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Final Report**Peanut Genetics**
March 13, 2005**Accelerating Development of Peanut Varieties through Molecular Markers**Mark D. Burow^{1,2}, Yolanda López¹, Arun M. Jesubatham³, and Charles E. Simpson⁴¹ Texas Agricultural Experiment Station, Texas A&M University, Lubbock, Texas 79403² Department of Plant and Soil Science, Texas Tech University, Lubbock, Texas 79409³ Department of Computer Science, Texas Tech University, Lubbock, Texas 79409⁴ Texas Agricultural Experiment Station, Texas A&M University, Stephenville, Texas 76401**Problem and Need**

Enhanced resistance to disease, early maturity, water-use efficiency, and oleic:linoleic ratios are important peanut traits requiring improvement in Texas. Breeding for these traits is difficult because of our lack of understanding of the genetics of these traits, and the variability in field conditions which means that the needed weather or pathogens are not present in some years. In all cases, research is needed to identify the genes controlling these traits and to develop molecular markers to accelerate varietal development for Texas producers.

Objectives

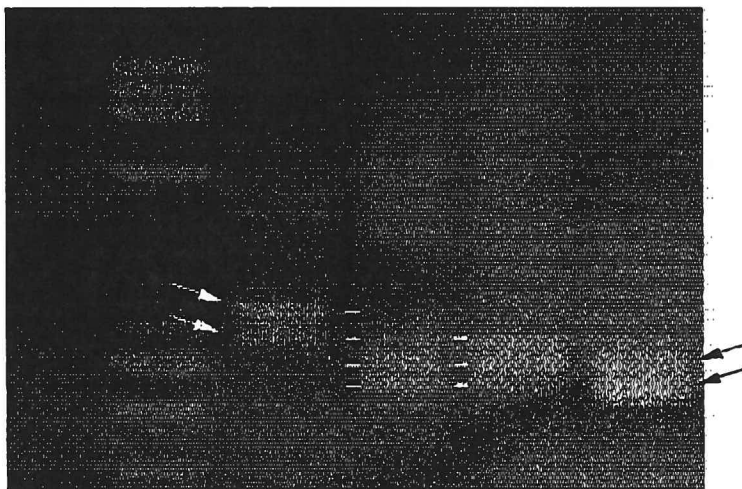
The proposed research aims to develop markers for cultivated × cultivated crosses to complement the peanut breeding programs in Texas. The applications expected to benefit the soonest are early maturity, disease resistance, and high O/L content.

Results

(1) **Test microsatellite primers for detection of polymorphism in cultivated peanut and begin mapping of markers on a peanut population.** Approximately 110 microsatellites have been reported to reveal differences among cultivated peanut have been synthesized commercially. We have been able to identify differences among the BC1 progeny of the Florunner × TxAG-6 mapping population. We will use this cross for mapping microsatellite markers on the RFLP map of peanut.

Figure 1. Use of markers to tell differences among parents (Florunner, TxAG-6, and progeny (BC1) of the mapping population.

Stds TxAG6 — BC1 — Flo



Many of these markers will also be useful for breeding work in cultivated peanut, with the potential to be associated with diverse traits including early maturity, nematode, leafspot, TSWV, and Sclerotinia resistance.

(2) **Development of markers for the high-O/L trait.** The high-oleic trait has known to be controlled by 2 recessive genes, but there is evidence that more genes are involved. This means additional complexity in breeding for this trait. We are in the process of developing markers that can be used for this trait. Also, success for this trait will signify that this approach is workable in peanut.

We have used differences in the sequences of the normal (low oleic) and mutant (high oleic) genes to design DNA primers for CAPS (cleaved amplified polymorphic sequence) markers. These markers can distinguish both high-O/L and low-O/L varieties (see figure below).

Figure 3. Use of markers to distinguish high-oleic varieties from low-oleic ones. Accessions are UF-435, Tamrun-OL01, Tamrun-OL02, Langley, Spanco, and New Mexico Valencia A. The digested samples ("C") have one band the same size as the uncut ("U") samples if high-oleic, but not if the variety is low-oleic.

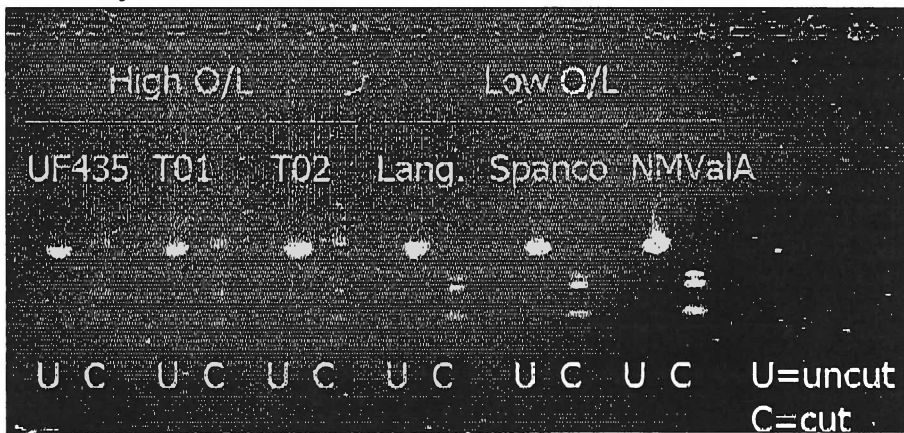
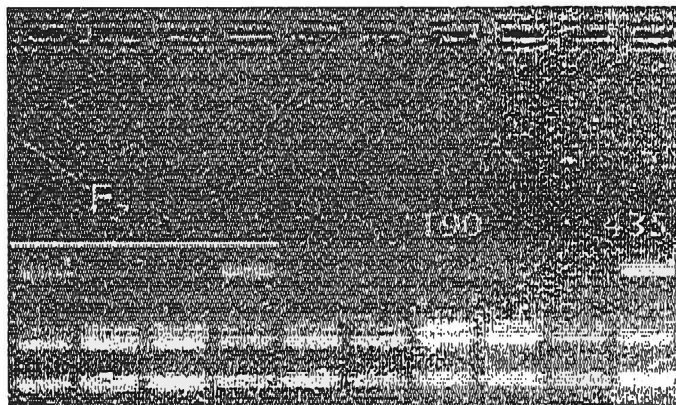


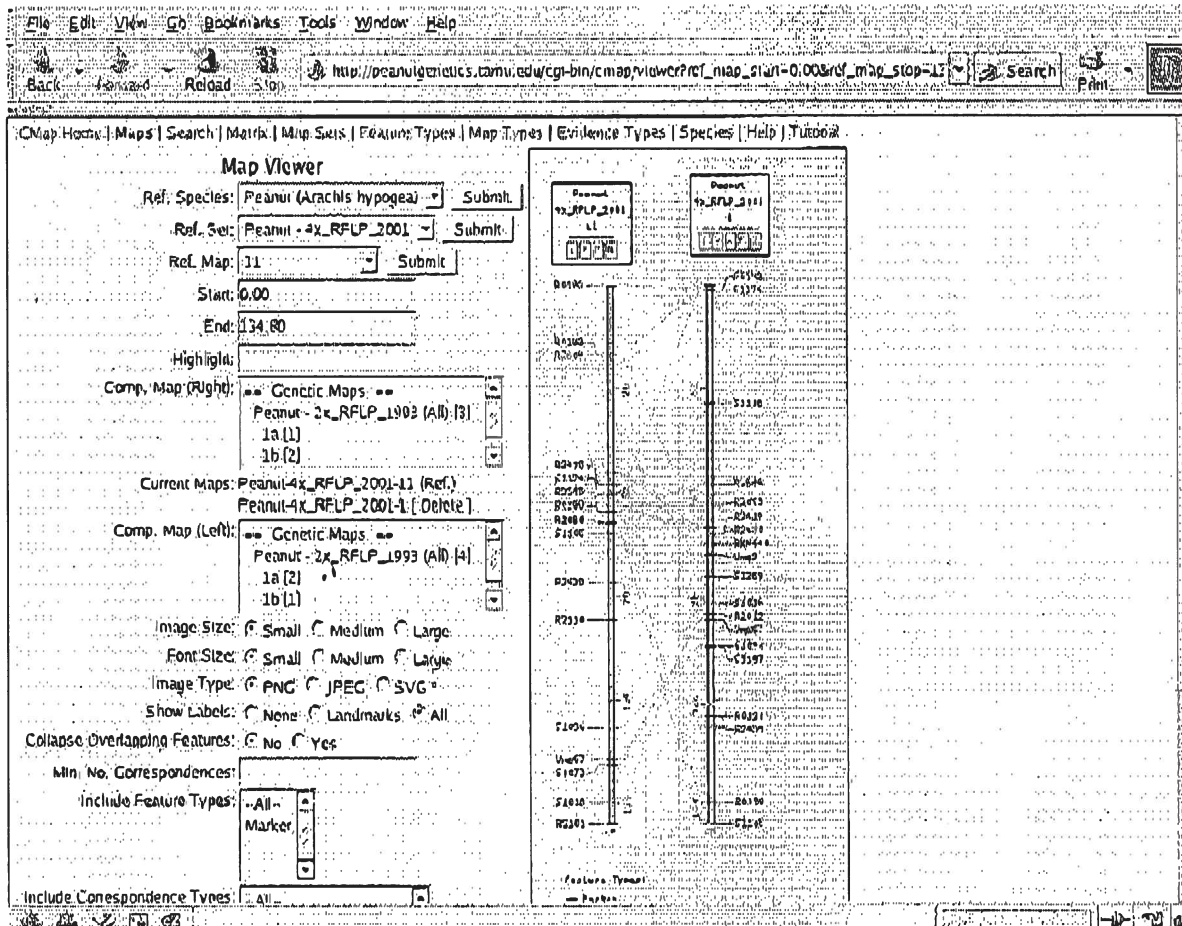
Figure 2. Segregation of digested marker patterns in an F2 population of peanut. The low-oleic variety Tamspan 90 is shown (T90) as is the high-oleic donor UF-435.



To test whether these work in a breeding population, we have made F2 crosses between high-O/L and low-O/L varieties, and are now testing the markers on DNA from this population (Figure 3).

(3) Development of a marker database and installation of DNA analysis software. We have published an online graphic-oriented database of DNA marker maps using the open source CMAP software. This is the only marker database for peanut, and data will be made available to the Legume Information System (LIS) database for comparison of peanut and other legumes. The benefit of this database is that it will allow easy access to peanut marker data for breeding and genetics work.

Figure 4. Screen shot of the peanut marker database.



We have added both marker maps of peanut (Halward *et al.*, 1993; Burow *et al.*, 2001). The database is publicly available on the internet at <http://peanutgenetics.tamu.edu/cmap>. The database shows the markers mapped on peanut, and places them on schematic drawings of peanut chromosomes.

ACKNOWLEDGMENTS

We express our sincere appreciation to the National Peanut Board and the Texas Peanut Producers Board for assisting our program in 2004. The work reported here would not have been possible without their generous support.