

## Improved understanding of thrips and TSWV ecology in the peanut production system of Georgia and implications for management

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A significant achievement in the past year has been the successful annotation and publication of the TSWV vector's (*Frankliniella fusca*) genome (Catto et al. 2023). Unlike the advancements in peanut genomics, thrips genomics was lagging behind. With both short and long read sequencing platforms, we have developed a high quality thrips genome that is now made available online. There are >7000 thrips species, and this is only the third thrips species genome that has been sequenced. We are currently working on another one as well (*Thrips tabaci*). This effort has opened avenues to conduct comparative genomics, and down the road identify virus-interacting partners in thrips that could be exploited for management.

On the ecology side, our research progress has been three-pronged. We have developed a TSWV detection (qRT-PCR based) protocol to successfully screen TSWV transmitters (individual thrips), even when obtained from sticky cards. We are planning to validate this protocol in the field in 2024. In addition, TSWV hosts' viromes are being developed to gain a more thorough picture of viruses infecting peanut and better comprehend the current status of TSWV resistance. The trial sample sequences obtained from last fall are currently being processed through a bioinformatics pipeline. Lastly, we have optimized a protocol to examine thrips gut contents and identify hosts of thrips. This protocol also can be useful for thrips specimens obtained from sticky cards. All of this research is currently being led by our doctoral student, Mr. Vamsi Reddy. Vamsi joined our laboratory in January 2023.

### Citation:

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