First Report of Saguaro Cactus Virus Infecting *Gymnocalycium mihanovichii* in South Korea

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Saguaro cactus virus (SgCV, genus *Carmovirus*, family *Tombusviridae*) was first isolated from an asymptomatic giant saguaro cactus (*Carnegiea gigantea*) in Arizona, U.S.A. (Milbrath and Nelson 1972). In November 2017, 30 asymptomatic grafted cactus plants (*Gymnocalycium mihanovichii* grafted onto *Hylocereus trigonus*) were randomly collected from a commercial market in Gyeonggi Province, South Korea. Total RNA was extracted from both the scions and rootstocks of the plants using an RNeasy Plant Mini Kit (Qiagen, Germany) then subjected to reverse transcription polymerase chain reaction (RT-PCR) using RevertAid reverse transcription (Thermo Scientific, U.S.A.), TaKaRa Taq (TaKaRa, Japan) and SgCV-CP primers (forward, 5'-ATGGA CGCTAAGTATGCG-3'; reverse, 5'-TCAGAGCCTAGCAACATA-3'). A validated SgCV stock (PV-0734, DSMZ, Germany) was used as an RT-PCR positive control. Out of 30 samples each of the rootstocks and scions, 21 and 8, respectively, produced an amplicon of the expected size of 1,035 bp. The amplicons from three samples were cloned into a pGEM-T easy vector (Promega, U.S.A.), and three clones of each sample were sequenced (Macrogen, South Korea). The amplicons shared 100% sequence identity with each other. BLASTn analysis showed that the sequence shared the highest identity at 66.3% with SgCV isolate Arizona (GenBank U72332). For a bioassay of the virus, sap from infected *G. mihanovichii* was mechanically inoculated on four indicator plant species. The virus induced local lesions in *Chenopodium*

amaranticolor, *C. quinoa*, and *Gomphrena globosa* and systemic necrosis including growth reduction in *C. capitatum*. These results are consistent with those reported for SgCV by Milbrath and Nelson (1972). For determination of the exact species of the virus, noninoculated leaves of *C. capitatum* were harvested 21 days after mechanical inoculation and subjected to total RNA extraction using the RNeasy Plant Mini Kit (Qiagen). A cDNA library was prepared using TruSeq RNA sample preparation v2, and sequenced on a NovaSeq 6000 system sequencer (Macrogen). A total of 137,393,766 raw reads were quality-trimmed and assembled into 120,408 contigs with sizes ranging from 201 to 15,898 nt using the Trinity program (r20140717). The assembled contigs were screened against the NCBI viral genome database using BLASTn, and a single contig of 3,858 nt matched the SgCV (acc. no. U72332, coverage 88%, identity 70.3%). The sequence was deposited in GenBank (SgCV-gm, MW590184) and contained five open reading frames (ORFs), which is consistent with those of SgCV reported by Weng and Xiong (1997). Using DNAMAN software (Lynnon Biosoft, Canada) the deduced amino acid sequences encoded by the ORFs were determined and their homology with respective ORF proteins of various carmoviruses were compared. The deduced protein sequences shared the highest identity of 68.2 to 81% with those of the SgCV isolate Arizona. King et al. (2011) suggested respective artificial host range reactions and percentage of coat protein and polymerase amino acid sequence identities of less than 52 and 57% as criteria for species demarcation in *Carmovirus*. These features suggest that SgCV-gm should possibly be designated a new SgCV isolate. To the best of our knowledge, this is the first report of SgCV naturally infecting *G. mihanovichii* in South Korea. Further research is needed to gain more in-depth insight into the biological and pathological properties of this virus.

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The author(s) declare no conflict of interest.

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