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Annual Report & Summary  
2014

**NATIONAL PEANUT BOARD / SOUTHEAST PEANUT RESEARCH INITIATIVE**

FINAL REPORT for WORK DONE UNDER RESEARCH AGREEMENT APPA-RIA03-PID  
388 BID 1286

PROJECT PERIOD: 1 January 2014–30 June 2015

INSTITUTION: Auburn University

PROJECT TITLE: Association mapping of DNA markers to leaf spot resistance in cultivated peanut that can be used in breeding program

RES. AGR. NO.: APPA-RIA03-PID 388 BID 1286

PROJECT LEADER: Drs. Charles Chen, Austin Hagan, and Kira Bowen

EXPIRATION DATE: 30 June 2015

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**FINAL REPORT FOR YEAR 2:**

Peanut growers in the United States rely on new cultivars to combat biotic and abiotic stress. Research gaps exist for the identification of molecular markers that can be associated with yield and disease resistance. As a serious concern, early and late leaf spots in peanut can reduce anticipated yield by 10-20% and up to 50% if not controlled. Currently fungicides can manage both pathogens; however, disease resistant cultivars would provide more cost-effective control. From a breeding's perspective, high yield combined with high levels of resistance to leaf spot diseases while maintaining acceptable market traits has proven very difficult to achieve. Therefore, the discovery of various alleles contributing to leaf spot resistance in *Arachis* germplasm is necessary for further breeding toward a high level of resistance to leaf spot through pyramiding alleles/genes, a strategy to overcome partial resistance to a disease. These resistant allele-specific makers will be applied in the peanut breeding program to improve leaf spot resistance. The objective for Year 2 of the proposed three-year project was to discover desirable alleles contributing to leaf spot resistance in *Arachis* germplasm through association analysis.

**Materials and Methods**

A peanut genotype collection containing a 132 accessions from plant introductions (PIs), advanced breeding lines, and released cultivars with known reactions to early and late leaf spot will be evaluated. Phenotyping of the 132 lines will be conducted in field with none fungicide treated program. A set of 200 SSR primers from peanut genetic linkage maps will be utilized to genotype the 132 accessions. Software programs STRUCTURE and TASSEL will be used to analyze both the genotypic and phenotypic data to associate the markers and disease resistances.

## Results

We have confirmed the accessions of PI 576614, PI 576634, PI 371521, and PI 268868 as sources of leaf spot resistance from previous year results and we also confirmed that the breeding lines of S518, T012, T065, T087, T109, T111, T118, 12H-10\_09,10, and 12H-13\_09,10 have strong leaf spot resistances.

Nine effective markers were associated with leaf spot resistance in *Arachis* germplasm by GLM and MLM analysis of TASSEL (Table 1). Among them, three markers, pPGPseq2D12B, pPGSseq19B1, and TC04F12, were confirmed in both years. The marker 'TC20B05' can explain 15% phenotypical variation.

Table 1. The markers associated with the trait at the significance threshold by MLM analysis of TASSEL.

Trait	Marker	P value	MarkerR2	Effect
2013 Early Rating	pPGPseq2D12B	0.0026	0.0638	2.3538
	TC04F12	0.0177	0.0390	0.9612
	pPGPseq3E10	0.0363	0.0302	-0.7025
	pPGSseq19B1	0.0406	0.0289	-0.6935
2013 Late Rating	TC20B05	0.0001	0.1074	1.7354
	TC04F12	0.0045	0.0527	2.4317
	pPGSseq13A10	0.0115	0.0413	-1.7126
	TC21C10	0.0360	0.0282	0.8207
	pPGSseq19B1	0.0384	0.0275	-1.4724
2014 Early Rating	GM2831	0.0083	0.0513	2.5647
	pPGPseq2D12B	0.0152	0.0432	1.7941
	XIP108	0.0464	0.0288	-1.3276
2014 Late Rating	pPGSseq19B1	0.0273	0.0281	-0.9599
	GM2745	0.0378	0.0249	-1.9447
	pPGPseq2D12B	0.0475	0.0226	1.9630