

Research report: Expansion of resistance sources to leaf spots and TSWV for peanut breeding

Peggy Ozias-Akins (pozias@uga.edu), Ye Chu, Institute of Plant Breeding, Genetics & Genomics, University of Georgia Tifton Campus, Tifton, GA 31793; C. Corley Holbrook, USDA-ARS, Tifton, GA 31793; David Bertoli, Institute of Plant Breeding, Genetics & Genomics, University of Georgia, Athens; Soraya Leal-Bertoli, Department of Plant Pathology, University of Georgia, Athens, GA, 30602; Tom Stalker, Department of Crop and Soil Sciences, North Carolina State University, Raleigh, NC, 27695

Multiple disease resistance sources to leaf spots (LS) and TSWV were tested at the Gibbs farm, Tifton Georgia in year 2019, to compare new with established sources of resistance in the same test. For the TSWV field test, in order to maximize the disease pressure, all of the genotypes were planted in April and at a low seeding rate of 4 seeds/ft. As for the LS field test, all genotypes were planted between late May and early June at 6 seeds/ft. Insecticides and fungicides were withheld for the TSWV and LS tests, respectively, to allow the natural field infection to occur. Complete randomized block design was applied for both experiments and each block consisted of a 10 ft plot. Two disease ratings of the percentage of canopy with TSWV symptoms were taken at 123 and 129 DAP. Average of the disease rating was used for data analysis. For LS, disease scouting was performed between August and early September until obvious emergence of LS disease was confirmed. Four disease ratings were taken at 102, 112, 122 and 133 DAP. Daily AUDPC (area under the disease progress curve) was calculated for all of the tested lines. Normality of the data sets was assessed by Shapiro-Wilk test and both TSWV and LS data sets significantly deviated from a normal distribution; therefore, Kruskal-Wallis non-parametric analysis was performed to separate the means (Fig. 1).

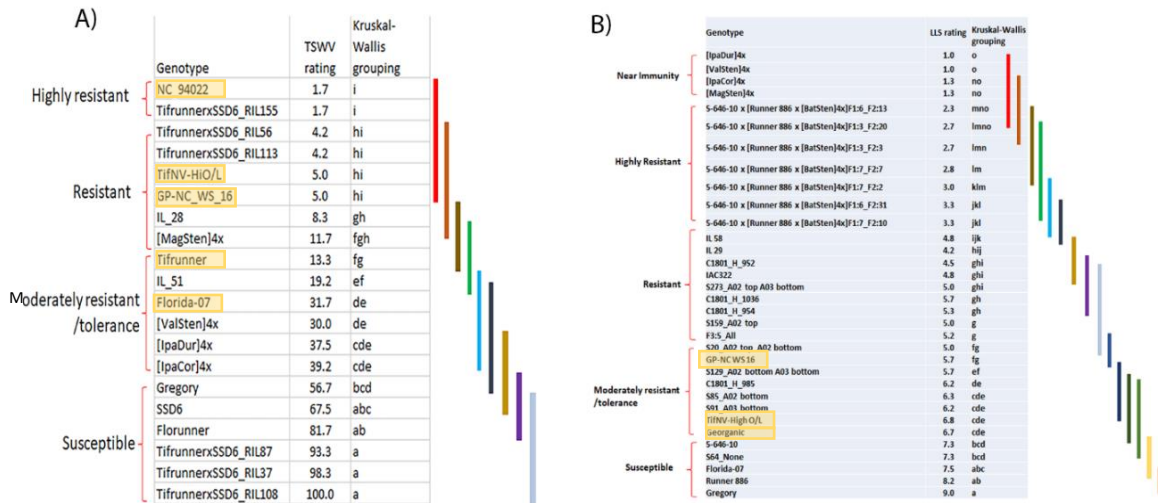


Figure 1. Diverse ranges of host resistance to TSWV (A) and LS (B) were identified in year 2019 field test. Means covered by the same bar are not statistically significant (P=0.05). Current resistance sources are highlighted in yellow.

In both TSWV and LS tests, significantly stronger sources of disease resistance than current resistant cultivars were identified. The highest level of resistance to TSWV was found in the RILs from Tifrunner x SSD 6 population and NC_94022. The introgression line (IL 28) descending from Gregory x *A. diogeni* and the new amphidiploid [MagSten]^{4x} also demonstrated TSWV resistance similar to the resistant checks TifNV-high OL and GP-NC WS 16. All four of the new amphidiploids ([IpaDur]^{4x}, [IpaCor]^{4x}, [MagSten]^{4x} and [ValSten]^{4x}) demonstrated near immunity to LS infection. The BC₁F₃ families from [BatSten]^{4x} were highly resistant to LS. Introgression lines (IL 58 and 29) from *A. diogeni*, the RILs harboring LS resistance QTLs from both Florida 07 x GP-NC WS 16 and selected lines from Tifguard x IAC 322 populations were also superior to the cultivated checks. Integrating these diverse sources of disease resistance into peanut cultivars will enhance the competitiveness of peanut production.