



# First report of cucumber mosaic virus infecting bitter melon (*Momordica charantia*) in Korea

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Bitter melon (*Momordica charantia*) is a widely grown tropical and subtropical vine of the family Cucurbitaceae that has long been used in herbal medicines in Asia and Africa (Grover and Yadav 2004). In June 2021, we collected 10 bitter melon leaves exhibiting virus-like symptoms including yellow spots and rugose texture from a greenhouse in Gangin, Jeollanam Province, Korea. We tested symptomatic plants for infection by major viruses of cucurbit crops, including cucumber mosaic virus (CMV), cucumber green mottle mosaic virus, and watermelon mosaic virus by RT-PCR (Pozzi et al. 2020). Positive test results were obtained only for CMV with total RNA extracted from the collected leaves and specific primers for the CMV coat protein (CP) gene (CMV CP 1257F: ATGGACAAATCTGAATCAAC and CMV CP 1913R: TCAGACTGGGAGCACTCCA). CMV was detected in two of the 10 sampled leaves. Sequences of RT-PCR products (expected size: 657 bp) were analyzed against the National Center for Biotechnology Information (NCBI) plant virus genome database. The two CMV isolates exhibited 99.24% nucleotide homology with a CMV isolate obtained from *Cucurbita pepo* in Japan (LC626020) and 99.09% nucleotide homology with CMV isolates from both *Passiflora edulis* in Korea (LC654689) and *Trifolium repens* in Japan (LC626022). A consensus complete CP gene sequence of CMV (CMV-BGK) from bitter melons in Korea was deposited in GenBank (accession

no. LC701732). A sap transmission test using *Nicotiana benthamiana* as an indicator species demonstrated that CMV-BGK caused leaf curling, mottle, and mosaic symptoms typical of CMV on systemic leaves at 7 days post-inoculation. Finally, CMV was confirmed in a symptomatic herbaceous host using RT-PCR with CMV-specific primers. To our knowledge, this is the first report of CMV infecting bitter melon in Korea.

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