

## **Inheritance of Tomato Spotted Wilt Virus Resistance Derived from *Solanum chilense* Accession LA1938**

*John W. Scott*<sup>1\*</sup>, *Steve M. Olson*<sup>2</sup> and *Mikel L. Stevens*<sup>3</sup>

<sup>1</sup> Gulf Coast Research and Education Center, University of Florida, 14625 CR 672, Wimauma, FL 33598 USA

<sup>2</sup> North Florida Research & Education Center, University of Florida, 30 Research Road, Quincy, FL 32351 USA

<sup>3</sup> Department of Plant and Animal Sciences, Brigham Young University, 287 Widstoe Bldg. Box 25183, Provo, UT 84602 USA

Previously we reported that resistance to tomato spotted wilt virus (TSWV) from Fla. 8516, a breeding line derived from LA1938, was conferred by one or two dominant genes (Rept. Tomato Genetics Coop. 2005). Fla. 8516 was backcrossed into 21 recurrent parents including Fla. 8124D which has the *Sw-5* gene. In Spring 2006 F<sub>1</sub>s were advanced to the F<sub>2</sub> and 106 selections were made for horticultural performance without TSWV disease pressure in Fall 2006. These 106 F<sub>3</sub> selections plus resistant and susceptible controls, Fla. 8516 and Fla. 8153 respectively, were planted in a completely randomized block design with 3 blocks and 10 plant plots at the North Florida Research & Education Center in Quincy in Spring 2007. Late in the season incidence of TSWV was evaluated from a natural TSWV infection by a virus strain controlled by the *Sw-5* gene. Disease incidence for Fla. 8153 was 76.6% and for Fla. 8516 was 3.4% (1/29). Conservatively, there were 20 or 18.9% of the F<sub>3</sub> lines rated as resistant based on an incidence of 0 or 1 infected plants. There were 27 resistant lines (25.5% of F<sub>3</sub>s) if lines with 2 infected plants (<8% incidence) are considered. There were 26 lines that were susceptible based on >50% disease incidence. There were 35 lines rated as clearly segregating but incidence was variable and thus 20 lines had segregation ratios that were more difficult to delineate. Nevertheless, the data clearly indicate that resistance was conferred by a single dominant gene as opposed to two dominant genes where only 6.25% of the lines would be expected to breed true for resistance. We will name this gene *Sw-7*. Four lines were from the cross with *Sw-5* resistance and none were rated as resistant indicating that *Sw-7* is not allelic or linked to *Sw-5*. Breeding implications will be discussed.