

First Report of TYLCV-IS141, a Tomato Yellow Leaf Curl Virus Recombinant Infecting Tomato Plants Carrying the *Ty-1* Resistance Gene in Sardinia (Italy)

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Tomato yellow leaf curl virus (TYLCV), tomato yellow leaf curl Sardinia virus (TYLCSV), and interspecies recombinants derived from them were detected in tomato (*Solanum lycopersicum*) in Italy (Panno et al. 2018). Cultivars carrying the *Ty-1* gene are a key component in the control of tomato yellow leaf curl disease (TYLCD); *Ty-1* prevents symptom expression and reduces virus accumulation. During a survey in September 2016 in Sardinia (Italy), symptomatic infections typical of TYLCD were observed on tomato plants of the resistant cultivar Parioli, in commercial greenhouses of the province of Cagliari, suggesting infection with TYLCV/TYLCSV recombinants (Belabess et al. 2015; Panno et al. 2018) or betasatellite (Conflon et al. 2018), which were both associated with the break of *Ty-1* resistance. Total DNA was extracted from leaf samples of three symptomatic and one nonsymptomatic plants collected in a single greenhouse. Using polymerase chain reaction (PCR) tests, all four samples were positive for the presence of the *Ty-1* gene at the heterozygous state (Verlaan et al. 2011) but negative for the presence of betasatellite DNA (Bridson et al. 2002). According to multiplex PCR tests (Belabess et al. 2015), the nonsymptomatic sample was negative for the detection of TYLCV, TYLCSV, and TYLCV/TYLCSV recombinants; one symptomatic sample was positive for all three types of genomes, and the other two were positive for TYLCSV and TYLCV/TYLCSV recombinants. These latter two DNA extracts were used in rolling circle amplification (RCA). To select recombinant genomes for cloning, the RCA product was digested with *SacI*, because this restriction site is unique in TYLCV and absent in TYLCSV genomes. A 2.8-kb restricted fragment was cloned in the *SacI*-linearized plasmid pBC, and three clones, obtained from the two DNA extracts, were sequenced. The three sequenced genomes had 2,773

nucleotides (nt) and shared 99% identity to each other. Like TYLCV-IL-[IT:Sic23:16], a TYLCV/TYLCSV recombinant recently detected from *Ty-1* resistant plants sampled in Sicily in 2016 (Panno et al. 2018), the Sardinian genomes were composed mostly of a TYLCV-IL sequence, except 124 nt (nt 16 to 139) between the origin of replication and the ATG codon of the V2 gene, which were derived from TYLCSV. The highest nt identity of the TYLCSV sequence was detected with a TYLCSV isolate from Sicily, accession no. Z28390 (92%), and that of the TYLCV sequence was detected with TYLCV-IL-[IT:Sic:04], DQ144621 (98%). Because the sequence identity of Sardinian and Sicilian recombinants was higher than 94% (97.6%), they were considered to belong to the same group of TYLCV-IL isolates previously named TYLCV-IS141 (Belabess et al. 2018). For the sake of clarity, we propose to give this name to all recombinants with the same recombination event. Thus, the sequence deposited to GenBank (MH817479) was called TYLCV-IS141 (TYLCV-IL-[IT:Sar IS141:16]). Because this recombinant was detected in coinfection with TYLCSV or TYLCV, it cannot be stated that it caused TYLCD symptoms on resistant plants. Moreover, these symptoms were not observed during the following year. However, TYLCV-IS141 recombinants were already detected from plants collected in 2012 and 2016 in Sicily (Belabess et al. 2015, 2018; Panno et al. 2018), and it was found to be positively selected in *Ty-1* resistant plants (Belabess et al. 2018). Further samplings are needed to estimate the prevalence of TYLCV-IS141 recombinants in Sardinia and Sicily and to test their fitness in *Ty-1* resistant plants.

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