

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

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Enhancing genetic diversity is critical for ensuring the continued success of plant breeding programs. Making crosses between genetically similar individuals limits potential genetic gain and a narrow genetic base makes a crop vulnerable to threats such as new diseases, pests, or climatic conditions. The objectives of this ongoing project are to (1) evaluate genetic distance among cultivars, breeding lines, and external germplasm to assist in parental selection and to make more effective cross combination decisions; (2) explore and develop new germplasm resources to incorporate novel alleles for important traits; and (3) develop mapping populations to identify new DNA markers for genes controlling disease resistance, agronomic, or quality traits important to Georgia peanut growers.

In 2019 and 2020 we conducted a replicated yield trial evaluating 16 runner type cultivars released by the University of Georgia (UGA) peanut breeding program, from Southeast Runner 56-15 (released in 1947) to Georgia-18RU (released in 2018). The purpose of the experiment was to quantify genetic gain attributed to breeding at UGA and to catalogue genetic and phenotypic diversity of the cultivars. Improvement for yield, dollar value, disease resistance, and other traits were significant (Fig. 1). We were also able to show that UAV-based imaging could be used effectively to detect differences for plant growth characteristics like plant height and plant vigor (canopy closure) among elite runner cultivars which have subtle phenotypic differences.

We are currently developing a diverse set of populations for phenotypic evaluation and selection to improve resistance for late leaf spot disease (LLS) and tomato spotted wilt virus (TSWV). Some of the parents we are using include WS-16, an *A. cardenasii* introgression line with good resistance to LLS; NC 94022, an *A. hypogaea* subsp. *hypogaea* var. *hirsuta* line with high levels of resistance to TSWV; TxAG-6, a synthetic tri-species hybrid with resistance to root knot nematode (RKN) and LLS; and TifGP-3 and TifGP-4 for marker-assisted introgression of LLS resistance.

Additionally, we have initiated several quantitative trait locus (QTL) mapping populations to investigate the genetic control of several traits of agronomic and economic importance and develop DNA markers for selection. One of these, an F₂ population created by crossing Georgia-14N and Georgia-18RU was planted at UGA's Gibbs Research Farm, Tifton, GA in 2020 (Fig. 2). Georgia-14N is a nematode-resistant cultivar with small to moderate plant size at maturity and is susceptible to leaf scorch/pepper spot disease (LS-PS). Georgia-18RU is a recently released cultivar with vigorous early-season growth, moderate plant size at maturity, and a high level of resistance to LS-PS. We saw good disease pressure and segregation for susceptibility to LS-PS disease and some agronomic characteristics. Plants were individually genotyped for mapping these disease resistance and agronomic characteristics. The genotypic data is currently being analyzed, however, it appears that the inheritance of resistance to LS-PS in this population may be controlled by a single gene. Other traits of interest include various shelling characteristics and plant vigor.

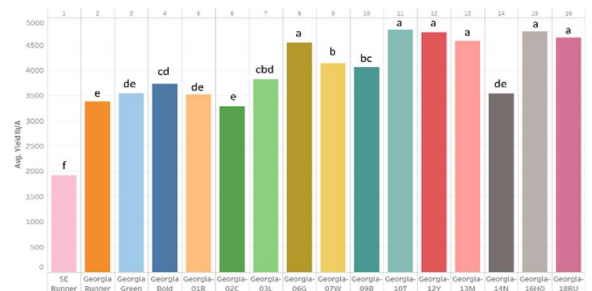


Figure 1. Average yield of Georgia runner peanut cultivars in 2019 and 2020 at Tifton, GA.



Figure 2. Evaluation plots for an F₂ mapping population segregating for leaf scorch/pepper spot susceptibility and other quantitative traits.