

### Accelerating Development of Peanut Varieties through Molecular Markers

Mark D. Burrow<sup>1</sup>, Yolanda López<sup>2</sup>, Charles E. Simpson<sup>3</sup>

<sup>1</sup> Department of Plant and Soil Science, Texas Tech University, Lubbock, Texas 79409

<sup>2</sup> Texas Agricultural Experiment Station, Texas A&M University, Lubbock, Texas 79403

<sup>3</sup> 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, however, can be difficult. Research is needed to identify the genes controlling these traits and to develop molecular markers to accelerate varietal development for Texas producers. Molecular markers are a method of helping breeders select for plants with desirable traits. DNA markers can assist selection of superior plants by scoring for the "DNA fingerprint" associated with desired traits obtained from one peanut parent or the other.

#### Plan of Action

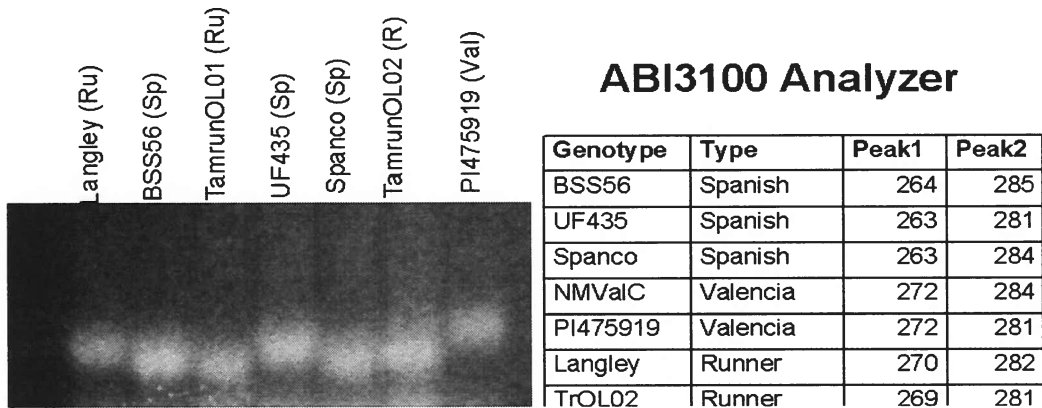
**Objectives:** The proposed research aims to develop markers for cultivated × cultivated crosses to complement the peanut breeding programs in Texas. In the past, we have identified RFLP (restriction fragment length polymorphism) markers in wild species for nematode resistance and are currently evaluating markers for resistance to leafspot resistance. In this continuing project, we will proceed with developing markers for cultivated × cultivated crosses. The applications expected to benefit the soonest are early maturity, disease resistance, and high O/L content.

#### Results:

**In Year 1**, we developed cultivated × cultivated crosses segregating for maturity, botanical type, O/L ratios, and possibly TSWV resistance. We are now focused on developing molecular markers for use with these populations.

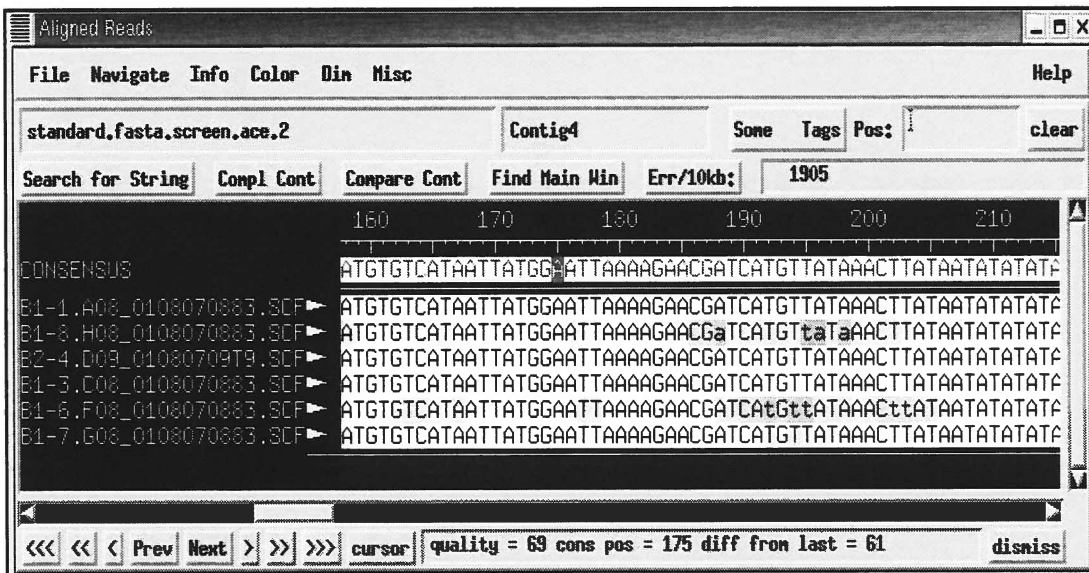
**(1) Begin mapping microsatellites on the Florunner x TxAG-6 mapping population.** This is the goal for this year and the next. We have extracted DNA from the mapping population, and have shown that the markers tested can distinguish wild and cultivated species. This project has waited for the publication of microsatellite primer sequences, which were made available in December 2003. We expect to use these primers for mapping using the same BC1 population that the RFLP map was made from.

**(2) Test microsatellite primers for detection of polymorphism in cultivated peanut.** We have been able to distinguish several varieties by separation and detection on both agarose gels and on an ABI3100 DNA analyzer (Figure 1.) We expect that this will allow us to use microsatellite markers to map traits such as maturity and disease resistance in cultivated crosses.



**Figure 1. Differences in DNA fingerprint of cultivated peanut, using microsatellite primers.** In the panel at left, separation is by agarose gel electrophoresis; at right, using an ABI 3100 DNA Analyzer at the USDA Plant Stress Laboratory (Lubbock). Fragment sizes are given for the two bands, sorted by market class. Data in the two panels are from different primer pairs.

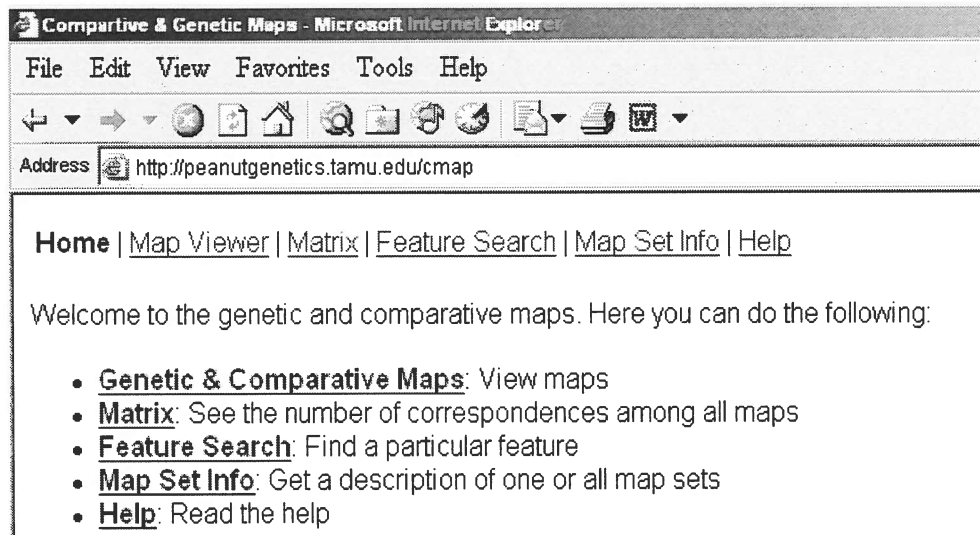
**(3) Begin converting RFLP markers to PCR-based ones and fill in the gaps in the microsatellite collection.** We are currently sequencing mapped RFLP markers and other peanut DNA clones. To date, we have sequenced approx. 100 of the 220 cDNA clones. The following figures is an example of one of the sequences:



We are also in the preliminary stages of developing a peanut seed cDNA gene library and have 51 clones with confirmed peanut genes and 500 more clones with unconfirmed inserts.

**(4) Continue development of a marker database and installation of DNA analysis software.**

The goal is to allow interactive display of any gene sequence, marker, trait, or clone with its genetic variation. We have set up a UNIX server running RedHat Linux, and installed the CMAP software for displaying molecular marker maps of peanut, and will begin entering data. The following figure shows one of the web pages:



**Summary.** We have performed the groundwork to show that microsatellite markers can be used for crosses in cultivated peanut. We are also making libraries of peanut genes for developing additional markers. This year we will focus on making a map of peanut using the microsatellite markers.