First Report of Melon Aphid-Borne Yellows Virus Infecting Watermelon in Korea

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Watermelon (*Citrullus lanatus*) is one of the most popular crops in Korea, with over 100 million units produced annually. As watermelon cultivation increases, the damage caused by plant viruses in watermelon farms is also increasing. In July 2020, some watermelons cultivated on farms in Uiryeong showed typical viral symptoms, such as yellowing and necrosis. In previous studies, two plant viruses, *Cucurbit aphid-borne yellows virus* and *Cucurbit chlorotic yellows virus*, have been reported as causal agents of yellowing disease in the Cucurbitaceae plant in Korea. To identify the virus(es) associated with the symptomatic watermelon plants, 11 samples were collected. Total RNA was extracted from each sample using the Plant RNA Prep kit (Biocube System, Gwacheon, Korea). RT-PCR was performed using primer sets specific to cucurbit aphid-borne yellows virus (CABYV) and cucurbit chlorotic yellows virus (CCYV) to detect each virus (Kwak et al. 2018; Wintermantel et al. 2019). CABYV was detected in one sample, and CCYV was detected in eight samples. Every sample presented similar yellowing symptoms; however, neither virus was detected in the remaining two samples. To investigate unknown viruses, a transcriptome library was constructed using total RNA of the watermelons and sequenced using a NovaSeq

6000 sequencer (Illumina, San Diego, CA). The reads were de novo assembled and annotated using the KEGG virus genome database with the NCBI BLAST utility. All procedures of next generation sequencing were performed by Macrogen (Seoul, Korea). Three large viral contigs were identified, and additional BLAST analyses for nucleotides (nt) and proteins indicated that they were CABYV, CCYV, and melon aphid-borne yellows virus (MABYV). A total of 247,198 reads were mapped to the reference MABYV sequence (GenBank accession no. NC_010809), and the sequencing depth was 6,575x. The contig (MW505927) had a size of 5,677 nt and showed 100% coverage and 96% identity with known complete MABYV sequences (JQ700307 and EU000534). To confirm the presence of MABYV, RT-PCR was performed using specific primer sets targeting MABYV (MABYV-262-F, 5'-GAACCGTCGACGCACTTCAAAGAGTA-3', and Polero-uni-R, 5'-GATYTTATAYTCATGGTAGGCCTTGAG-3'; Knierim et al. 2010). The expected size of 262 bp was obtained from 5 out of 11 samples, including the two samples mentioned above. *Melon aphid borne yellows virus* belongs to the genus *Polerovirus* and has been reported in cucurbit crops in China, Taiwan, and Thailand (Cheewachaiwit et al. 2017; Knierim et al. 2010; Xiang et al. 2008). According to the farmer, an outbreak of aphids had previously occurred and was controlled with pesticides. Since aphids are known to be vectors of poleroviruses, we surmise that the watermelons were infected with MABYV by the aphids at that time. To monitor the outbreak of MABYV, watermelon farms in Uiryeong will be continuously investigated. To our knowledge, this is the first report of MABYV in Korea.

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