

Research Report (2009) to  
The Georgia Peanut Commission  
February 10, 2010

**TITLE: A Rapid and Accurate Detection of High Oleic Genotypes of Peanuts Using Real-Time PCR**

**INVESTIGATORS:** N. A. Barkley\*, M. L. Wang, and R. N. Pittman, USDA-ARS, PGRCU, Griffin Experiment Station, Griffin, GA 30223.

**OBJECTIVES:** 1) Using parents and advance F1 material involving crosses with high oleic parents develop an accurate fast method of detection, 2) Develop a method of extracting DNA from either seeds or leaves of peanuts, 3) Develop a method detection that can easily be interpreted, and 4) Procedure must identify each genome's genotype.

**PROGRESS:** In attempt to increase genetic diversity (specifically disease resistance) of high oleic acid lines, crosses were made between lines containing high oleic to linoleic ratios and cultivated botanical varieties. Therefore, a Real-time PCR assay was developed to identify the high oleic genotype in high oleic parents or the normal genotype in the non-high parents. In addition to developing the real-time PCR procedure, we developed a DNA extraction for either single seed or leaves.

**RESULTS:** 1) We were able to detect hybrid seeds collected from a cross and parents could be either the male or the female and plant only hybrid seeds for evaluation and increase. Using seed (F2 seed) collected from F1 plants, we were able to identify specific genotypes that were high oleic, identify new genotypes which could not be previously identified and keep for future crosses with other high oleic parents and again eliminate material that was not desirable. In addition, after DNA is collected we are able to get results within one to two hours using either a 48 or 96-well format for PCR.

2) We were able to confirm the inheritance the high oleic as previously reported and for the first time identify each genotype possible from the cross.

**FUTURE OBJECTIVES:** Expand the use of the procedure to larger and more diverse populations from crosses to identify the high oleic genotype so that selection can be followed for high yield and other desirable characters. Also, identify in the germplasm accessions which carry one of the genome markers for the high oleic trait.