



Natural occurrence of *Bhendi* yellow vein mosaic virus on *Litsea* spp. in India

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Received: 07 Jan 2015. Published: 15 Feb 2015. Keywords: Geminivirus, natural host, India, detection, Begomovirus

Abelmoschus esculentus (Malvaceae) commonly called okra, lady's finger, bhendi or bindi is an important vegetable crop grown in West Bengal, India. The plant is susceptible to a most important and destructive *Begomovirus*: *Bhendi yellow vein mosaic virus* (BYVMV) that causes severe economic losses. BYVMV was first reported from Mumbai in India (Kulkarni, 1924). Okra infected with BYVMV has been reported in Asia in Bangladesh, India, Pakistan, Thailand, Sri Lanka and China (Kulkarni, 1924; Tsai *et al.*, 2013). During summer season surveys in Barasat, West Bengal, India in 2013 and 2014, both *Litsea apetala* and *L. sebifera* (Lauraceae) exhibited typical symptoms of geminivirus infection, including leaf curling, deformation, leaf yellowing, vein clearing, mosaic and stunted growth (Fig. 1). Total DNA was isolated from diseased leaves using a modified CTAB procedure (Ghosh *et al.*, 2009) and the extract tested for the presence of geminiviruses by PCR using a pair of degenerate geminivirus-specific primers (GEM-F: 5'-ATRRHTHTGGATGGAYGARAACAT-3'; GEM-R: 5'-AAATCCCCTNTATTTCAAARAT-3') amplifying approximately 760 bp of sequence partially overlapping the putative AV1, AC3 and AC2 genes (Fig. 2). The sequences from both *L. sebifera* and *L. apetala* share 93-99% identity with the sequences of several BYVMV isolates, while they share 98% identity with each other at the nucleotide level. Both viral sequences from *L. apetala* and *L. sebifera* were submitted to the DDBJ sequence database as *Bhendi yellow vein mosaic virus*, isolate Barasat1 (GenBank Accession No. LC010941) and *Bhendi yellow vein mosaic virus*, isolate Barasat7 (LC010947), respectively. To the best of our knowledge this is the first report of *L. apetala* and *L. sebifera* as natural and alternative

hosts of BYVMV in India. This result supports the notion that geminiviruses are important emerging and devastating viruses causing threats to crops (Varma & Malathi, 2003). Therefore, there is a need for further detailed study on the diversity of BYVMV, viral disease management, and identification of alternative hosts that may act as virus reservoirs.

Acknowledgements

The authors would like to thank Prof. G.G. Maiti for his excellent expertise in the identification of the host plants.

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Figure 1

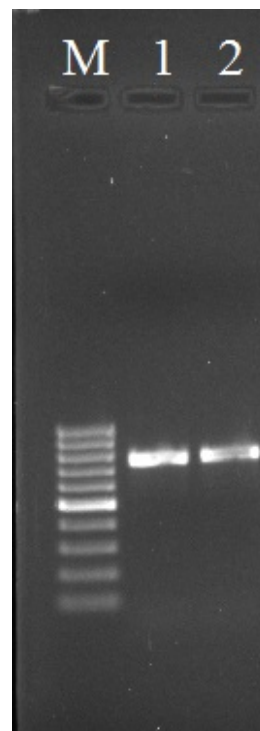


Figure 2

To cite this report: Roy B, Chakraborty B, Mitra A, Sultana S, Sherpa AR, 2015. Natural occurrence of *Bhendi* yellow vein mosaic virus on *Litsea* spp. in India. *New Disease Reports* **31**, 7. <http://dx.doi.org/10.5197/j.2044-0588.2015.031.007>

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