



# First report of sweet potato feathery mottle virus infecting *Amaranthus blitum* in China

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Received: 29 September 2019 / Accepted: 27 February 2020 / Published online: 5 March 2020  
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**Keywords** Sweet potato feathery mottle virus · *Amaranthus blitum* · RT-PCR

Sweet potato feathery mottle virus (SPFMV, genus *Potyvirus*) is the most common viral agent of cultivated sweet potato worldwide. SPFMV alone causes no or mild symptoms in most sweet potato cultivars, while the co-infection with sweet potato chlorotic stunt virus causes sweet potato virus disease (SPVD), the most serious disease in sweet potato globally (Clark et al. 2012). Weed species had previously reported to act as natural hosts for SPFMV (Tugume et al. 2008). In April 2019, seven plants of the three most common weed species, namely, *Amaranthus blitum* (four), *Convolvulus arvensis* (two) and *Chenopodium album* (one), were randomly collected in a field planting sweet potato seedlings in Xinxiang, Henan Province, China. SPFMV was tested in all samples by RT-PCR with a SPFMV-specific primer set (SPFMV-F1, 5'-TGGGGTTATGATGAACTTCTTC-3'; SPFMV-R1, 5'-TTCTGGAATGRYTGCGGGTTG-3'). An approximately 400-bp product of the expected size was obtained in one *A. blitum* plant displaying mottle symptoms on leaves and sequenced. The resulting 405-bp sequence was deposited in GenBank (accession No. MK953929) and analyzed by BLASTn, showing a 97.28% nucleotide sequence (nt) identity to SPFMV isolate TM64B (MF572053). The presence of

SPFMV in *A. blitum* was further confirmed by a nitrocellulose membrane enzyme-linked immunosorbent assay with rabbit polyclonal anti-SPFMV antibodies (Zhang et al. 2000). Additionally, using sap from SPFMV-infected *A. blitum*, mechanically inoculated *Ipomoea setosa* plants were asymptomatic, but positive for SPFMV by RT-PCR. To examine the incidence of SPFMV in *A. blitum*, 26 plant samples were collected from four different sweet potato fields in Henan Province in July 2019. SPFMV, showing a 19.23% (5/26) of incidence, was detected in both symptomatic (mottling and mosaic) and asymptomatic plants from three surveyed fields by RT-PCR using primer set SPFMV-F1/R1. Sequencing of the five amplified fragments generated four distinct SPFMV sequences (MN508224-MN508227). The nt identity of 85.93–100.00% was obtained when comparing the sequences of PCR amplicons from the six SPFMV-infected samples, suggesting the genetic diversity of SPFMV in *A. blitum* plants. To our knowledge, this is the first report of SPFMV infecting *Amaranthus blitum*.

**Electronic supplementary material** The online version of this article (<https://doi.org/10.1007/s42161-020-00533-2>) contains supplementary material, which is available to authorized users.

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