Diseases Caused by Viruses

First Report of Cucurbit Chlorotic Yellows Virus Infecting Cucumber in South Korea

H.-R. Kwak,¹ H.-S. Byun,¹ H.-S. Choi,¹ J.-W. Han,² C.-S. Kim,³ W. M. Wintermantel,⁴ J.-E. Kim,⁵ and M. Kim^{5,†}

¹Rural Development Administration, National Institute of Agricultural Science, Wanju 55365, South Korea

²Chungcheongbuk-do Agricultural Research and Extension Services, Cheongju 28130, South Korea

³Rural Development Administration, Highland Agriculture Research Institute, Pyeongchang 25342, South Korea

⁴United States Department of Agriculture, Agricultural Research Service, Salinas, CA, U.S.A.

⁵Department of Plant Medicine, Chungbuk National University, Cheongju 28644, South Korea

H.-R. Kwak and J.-W. Han contributed equally to this work.

Funding: This research was supported by grants from the Agenda Program funded by the Rural Development Administration of Korea (PJ01530804). Plant Dis. 105:1862, 2021; published online as <https://doi.org/10.1094/PDIS-10-20-2254-PDN>. Accepted for publication 5 January 2021.

In October 2018, cucumber plants showing yellowing and chlorotic mottle symptoms were observed in a greenhouse in Chungbuk, South Korea. The observed symptoms were similar to those caused by cucurbit aphid-borne yellows virus (CABYV), which has been detected on cucumber plants in the region since it was reported on melon in Korea in 2015 (Lee et al. 2015). To identify the potential agents causing these symptoms, 28 samples from symptomatic leaves and fruit of cucumber plants were subjected to total RNA extraction using the Plant RNA Prep Kit (Biocubesystem, Korea). Reverse transcription polymerase chain reaction (RT-PCR) was performed on total RNA using CABYV-specific primers and protocols (Kwak et al. 2018). CABYV was detected in 17 of the 28 samples, whereas 11 symptomatic samples tested negative. To identify the cause of the symptoms, RT-PCR was

performed using primers specific for cucurbit chlorotic yellows virus (CCYV) and cucurbit yellow stunting disorder virus (CYSDV) (Wintermantel et al. 2019). Eight of the 28 samples were positive using the CCYV-specific primers, whereas seven samples were infected with only CCYV and one contained a mixed infection of CABYV with CCYV. None of the samples tested positive for CYSDV. The expected 373-nt amplicons of CCYV were bidirectionally sequenced, and BLASTn analysis showed that the nucleotide sequences shared 98 to 100% identity with CCYV isolates from East Asia, including NC0180174 from Japan. Two pairs of primers for amplification of the complete coat protein and RNA-dependent RNA polymerase (RdRp) genes (Wintermantel et al. 2019) were used to amplify the 753-bp coat protein and 1,517-bp RdRp genes, respectively. Amplicons of the expected sizes were obtained from a CCYV single infection and ligated into the pGEM T-Easy vector (Promega, WI). Three clones from each amplicon were sequenced and aligned using Geneious Prime and found to have identical sequences (GenBank accession nos. MW033300 and MW033301). The CP and RdRp sequences demonstrated 99% nucleotide and 100% amino acid identity with the respective genes and proteins of the CCYV isolates from Japan. This study documents the first report of CCYV in Korea. Since CCYV was first detected on melon in Japan, it has been reported in many other countries including those in East Asia, the Middle East, Southern Europe, North Africa, and recently North America. CCYV has the potential to become a serious threat to production of cucurbit crops in Korea, particularly due to the increasing prevalence of the whitefly, *Bemisia tabaci*, in greenhouse production systems. It will be important to continue monitoring for CCYV and determine potential alternate hosts in the region to manage and prevent further spread of CCYV in Korea.

References:

- Kwak, H.-R., et al. 2018. Plant Pathol. J. 34:532.
- Lee, H. J., et al. 2015. Kor. J. Hort. Sci. Technol. 33:210.
- Wintermantel, W. M., et al. 2019. Plant Dis. 103:778.

The author(s) declare no conflict of interest.

e-Xtra

Keywords: crinivirus, cucurbita, virus detection, whitefly, *Cucumis sativus*

[†]Indicates the corresponding author.
M. Kim; mkim00@korea.kr