Understanding Viruliferous Thrips Dispersal into Peanut Fields and TSWV Epidemics

Rajagopalbabu Srinivasan[1] and Mark Abney[2]
[1] Department of Entomology, University of Georgia, 30215Griffin, GA 30223
[2]Department of Entomology, University of Georgia, Tifton, GA 30215

Thrips-transmitted tomato spotted orthotospovirus (TSWV) continues to be an important production issue despite adopting the risk management recommendations including planting resistant cultivars, insecticide applications, and incorporating cultural practices. Research in our programs has examined factors that could be influencing TSWV incidences in our production system. Our research has indicated that TSWV infections could continue to occur throughout the season; however, past a certain date (~ 75 DAP) these infections might not be yield-limiting. With that background, our objectives were to identify the viruliferous thrips dispersing into the fields and within fields as well as identify inoculum sources both outside and within peanut fields. These are not new questions but with the availability of new diagnostic techniques and tools it might be feasible to address them.

Doctoral student Ms. Yi-Ju Chen took the lead in addressing these two objectives. Her work in 2020 was constrained due to the ongoing pandemic-related lab closures and lab personnel space-related restrictions. Nevertheless, Yi-Ju has made some good progress, especially with the first objective (tracking viruliferous thrips). Yi-Ju's goal was to design a quantitative RT-PCR test to assay thrips (individual or in small batches). For this purpose, Yi-Ju attempted to use two sets of primers (targeting the N-gene as well as the NSs gene), and optimize multiple RNA extraction techniques, and multiple thrips sample numbers. Several permutations were attempted. Overall, the RNeasy Microkit-based TSWV extraction seems to work better for TSWV detection and quantitation in thrips, especially when using N-gene specific primers followed by absolute quantitation. Individual thrips were not amenable for TSWV detection and/or quantitation with either sets of primers. However, a pooled sample of 5 to 7 thrips consistently resulted in TSWV detection and/or quantitation using qRT-PCR. The student has also attempted to use sticky card-trapped thrips under greenhouse/laboratory conditions for TSWV detection and/or quantitation, and a preliminary attempt was also made with thrips collected from sticky cards in the field. With some more optimization, this technique should be ready for field sampling of thrips for TSWV in 2021.

The second objective utilized thrips gut contents and generic/universal primers to identify plant species that were ingested by thrips. Primer sets targeting the ITS region and the chloroplast region were used for this purpose and was followed up by Sanger sequencing. However, this technique was not very robust and/or reliable. Yi-Ju is currently working on this objective to improve it. She intends to use a more robust Next Generation Sequencing technique to assess plant species in thrips gut contents. While this technique might not be optimized by the beginning of 2021 field season, she intends to complete the optimization as soon as possible. When optimized, this approach would play a key role in identifying non-peanut TSWV inoculum sources both in the presence and absence of the peanut crop. This will also assist us in assessing the relevance of the peanut crop itself as an inoculum source during the growing season. We anticipate completion of this work by the summer/fall of 2021.