

## **Genotypic Variation in Tomato Spotted Wilt Virus Infection in Peanut and Methods of Estimating Infection Frequency**

Y-C. TSENG, **B. L. TILLMAN\***, J. WANG, and D. L. ROWLAND, Agronomy Department, Univ. of Florida, FL.

Breeding peanut for resistance to spotted wilt has been successful in the southern US. Cultivars with moderate resistance have reduced the risk of disease losses. The source of resistance appears to be PI203396, Southern Runner, and C-99R which are in the pedigree of cultivars with moderate resistance including DP-1, York, Georgia-06G, Georgia-07W, Florida-07, and Tifguard. Each of these cultivars has an index score of 10 on the TSWV Index. Only the cultivar Georgia-12Y has a lower index score of 5. Georgia-12Y has PI203396 and Southern Runner in its pedigree. However, research has shown that there is a high incidence of asymptotically infected plants within this germplasm group. This means that there was greater potential for disease to occur than symptoms would predict. This strongly indicates that the resistance/tolerance derived from PI203396, Southern Runner, and C-99R is not a resistance to infection but a resistance to disease expression. In some seasons, these cultivars have succumbed to spotted wilt, indicating that their resistance may not be sufficient in the most severe disease environments.

A new source of resistance based on genotypes with *hirsuta* background has shown outstanding resistance. In over 15 years of testing, even under severe spotted wilt epidemics, these genotypes have not succumbed to spotted wilt. The incidence of TSWV infection in these genotypes was 10% or less compared to 44% in Florida-07 and 67% in Georgia Green. Work with Florida-EP™ '113', a derivative these lines, showed that the frequency of infected plants was 10% or less even in the most risky situations. This source of resistance could drastically reduce the risk of spotted wilt because over 90% of the plants are not infected and are therefore at no risk of disease development. This presentation describes potential methods (ELISA, seed coat symptomology and marker assisted selection) to identify genotypes with low infection frequency characteristic of the *hirsuta*-derived types.