

## Research report

### Marker-assisted breeding to diversify alleles for late leaf spot resistance

Peggy Ozias-Akins, Ye Chu, Institute of Plant Breeding, Genetics & Genomics, University of Georgia Tifton Campus, Tifton, GA 31793; David Bertioli, Soraya Bertioli, Josh Clevenger, Institute of Plant Breeding, Genetics & Genomics, University of Georgia, Athens, GA 30602; Albert Culbreath, Department of Plant Pathology, University of Georgia Tifton Campus; Thomas G. Isleib, North Carolina State University, Raleigh, NC; C. Corley Holbrook, USDA-ARS, Tifton, GA 31793

Late leaf spot and early leaf spot are the major fungal diseases plaguing peanut production. Fungicide applications to control these foliar diseases are not only costly to peanut producers but also compromise environmental safety. Host resistance to both diseases is highly desirable to protect peanut yield. GP-NC WS 16 was found to have strong resistance to early leaf spot and moderate resistance to late leaf spot. Florida-07 is a high oleic peanut cultivar susceptible to late leaf spot. We identified QTL on chromosomes A05, B05, and B03 in a recombinant inbred population from Florida-07 x GP-NC WS16 (C1801) using two methods, 1) SNP-array genotyping and genetic mapping and 2) QTL-seq of resistant and susceptible pools (Clevenger et al. 2018. *Frontiers in Plant Science*). Population development was initiated in Tifton, GA and split into half for advancement in Tifton and North Carolina (NCSU). The entire population was genotyped by the *Arachis* Axiom Affymetrix SNP array. The population was phenotyped for early leaf spot disease for two years in North Carolina and for late leaf spot disease for three years in Georgia. Both QTL discovery methods identified overlapping QTL on A05 and B05 for LLS while QTL-seq also identified a QTL for LLS on B03 and genetic mapping identified a QTL for ELS on B03, but in a different chromosomal region. Selection with markers designed for LLS QTL showed that marker-assisted selection could identify lines that subsequently demonstrated high levels of LLS resistance in field tests. To introduce a novel source of LLS resistance into the breeding program, advancement of materials containing marker-selected *Arachis cardenasii* introgressed regions (Clevenger et al. 2017. *Peanut Science*) from breeding line IAC322, likely associated with late leaf spot resistance, led to the recovery of materials with one, different combinations of two, or all three introgressed regions. A second round of backcrossing using marker-assisted selection to retain all three regions in male parents has been conducted. Based on preliminary detached leaf inoculation assays, it does not appear that all three regions are needed to confer resistance. Therefore, families from different generations containing combinations of introgressed regions due to recombination will be phenotyped in the field in 2018. Further analysis will determine the extent of linkage drag associated with each segment and level of associated LLS resistance.