**Title:** To investigate the re-emergence of *Tomato spotted wilt orthotospovirus* and its role in increasing yield loss on Peanut in GA.

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## Layman's Summary:

The research was severely impacted due to the COVID-19 restrictions until August 2020.

The incidence and disease severity of spotted wilt diseases is increasing steadily since 2012 and has been a constraint to peanut production. The estimated yield loss is doubled from 3.5% in 2018 to 7% in 2019 with an approximate value of 25 million USD. The disease incidence in 2020 is comparatively less than 2019 (as discussed in Peanut Rx Meeting). Peanut plants showing characteristic concentric ring spots, dwarf, bud necrosis as well as some new symptoms as heart or claws shaped symptoms on leaves were collected from peanut fields and subjected to molecular and molecular analysis. TSWV was detected from all the different symptomatic tissues using RT-PCR targeting the nucleocapsid protein (NP) gene encoded



Figure 1: Graph showing the losses to Tomato spotted wilt orthotospovirus in Peanut in Georgia, 1990-2019.

by S RNA. TSWV is known to have wide host range and cause disease on different crops. To understand the genomic diversity on the S RNA encoding NP and NSs gene, an attempt was made to sequence six isolates from GA. Freeze-dried samples of infected peanut tissues collected in 1997 were compared with the samples collected in 2018, 2019, and 2020. TSWV infected tobacco (2019, 2019) and tomato (2019) were also included for the sequence comparison. The S RNA was using the Sanger sequencing technique and annotated with Bio-Edit and MEGA X software. The sequence analysis reveals that the NP gene from Peanut collected from Lang Farm in 1997 is changes in 23 different amino acid positions and one amino acid position in NSs compared to other peanut isolates from 2018-2019. The role of these changes on disease incidence is unknown. The samples collected from peanut fields in 2019-2020 were also tested for the presence of other thrips transmitted viruses, including GRSV and TCSV that were reported from Florida. We have not detected the presence of either of the virus in the samples tested.