First Report of Zucchini Yellow Mosaic Virus Infecting Bitter Melon (*Momordica charantia*) in South Korea

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Bitter melon (*Momordica charantia* L., family Cucurbitaceae) is used in traditional medicine in Asia and tropical Africa for diabetes, cancer, and inflammation-associated diseases due to its bioactive compounds (Bortolotti et al. 2019). In July 2021, approximately 10% of bitter melon plants in the field showed symptoms such as mosaic, yellowing, and deformation on the leaves in Samchuk, South Korea. Cucumber and zucchini plants growing in the same field exhibited symptoms like those of bitter melon plants (Ali et al. 2012). To investigate the causative virus, leaf dip preparations from three symptomatic bitter melon leaf samples were analyzed by transmission electron microscopy (TEM). *Potyvirus*-like particles (approximately 680 to 730 nm in length and 11 to 13 nm in diameter) were observed in all samples. To further identify the causal viral pathogens, leaf extracts from five symptomatic bitter melon plants were tested by DAS-ELISA using specific antibodies (Agdia, Elkhart, IN, U.S.A.) against cucumber mosaic virus, zucchini yellow mosaic virus (ZYMV), watermelon mosaic virus, and papaya ring spot virus. Positive controls from commercial kits and negative controls from healthy bitter melon plants were included in the ELISA assay. The serological assay revealed that all five symptomatic samples positively reacted with the antiserum against ZYMV, but not for other viruses. Total RNA extracted from the five ELISA-positive samples and two healthy

bitter melon plants (as negative controls), using Clear-S Total RNA extraction kit (InVirusTech, Gwangju, Korea), was tested by RT-PCR with ZYMV-specific primers as previously described (Cho et al. 2011). All amplicons of the expected size (~822 bp) were individually cloned into the pGEM-T Easy Vector (Promega, Madison, WI), and sequenced in both orientations. Thereafter, all the sequenced clones shared 100% nucleotide identity. The sequence of ZYMV-MC1 isolated from bitter melon was deposited in GenBank (accession no. LC652434). Pairwise comparison of the nucleotide sequence with that of ZYMV isolates in GenBank revealed 99% sequence identity with ZYMV-chk (MG020559) from Korea, 98% with ZYMV-14-HY-SCS (KU743321) from China, 97% with ZYMV-Y21 (MW345249) from Turkey, and 96% with ZYMV-AUIKTPK (KR261951) from Pakistan. Leaf saps from the ZYMV-positive bitter melon samples, prepared in 10 mM phosphate buffer (pH 7.0), were mechanically inoculated in five young, healthy bitter melon plants to fulfill Koch's postulates. ZYMV-MC1 isolate caused mosaic and leaf deformation on bitter melon plants 10 days postinoculation. The presence of ZYMV in the symptomatic leaves was confirmed by RT-PCR using the primers mentioned above followed by nucleotide sequencing of the amplicons. Several cotton aphids (*Aphis gossypii*) were observed in the bitter melon field, which indicated that they might transmit the virus from ZYMV-infected cucumber or zucchini plants. ZYMV is an economically important virus of cucurbits worldwide and has been recently reported from various crops as natural hosts, including chayote (Yoon et al. 2018) and balloon flowers (Kim et al. 2021). To the best of our knowledge, this is the first report of ZYMV naturally infecting bitter melon in South Korea. Further large-scale surveys are required to determine its incidence, yield losses, and management in bitter melon in Korea.

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