

LONG-TERM GERMLASM ENHANCEMENT AND DEVELOPMENT OF DNA MOLECULAR MARKER RESOURCES FOR PEANUT

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Growers are continuously faced with biotic and abiotic constraints on production. Some of those constraints can be mitigated with improved genetics, such as improved disease resistance, higher yields, better yield stability, and other genetically influenced traits. Our goal, since the beginning of this project has been to (1) evaluate and improve genetic diversity in order to make better-informed genetic combinations; (2) identify and utilize germplasm with improved resistance to biotic and abiotic stresses; (3) map genes that are important to peanut growers and develop DNA molecular markers to use within peanut breeding programs to improve breeding efficiency. During the 2021 growing season, we continued projects involving improving and evaluating genetic diversity, improving disease resistance, and improving plant vigor.

Initial data from our genetic distance study will be generated during the 2022 growing season. We are currently evaluating several unique and diverse sources of late leafspot (LLS) resistance and tomato spotted wilt virus (TSWV) resistance. Germplasm lines being used for improving LLS resistance include TxAG-6, a multi-species hybrid; GP-NC WS 16 (WS 16), TifGP-3, and TifGP-4, germplasm lines with interspecific introgressions. A germplasm line with excellent TSWV resistance, NC 94022 has also been incorporated for introgression of improved resistance to the disease. TxAG-6 (Simpson et al., 1993) is the original donor parent of root-knot nematode resistance in cultivated peanut, but the high level of LLS resistance in TxAG-6 has not been thoroughly explored. In 2021, we evaluated segregating F_3 and BC_1F_2 populations under non-sprayed, moderate to high LLS-pressure and made several selections. DNA marker resources have been developed by researchers at UGA for tracking resistance loci in WS 16, TifGP-3, and TifGP-4. Crosses were made in the 20/21 greenhouse season, and F_1 progeny were screened using markers to ensure presence of desired resistance (except for NC 94022). The resulting F_2 populations will be screened for LLS and TSWV resistance in 2022.

Multiple QTL mapping projects are ongoing. A mapping project involving resistance to leaf scorch/pepper spot disease caused by the fungus *Leptosphaerulina crassiasca*, was in the F_3 progeny row stage in 2022 and mapping analysis is being completed now using this phenotypic data. We are also using this population to map other characteristics of interest such as early- and mid-season plant vigor (Fig. 2). An F_2 population will be genotyped this winter for identifying QTL involved with seed size. Additional populations are currently under development to map shelling quality characteristics, and other agronomically and economically significant QTL.



Figure 1. LLS-susceptible cultivar on left with TxAG-6-derived populations segregating for LLS-resistance on right.

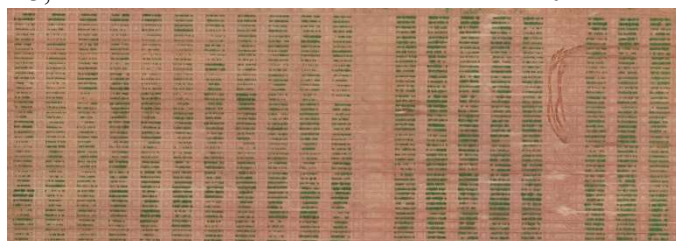


Figure 2. Aerial image used to analyze early- and mid-season plant vigor in F_3 progeny rows at Plains, GA.