

Cultivar x Environment Interactions in Peanut Yield Tests¹

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ABSTRACT

Cultivar x environment interactions for yield and several fruit traits were estimated from two groups of Virginia peanut (*Arachis hypogaea* L.) cultivar yield trials conducted in the Virginia-North Carolina production area.

A substantial cultivar x location x year second-order interaction was observed for yield in both studies. Both cultivar x location and cultivar x year interactions were small when compared to the variation among cultivars.

No advantage could be gained by subdividing the production area into subareas for breeding or testing purposes. However, a reallocation of the number of plots presently used could give comparable estimates of cultivar performance and reduce the time necessary for cultivar evaluation.

Key Words: *Arachis hypogaea*, variance components, cultivar evaluation.

Cultivar by environment interactions have been reported for many self-pollinated crop plants and the implications of these interactions on selection, estimation of genetic variance and testing procedures have been discussed (2, 3, 4, 5, 6, 7, 8, 9).

It is difficult to make general conclusions about the importance of genotype x environment interactions for all self-pollinators because estimates vary considerably among crops. However, it does appear that the genotype x year x location interaction is usually larger than either of the first-order interactions (2, 5, 6, 7). This suggests that each individual experiment is unique and the environmental conditions differentiating these studies cannot be grouped according to years or locations (4, 5, 6, 7).

Even though numerous genotype x environment interaction studies for self-pollinators have been reported, there is little information on the importance of genotype x environment interactions for the autogamous peanut (*Arachis hypogaea* L.). Chen and Wan (3) in Taiwan and Tai and Hammons (9) in Georgia, U. S. A. found large and significant cultivar x location x year interactions and small year x cultivar and location x cultivar interactions for peanuts grown in two-year field trials.

The purpose of this paper is to present estimates of genotype x environment interactions for Virginia (ssp. *hypogaea* var. *hypogaea*) cultivars from two separate studies conducted in the North Carolina-Virginia production area and discuss their implications in peanut cultivar evaluations.

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Materials and Methods

Field Procedures

Study 1. Nine Virginia cultivars were evaluated at three locations in northeastern North Carolina and southeastern Virginia during the 5-year period, 1963-1967. Five of the nine cultivars were commercial releases developed for the North Carolina-Virginia production area. The other four cultivars were late generation breeding lines. All nine cultivars were adapted to the North Carolina-Virginia area.

A randomized complete block design with three replicates was used for each test. Plots consisted of two rows of 50 plants each. Rows were 90.4 cm apart and plants within a row were approximately 25.4 cm apart. Standard cultural practices were employed in each test.

Data were obtained on percentage of fancy size pods, FS (% pods that ride 1.34 x 7.62-cm screen); percentage of extra large kernels, ELK (% seeds which ride a 0.85 x 2.54 cm screen); meat content (ratio of total seed weight to total fruit weight); weight of 100 seeds in g; and yield in kg/ha.

Study 2. Six Virginia cultivars were evaluated at four locations in North Carolina during the 3-year period from 1975-1977. All six cultivars were commercial releases adapted to North Carolina growing conditions. A randomized complete block design was used for each test. Nine of the 12 tests had four replicates. One test was replicated five times and two tests were replicated three times. Plot size and plant spacing were the same as in the first study. Yield was measured for all replicates but FS, ELK, meat content, and g/100 seed were measured on two to five replicates depending upon the location.

Statistical Analysis

The importance of the cultivar x environment interactions was obtained by conducting an analysis of variance on the data for each study and then examining the relative magnitudes of the variation arising from different sources. The sources of variation and the expectation of mean squares (Table 1) were similar for both studies

Table 1. Form of analysis of variance and expected mean squares.

Source	Mean square	Mean square expectation*
Years		$\sigma_e^2 + c\sigma_r^2 + r\sigma_{c\ell y}^2 + r\ell\sigma_{cy}^2 + cr\ell\sigma_y^2$
Locations		$\sigma_e^2 + c\sigma_r^2 + r\sigma_{c\ell y}^2 + ry\sigma_{c\ell}^2 + cry\sigma_{\ell}^2$
Years x locations		$\sigma_e^2 + c\sigma_r^2 + r\sigma_{c\ell y}^2 + cr\sigma_{\ell y}^2$
Reps in loc and yr		$\sigma_e^2 + c\sigma_r^2$
Cultivars	M ₅	$\sigma_e^2 + r\sigma_{c\ell y}^2 + ry\sigma_{c\ell}^2 + r\ell\sigma_{cy}^2 + r\ell y\sigma_c^2$
Cultivar x yr	M ₄	$\sigma_e^2 + r\sigma_{c\ell y}^2 + r\ell\sigma_{cy}^2$
Cultivar x loc	M ₃	$\sigma_e^2 + r\sigma_{c\ell y}^2 + ry\sigma_{c\ell}^2$
Cultivar x yr x loc	M ₂	$\sigma_e^2 + r\sigma_{c\ell y}^2$
Error	M ₁	σ_e^2

*c, r, ℓ, and y are numbers of cultivars, replicates, locations, and years, respectively. For study 1, c, r, ℓ, and y were 9, 3, 3, 5, respectively. For study 2, the coefficients of variance components were not constant due to unbalanced data, and the year and cultivar x year lines contained portions of the location and cultivar x location components, respectively.

except the number of cultivars, years, locations and replicates were not constant for the two studies.

Data from the first study were balanced while those from the second study were unbalanced because of the unequal replication at different locations. Therefore, the second study was analyzed using generalized least squares. The VARCOMP procedure of SAS (1) was used to generate the coefficients of the expected mean squares, which for the second study were not whole numbers and were not constant for the different sources of variation. Because the VARCOMP procedure calculates sequential mean squares, the magnitudes of variance component estimates from unbalanced data are affected by the order in which effects are added to the statistical model, although each estimate is unbiased. In this case, there were only two possible sequences in which the effects could be arranged so both models were used to estimate variance components. Each pair of estimates, *i.e.*, for each effect in each trait, was tested for equality using the F-test. No pair of estimates was found to differ significantly; therefore, only one set of estimates was reported for the second study.

The analyses of the two studies were combined to provide a single estimate for each variance component. Expected sums of squares were calculated for each study and added to provide the expected sums of squares for the combined analysis. Mean square expectations were then computed, and the matrix of coefficients from the expectations was inverted and multiplied by the vector of combined mean squares to calculate estimates of the variance components.

Significance levels were attached to variance component estimates using F-tests of the appropriate mean squares. Exact tests were not available for some effects, so approximate F ratios were constructed where needed. Error variances at different environments were expected *a priori* to be heterogeneous. Heterogeneity was confirmed for all traits using Bartlett's test. This finding affected the significance level associated with the F-test of the second-order interaction but not of other effects. For yield and meat content, the outlying estimates of σ_e^2 contributing most to heterogeneity were smaller than the pooled estimates.

The theoretical variance of a cultivar mean for this study is:

$$\sigma_x^2 = \frac{\sigma_{cy}^2}{y} + \frac{\sigma_{cl}^2}{l} + \frac{\sigma_{c\ell y}^2}{\ell y} + \frac{\sigma_e^2}{r\ell y}$$

in which *y*, *l*, and *r* equal the number of years, locations and replicates, respectively. Estimates of the variances for cultivar means arising from different allocations of plots to years, locations and replicates were made for yield using the estimates of the variance components from the combined analysis.

Results and Discussion

The relative magnitude of the variance component estimates were similar for the same traits of the two independent studies (Table 2). In the first study, cultivar effects were significant for all traits and were greater in magnitude than any of the interactions for FS, ELK, meat content, and weight of 100 seeds, all of which are traits associated with fruit size and weight. Similar results were obtained from the second study, except that there were no significant cultivar effects for meat content. In general, there was less variation for fruit size among the cultivars in the second study, possibly because the six lines used had been subjected to commercial uniformity standards before release, whereas the breeding lines used in the first study had not.

In both studies, the second-order interaction was greater in magnitude than either of the first-order interactions for fruit characters with the exception of ELK in the second study where both first-order interactions

Table 2. Estimates of variance components and their standard deviations from separate and combined analyses of two field studies.

Character	Study	$\hat{\sigma}_c^2$	$\hat{\sigma}_{cy}^2$	$\hat{\sigma}_{cl}^2$	$\hat{\sigma}_{c\ell y}^2$	$\hat{\sigma}_e^2$
% Fancy size pods	1+	253.24±115.91**	12.18±6.12**	3.42±3.68	22.61±6.19**	37.01±3.36
	2	46.77±27.11**	5.69±4.97	-0.21±3.20	10.10±5.97*	34.72±4.64
	Combined	186.85±70.21**	10.58±4.57**	1.64±2.57	18.88±4.62**	36.29±2.74
% Extra large kernels	1	58.45±27.62**	9.81±4.05**	0.21±1.47	11.42±3.33**	21.99±2.00
	2	22.48±14.04**	5.86±3.30**	3.68±2.34*	0.74±2.36	21.05±2.81
	Combined	46.70±18.39**	8.90±3.02**	0.93±1.31	8.24±2.33**	21.69±1.64
% Meat content	1	1.69±1.14*	1.02±0.47**	1.33±0.61**	1.40±0.44**	3.11±0.28
	2	0.11±0.44	-0.66±0.73	-0.08±1.05	3.93±1.94**	9.73±1.30
	Combined	1.14±0.71*	0.45±0.40	1.05±0.52**	2.17±0.59**	5.19±0.39
g/100 seeds	1	20.55±9.64**	1.14±1.33	0.04±0.84	6.97±1.96**	12.22±1.11
	2	15.00±9.22**	2.48±2.50	0.81±2.05	4.96±3.37*	21.27±2.84
	Combined	18.80±7.36**	1.48±1.21	0.35±0.89	6.39±1.71**	15.07±1.14
Yield (kg/ha)	1	64,103±31,991**	20,633±9,931**	-1,520±3,660	24,432±9,879**	90,299±8,209
	2	107,546±66,414**	14,363±23,802	-8,773±19,674	105,429±38,933**	185,253±19,976
	Combined	86,564±33,497**	-7,206±6,023	312±6,688	51,748±13,510**	129,611±9,030

+Study 1 included nine cultivars grown at three locations for five years, while study 2 included six cultivars grown at four locations for three years.

*,**Mean square significant at the .05 and .01 probability levels, respectively.

were greater than the second-order interaction. For yield, the second-order interaction in both studies was larger than either first-order interaction, although the cultivar x year interaction in the first study was almost equal in magnitude to the second-order interaction. The cultivar x location interaction component in both studies was not significant and estimates were small and negative.

Although cultivar x environment interactions were present for fancy size pods, extra large kernels and g/100 seeds, the interactions, although frequently significant, were relatively unimportant because of the much larger variation attributable to cultivars. However, for meat content and yield, the most economically important traits, the magnitudes of the interaction components in relation to the cultivar component were large, particularly in the second study.

Combining the two analyses provided estimates of variance components based on larger samples of cultivars, years and locations. The results from the combined analysis followed those from the first study rather closely, but with a few differences. Cultivar x year interactions for meat content and yield were significant in the first study. When both studies were combined, these interactions were not significant.

The large second-order interaction for yield agreed with previous reports for several crop species (5, 6, 7) including peanuts (3, 9). Thus the yield of peanuts in each individual experiment is unique and the environmental conditions differentiating the tests cannot be grouped according to years or locations.

The lack of a significant cultivar x location interaction for most traits, including yield, indicates that there would be no advantage gained from dividing the production area into subareas for breeding and testing purposes. These results are in agreement with those reported for cotton and tobacco studies conducted in North Carolina (4, 6). Similar conclusions can be made from the peanut data collected in Georgia (9) and Taiwan (3). The cultivars in both studies might be expected to show little cultivar x location interaction since the lines had all been selected for adaptation to North Carolina. Previously untested breeding materials might show a greater genotype x location interaction.

The presence of a large cultivar x location x year interaction for yield indicates that it is imperative to test peanut cultivars at a number of environments in North Carolina. In the combined study the lack of a significant cultivar x year interaction indicated that the relative performance of the cultivars averaged over locations was nearly the same in each of the years of testing. Thus the test locations in any one year must have represented the environments encountered during the other years of testing. Therefore, the evaluation of new materials can probably be accomplished by substituting locations for years in a testing program.

The predicted effects of different allocations of plots over years, locations and replicates on the theoretical standard deviation of the mean for the yield of a culti-

Table 3. Predicted standard deviations (kg/ha) of the mean yield of a cultivar tested over varying numbers of years, locations, and replicates.

Years	Locations	Replicates				
		2	3	4	5	6
1	1	331	297	278	266	258
	2	226	201	187	178	172
	3	178	157	145	137	132
	4	148	129	118	111	106
2	1	234	210	197	189	183
	2	160	142	133	126	122
	3	126	111	103	97	93
	4	105	91	84	79	75
3	1	192	172	161	154	150
	2	131	117	109	103	100
	3	103	91	84	80	76
	4	86	75	68	64	62

var is given in Table 3. Predictions were based on the variance component estimates from the combined analysis. The present testing program in North Carolina uses two locations and two years with three replicates in each of the four tests to evaluate peanut breeding lines for inclusion in regional testing programs. Such a program results in a theoretical standard deviation for a cultivar mean of 142 kg/ha (Table 3). The 12 plots now being used to evaluate a peanut line could be reallocated to one year, three locations with four replicates each and give a comparable estimate (145 kg/ha) of the relative performance of peanut cultivars at a considerable savings in time. Reallocation of the 12 plots to four locations with three replications each would lower the standard deviation to 129 kg/ha, resulting in more efficient evaluation of peanut cultivars. Similar results were obtained for meat content. The precision of meat content measurement is such that reallocation of the 12 plots to one year, three locations, and four replicates does not result in a significant loss of precision. Allocation of the plots to four locations with three replicates in one year would result in a slight, nonsignificant increase in precision.

The ingrained conservatism of plant breeders precludes the commercial release of a cultivar based on one year's testing. Nevertheless, these results may pertain to the evaluation of late generation breeding materials prior to their inclusion in extensive regional testing programs.

The data from these studies may be biased by the small sample of cultivars and the small number of locations in each study. However, since the estimates of variance components from the two independent studies were similar, greater confidence can be placed in the conclusion from these data.

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