

ACQUISITION AND INOCULATION OF *TOMATO YELLOW LEAF CURL VIRUS* FROM RESISTANT GENOTYPES BY *BEMISIA TABACI*: RESISTANT GENOTYPES ARE RESERVOIRS OF THE VECTOR AND THE VIRUS

Rajagopalbabu Srinivasan¹; David Riley¹; Stan Diffie¹; Stormy Sparks¹; Scott Adkins².

¹*Department of Entomology, University of Georgia, 2360 Rainwater Road, Tifton, GA. 31793-5766; babusri@uga.edu*

²*USDA-ARS, 2001 South Rock Road, Fort Pierce, FL 34945.*

Tomato yellow leaf curl virus (Family *Geminiviridae*, Genus *Begomovirus*) is transmitted by sweet potato whitefly, *Bemisia tabaci* (Gennadius). One of the main management options includes planting of *Tomato yellow leaf curl virus* (TYLCV) resistant genotypes. Resistant genotypes possess a semi-dominant gene (*Ty-1*) that confers resistance against TYLCV. However, they do not possess desirable horticultural characteristics and are also not available for all tomato fruit types. As a consequence, resistant and susceptible genotypes are often planted in close proximity. Resistant genotypes also do not provide any resistance against whiteflies. Field studies were conducted in 2009 and 2010 to evaluate the effect of resistant genotypes on TYLCV incidence and whitefly populations. Visual observations indicated that there was no TYLCV infection in resistant genotypes, the infection rates ranged from 45 to 85% in susceptible cultivars. However, further testing with PCR using degenerate *Begomovirus* primers followed by sequencing indicated that the resistant cultivars were actually infected with TYLCV, but were symptomless. Greenhouse inoculations using viruliferous whiteflies followed by PCR testing indicated that the resistant genotypes were infected up to 100% without exhibiting symptoms. Acquisition ability of whiteflies was tested on various genotypes. Results indicated that resistant genotypes differentially affected acquisition. Whitefly acquisition rates were lower when they fed on resistant genotypes than on susceptible genotypes. Nevertheless, this difference did not affect TYLCV inoculation from resistant genotypes to susceptible genotypes. Whitefly population densities in resistant and susceptible genotypes were similar. Results emphasize that resistant genotypes can potentially serve as inoculum sources for TYLCV and may influence its epidemiology.