First report of tobacco vein banding mosaic virus infecting *Solanum lyratum* Thunb in China

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Received: 28 August 2019 / Accepted: 1 October 2019 / Published online: 10 November 2019
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Keywords *Solanum lyratum* Thunb · Vein banding and mosaic symptoms · Tobacco vein banding mosaic virus

Solanum lyratum Thunb, a species of the genus *Solanum* in the family *Solanaceae*, is a common Chinese herbal medicine. Tobacco vein banding mosaic virus (TVBMV) is a member of the genus *Potyvirus* and was first discovered in Taiwan in 1964 (Habera et al. 1994). In July 2018, several *S. lyratum* plants growing naturally along a roadside exhibited virus-like symptoms including dark green vein banding and mosaic in Zhenjiang, Jiangsu province, China. The crude sap from the symptomatic leaves of *S. lyratum* was rubbed onto leaves of *Nicotiana benthamiana* plants, resulting in mild downward leaf curling and mild mosaic symptoms at 9 days post inoculation (dpi) and severe downward leaf curling, yellowing and plant stunting at 20 dpi, indicating mechanical transmission of a virus. Mock-inoculated *N. benthamiana* plants did not exhibit any symptoms at 9 or 20 dpi. Double-stranded (ds) RNA was extracted from the symptomatic leaves of *S. lyratum* (Morris and Dodds 1979), and used as a template for sequence-independent amplification (SIA) (Agindotan et al. 2010). Polymerase chain reaction (PCR) products were ligated into pUCm-T Vector (Sangon, Shanghai, China) and sequenced (Sun Ya, Shanghai, China). BLAST analysis showed that the nucleotide sequence (nt) of seven fragments were 92–

94% identical to a TVBMV isolate from Shandong, China (JN630469). The presence of TVBMV was further confirmed in the symptomatic *S. lyratum* and *N. benthamiana* plants inoculated with crude sap by reverse transcription (RT) PCR using virus-specific primers (forward, 5'-GGATATTG GTGAGCAGATGC-3'; and reverse, 5'-CGTTTTTCG ATGCACCACACCATC-3') designed on the sequences obtained by SIA. The expected 1109 nt product was not amplified from the asymptomatic or the mock-inoculated *N. benthamiana* plants. Subsequently, the complete genome of this isolate (tentatively named TVBMV-lyr) was determined by sequencing RT-PCR products obtained using degenerate TVBMV primers designed from the results of multiple sequence alignments of TVBMV isolates along with TMV-lyr-specific primers designed from sequences obtained by SIA. The complete genomic sequence of TVBMV-lyr was deposited in GenBank as accession number MH898883. It is 9570 nt in length and shares the highest nucleotide identity (94.32%) with TVBMV-SDZC1 (HQ396793). To our knowledge, this is the first report of TVBMV infection in *S. lyratum*.

Acknowledgements This work was partially granted by the Natural Science Foundation of the Jiangsu Higher Education Institutions of China (No. 18KJA210001).

Electronic supplementary material The online version of this article (<https://doi.org/10.1007/s42161-019-00419-y>) contains supplementary material, which is available to authorized users.

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