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2016

NATIONAL PEANUT BOARD/SOUTHEAST PEANUT  
RESEARCH INITIATIVE  
FINAL REPORT FOR WORK  
DONE UNDER RESEARCH AGREEMENT

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**Final Report**

INSTITUTION: UGA Research Foundation

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PROJECT TITLE: Gene-based Markers for Breeding of Nematode and Leaf Spot Resistance

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RES. AGR. NO.: 25-21-RF324-393 PROJECT LEADER: Dr. Peggy Ozias-Akins

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EXPIRATION DATE: June 30, 2016 NPB CONTACT: Maria Mehok or D Wilson  
NPB Control NO.: 407

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**FINAL REPORT:**

The research supported by this funding addressed several goals of the Peanut Genomic Initiative Strategic Plan including: Genetic Tools and Breeding Methods, Genomic Sequencing & Gene Discovery, and Functional Genomics & Proteomics. Sequencing of expressed genes is essential to extract the portion of the genome that is largely responsible for the phenotype of the plant. Quantitative analysis of gene expression also allows evaluation of differential gene expression across tissues and between duplicated genes, particularly with respect to whole genome duplications, which is important for understanding the genetic contributions of the subgenomes of tetraploid peanut. We accomplished the objectives to 1) complete gene expression profiling using RNA-Seq for resistant and susceptible genotypes challenged with late leaf spot and previously nematode; and 2) identify additional single nucleotide polymorphisms (SNPs) in differentially expressed genes for genetic mapping in populations segregating for these disease resistance traits.

Experimental materials were late leaf spot infected tissues of two parental lines of a recombinant inbred line mapping population, SPT-06-06 and Florida-07. Time points after infection included 0h, 2,4,5,8,20 days so that different stages of host-pathogen interaction could be captured in the gene expression analysis. Sequence analysis identified groups of genes that were up- or down-regulated in response to infection. Recombinant inbred lines segregating for nematode or leaf spot resistance were used to genetically map these traits. Single nucleotide polymorphisms identified from these data sets that discriminate between nematode resistant/susceptible or leaf spot resistant/susceptible parents of populations have been mapped in respective segregating populations to determine association with a resistance trait. Markers tightly linked with a trait locus are being used to screen breeding materials for selection of lines that have a high probability of carrying the resistance traits. Markers for both traits have been validated by phenotyping selected lines in the greenhouse (nematode) or field (leaf spot). Validated markers are now being routinely used in the breeding program with materials that are derived from these genetic backgrounds.