


NEW DISEASE REPORT

First report of *Maize striate mosaic virus*, a mastrevirus infecting *Zea mays* in Argentina

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Geminiviridae, saccharata, zea mays convar

During 2021, sweet corn plants cultivated for human consumption in a 400-ha area in Santa Fe province, Argentina, showed severe virus-like symptoms, including marked dwarfism, plant deformation, nerval or internerval vein yellowing, chlorotic rings, chlorosis along leaf edges, and vein thickening (Figure 1–2). Abundant populations of the corn leafhopper *Dalbulus maidis*, a vector of several pathogens (Carloni *et al.*, 2013), were also observed (Figure 3). Ten diseased plants collected in Helvecia, Santa Fe (31°07′47″S, 60°08′48″W) were tested by leaf dip and serology (DAS-ELISA or PTA-ELISA) against: *Maize yellow striate virus*, *Mal de Río Cuarto virus*, *Spiroplasma kunkelii*, *Sugarcane mosaic virus* (JM isolate) (IPAVE, Córdoba, Argentina), *Maize rayado fino virus* (MRFV) (provided by Castillo Loayza, UNALM, Perú), *Maize chlorotic mottle virus* (MCMV), *Maize dwarf mosaic virus* (BIOREBA, Switzerland), *Wheat streak mosaic virus* (DSMZ, Germany), *Cucumber mosaic virus*, *High Plains wheat mosaic virus* (HPWMoV), *Maize streak virus* (MSV) and *Sugarcane mosaic virus* (SCMV) (Agdia, USA).

The samples tested by serology were positive for one or more of the following pathogens: HPWMoV, MCMV, MRFV, SCMV or *S. kunkelii*, and six of them had a mild reaction when tested for MSV (Table 1). Furthermore, electron microscopy detected geminivirus-like particles in sample 4, one of the six samples with a mild reaction for MSV (Figure 4). The DNA of this sample was extracted using the CTAB

method, amplified by rolling circle amplification (Inoue-Nagata *et al.*, 2004) and sequenced using a MinION Mk1B device with the Rapid Barcoding kit (Oxford Nanopore Technologies, UK). Raw sequences were filtered using the FilTlong (<https://github.com/rrwick/FilTlong>) software, and assembled using minimap2/miniasm (<https://github.com/lh3/minimap2>). Contigs of *Maize striate mosaic virus* (MSMV) were identified using BLASTn against a local viral reference database available from NCBI and polished with Medaka v1.2.3 (<https://github.com/nanoporetech/medaka>). MSMV has 96.6% amino acid identity in the coat protein with MSV, hence the cross-reaction observed in ELISA.

Thirty-seven sequences, including dicot- and monocot-infecting species, were aligned with MAFFT, and a maximum-likelihood phylogenetic tree was constructed in IQ-TREE (<http://www.iqtree.org/>) with 1000 bootstrap replications. The sequence of the Argentinian MSMV isolate (GenBank Accession No. OP811251) has 2746 bp, shares 99% identity with all the previously described MSMV isolates, and the final tree showed that the Argentinian isolate branches with representative sequences of the virus (Figure 5)

MSMV was first detected in maize and sugarcane in Brazil (Fontenele *et al.*, 2018, Batista *et al.*, 2021). The high population levels of the leafhopper vector and the effects of MSMV on plant growth and yield in susceptible cultivars (Vilanova *et al.*, 2022) warrant

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FIGURE 1 Severe stunting symptom observed in the field in Helevecia, Santa Fe province, Argentina.



FIGURE 2 Symptoms of vein thickening (left) and interveinal yellowing (right) observed in the field in Helevecia, Santa Fe province, Argentina.



FIGURE 3 Abundant populations of the corn leafhopper (*Dalbulus maidis*) observed on sweet corn leaves.

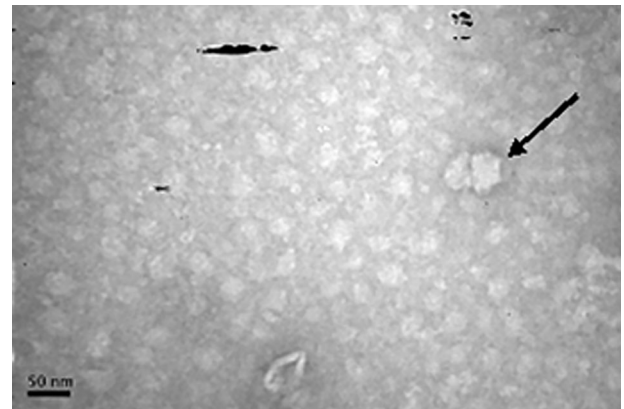


FIGURE 4 Geminivirus-like particle observed under electron microscopy.

TABLE 1 Results of the serological analysis conducted on ten sweet corn samples collected in Helevecia, Santa Fe province.

	1	2	3	4	5	6	7	8	9	10
<i>High Plains wheat mosaic virus</i>	-	-	-	-	-	-	-	-	+	-
<i>Maize chlorotic mottle virus</i>	-	-	-	-	-	+	+	-	-	-
<i>Maize rayado fino virus</i>	+	+	-	+	+	+	+	+	+	+
<i>Maize streak virus</i>	-	+/-	-	+/-	-	+/-	-	+/-	+/-	+/-
<i>Sugarcane mosaic virus</i>	+	+	+	+	+	+	+	+	+	+
<i>Spiroplasma kunkelii</i>	-	-	-	-	-	-	-	+	-	+

+ positive reaction, - non-reaction, +/- mild reaction

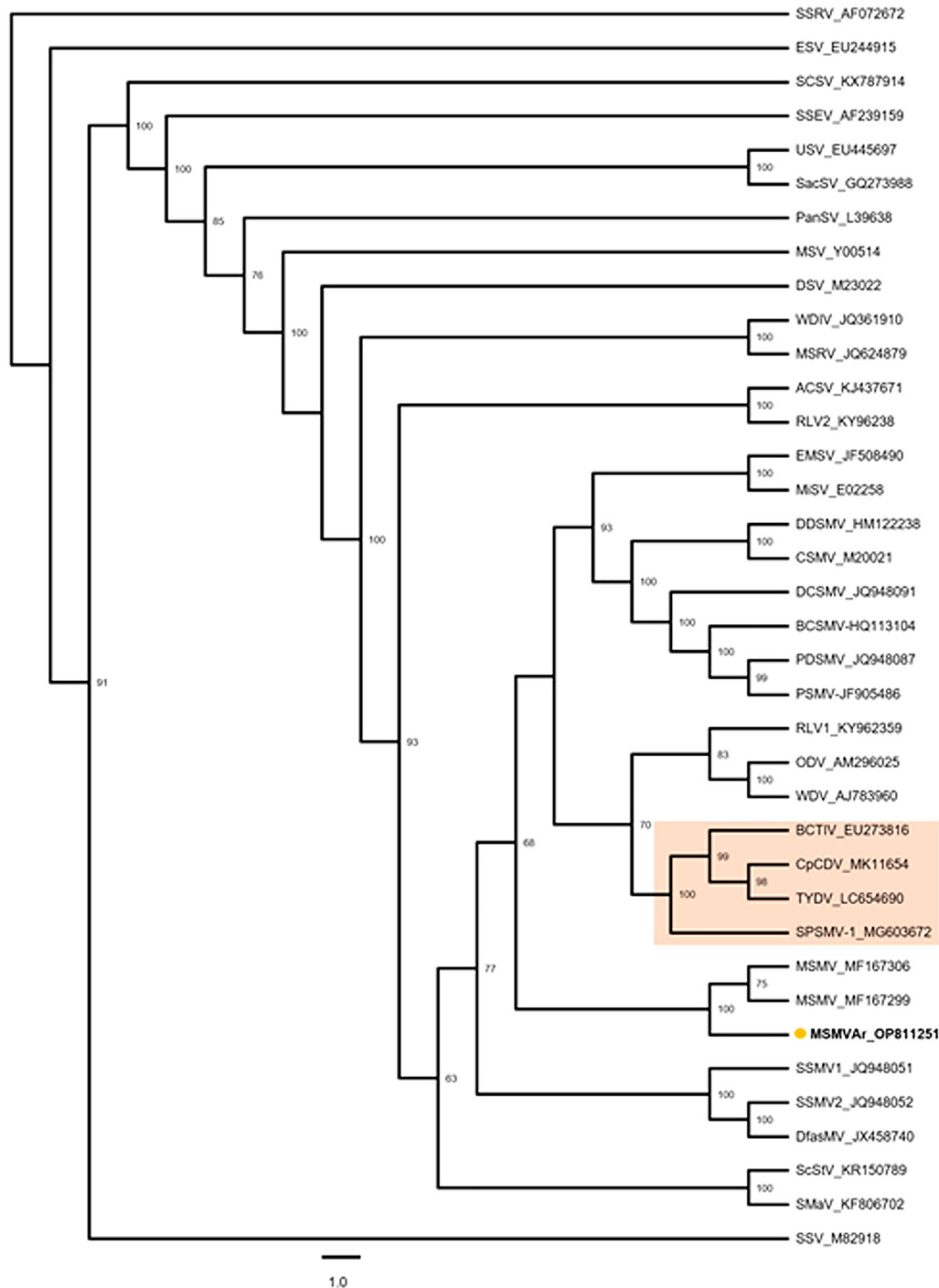


FIGURE 5 Phylogenetic tree showing the relationship between the studied isolate (MSMV-Ar) and 37 different mastrevirus isolates. The evolutionary history was inferred using the maximum-likelihood method (1000 bootstraps). Accession numbers are indicated for each virus isolate. MSMVAr GenBank OP811251 is highlighted in bold and with a yellow circle. Mastrevirus isolates related to dicots are highlighted in orange.

further epidemiological studies to assess the importance of this pathogen in Argentina. To our knowledge, this is the first report of MSMV (*Mastrevirus*, *Geminiviridae*) infecting *Zea mays* in Argentina.

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