

# First Report of a Resistance-breaking Isolate of *Tomato spotted wilt virus* Infecting Sweet Pepper Harboring the *Tsw* Gene in Argentina

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## ABSTRACT

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The disease caused by *Tomato spotted wilt virus* (TSWV) is endemic on vegetable crops in the Buenos Aires green belt, the most important vegetable-production area in Argentina (18,000 ha). Approximately half of the greenhouse surface planted with sweet pepper (*Capsicum annuum* L.) in the country is located in La Plata (Buenos Aires). In this area, TSWV had limited sweet pepper production until the introduction of resistant genotypes harboring the *Tsw* resistance gene that replaced 100% of the susceptible cultivars. However, in November 2013, resistant peppers showing typical *Tospovirus* symptoms were observed in La Plata. Symptoms appeared 20 days after transplanting in early spring, and by midsummer 100% of the plants were affected in many greenhouses, causing important economic losses in this season. Samples from symptomatic plants were analyzed by ELISA with antisera against the viruses: TSWV, *Groundnut ringspot virus* (GRSV), *Tomato chlorotic spot virus* (TCSV), *Potato virus Y* (PVY), *Cucumber mosaic virus* (CMV), and *Tobacco mosaic virus* (TMV). All samples were positive only for TSWV. Presence of TSWV was confirmed by RT-PCR with primers designed from a conserved sequence of the *N* gene that amplified a fragment of about 450 bp. Further, RFLP using *Bst*NI and *Hin*CII enzymes that cut the 450-bp fragment specifically ([Dewey et al. 1996](#)) showed the typical restriction pattern of TSWV. To test the ability to overcome the resistance, this greenhouse-isolate, named TSWV-A2, was mechanically transmitted to two commercial pepper cultivars carrying the *Tsw* gene, cvs. Almuden and Platero (10 plants each). After two weeks, all plants were systemically infected, showing the typical symptoms of TSWV infection. RT-PCR (as

previously described) from total RNA extracted from symptomatic leaves of these plants confirmed the presence of TSWV-A2. Therefore, we demonstrated that TSWV-A2 is able to overcome *Tsw* gene resistance. Furthermore, to amplify the complete *N* gene of TSWV-A2 isolate, a new RT-PCR was carried out ([Lovato et al. 2008](#)). A specific 800-bp product was cloned and sequenced (GenBank Accession No. KP719131). BLAST analysis showed that the sequence was 99% homologous at the nucleotide as well as the amino acid sequence to the *N* gene of isolates EF195230 and EF195224 from South Korea ([Kim et al. 2004](#)). In addition, TSWV-A2 shared common characteristics with the resistant-breaking isolates infecting sweet pepper cultivars carrying the *Tsw* gene, previously reported in Italy ([Roggero et al. 2002](#)) and Spain ([Margaria et al. 2004](#)). Overall, based on biological, serological, and molecular features, this is the first report of a local isolate of TSWV breaking the *Tsw*-resistance in sweet pepper in Argentina.

## References:

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