Annual Research Report to the Georgia Peanut Commission Board (2/15/14)

Title: Characterization, evaluation, and regeneration of the US peanut core collection

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Objectives: The entire core collection (approximately 800 lines) will be evaluated over a two year period, assessing phenotypic (yield, grade, disease resistance, morphological characteristics), biochemical (fatty acids, oil, and protein), and genetic parameters (*ahFAD2* and SSR genotyping). This project will produce a publicly available, comprehensive catalog that more thoroughly describes the traits within the core collection desired by the peanut community.

Results: The entire core collection along with commercial standards of each market type (runner, Spanish, Valencia, and Virginia) were planted at Plant Science Research and Education Unit in Citra, FL for a total of 1098 plots. An augmented design was employed with replications of the commercial standards and the U.S. mini core in order to evaluate block variability. Phenotypic traits were collected at mid season which included standard descriptors, height and width of the canopy of each plot, stem pigmentation, and leaf length and width. In addition, when the plots were harvested mainstem height, disease prevalence, presence or absence of flower or pegs on the mainstem in order to distinguish subspecies, and stand counts were also collected. Currently, the harvested pods are being evaluated for yield and grade. The total yield and grade on the entire mini core and the commercial standards has been completed. (Yield data on the core are still being collected). The yield and grade ranged from 500 -5300 lbs/acre and TSMK were 69-81%, respectively. Digital images were collected of all the plots (1098), flowers (265), a single plant post digging (1097), and pod and seed images will also be taken. All of these images will be submitted to GRIN for the peanut community to access.

Each line from the core and the commercial standards are also being evaluated by genotyping to assess genetic diversity and to associate markers with agronomic traits. All of the accessions had DNA extracted and quantified. A combination of SSR and SNP genotyping were employed. A set of 30 SSR markers were evaluated on a subset of peanut lines and 22 of these markers were successful in distinguishing variability among accessions. The majority of the core has now been assessed with these 22 SSR markers. The number of alleles range from two to 14 per marker. Further, we have evaluated the core for variability of the *ahFAD2* alleles which control the high oleic trait (G448A in ahFAD2A and Ains442 in ahFAD2B). No high oleic lines have been detected; however, 36% of the lines are fixed for the *ahFAD2A* mutation which

has been known to occur fairly frequently in runner and Virginia type peanuts. This information will allow breeders to select germplasm that contains the ahFAD2A mutation and make crosses with a high oleic line in order to obtain a higher frequency of high oleic progeny in their segregating populations (3 normal oleic: 1 high oleic versus 15 normal:1 high oleic).

Biochemical parameters such as total oil, total protein, and fatty acid profiling are currently underway for the mini core and commercial standard lines. Samples for all these lines have been separated into whole seeds for NIR analysis and ground into a fine powder for biochemical analysis. Total protein collected to date ranges from 25-35% and the total oil is ranging from 50-61%. While only 15% of the mini core and standard lines have been analyzed, high oleic fatty acid content has only been detected in the standard lines, which is in agreement with the molecular data.