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Final Report for CY 2012

I. **Abstract**

Project Title: Development of Peanut Cultivars with Resistance to Diseases and Improved Water Use Efficiency and Development and Use of Molecular Markers for Marker Assisted Selection

Project Investigators:

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Summary:

Previous progress from this project has resulted in the development of peanut genotypes with relatively high yield and relatively low aflatoxin contamination when grown under drought and heat stress conditions. Continued breeding efforts are needed to improve the yield and grade to develop drought tolerant peanut cultivars. During this year we continued these breeding efforts and conducted numerous field tests containing breeding lines that we are evaluating to access their tolerance to drought, yield, and grade. These lines were planted in replicated studies at our field at the Gibbs Farm that has ten rain out shelters, and in our field at the Bowen Farm that has three rain out shelters. The shelters were then used to impose heat and drought stress for the 40 days immediately prior to harvest. Plots were visually rated for drought stress, and the yield and aflatoxin contamination were measured. Breeding lines that had relatively high yield and relatively low aflatoxin were indentified.

Molecular markers are widely used in other crops to improve breeding efficiency and effectiveness. Use of molecular marker assisted selection (MAS) in peanut breeding has lagged other crops because of a lack of molecular markers for important traits. We have recently developed molecular markers for resistance to the peanut root-knot nematode, and molecular markers for both genes controlling the high oleic acid trait in peanut. We are actively using these markers to enhance our breeding efficiency. We are also developing segregating populations that should be useful in developing molecular markers for several other important traits in peanut.

II. Main Body of Report

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Objectives:

1) Development of peanut cultivars with resistance to diseases.
2) Development of peanut cultivars with improved water use efficiency.
3) Development and use of molecular markers for marker assisted selection.

Procedures:

1) Crosses were made and progeny were selected for resistance to leaf spot, tomato spotted wilt virus, white mold, and Cylindrocladium Black Rot. Late generation breeding lines were evaluated for yield and disease resistance in replicated field studies.
2) Crosses were made and progeny were selected for drought tolerance. Late generation breeding lines were grown under late season heat and drought stress, and evaluated for yield and pre-harvest aflatoxin contamination.
3) Recombinant inbred line populations are being developed and will be phenotyped for economically significant characteristics.

Results and Discussion:

Sources of resistance to disease and sources of improved drought tolerance were crossed with breeding lines and cultivars that have more acceptable agronomic characteristics. The resulting breeding populations are advanced using single seed descent to the F_4 generation when individual plants are harvested. Selection for disease resistance, drought tolerance, and improved agronomic characteristics begins in the F_5 generation. Table 1 (Below) shows the performance with no fungicide sprays of late generation breeding lines selected using this procedure. Breeding lines (C1805-3-43-37 and E88) were identified that had greater yield and lower disease severity in comparison to commonly grown cultivars.

Some of our results from testing late generation breeding lines under late season heat and drought stress are presented in Table 2 and 3. Several breeding lines were identified that exhibited relatively high yield under late season drought, and some of these also exhibited relatively low aflatoxin. For example, C321-2-2 (Table 2) and C76-16 (Table 3) both exhibited high relative yield and low relative aflatoxin contamination.

For the past several years we have been actively involved in the development of several late generation Recombinant Inbred Line (RIL) Populations. The parents for these populations were selected to provide populations containing a wide range of segregation for several economically important traits in peanut. We have begun to phenotype these populations, and other groups will soon begin to genotype these populations. The resulting data will be used to attempt to develop molecular markers and quantitative trait loci (QTLs) that can be used to improve the efficiency and effectiveness of peanut cultivar development.

Table 1. 2012 Test 40 LS

Entry	LFSPT1	LFSPT2	Entry	Yield lb/ac
Georgia-06G	7.2	8.3	C1805-3-43-37	4430
C1805-2-9-34	6.5	7.8	C1805-794-9	4412
Florida-07	6.3	8.0	E88	4408
Ga Greener	6.0	7.3	E62	4303
C1805-794-9	5.2	6.8	E36	4266
E36	5.2	7.0	C1805-2-9-34	4258
E62	4.8	6.3	Tifguard	4052
Tifguard	4.3	6.0	Ga Greener	3837
E88	4.2	5.8	Florida-07	3126
C1805-3-43-37	4.0	6.2	Georgia-06G	3126
LSD 0.05	1.0	1.0		563

Table 2. 2013 Test 07 Date 1 Shelter 10

Entry	Yield g/plot	Entry	Aflatoxin ppb
C321-2-2	482	ICGV93305	696
A137	329	ICGV93280	400
C448-1	318	458CC	321
C76-16	284	A47	311
ICGV93305	277	C448-1	226
479CC	272	A137	220
458CC	268	ICG23	170
ICGV93280	263	479CC	156
ICG23	258	C321-2-2	71
A47	250	C76-16	46
LSD (0.05)	97		605

Table 3. 2012 Test 07 Date 1 Shelter 7

Entry	Yield g/plot	Entry	Aflatoxin ppb
C76-16	511	ICG1105	2056
ICG1105	406	ICG884	1427
ICG2266	398	ICG369	1379
ICG369	346	ICG558	640
ICG2800	335	ICG4750	587
ICG1102	326	ICG2266	502
ICG45	304	ICG1102	482
ICG558	304	ICG2800	471
ICGV4750	246	C76-16	382
ICG884	245	ICG45	148
LSD (0.05)	105		ns