

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 these constraints can be mitigated with improved genetics, such as improved disease resistance, higher yields, better yield stability, and others. Our goal for this project is to (1) improve genetic diversity; (2) incorporate germplasm with improved resistance to biotic and abiotic stresses; (3) and map genes that are important to peanut growers for DNA marker-assisted breeding.



Figure 1. C20019-16 (left), derived from a cross with NC 94022, is pictured with a check cultivar (right) in early-planted, space-planted F_2 nursery plots in 2022.

We are currently incorporating a number of unique sources of late-leaf spot (LLS) resistance into the breeding pipeline. These include TxAG-6 (Simpson, 1993), a multi-species hybrid that has high levels of LLS-resistance, and is also the donor parent of root-knot nematode resistance in commercially-available cultivars. Initial crosses with elite Georgia breeding material were made in 2018. From 54 plots (2000 plants) of the F_4 progenies grown in a no-fungicide, LLS nursery in 2022, 57 plants were selected based on visual LLS-resistance and agronomic performance compared to elite cultivar checks. Further selections will be made based on shelling characteristics prior to planting F_5 seed increase plots in 2023. Replicated yield trials will begin in 2024. Other sources of LLS-resistance currently being used include germplasm lines GP-NC WS 16 (Tallury et al., 2013), developed at NC State, and TifGP-3 and TifGP-4 (Hollbrook et al., 2021), developed at USDA in Tifton, GA. Families developed from crosses with these germplasm lines in 2019 and 2020 were planted in a no-fungicide, LLS F_2 nursery in 2022 consisting of 68 plots. A total of 98 individual plants were visually selected based on LLS resistance and agronomic performance compared to cultivar checks. Further selections will be made based on shelling characteristics prior to planting the F_3 nursery plots in 2023. Replicated yield trials will begin in 2026.

For improving resistance to tomato spotted wilt virus (TSWV), we are using NC 94022, an interspecific germplasm line developed at NC State, further selected at Univ. of Florida, and tested by Cullbreath et al. in 2005. Initial crosses with this line were made in 2020. In 2022, the TSWV F_2 nurseries were planted in early April, with seeds spaced 1 ft apart to maximize TSWV pressure (**Figure 1**). From a total of 75 F_2 plots (3000 plants), 401 plants were visually selected for TSWV resistance and agronomic performance compared to cultivar checks. Further selections will be made based on shelling characteristics prior to planting the F_3 nursery plots in 2023. Replicated yield trials will begin in 2026.

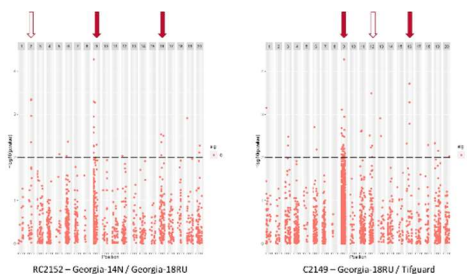


Figure 2. QTL mapping analysis indicating large effect QTLs (red arrows) and potential small effect QTLs (white arrows) for leaf scorch/pepper spot -resistance in two mapping populations.

Multiple quantitative trait loci (QTL) mapping projects are ongoing, however, this year the final mapping analysis was completed for resistance to leaf scorch/pepper spot disease caused by the fungus *Leptosphaerulina crassiasca*. Two major QTL and several small effect QTLs were identified (**Figure 2**). These will be validated in 2023 prior to publication. Other mapping projects are also ongoing.