Diseases Caused by Viruses

First Report of *Cnidium officinale* as a Natural Host Plant of Apple Stem Grooving Virus in South Korea

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Cnidium officinale is a perennial plant in the family Apiaceae. It is native to China and cultivated in China, Japan, and Korea for its roots for medicinal purposes. In August 2019, 63 *C. officinale* plants showing symptoms of vein chlorosis, yellowing, and chlorotic spots were collected from commercial farms in Bonghwa and Youngyang, Gyeongsangbuk-do, South Korea. Reverse transcription polymerase chain reaction (RT-PCR) was performed to confirm the presence of apple stem grooving virus (ASGV), cnidium vein yellowing virus 1, cnidium vein yellowing virus 2, lychnis mottle virus, and cnidium virus X with specific primers. Forty-one out of the 63 samples were positive for ASGV in mixed infection with one or more of the other four viruses. *Nicotiana benthamiana* plants mechanically inoculated with the crude sap of one of the ASGV-infected *C. officinale* plants showed mosaic symptom on upper leaves 10 days postinoculation (dpi). Infection was confirmed by RT-PCR and Sanger sequencing. *N. benthamiana* plants systemically infected with ASGV-CO-kr1 isolate alone were used for subsequent sequencing and host range test. Twenty-day-old seedlings of 23 species of plants (two to 14 species for each family) from the families Solanaceae, Chenopodiaceae, Cucurbitaceae,

Fabaceae, and Amaranthaceae were mechanically inoculated with sap of ASGV-CO-kr1-infected *N. benthamiana* plants. ASGV-CO-kr1 infected all 23 tested species as confirmed by symptomology, RT-PCR, and Sanger sequencing at 10 to 20 dpi. The MP and CP genes of ASGV-CO-kr1 were amplified by RT-PCR with specific primers 4300–4325F/5642–5666R and 5592–5612F/6475–6499R, respectively. The amplicons were cloned and sequenced (GenBank accession nos.: MP, MW889883; and CP, MW889884). Multiple sequence alignment using the MegAlign program in DNASTAR showed that the complete CP and MP genes of ASGV-CO-kr1 shared 89.9 to 99.7% and 83.1 to 99.5% identities, respectively, at the nucleotide level, and they shared 92.4 to 99.6% and 93.8 to 99.4% identities, respectively, at amino acid (aa) level with corresponding sequences of 34 other ASGV isolates from various host plants and countries. Phylogenetic analysis with the maximum likelihood method using the MEGA X program (Kumar et al. 2018) showed that ASGV-CO-kr1 grouped with isolates Cuiguan (KR185346), BH (LC480456), and YY (LC480457) based on the CP aa sequences, whereas it grouped with isolates SG (LC475148) and TL101 (MH108976) based on the MP aa sequences. ASGV is known to naturally infect apples, European pear, Asian pear, citrus, apricot, cherry, kiwifruit, loquat, lily, and lotus (Clover et al. 2003; He et al. 2019; Hu et al. 2017; Liu et al. 2019; Yanase et al. 1975). To the best of our knowledge, this is the first report of the natural infection of ASGV in *C. officinale*. *C. officinale* plants are propagated by root division, so they are susceptible to infection with viruses. The result of this study is important for generating virus-free seedlings to produce *C. officinale*.

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