New Disease Reports

WILEY

NEW DISEASE REPORT OPEN ACCESS

Vasconcellea cauliflora: A New Host of Chilli Leaf Curl Virus

S. Tripathi | A. Verma | R. Verma | A. Khar

ICAR-Indian Agricultural Research Institute, Regional Station, Pune, India

Correspondence: S. Tripathi (savarni_pune@iari.res.in)

Received: 26 June 2025 | **Accepted:** 15 August 2025

Keywords: Begomovirus | leaf curl | highland papaya | India

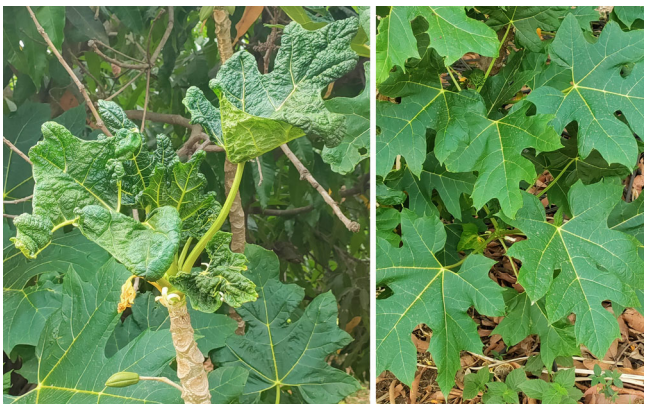


FIGURE 1 | Infected *Vasconcellea cauliflora* plant showing crinkling, mottling and downward curling of leaves (left), healthy plant (right).

Vasconcellea cauliflora is a member of the family Caricaceae and is known as highland or mountain papaya due to its resemblance to papaya and its adaptation to grow in elevated or mountainous regions with cooler climates (Scheldeman et al. 2007). In spite of its name and appearance, it is not closely related to papaya as evidenced by significant genetic differences between the two species (Kyndt et al. 2005).

Vasconcellea cauliflora plants showing symptoms of crinkling, mottling and downward curling of leaves, indicative of a possible begomovirus infection, were observed in November 2023 in the experimental research field of IARI Regional Station, Pune, Maharashtra, India (Figure 1). The overall average disease incidence was 12% across the 1-acre field. The plants were growing in the vicinity of tomato and chilli plantations. Five diseased and five asymptomatic leaf samples were collected to identify and characterise the associated virus.

Total DNA was extracted from the leaf samples (100 mg) using a DNeasy Plant Mini Kit (Qiagen, Germany). PCR was done using the extracted DNA and universal degenerate primers for begomovirus detection (Deng 540/541) that amplify part of the coat protein gene (Deng et al. 1994). Amplicons of the expected size, c. 500 bp, were detected in all five diseased samples. No amplification was recorded in asymptomatic samples. All amplicons were found to be identical on sequencing and one of the sequences (VCP1) was deposited in GenBank (Accession No. PP748834). No amplification was obtained when the samples were tested for the presence of DNA-B using the specific degenerate primer pair PBL1v2040/PCRc1 (Rojas et al. 1993) indicating that the virus is monopartite. Amplification was also not obtained for alpha and beta satellites using specific primers DNA101/DNA102 and β01/β02, respectively (Bull et al. 2003). BLASTn analysis revealed more than 98% identity with chilli leaf curl virus (ChiLCV) sequences reported in chilli from the neighbouring states of Karnataka (MW760302; MW760329) and Gujarat (JN663846), and tomato (MH577034) from Rajasthan (Table 1). In a phylogenetic analysis, the sequence clustered with other ChiLCV sequences (Figure 2).

Recently, cucumber mosaic virus has been reported to infect *V. cauliflora* (Verma et al. 2023). To the best of our knowledge, this is the first report of ChiLCV causing leaf curl disease in *V. cauliflora*. The finding is of considerable epidemiological importance as it provides evidence for an expansion in the known host range of this economically important virus. It has critical relevance for the global papaya industry, especially given the use of *V. cauliflora* as a parent in the development of disease-resistant varieties.

This is an open access article under the terms of the Creative Commons Attribution License, which permits use, distribution and reproduction in any medium, provided the original work is properly cited.

© 2025 The Author(s). *New Disease Reports* published by British Society for Plant Pathology and John Wiley & Sons.

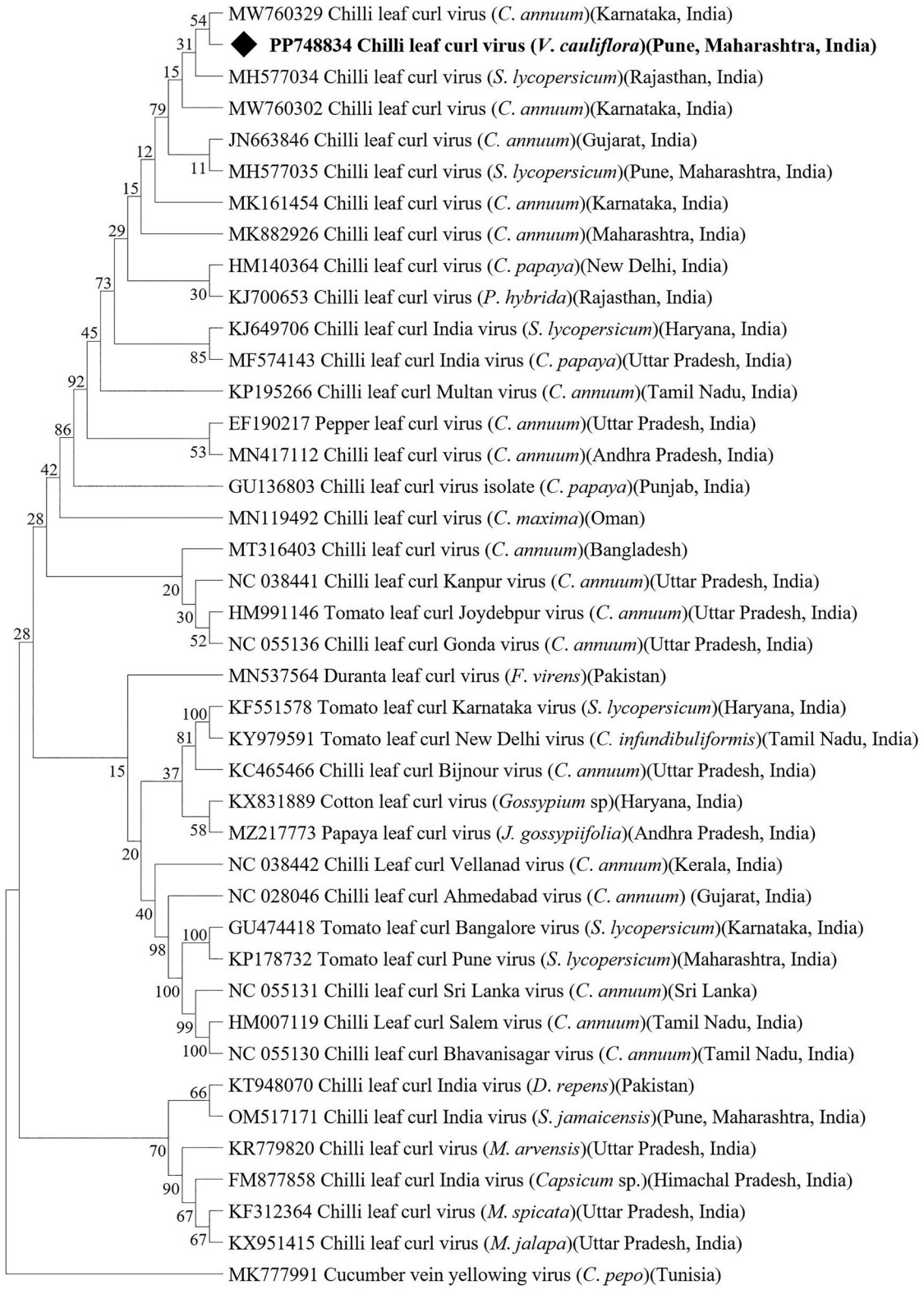


FIGURE 2 | Phylogenetic tree showing the relationship between the sequence in the present study (PP748834, marked with a diamond symbol) with other begomovirus sequences. The tree was constructed using the neighbour-joining method and bootstrap values obtained for 1000 replicates. Cucumber vein yellowing virus was used as an outgroup to root the tree.

TABLE 1 | Begomovirus sequences used in the bioinformatic analysis and their percentage identity with the viral sequence obtained from *Vasconcellea cauliflora* in Pune, Maharashtra, India (PP748834).

GenBank accession number	Begomovirus	Host species	Origin	Percentage identity
NC_028046	Chilli leaf curl Ahmedabad virus	*Capsicum annuum*	Gujarat, India	78.24
NC_055130	Chilli leaf curl Bhavanisagar virus	*Capsicum annuum*	Tamil Nadu, India	75.06
NC_055136	Chilli leaf curl Gonda virus	*Capsicum annuum*	Uttar Pradesh, India	81.53
NC_038441	Chilli leaf curl Kanpur virus	*Capsicum annuum*	Uttar Pradesh, India	89.49
NC_055131	Chilli leaf curl Sri Lanka virus	*Capsicum annuum*	Sri Lanka	74.40
NC_038442	Chilli leaf curl Vellanad virus	*Capsicum annuum*	Kerala, India	82.34
HM007119	Chilli Leaf curl Salem virus	*Capsicum annuum*	Tamil Nadu, India	75.00
KC465466	Chilli leaf curl Bijnour virus	*Capsicum annuum*	Uttar Pradesh, India	82.07
KT948070	Chilli leaf curl India virus	*Duranta repens*	Pakistan	85.31
MF574143	Chilli leaf curl India virus	*Carica papaya*	Uttar Pradesh, India	95.56
KJ649706	Chilli leaf curl India virus	*Solanum lycopersicum*	Haryana, India	96.77
KF312364	Chilli leaf curl India virus	*Mentha spicata*	Uttar Pradesh, India	84.71
KX951415	Chilli leaf curl India virus	*Mirabilis jalapa*	Uttar Pradesh, India	85.31
FM877858	Chilli leaf curl India virus	*Capsicum sp.*	Himachal Pradesh, India	85.51
KR779820	Chilli leaf curl India virus	*Mentha arvensis*	Uttar Pradesh, India	82.36
OM517171	Chilli leaf curl India virus	*Stachytarpheta jamaicensis*	Pune, Maharashtra, India	87.22
MH577035	Chilli leaf curl virus	*Solanum lycopersicum*	Pune, Maharashtra, India	97.78
MN119492	Chilli leaf curl virus	*Cucurbita maxima*	Oman	87.35
MN417112	Chilli leaf curl virus	*Capsicum annuum*	Andhra Pradesh, India	94.15
MK882926	Chilli leaf curl virus	*Capsicum annuum*	Maharashtra, India	97.78
GU136803	Chilli leaf curl virus	*Carica papaya*	Punjab, India	92.74
HM140364	Chilli leaf curl virus	*Carica papaya*	New Delhi, India	96.37
MK161454	Chilli leaf curl virus	*Capsicum annuum*	Karnataka, India	97.78
KJ700653	Chilli leaf curl virus	*Petunia hybrida*	Rajasthan, India	97.78
MT316403	Chilli leaf curl virus	*Capsicum annuum*	Bangladesh	87.32
MW760302	Chilli leaf curl virus	*Capsicum annuum*	Karnataka, India	98.38
MW760329	Chilli leaf curl virus	*Capsicum annuum*	Karnataka, India	98.38
JN663846	Chilli leaf curl virus	*Capsicum annuum*	Gujarat, India	98.38
MH577034	Chilli leaf curl virus	*Solanum lycopersicum*	Rajasthan, India	98.38

(Continues)

TABLE 1 | (Continued)

GenBank accession number	Begomovirus	Host species	Origin	Percentage identity
KP195266	Chilli leaf curl Multan virus	*Capsicum annuum*	Tamil Nadu, India	96.57
MN537564	Duranta leaf curl virus	*Ficus virens*	Pakistan	80.24
GU474418	Tomato leaf curl Bangalore virus	*Solanum lycopersicum*	Karnataka, India	74.16
HM991146	Tomato leaf curl Joydebpur virus	*Capsicum annuum*	Uttar Pradesh, India	90.36
KF551578	Tomato leaf curl Karnataka virus	*Solanum lycopersicum*	Haryana, India	74.23
KY979591	Tomato leaf curl New Delhi virus	*Crossandra infundibuliformis*	Tamil Nadu, India	77.54
KP178732	Tomato leaf curl Pune virus	*Solanum lycopersicum*	Maharashtra, India	73.62
EF190217	Pepper leaf curl virus	*Capsicum annuum*	Uttar Pradesh, India	93.60
MZ217773	Papaya leaf curl virus	*Jatropha gossypiifolia*	Andhra Pradesh, India	82.34
KX831889	Cotton leaf curl virus	*Gossypium* sp.	Haryana, India	85.47

Moreover, the infected plants could serve as natural reservoirs of the virus aiding its transmission to other important vegetable crops cultivated in the vicinity.

Acknowledgements

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

References

Bull, S. E., R. W. Briddon, and P. G. Markham. 2003. "Universal Primers for the PCR-Mediated Amplification of DNA1: A Satellite-Like Molecule Associated With Begomovirus-DNA β Complexes." *Molecular Biotechnology* 23: 83–86. https://doi.org/10.1385/MB:23:1:83.

Deng, D., P. F. McGrath, D. J. Robinson, and B. D. Harrison. 1994. "Detection and Differentiation of Whitefly-Transmitted Geminiviruses in Plants and Vector Insects by the Polymerase Chain Reaction With Degenerate Primers." *Annals of Applied Biology* 125: 327–336. https://doi.org/10.1111/j.1744-7348.1994.tb04973.x.

Kyndt, T., E. Romeijn-Peeters, B. Van Droogenbroeck, J. P. Romero-Motochi, G. Gheysen, and P. Goetghebeur. 2005. "Species Relationships in the Genus *Vasconcellea* (Caricaceae) Based on Molecular and Morphological Evidence." *American Journal of Botany* 92: 1033–1044. https://doi.org/10.3732/ajb.92.6.1033.

Rojas, M. R., R. L. Gilbertson, D. R. Russel, and D. P. Maxwell. 1993. "Use of Degenerate Primers in the Polymerase Chain Reaction to Detect Whitefly-Transmitted Geminiviruses." *Plant Disease* 77: 340. https://doi.org/10.1094/PD-77-0340.

Scheldeman, X., L. Willemen, G. Coppens d'Eeckenbrugge, et al. 2007. "Distribution, Diversity and Environmental Adaptation of Highland Papayas (*Vasconcellea* spp.) in Tropical and Subtropical America." *Biodiversity and Conservation* 16: 1867–1884. https://doi.org/10.1007/s10531-006-9086-x.

Verma, R., A. Verma, S. S. Kushwah, and S. Tripathi. 2023. "*Vasconcellea cauliflora*—A New Natural Host of Cucumber Mosaic Virus." *Archives of Phytopathology and Plant Protection* 56: 1300–1310. https://doi.org/10.1080/03235408.2023.2279944.