

Genome Wide Association Study (GWAS) on Root-Knot Nematode Resistance in Cultivated Peanut

F.E. KUMRAL*, C.Y. CHEN, Department of Crop Soil and Environmental Sciences, Auburn University, AL 36849; and B.R. LAWAJU, K. LAWRENCE, Department of Entomology and Plant Pathology, Auburn University, AL 36849.

The peanut root-knot nematode, *Meloidogyne arenaria*, is one of the major soil-borne pests for peanut (*Arachis hypogaea* L.). It causes economic losses in the production of peanut in the southeastern region, especially in Alabama, Georgia, and Florida, and in Texas as well. Losses due to root-knot nematodes can reach up to 50% at dense infested fields without using nematicides. The application of nematode resistant cultivars is the most convenient economical way of the biological control method for producers. The identification of resistant peanut germplasm to nematode diseases is a fundamental task for breeding nematode resistant cultivar. The objectives of this research are to evaluate 161 accessions of peanut germplasm in the greenhouse for resistance and to identify SNP markers associated with root-knot nematode resistance via genome-wide association study (GWAS). Randomized complete block design with three replications for each genotype is performed for phenotyping by using greenhouse inoculation techniques. The genetic diversity panel was genotyped by Affymetrix version 2.0 SNP assay. Forty-six quantitative trait loci (QTLs) located on twelve different chromosomes underlying root-knot nematode resistance were determined with phenotypic variation explained (PVE) between 7.8% and 17% by GWAS. The associated markers could be applied in breeding programs for marker assisted selection.