

Fine-Mapping and Cloning of *Ty-1* and *Ty-3*; and Mapping of a New TYLCV Resistance Locus, “*Ty-6*”

Sam F. Hutton and Jay W. Scott

IFAS, University of Florida, Gulf Coast Research & Education Center, 14625 CR 672, Wimauma, Florida, 33598 email sfhutton@ufl.edu



Fine-mapping efforts for *Ty-3* focused on an allele derived from the *S. chilense* accession LA2779, and on an allele derived from *S. chilense* LA1969 for *Ty-1*. In total, nearly 12,000 plants were screened for recombination, and multiple molecular markers were developed and used in combination with disease screens to map both resistance alleles to an approximately 70 Kb interval. This region was predicted to contain five genes, three of which were considered candidates for *Ty-1/Ty-3*. Using a Tobacco Rattle Virus-Virus Induced Gene Silencing approach, the resistance gene was identified. It was determined that *Ty-1* and *Ty-3* are allelic and that they code for a RNA-dependent RNA polymerase (RDR). Fla. 8383 has a moderately-high level of resistance to tomato yellow leaf curl virus (TYLCV), but lacks all of the previously identified resistance loci (*Ty-1*, *Ty-2*, *Ty-3*, *Ty-4*, and *ty-5*). In spring 2010, 203 plants of an F₂ population derived from the cross between Fla. 8383 and the susceptible breeding line, Fla. 7776, were inoculated with TYLCV and evaluated for disease severity. Each plant was genotyped with 158 polymorphic snps developed through the SolCAP project. Chi-Square analysis using the most resistant most susceptible plants in the population identified two significant regions on chromosomes 4 and 12, and a highly significant region on chromosome 10, the latter of which is tentatively named “*Ty-6*.”