Foundational Genotyping for Multipronged Breeding against Tomato Spotted Wilt Virus (TSWV) in Peanut

Project Report - UGAT-45-26/26

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Introduction

Tomato spotted wilt virus (TSWV) remains one of the most significant threats to peanut production in Georgia, accounting for over $55 million in crop losses in 2022 alone. While the University of Georgia (UGA) breeding program has historically provided varieties with excellent resistance, such as 'Georgia Green' and 'Georgia-06G,' recent years have seen an increase in TSWV pressure within both research plots and commercial farms. Because this pathogen has demonstrated the ability to overcome resistance in other crops, it is critical to identify and incorporate new resistance alleles from diverse genetic sources to safeguard the industry. This project establishes the genetic foundation necessary for a multipronged breeding approach to enhance TSWV resistance. We will identify new and old sources of genetic resistance and test advanced "genomic selection" methodologies—using genetic data from all parts of the genome—for accelerating development of resistant, elite breeding lines.

Project Summary

This project aims to accelerate the development of resistant breeding lines using modern genomic tools. The primary focus of the funded activities thus far is to provide high-resolution genetic data for the breeding program. This involved getting genetic data (this year's goal), field evaluations (future years), and combining them into a predictive computer model to "learn" how to connect the genetics to the final trait. (This is a form of AI, but less complex than ChatGPT and the like.)

Activities in 2025

- Three populations were previously developed by crossing highly susceptible cultivar, Georgia Runner, with 3 cultivars of varying levels of resistance to TSWV. The cultivars C-99R and Georgia-06G have moderate resistance to the disease, while Georgia-12Y is highly resistant to TSWV. These populations were advanced in the field since 2022, and the F_4 generation was advanced in the greenhouse during the winter of 24/25. The F_4 plants were harvested using single seed descent, and in 2025 the resulting F_5 populations were grown in Tifton at UGA's Animal Science Farm in space-planted nursery plots.
- The individual F_5 plants were harvested to develop recombinant inbred lines for the planned replicated field trials.
- A total of 768 F_5 lines were sampled and submitted for genotyping-by-sequencing through Freedom Markers. (The original plans for long-read genotyping had to be changed because the quote for this service came back much higher than we were originally told.) All sequencing data has been collected and is in queue for processing.