

I.

Abstract

Project Title: (i) Development of Peanut Cultivars with Resistance to Diseases and Improved Water Use Efficiency; and (ii) Development and Distribution of Recombinant Inbred Line (RIL) Populations for Use in Genomics Projects to Develop Molecular Markers for Marker Assisted Selection

Project Investigators:

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Dr. Tom Isleib, Peanut Breeder, NCSU, Raleigh NC

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. 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 was 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. Recent advances in peanut genomic research have resulted in the development of a few markers that can be used in peanut breeding. In order for the peanut industry to reap the maximum benefits from MAS, additional markers need to be developed for important traits. This should improve the efficiency and effectiveness of all U.S. peanut breeding programs. We have been advancing several recombinant inbred lines (RIL) populations that should be segregating for numerous economically important traits. Seed for these lines were distributed to eight research groups for phenotyping. These data will then be associated with genotypic data to identify QTL (molecular markers) for these traits.

II. Main Body of Report

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Objectives:

- 1) Develop high yielding peanut germplasm with resistance to biotic and abiotic stresses.
- 2) Develop populations that can be used to identify additional genetic markers for valuable traits in peanut.

Procedures:

- 1) Crosses have been made and progeny will be selected for resistance to leaf spot, tomato spotted wilt virus, white mold, and *Cylindrocladium* Black Rot. Late generation breeding lines will be evaluated for yield and disease resistance in replicated field studies.
- 2) Crosses have been made and progeny will be selected for drought tolerance. Late generation breeding lines will be 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. Seed will be increased and distributed for research to phenotype and genotype 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 F₄ generation when individual plants are harvested. Selection for disease resistance, drought tolerance, and improved agronomic characteristics begins in the F₅ generation. Breeding lines were identified that had greater yield and lower disease severity in comparison to commonly grown cultivars. Several breeding lines were also identified that exhibited relatively high yield under late season drought, and some of these also exhibited relatively low aflatoxin.

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 distributed seed of these lines to eight research groups to begin phenotyping these population. These data will then be analyzed with genotypic data to identify associations. These results will be used to develop molecular markers and quantitative trait loci (QTLs) that can be used to improve the efficiency and effectiveness of peanut cultivar development.