus Infecting *Cucumis melo* (Muskmelon and Oriental Melon) in Korea

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In December 2018, virus-like symptoms (yellowing, vein clearing) were observed on 2% of muskmelon (*Cucumis melo* L.) plants in plastic houses on a farm in Gyeongsang province, Korea. Total RNA from two symptomatic and two asymptomatic plants was extracted using an RNeasy Plant Mini Kit (Qiagen, Germany) for high-throughput sequencing (HTS). After preprocessing and Ribo-Zero rRNA removal, a cDNA library was prepared (Illumina TruSeq Stranded Total RNA kit) and sequenced (Illumina NovaSeq 6000 system; Macrogen, Korea). De novo assembly of 88,222,684 HTS reads with Trinity software (r20140717) yielded 146,269 contigs of 201 to 28,442 bp, which were screened against the NCBI viral genome database by BLASTn. Contigs from cucumber mosaic virus (CMV), melon necrotic spot virus (MNSV), tobacco mosaic virus (TMV), and watermelon mosaic virus (WMV) were identified, all previously reported in Korea. Two contigs (8,539 and 8,040 bp) with 99.9% sequence identity to distinct cucurbit chlorotic yellows virus (CCYV) isolates (JN641883, RNA1, Taiwan; MH819191, RNA2, China) were also identified. The 10 sequences most closely related to each RNA of the Korean isolate (≥99% coverage, ≥99.6% nt identity) were from Japan, China, Taiwan, or Israel. CCYV presence was confirmed by reverse transcription polymerase chain reaction (RT-PCR) using newly designed specific primers, RdRp-F/RdRp-R (5'-ACCGAACACTTGGCTATCCAA-3'/

5'-CTTAATGCCGCGTATGAACTCA-3') and HSP-F/HSP-R (5'-TGAACGACACTGAGTTCATTCTCA-3'/5'-CGCCAAGATCGTACATGAGGAA-3'), against RNA dependent RNA polymerase (RdRp; RNA1) and the heat shock protein 70 homolog (HSP70h; RNA2). Symptomatic samples yielded products of expected sizes (RdRp, 450 bp; HSP70h, 510 bp), whereas asymptomatic samples did not. The amplicons were cloned, and two clones of each were sequenced (Bioneer, Korea; GenBank nos. LC592226 and LC592227), showing 100 and 99.2% nt identity with RdRp and HSP70h genes of Chinese CCYV isolate SD (MH819190 and MH819191, respectively) and other Asian isolates. Primers specific for CMV, WMV, beet pseudo-yellows virus (Okuda et al. 2007), TMV (Kim et al. 2018), MNSV (F/R, 5'-ATCTCGCATTGGCATTACTC-3'/5'-ATTTGTAGAGATGCCAACGTA-3'), cucurbit yellow stunting disorder virus (Zeng et al. 2011), and cucurbit aphid-borne yellows virus (F/R, 5'-CGGTCTATTGTCTGCAGTACCA-3'/5'-GTAGAGGATCTTGAA TTGGTCCTCA-3') were also used. None of these viruses were detected in the symptomatic samples, but both asymptomatic plants were positive for CMV and WMV, and one also for MNSV. In June and September 2020, muskmelon and oriental melon (*C. melo* var. *makuwa*) plants with yellowing disease (incidence 80 to 90%) and whiteflies were observed in all investigated plastic houses of one muskmelon and one oriental melon farm in Gyeonggi and Jeolla provinces. Symptomatic samples (14 muskmelon; six oriental melon) were collected and RT-PCR tested as above; 19/20 samples were positive for CCYV but none for the other viruses. The oriental melon sequence (LC592895, LC592230) showed 99.7 and 100% nt identity with the RdRp and HSP70h genes of Chinese isolate SD, respectively. CCYV was first reported in Japan (Okuda et al. 2010), Taiwan, and China (Gu et al. 2011; Huang et al. 2010); to our knowledge, this is the first report of CCYV infecting muskmelon and oriental melon in Korea. Whitefly-transmitted CCYV could present a serious threat of yield losses to cucurbit crops in Korea, requiring control of vector populations to prevent spread of CCYV.

References:

- Gu, Q. S., et al. 2011. Plant Dis. 95:73.
- Huang, L. H., et al. 2010. Plant Dis. 94:1168.
- Kim, E. K., et al. 2018. Res. Plant Dis. 24:81.
- Okuda, M., et al. 2007. Kyushu Pl. Prot. Res. 53:9.
- Okuda, M., et al. 2010. Phytopathology 100:560.
- Zeng, R., et al. 2011. Plant Dis. 95:354.

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