

FINAL

#137
2005
TX

(Changes to 2004)

Subject: Peanut Breeding

March 13, 2006

Title: Heritability Estimates for High Yield Traits transferred from Wild Species Hybrids to a Conventional Variety

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Progress Report

The original strategy for this study included four F₂ generation populations arising from four individual F₁ generation crosses between our disease resistant high O/L lines and high yielding wild species derived hybrids. We had planned to use 80 F₂ plants, 20 F₁ plants, 20 P₁ (Parent 1) plants, and 20 P₂ (Parent 2) plants. Upon an extended literature review, it was determined that the F₂ populations needed to be much larger than the original 80 specified in the proposal due to the variability expected within the population. So, on June 19, 2005 the experiment was planted at the College Station nursery using two F₂ populations instead of the original four with 220 F₂ plants, 20 F₁ plants, 20 P₁ plants and 20 P₂ plants for each population. Only two populations were used because the size of each population was doubled from the original strategy and this limited space availability and labor.

The pedigree of P₁ in population one is Tamrun OL 01 and P₂ is TP301-209. The pedigree of P₁ in population two is also Tamrun OL 01 and P₂ is TP301-33. These two populations were chosen because they had the highest measured F₁ hybrid vigor in terms of yield. The plants from each population are planted on a 36" row spacing at 36" apart. The test plots consisted of 14 plants per range (F₂=11 plants, F₁=1 plant, P₁=1 plant, P₂=1 plant, all randomized for each range) and 20 ranges deep for a total of 280 plants.

All plants were hand harvested and picked by hand to determine individual plant yields. Yields were measured in grams of pods harvested. SAS Proc Means was used to analyze the means and the standard deviations for each of the groups; F₁'s, F₂'s, P₁'s and P₂'s.

Theoretically, the (F₁'s, P₁'s, and P₂'s) are each homozygous within their respective group, so, all of the phenotypic variation is due to environmental effects. Therefore, if $V_G=0$, then $V_E=V_P$. The average environmental effect for the entire experiment can be estimated by averaging the variation of the three homozygous groups. The first population had the following variances recorded. The variation for the F₁ group was 66.46. The variation for the P₁ group was 45.7 and the P₂ group was 37.2. The average environmental variation for these three groups was $(66.46+45.7+37.2)/3=49.77=V_E$. This

value is an estimate of the V_E for the F_2 group which had a phenotypic variance of 70.5 because this group was grown under the same environment.

To get a Broad-sense (H^2) heritability estimate for the high yield trait, we simply modify the equation to read $V_G = V_P - V_E$ ($V_G = 70.5 - 49.77 = \mathbf{20.73}$). $H^2 = V_G / (V_G + V_E)$ so, $H^2 = 20.73 / 70.5 = \mathbf{.294}$. This indicates that about 29.4% of the phenotypic variation that is measured in the individual plant yields can be attributed to genetics while the remaining 70.6% of the variation can be attributed to environmental effects. The second population was very similar with a $H^2 = .313$ or 31.3% of the variation due to genetics.

These numbers indicate that there is a low rate of heritability for selecting high yields in early generation material such as the F_2 's and that environmental variation could cause plants with good yield potential to be discarded during selection and plants with poor yield potential to be retained.

The study will be conducted again in 2006 to confirm these findings. Additionally, single seed decent is being performed on all of the harvested plants in the winter nursery. These generation advances will be carried out until the 5th generation which will enable us to run a generation means analysis to determine which generation would be the ideal generation of selection in terms of selecting for higher yield potential.

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March 1, 2005

Subject: Peanut Breeding

Title: Heritability Estimates for High Yield Traits Transferred from Wild Species Hybrids to a Conventional Peanut.

Researchers: M.R. Baring, C.E. Simpson, and M.D. Burow

Final Report for 2004:

The crossing program to transfer high yield potential from wild species derived hybrids to conventional peanuts began in the spring greenhouse of 2004. Approximately 275 pollinations were made with positive results on 70% of the attempts. The resulting F₁ populations were planted in the College Station nursery in June of 2004. There were 191 F₁'s planted in the nursery with the pedigrees listed in the following table.

#F ₁ 's	Pedigree	#F ₁ 's	Pedigree
5	Tamrun OL 01 X TP301-81	4	01F5404 XTP301-81
4	Tamrun OL 01 X TP301-95	10	01F5404 X TP301-209
10	Tamrun OL 01 X TP301-33	10	01F5404 X TP301-112
12	Tamrun OL 01 X TP301-112	2	TP301-112 X 01F5404
10	Tamrun OL 01 X TP301-81	7	01F5404 X TP301-95
6	TP 301-89 X Tamrun OL 01	16	01F6212 X TP301-112
12	TP301-89 X Tamrun OL 01	4	02F3813 X TP301-95
4	TP301-112 X Tamrun OL 01	3	02F3813 X TP301-112
4	Tamrun OL 01 X TP301-209	1	02F3846 X TP301-112
1	Tamrun OL 02 X TP301-33	1	02F3820 X TP301-89
4	Tamrun OL 02 X TP301-81	2	02F3820 X TP301-95
14	Tamrun OL 02 X TP301-112	3	01F5415 X TP301-95
8	Tamrun OL 02 X TP301-209	2	01F5415 X TP301-209
6	Tamrun OL 02 X TP301-95	6	TP301-89 X 01F5415
6	TP301-112 X Tamrun OL 02	2	01F5415 X TP301-112
7	TP301-112 X 03T4204	3	TP301-89 X 03T4202

The F₁ yields and seeds are being evaluated and a select number of F₂ populations will be grown out for the purpose of estimating the heritability of high yield traits as compared to parent 1, parent 2, and the F₁ progeny. This will give a preliminary idea as to whether or not the study should progress and lines should be carried out to the fifth or sixth generation for a generation means analysis. Crosses will be made in the 2005 spring greenhouse to make duplicate F₁'s from last years crosses so that the individual F₂ population variances can be measured against both the F₁ and Parental variances.