Diseases Caused by Viruses

First Report of Dasheen Mosaic Virus Infecting *Typhonium giganteum* (Baifuzi) in Henan Province of China

Y. H. Qin,^{1,2,3} S. X. Gao,^{1,2,3} Y. X. Liu,^{1,2,3} Y. Wen,^{1,2,3} C. T. Lu,^{1,2,3} F. Wang,^{1,2,3,†} J. Yang,^{1,2,3} X. M. Li,^{1,2,3} and W. P. Qi^{1,2,3}

¹ Institute of Plant Protection, Henan Academy of Agricultural Sciences, Zhengzhou 450002, China

² Henan Key Laboratory of Crop Pest Control, Zhengzhou 450002, China

³ IPM Key Laboratory in Southern Part of North China for Ministry of Agricultural and Rural Affairs, Zhengzhou 450002, China

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Typhonium giganteum Engl. (baifuzi) is a perennial plant of the family Araceae. In China, its root is commonly used as an antispasmodic for stroke and cancer treatment (Chi et al. 2010; Gao et al. 2014; Khalivulla et al. 2019). Yuzhou city in Henan Province is the main producing area of *T. giganteum*, and in July 2020, a survey of viral disease infecting *T. giganteum* was conducted in the city. In the surveyed fields ($n = 5$), over 60% of plants displayed varying levels of virus-like symptoms, including mosaic, chlorosis, and leaf distortion. To identify possible viral pathogens associated with the disease symptoms afflicting *T. giganteum*, one leaf was collected from each of 25 symptomatic plants and analyzed by high-throughput sequencing (HTS) as well as polymerase chain reaction (PCR). For HTS analysis, total RNA was extracted from one pooled sample containing a portion of all above-mentioned leaves using an RNAPrep Pure Plant Plus Kit (Tiangen Biotech, Beijing, China). After removing ribosomal RNA with a Ribo-off rRNA depletion kit (Vazyme Biotech, Nanjing, China), a sequencing library was generated using a NEBNext Ultra RNA Library Prep Kit for Illumina (NEB, Ipswich, MA, U.S.A.) and sequenced on an Illumina Novaseq6000 sequencing system at Berry Genomics Corporation (Beijing, China). A total of 6,899,143 high-quality clean reads were obtained after trimming and used for contig assembly. BLASTn and BLASTx analyses on the contigs

($n = 128,400$) showed that one contig (9,245 bp in length) exhibited a sequence identity of 84.0% with the reference sequence of dasheen mosaic virus (DsMV, NCBI reference seq. NC_003537, genus *Potyvirus*, family *Potyviridae*), suggesting infection of the plants by DsMV. No other viral sequences were detected in the sample. To confirm these results, a near full-length genomic sequence of DsMV was obtained from one sample (sample no. 39) by reverse transcription PCR (RT-PCR) of three overlapping fragments with the following primer pairs: DsMV-1F (5'-AAATTAAACATCTCAACAAAACCTACA-3')/DsMV-4130R (5'-TTCATGGTCCTCGTGGAGTATA-3'), DsMV-3870F (5'-GAGGACGTGAGAATTCAAAGTCT-3')/DsMV-8250R (5'-GTCCACCTTGCTTGATGCATGC-3'), and DsMV-7690F (5'-GGAGCGACTCCTCTTCCAAAGTTGTG-3')/DsMV-10100R (5'-TGAACACCGTGCACGAAGCATCTC-3'). The PCR products were cloned into pMD19-T vector (Takara Biotech, Dalian, China) and sequenced. The near full-length genomic sequence of the isolate (DsMV-BF39) was 9,737 nt in length and deposited into GenBank under the accession number MZ043618. BLASTn analysis of this sequence demonstrated that it shared an identity ranging from 78.6% (MG602234) to 85.6% (MG602227) with various DsMV isolates. To determine whether DsMV was closely associated with the symptoms observed in *T. giganteum*, leaf tissues from 30 symptomatic plants and 22 asymptomatic plants were analyzed by RT-PCR using primer pairs DsMV-CPF (5'-TGTTCTGTGAACATGATGAAGTTG-3', sense) and DsMV-CPR (5'-GTAAGTGTGGCCTGTTTACCAG-3', antisense) targeting a 916-bp fragment of the CP gene of DsMV. Amplicons with the expected size were detected from the 30 symptomatic plants but not from the 22 asymptomatic plants, suggesting a close association between DsMV infection and the observed symptoms. To our knowledge, this is the first report of DsMV infecting *T. giganteum*. Further study is needed to identify the specific symptoms induced by this virus in *T. giganteum* and to understand the biological characteristics, epidemiology, and prevalence of this virus in China.

References:

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[†]Indicates the corresponding author.
F. Wang; yunfeiren@163.com