Precision breeding for multiple disease resistance

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Tomato spotted wilt virus (TSWV) is a disease that significantly affects Georgia peanut production, causing yield and economic losses each season. Genetic resistance is essential to maintain yield and quality of the crop as recognized by the weight given to cultivar in the peanut risk index (peanutrx.org). Breeding programs have obtained resistance to TSWV through PI 203396 with great success for many years. A second source of resistance was identified via PI 576638 (SSD6) and its highly resistant offspring, NC94022. A major quantitative trait locus (QTL) was identified on chromosome A01 in a SunOleic 97R (TSWV susceptible) x NC94022 population (Agarwal et al. 2019. Sci Rep 9). To further understand this resistance, a single recombinant inbred line (RIL_F155) produced from Tifrunner x SSD6 (resistant parent of NC94022) was crossed with eight unique breeding lines and progeny were screened with molecular markers to identify presence or absence of the QTL region on A01. These progenies have been evaluated over four field seasons (2022-2025) under varying environmental conditions for their resistance to TSWV and agronomic traits, including yield. From 2022 to 2024, progenies with the highest TSWV field resistance and favorable agronomic traits were advanced for further development. In 2024, 31 lines at the F_5 generation were planted in replicated 10-foot, two-row plots at Gibbs Farm in Tifton, GA on April 9th. A seeding rate of four seed per foot and early planting date were used to enhance TSWV pressure. Georgia-06G, TifNV-HG and TifGP-2 were used as check lines. TSWV ratings were taken as a percent of the plot canopy showing typical TSWV symptoms represented as a one to ten score. Final TSWV ratings were taken at 122 days, and all plots were harvested at 132 days post planting. Ten selections from this trial were further tested in 2025 along with resistant checks RIL155, NC94022, Arnie, and TifNV-HG and susceptible check TufRunner 511.

Lines containing the identified QTL insertion region on A01 showed significantly greater TSWV resistance as compared to lines lacking this region (Figure 1), including Georgia-06G and other check lines. A glutamate receptor-like (GLR) gene is present within this insertion in varying copy numbers. There are four copies in the highly resistant RIL155 and NC94022, but no copy in Tifrunner or the population parents crossed with RIL155. The lines within the populations vary in their GLR gene copy number, and the level of resistance is correlated with copy number (Figure 1). Crosses have been made between selected lines and recent releases, TifNV-HG, TifTB, and 17-2214 to stack A01 TSWV resistance, nematode resistance, leaf spot resistance and high or normal oleic acid by selection with molecular markers when possible.

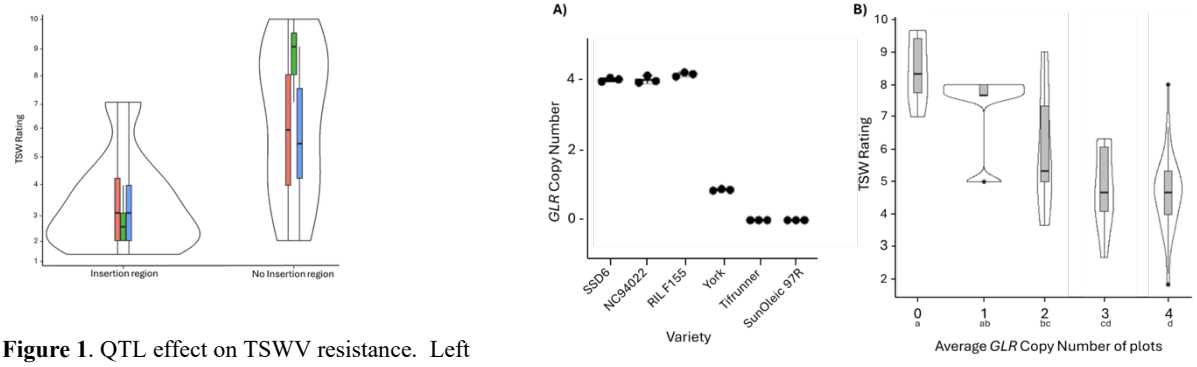

Figure 1. QTL effect on TSWV resistance. Left panel: Comparison of TSWV ratings in lines with and without the insertion region, across three populations with both genotypes. TSWV scores from replicated plot studies in 2024. p-value <0.001. Right panel: A) Determination of *GLR* copy number by ddPCR in SSD6, NC94022 and RIL F155 compared to released varieties. B) Distribution of average TSW disease ratings of $F_{3:4}$ plots for each *GLR* copy number. Significance groups are identified under x-axis; p-value <0.001.