An Anomalous Detection of Tomato Yellow Leaf Curl Virus in Tomato in New York State

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Funding: Funding was provided by Cornell University. Plant Dis. 105:3312, 2021; published online as <https://doi.org/10.1094/PDIS-02-21-0356-PDN>. Accepted for publication 26 April 2021.

In August 2020, a New York (NY) State vegetable grower sought assistance to identify a malady of tomato (*Solanum lycopersicum*). The plants were grown from saved seed that had been planted annually in NY and/or Florida for over 15 years without significant disease problems, but the identity of the cultivar was not known. Submitted photos showed severely stunted plants with distorted leaves (crinkling, cupping, twisting); leaves were reduced in size and showed interveinal yellowing. Although the most likely explanation given the growing region was herbicide damage, the symptoms bore a striking resemblance to those presented by tomato yellow leaf curl virus (TYLCV)-infected tomato plants. TYLCV has not been reported from NY, as the whitefly vector (*Bemisia tabaci*) does not overwinter in the region. Stem tissue from a symptomatic plant was grafted onto a greenhouse-grown rootstock of tomato breeding line 201231 (Cornell University); shoots emerging from grafted rootstocks showed symptoms consistent with those on the scion within 21 days of grafting. Total nucleic acid was extracted (Gambino et al. 2008), and a polymerase chain reaction assay to detect TYLCV was performed using primers AV632 and AC1048 (Martínez-Culebras et al. 2001). Sanger sequencing of the expected size ~460-bp product from a representative sample showed 98% nucleotide identity with the sequence of over 52 isolates of TYLCV (BLASTn analysis using default parameters; Altschul et al. 1990). The total nucleic acid preparation was subjected to rolling circle

amplification followed by restriction enzyme *SphI* digestion (Haible et al. 2006). An approximately 2.8-kb DNA fragment was resolved by agarose gel electrophoresis, gel purified, inserted into the cloning vector pUC19, and sequenced. Two clones yielded a sequence of 2,781 nt with only 1 nt mismatch (accession nos. MW373746, MW373747). BLAST analysis showed the sequence to be most closely related to TYLCV-IL from papaya in Texas (accession KX024647.1) with 99% identity (2,752 of 2,781 nt). Further inquiry revealed that the vegetable grower's plants had been seeded and grown in Florida prior to transplanting in NY; Florida is a production region where the virus and vectors are endemic. Although the virus has been shown to be associated with seed (Pérez-Padilla et al. 2020) and seed transmission has been reported (Kil et al. 2016), this subject is controversial and the epidemiology of the disease is not consistent with a seed-transmitted virus (Rojas et al. 2018). In this reported occurrence, the most plausible explanation is that the virus was introduced into NY with transplants. All of the field-grown transplants of this cultivar were infected, but no local disease spread in NY was reported, nor were there reports of the vector. The significance of this report is to highlight the importance of phytosanitation in the movement of plants and plant materials. The long-distance movement of TYLCV via infected transplants in the United States and globally is well-established. The presence of a pathogen may be transient, and their establishment will depend on the epidemiology of the pathogen, in this case, the presence of the vector.

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The author(s) declare no conflict of interest.

Keywords: viruses and viroids, vegetables, pathogen detection, epidemiology

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