Received: 22 December 2023 | Accepted: 2 June 2024

DOI: 10.1002/ndr2.12288

New Disease Reports Open Access BSPP WILEY

NEW DISEASE REPORT

First report of *Zucchini tigré mosaic virus* naturally infecting two different cucurbit species in Argentina

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KEYWORDS
Cucurbita maxima, PRSV Cluster, ZTMV

In Argentina, *Cucurbita maxima* cv. Zapallo Plomo, an indigenous variety, and the hybrid *Cucurbita maxima* × *Cucurbita moschata* cv. Tetsukabuto contribute significantly to regional economies, being the fourth most popular vegetable in the domestic market. In March 2022, leaves showing virus-like symptoms, including discolouration, blistering, distortion and mosaics were collected from both cultivars in Balcozna, Catamarca province (Figure 1). The fruits were severely affected, being covered in knobbly warts, blotches and brown bumps (Figure 2).



FIGURE 1 *Cucurbita maxima* cv. Zapallo Plomo leaf showing symptoms caused by *Zucchini tigré mosaic virus*.



FIGURE 2 *Cucurbita maxima* cv. Zapallo Plomo fruit showing symptoms caused by *Zucchini tigré mosaic virus*.

Samples were tested by DAS-ELISA using commercial *Papaya ringspot virus* (PRSV) antisera (BIOREBA AG, Switzerland), following

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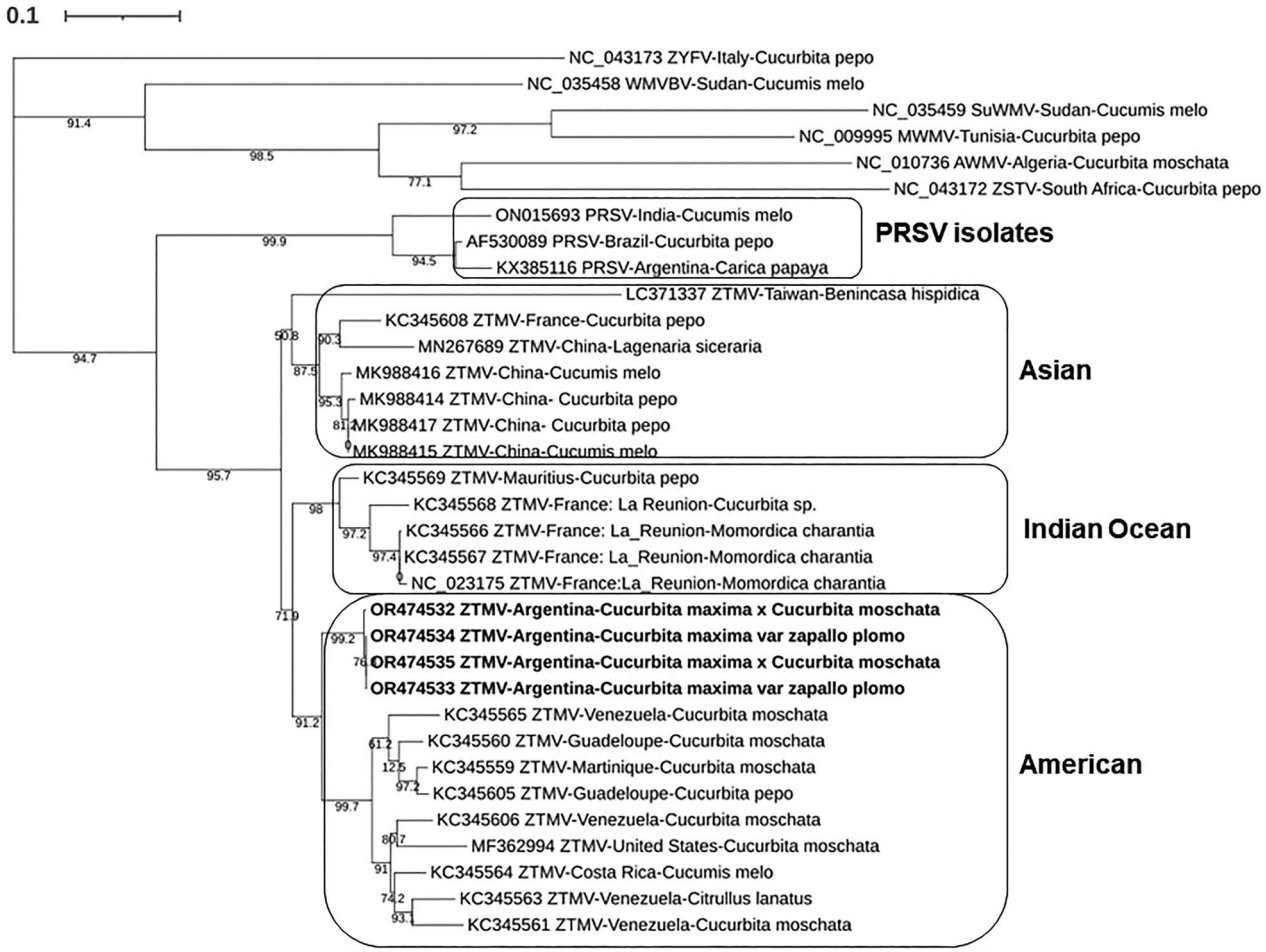


FIGURE 3 Phylogenetic tree of the coat protein region of *Zucchini tigré mosaic virus* (ZTMV) isolates from this study (in bold font) and 21 sequences available in GenBank. The TIM2+F+I+G4 model was chosen according to Bayesian Information Criterion, and 10,000 ultrafast bootstrap repetitions. Nine isolates from the PRSV cluster were used as outgroups. The tree showed: GenBank accession number, viral species, country and host. The numbers on the branches are bootstrap values. The horizontal scale indicates genetic distance. ZTMV isolates were grouped into three subgroups: Asian, American and the Indian Ocean, related to their geographical origins.

the manufacturer's instructions. Four ELISA-positive samples were tested by RT-PCR for the PRSV coat protein (CP) gene (Cabrera Mederos et al., 2016) but failed to generate the expected amplicon, suggesting the plants were infected with a different virus in the PRSV cluster. There are seven viruses that are closely related to PRSV which form the PRSV cluster. Cross-reaction with polyclonal antisera between the species of the PRSV cluster has been reported, resulting in misdiagnosis (Desbiez & Lecoq, 2021). While most members of the cluster are geographically restricted, *Zucchini tigré mosaic virus* (ZTMV) is distributed across Asia, Europe, and the Americas, including the United States, Costa Rica and Venezuela, as well as several islands in the Caribbean Sea and Indian Ocean (Cabrera Mederos et al., 2023).

Two-step RT-PCR was done using ZTMV-specific primers which amplify c. 830 bp of the CP region (Romay et al., 2014). The obtained amplicons were sequenced (Macrogen Inc., South Korea). Sequence comparison using BLASTn showed the highest nucleotide identity values (91.37 %, 100% query coverage) with a ZTMV isolate from Martinique (GenBank Accession No. KC345559). The obtained sequences were submitted to GenBank (OR474532-OR474535). Phylogenetic analysis of the CP region of ZTMV were performed using the maximum likelihood method in the IQ-TREE software (Figure 3). All four sequences from Argentina clustered together with those from America.

This finding suggests ZTMV might be more widespread than previously thought, potentially explaining recent yield losses in Balcozna due to reduced fruit growth and quality. The virus poses a significant threat to cucurbit crop yields in Argentina, highlighting the importance of characterising viral pathosystems to develop sustainable management practices and anticipate future outbreaks. Here, we report the first detection of ZTMV infecting cucurbits in Argentina, with *Cucurbita maxima* and *Cucurbita maxima* × *Cucurbita moschata* identified as novel hosts.

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How to cite this article: Brugo Carivali, M.F., Luciani, C.E., Celli, M.G., Carrasco, F., Silva, M.I., Cabrera Mederos, D. et al. (2024) First report of *Zucchini tigré mosaic virus* naturally infecting two different cucurbit species in Argentina. *New Disease Reports*, 49, e12288. https://doi.org/10.1002/ndr2.12288