



NEW DISEASE REPORT

Musk mallow (*Abelmoschus moschatus*): a new host of Cucurbit aphid-borne yellows virus

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E-mail: savarni.tripathi@icar.gov.in**KEYWORDS**

CABYV, musk okra, ornamental okra, Polerovirus

Musk mallow (*Abelmoschus moschatus*, family Malvaceae) is a medicinal plant cultivated across Asia, Africa and South America. It is found as a weed all over the Deccan region of India (Pawar & Vyawahare, 2017). The seeds of the plant are used for medicinal purposes and as a source of fragrant compounds (Gul *et al.*, 2011).

Musk mallow plants exhibiting yellowing of older leaves, midvein clearing, leaf reduction, mottling and slight downward curling (Fig. 1) were observed in October 2022 at the experimental research farm of the Indian Agricultural Research Institute in Pune, Maharashtra, India. The plants occurred as weeds and the disease incidence was 4% (c. 16 plants) in an eight-acre area. Ten diseased and four asymptomatic plants were sampled to ascertain the viruses associated with the symptoms.

ELISA was done using antisera against Cucurbit aphid-borne yellows virus (CABYV) (DSMZ, Germany), Cucurbit yellow stunting disorder virus (CYSDV) (Arsh Biotech, India), Cucumber mosaic virus (CMV), Papaya ringspot virus (PRSV) and Zucchini yellow mosaic virus (ZYMV) (Agdia, USA). CABYV was detected in all diseased samples but CMV, CYSDV, PRSV and ZYMV were not detected. None of the five viruses were detected by ELISA in the asymptomatic samples.

Total RNA was extracted from both diseased and asymptomatic samples using an RNeasy Plant Mini Kit (Qiagen, USA). Two-step RT-PCR assay was done using the extracted RNA and CABYV-specific primers which amplify c. 484 bp of the partial coat protein region (Boubourakas *et al.*, 2006). RT-PCR was also performed using primers specific for CMV, CYSDV, PRSV, ZYMV, *Beet pseudo-yellows virus* and *Cucumber vein yellowing virus*. Amplicons of the expected size were obtained in all diseased plants with CABYV primers but not with



FIGURE 1 Musk mallow plant infected with *Cucurbit aphid-borne yellows virus* showing yellowing of older leaves, midvein clearing, leaf reduction, mottling and slight downward curling symptoms.

primers for any of the other viruses. No amplification was obtained in the asymptomatic samples for any of the viruses. The amplicons

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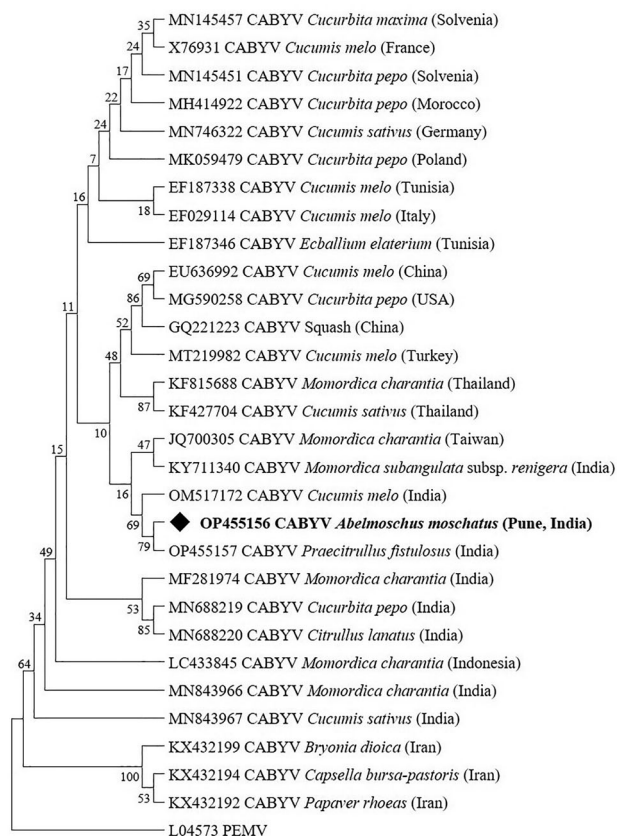


FIGURE 2 Phylogenetic tree constructed based on *Cucurbit aphid-borne yellows virus* (CABYV) sequences showing the relationship between the sequence from the current study (OP455156; diamond symbol) and other CABYV sequences. *Pea enation mosaic virus* was used as an outgroup. The tree was constructed using the neighbour-joining method and bootstrap values obtained for 1,000 replicates.

of five samples were Sanger sequenced bidirectionally and found to be identical (GenBank Accession No. OP455156). A BLASTn search of the sequence revealed that it shared 100% identity with an Indian CABYV sequence from *Praecitrullus fistulosus* (OP455157). A phylogenetic tree was constructed using the neighbour-joining method (MEGA X program) with CABYV sequences from different hosts and geographies, and the sequence clustered with other Indian CABYV sequences (Fig. 2).

CABYV primarily infects cucurbits but also infects other crops and weeds including three Malvaceae species, *Abutilon theophrasti*, *Gossypium hirsutum* and *Malva parviflora* (Lecoq *et al.*, 2022). To our knowledge, this is the first report of CABYV infecting *Abelmoschus moschatus* in the world. The present finding is of epidemiological importance as it indicates the further broadening of the host range of CABYV and the possibility of infecting other economically important Malvaceae members, such as *G. hirsutum* which is grown for cotton in India. Furthermore, musk mallow plants could serve as an alternative / reservoir host for CABYV aiding its transmission to other commercial crops.

ACKNOWLEDGEMENTS

The authors thank the Director, ICAR-IARI, New Delhi for providing lab facilities.

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How to cite this article: Verma, R., Verma, A. & Tripathi, S. (2023) Musk mallow (*Abelmoschus moschatus*): a new host of Cucurbit aphid-borne yellows virus. *New Disease Reports*, 47, e12185. <https://doi.org/10.1002/ndr2.12185>