



First report of cucumber green mottle mosaic virus infecting *Perilla frutescens* in Korea and the world

In-Sook Cho¹ · Ju-Yeon Yoon¹ · Bong-Nam Chung¹ · Hyoun-Sub Lim²

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Cucumber green mottle mosaic virus (CGMMV, genus *Tobamovirus*, family *Virgaviridae*), causes serious losses in cucurbit crops worldwide. In December 2017, virus-like symptoms of mosaic and malformed leaves were observed on 20–30% of perilla (*Perilla frutescens*, Lamiaceae) plants in a greenhouse in Yeongcheon, Korea. Total RNA from leaves of five symptomatic plants was extracted (BCS plant RNA prep kit, Biocube Inc, Korea) and prepared for high-throughput sequencing. After processing (mRNA purification kit and Ribo-Zero RNA removal kit), a cDNA library was prepared and sequenced (Illumina TruSeq Stranded Total RNA kit and NovaSeq 6000 system, Macrogen Inc. Korea) as 150 nt paired ends. *De novo* assembly of 76,231,370 reads was performed by Trinity software (r20140717), and BLASTn analysis against the NCBI viral database of the assembled 87,553 contigs resulted in identification of seven contigs of 293–1714 nt, sharing 96.83 to 99.32% nt identity to the CGMMV reference genome. CGMMV presence was confirmed by reverse transcription PCR using virus-specific primers 724F/724R (Cho et al. 2011). Amplicons of the expected 724 bp were obtained from the five symptomatic plants, and from *Nicotiana tabacum* inoculated from

perilla; the sequence (GenBank accession No. LC507614) shared 99.86% identity with CGMMV –TG (KP868653). *Perilla* is an important oilseed and vegetable crop in Korea, and other viruses are reported to infect perilla, including tomato spotted wilt virus, perilla mosaic virus, broad bean wilt virus 2 and turnip mosaic virus (Kubota et al. 2020; Park et al. 2020). To our knowledge, this is the first report of CGMMV infecting *P. frutescens* in Korea and the world. CGMMV is seed-borne on cucurbits, and highly transmissible. Use of CGMMV-free seed is necessary for prevention of disease in susceptible crops. Additional studies are needed of the effects of CGMMV on *P. frutescens*.

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✉ Hyoun-Sub Lim
hyounlim@cnu.ac.kr

In-Sook Cho
hyounlim@cnu.ac.kr

¹ National Institute of Horticultural & Herbal Science, RDA, Wanju 55365, Republic of Korea

² Department of Applied Biology, Chungnam National University, Daejeon 305-764, Korea