

## **Assessing the probable presence of a new thrips-transmitted *Tospovirus* in peanut in Georgia**

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Spotted wilt caused by *Tomato spotted wilt virus* (TSWV) has once again become a concern due to the increased incidences in 2014 and 2015 when compared with the recent past. Another concern has been the increase of spotted wilt incidence becoming more and more obvious in what is widely perceived as a TSWV resistant cultivar, GA-06G. The goal of this proposal was to assess if there are any new factors contributing to the observed spike in spotted wilt.

A number of reasons could have contributed to the recent spike of spotted wilt. Our goal was to assess if this spike was due to the introduction of a new thrips-transmitted virus, *Groundnut ring spot virus* (GRSV). GRSV is a close cousin of TSWV, it was found in Florida in 2010, and has been consistent in its occurrence in Florida. No recent surveys have been made in Georgia to assess the presence of GRSV in peanut. GRSV, similar to TSWV, has a wide host range and the potential to cause severe spotted wilt epidemics. Also, it is not clear if TSWV resistant cultivars would also be resistant to GRSV.

Last year, samples of peanut foliage from high spotted wilt incidence areas were brought to the vector biology laboratory in Tifton, GA. Foliar samples were tested for the presence of GRSV using commercially available antibodies with a double antibody sandwich enzyme linked immunosorbent assay (DAS-ELISA). Numerous microtiter plates were used for this testing, test results indicated that 5 to 30% (Avg. 21%) of the samples tested could be positive for GRSV. However, a close observation of the absorbance values indicated a consistent weak response. This prompted us to speculate that what we observed was cross-reaction of TSWV-positive foliar samples to GRSV. To test the same, the samples were retested using DAS-ELISA with specific antibodies for TSWV coat protein. Results revealed that the samples that tested weakly positive for GRSV were strongly tested positive for TSWV. This suggested that the virus was indeed TSWV and not GRSV.

To further confirm our results, a subsample of the positive samples was tested for both GRSV and TSWV with polymerase chain reaction (PCR) using primer sets targeting specific genes in both viral genomes. Results indicated that none of the samples tested were positive for GRSV, and all the analyzed symptomatic samples tested positive for TSWV.

Results revealed that, based on limited sampling, GRSV was not found in the peanut foliar samples in Georgia. This situation could however change quickly. As in 2015, we will be proactive and continue to test for GRSV throughout the next season. This, however, does not still explain the recent spike in TSWV incidence. A PhD student will soon be conducting whole genome sequencing to see if continuous usage of resistant cultivars is imparting any selection pressure on the virus leading to increased virulence.