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DISEASE NOTES

First Report of *Cucumber mosaic virus* Infecting *Wisteria sinensis* in Serbia

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Wisteria sinensis (Sims) DC (family Fabaceae), commonly known as Chinese wisteria, is a perennial vine that can live for 50 years or more. It is commonly found in natural forests, riparian zones, and ruderal areas, but in city parks as an ornamental plant as well. In some parts of the world, it is considered to be an invasive species (USDA 2016). Five samples of *W. sinensis* showing virus-like symptoms including mosaic accompanied by leaf deformation and severe shoestring were collected in 2010 from the Porodin locality (Braničevo District, Serbia). Because a large number of aphids were present on the leaves of naturally infected plants, collected samples were serologically tested for the presence of three commonly occurring aphid-transmitted viruses, *Cucumber mosaic virus* (CMV), *Alfalfa mosaic virus* (AMV), and *Potato virus Y* (PVY) (Delibašić et al. 2013). Double-antibody sandwich (DAS)-ELISA was performed using commercial diagnostic kits (Bioreba AG, Reinach, Switzerland). Commercial positive and negative controls were included in each ELISA. CMV was serologically detected in all five collected samples, while no other tested viruses were found. The ELISA-positive sample 540-10 was mechanically transmitted to


five plants of each of three common test plants. Chlorotic local lesions on *Chenopodium quinoa* and severe mosaic and leaf malformations were observed on all inoculated *Nicotiana tabacum* 'Samsun' and *N. glutinosa*. The inoculated plants were assayed by DAS-ELISA and all tested positive for CMV. The presence of CMV in *W. sinensis* as well as mechanically inoculated plants was further confirmed by RT-PCR. Total RNAs from naturally and mechanically infected plants were isolated using the RNeasy Plant Mini Kit (Qiagen, Hilden, Germany). RT-PCR was carried out using the One-Step RT-PCR Kit (Qiagen) with primer pair CMVCPfwd/CMVCPrev, which amplifies an 871-bp fragment of the entire coat protein (CP) gene and part of 3'- and 5'-UTRs of subgenomic RNA 4 (Milojević et al. 2012). Total RNAs obtained from the Serbian CMV pumpkin isolate (GenBank Accession No. HM065510) and healthy *W. sinensis* leaves were used as the positive and negative controls, respectively. All naturally and mechanically infected plants, as well as the positive control, yielded an amplicon of expected size. No amplicon was recorded in the healthy control. The amplified product derived from isolate 540-10 was purified (QIAquick PCR Purification Kit, Qiagen), directly sequenced in both directions and deposited in GenBank (KT270568). Sequence comparison of the complete CP gene (657 nt) with those available in GenBank, conducted with MEGA5 software (Tamura et al. 2011), revealed a maximum nucleotide identity of 99.1% (98.1% amino acid identity) with the Japanese isolate (AB006813). To our knowledge, this is the first report on the occurrence of CMV in *W. sinensis* worldwide. Considering that *W. sinensis* is an invasive, perennial plant with extreme longevity, it could act as a virus reservoir. This finding has potentially significant implications for the successful production of CMV susceptible crops.

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