Peanut Genetics
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NPB Final Report

Title: **Identification of Markers for Maturity and O/L Ratio, Leafspot Resistance, and Resistance to Heat and Drought for Varietal Development**

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Objectives.

The proposed research aims to develop markers for cultivated H 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 using lines developed from wild species. In this continuing project, we will develop markers for cultivated H cultivated crosses. The applications expected to benefit the soonest are early maturity, disease resistance, and high O/L content.

Results:

The experimental plan was to use microsatellite (SSR, simple-sequence repeat) markers to find differences that can be used for DNA fingerprints to identify plants that have specific traits.

(1) Identification of markers for pod and seed-related traits.

We used an 88 plant subset of an $F_{2:6}$ recombinant inbred (single-seed descent) population to identify markers for quantitative traits QTLs (quantitative trait loci). For the current experiment, markers were identified by bulk segregant analysis. Twelve pools were made for pod and kernel-related traits, including pod and seed length, width, and weight; pod constriction; maturity; and oil percentage. Bulks for analysis were made from separate pools of equal quantities of DNA from 8-10 individuals having high and low phenotypic values for each trait.

Marker analysis was performed with SSR markers. Parents (BSS56, Tamrun OL01) were screened with 112 peanut SSR primer pairs (He and Prakash, 1993; Hopkins et al., 1999; Ferguson et al., 2004), and banding patterns were resolved on PAGE gels.

1**Figure 1.** Bulked segregant analysis of a marker for pod length. Each lane contains DNA from a different plant or pool of plants. Lanes marked as "LOW" are from plant lines with the shortest pods, and lanes in the "HIGH" have the longest pods. "LB" is DNA pooled from the low bulk (plants with short pods), and "HB" is from plants from the high bulk (plants with the longest pods). P1 is Tamrun OL01, and P2 is BSS56. The arrows denote the markers for the alleles (bands) for short or long pods.

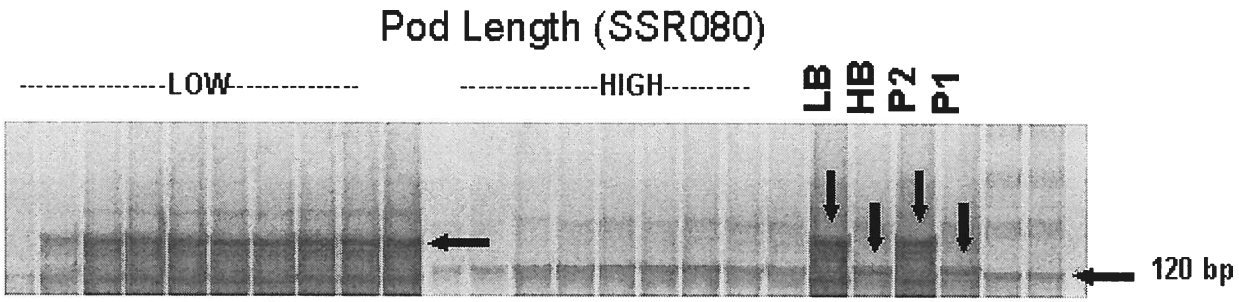

Table 1. List of markers identified for pod- and seed-related traits.

Trait	SSR marker	P-value	R_2 %	Recomb %
Seed length(mm)	SSR753	0.001	12.45	0
Pod length(mm)	SSR753	0.007	9.19	11.5
100 seed weight (g)	SSR753	0.004	10.17	0
Pod length(mm)	SSR098	0.006	9.50	0
Number of pods	SSR410	0.001	12.47	0
Plant weight(g)	SSR410	0.004	10.10	0
%Mat Pods(Br + Bl)	SSR450	<0.001	17.69	0
Oil content %	SSR360	0.003	11.03	16.6

Table 2. Trait scores associated with the two alleles of the markers in Table 1. It shows the

Trait	SSR markers	High bulk phenotypic mean	Low bulk phenotypic mean	Mean value of TamRunOL1 allele	Mean value of BSS56 allele
Seed length(mm)	SSR753	18.11(8)	13.00 (8)	15.62	14.18
Pod length(mm)	SSR753	35.22(9)	24.80(9)	32.39	29.61
100 seed wgt (g)	SSR753	85.58(8)	48.58(8)	75.56	65.44
Pod length(mm)	SSR098	35.22(9)	24.80(9)	32.12	29.38
Number of pods	SSR410	101.3(9)	14.50(9)	60.24	40.65
Plant weight (g)	SSR410	139.3(9)	19.39(10)	76.53	53.40
% Mat. Pods	SSR450	94.99(9)	18.03(9)	51.86	74.38
Oil content %	SSR360	50.63(9)	41.50(9)	45.85	47.56

Future work is needed is to identify more markers that distinguish between the parents, and test these markers against the trait pools. There are other traits that have not been tested, and these need to be included also.

(2) Identification of markers for leafspot resistance.
We have developed 4 populations from crosses between leafspot-resistant BC_3F_6 introgression lines developed from TxAG-6 and runner and Spanish parents. These lines were evaluated in the field for leafspot resistance in the summer of 2007.

(3) Advance populations segregating for resistance to heat and water stress.
We have developed three populations for studying the genetics of heat stress, and have tested polymorphism in two of these crosses, plus an additional population for mapping maturity and quality-related traits. We have >2000 F_2 seed from each of two of the three populations; F1 plants of the third population were sickly, and few seed were obtained from this population.

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