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Genotype X Environment Interaction Among Peanut Lines in Oklahoma[1]

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ABSTRACT

Data from Oklahoma peanut (*Arachis hypogaea* L.) performance tests from 1969 through 1978 were used to estimate genotype X environment interaction variance components for pod yield, % TSMK, % SS, % OK, and gross return per unit area. The objectives of this study were to determine if it would be advantageous to select cultivars for specific regions, and to determine the most efficient combination of years, locations, and replications to use when evaluating peanut lines.

Evidence was obtained that genotypes perform consistently between irrigated and nonirrigated locations for the traits studied. The variance of the difference between two cultivars or lines was calculated for % TSMK, pod yield, and gross return using various combinations of years, locations, and replications. Results indicate that, when testing for gross return, the time presently allotted for testing could be reduced without sacrificing accuracy.

Key Words: *Arachis hypogaea* L., Cultivar evaluation, Variance components, Water-management systems, Groundnut, Pod yield, Gross return, Sound mature kernels, Sound split kernels, Other kernels.

In Oklahoma, peanuts (*Arachis hypogaea* L.) are grown under two distinctly different management systems, i.e., irrigated or dryland. They are also grown on many different soil types. Climatic conditions vary from location to location in any one year and from year to year at any single location. It would be helpful to know if varieties should be developed for different areas or water-management systems and what combination of years, locations, and replications are required for an optimum performance testing program.

Many genotype X environment interaction studies have been reported (e.g., 3, 4, 5, 6, 7, 8). In Georgia, Tai and Hammons (7) reported that, for peanut pod yield and seed size factors, the cultivar component significantly exceeded the first- and second-order interactions indicating that the cultivar effect would be consistently expressed regardless of environment. In a peanut study conducted in the Virginia-North Carolina area, Wynne and Isleib (8) concluded that there would be no advantage to subdividing the production area into subareas for breeding or testing purposes, and that by reallocating the number of plots presently used, cultivar evaluation could be performed in less time while maintaining approximately the same accuracy.

For the study reported herein, the genotype X environment interaction variance components were estimated for peanuts grown in Oklahoma. The objectives were to determine if it would be advantageous to select for cultivars with superior performance for specific regions or management systems, and to determine the most efficient combination of years, locations, and replications to use when evaluating peanut lines.

Materials and Methods

Peanut performance tests were conducted at Fort Cobb, Perkins, and Stratford, Okla., from 1969 through 1978. The soil types at each location are given in Table 1. From the performance tests that were conducted at those locations in those years, four data subsets were organized in an attempt to maximize the number of lines, years, and locations and are described in Table 2. Because of the large number of lines being tested each year, it is impractical to include all lines in one large test. Therefore, a number of performance tests are conducted each year with smaller numbers of lines per test. The data subsets analyzed herein were statistically valid because, within a subset, all the lines were tested in the same experiment for the locations and years listed. A randomized, complete-block experimental design was used in each test. The traits measured included pod yield, percent total sound mature kernels (% TSMK), percent sound split kernels (% SS), percent other kernels (% OK), and gross return calculated using 1978 prices. Each performance trial had a minimum of three replications for pod yield and two replications for the other traits. Plot size was two rows spaced 91.4 cm apart X 5.2 m long. The cultural practices followed were those recommended to commercial peanut growers in Oklahoma.

Table 1. Description of soils used in the peanut performance tests.

Location and water-management system	Year	Soil description
Fort Cobb-irrigated	1969-1978	Cobb fine sandy loam-a member of the fine-loamy, mixed, thermic Udic Haplustalfs
Fort Cobb-dryland	1969-1977	Meno loamy fine sand-a member of the loamy, mixed, thermic Aquic Arenic Haplustalfs
	1978	Meno fine sandy loam-a member of the loamy, mixed, thermic Aquic Arenic Haplustalfs
Perkins-dryland	1969-1978	Teller loam-a member of the fine-loamy, mixed, thermic Udic Arguistolls
Stratford-dryland	1969-1975	Stidham fine sandy loam-a member of the loamy, mixed, thermic Arenic Haplustalfs
	1976-1978	Dougherty loamy fine sand-a member of the loamy, mixed, thermic Arenic Haplustalfs

An unweighted means analysis of variance was employed for data subsets 1 and 2 because number of replications among years and locations was not consistent. Analyses for data subsets 3 and 4 were calculated based on data from individual plots.

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Table 2. Description of the data subsets analyzed herein.

Data Subset 1

6 Lines: 'Comet', 'Florunner', 'Spanhoma', 'Starr', 'Tamnut 74', 'Tifspan'

5 Years: 1972-1976

4 Locations: Ft. Cobb - irrigated
Ft. Cobb - dryland
Perkins - dryland
Stratford - dryland

Data Subset 2

8 Lines: Comet, 'Dixie Spanish', 'Spancross', Spanhoma, P.I. 248759, P.I. 268644, P.I. 268684, P-74 (an 'Argentine' seln.)

4 Years: 1969-1970, 1973-1974

3 Locations: Ft. Cobb - irrigated
Perkins - dryland
Stratford - dryland

Data Subset 3

14 Lines: 'Chico', Comet, Florunner, Spanhoma, Tamnut 74, EM-3, EM-9, EM-12, 0-11, 0-14, 0-19, 0-20, 0-21, 0-22, (EM-3 through 0-22 are breeding lines)

2 Years: 1977-1978

2 Locations: Ft. Cobb - irrigated
Stratford - dryland

Data Subset 4

7 Lines: 'Pearl', Ga. 61-42, P.I. 234416 sel., P-1446 and P-1447 (P.I. 162538 sels.), P-29 and P-1451 (Argentine sels.)

3 Years: 1971-1973

3 Locations: Ft. Cobb - irrigated
Perkins - dryland
Stratford - dryland

The procedures used to calculate variance components were similar to those described by Comstock and Moll (2). The effect of water-management system (W) was considered fixed. The effects of location within water-management system [L(W)], years (Y), and genotypes (G) were considered random. It was assumed that the variance components were the same for the four data subsets. Since there was never more than one irrigated location, it was necessary to assume that the variance components for genotype X location and genotype X year X location within the non-irrigated system were the same as those within the irrigated system. Such an assumption is typical of such analyses. It could only be imprecisely checked unless a very large number of locations were available. Expected mean squares are shown in Table 3. The mean squares for a particular source of variation do not have the same expectations in all data subsets because of different numbers of observations and because data subset three does not have all sources contained in the others. The effects of locations and waer-management systems are confounded in data subset three, however, these are not ignored as can be seen from the expected mean squares. The variance of a mean square is

$$\frac{2 \text{ x } (\text{expected mean square})^2.}{\text{degrees of freedom}}$$

Thus an iterative weighted least squares solution to the equations formed by equating mean squares to their expected values was obtained for the variance components. Any variance component estimate that was negative was eliminated (set to zero) and the estimation process was repeated. The variance components are listed below:

σ^2_G = Variance due to genetic differences among genotypes;
σ^2_{GY} = Variance due to interactions among genotypes and years;
σ^2_{GW} = Variance due to interactions among genotypes and water-management systems;
σ^2_{GYW} = Variance due to interactions among genotypes, years, and water-management systems;
$\sigma^2_{GL(W)}$ = Variance due to interactions among genotypes and locations within a water-management system;
$\sigma^2_{GYL(W)}$ = Variance due to interactions among genotypes, years, and locations within a water-management system; and
σ^2_e = Variance due to error.

The $\sigma^2_{GL(W)}$ was estimated only for dryland locations because there was only one irrigated location in each data subset. For statistical purposes it was assumed that the $\sigma^2_{GL(W)}$ for irrigated locations was equal to $\sigma^2_{GL(W)}$ for dryland locations. There is no evidence to support or refute this assumption, but it would seem logical to expect the $\sigma^2_{GL(W)}$ for dryland locations to be equal to or greater than the $\sigma^2_{GL(W)}$ for irrigated locations because the environmental variance caused by water stress is controlled at irrigated locations.

Table 3. Expected mean squares for data subsets 1, 2, and 4 (A) and for data subset 3 (B).

A. Source of variation	Expected mean square
G	$\sigma^2_e + r\sigma^2_{GYL(W)} + yr\sigma^2_{GL(W)} + ar\sigma^2_{GY} + ayr\sigma^2_G$
G X Y	$\sigma^2_e + r\sigma^2_{GYL(W)} + ar\sigma^2_{GY}$
G X W	$\sigma^2_e + r\sigma^2_{GYL(W)} + br\sigma^2_{GYW} + yr\sigma^2_{GL(W)} + byr\sigma^2_{GW}$
G X Y X W	$\sigma^2_e + r\sigma^2_{GYL(W)} + br\sigma^2_{GYW}$
G X L(W)	$\sigma^2_e + r\sigma^2_{GYL(W)} + yr\sigma^2_{GL(W)}$
G X Y X L(W)	$\sigma^2_e + r\sigma^2_{GYL(W)}$
Error	σ^2_e

B. Source of variation	Expected mean square
G	$\sigma^2_e + wr\sigma^2_{GY} + ywr\sigma^2_G$
G X Y	$\sigma^2_e + wr\sigma^2_{GY}$
G X W	$\sigma^2_e + r(\sigma^2_{GYL(W)} + \sigma^2_{GYW}) + yr\ (\sigma^2_{GL(W)} + \sigma^2_{GW})$
G X Y X W	$\sigma^2_e + r(\sigma^2_{GYL(W)} + \sigma^2_{GYW})$
Error	σ^2_e

r = no. replications, y = no. years,a = total no'. locations, b = no. dryland locations, and w = no. water-management systems

The variance components were converted to a percent of the total calculated variance. Those values were then used in the following equation to estimate the relative merits of a cultivar testing program as the number of years, locations, water-management systems, and replications were varied:

$$\text{Variance } [\bar{Y} \text{ genotype}_1 - \bar{Y} \text{ genotype}_2] = \sigma^2_{GY}/y + \sigma^2_{GW}/w + \sigma^2_{GL(W)}/l + \sigma^2_{GYW}/yw + \sigma^2_{GYL(W)}/yl + \sigma^2_e/ylr$$

where

w = No. water-management systems,
l = No. locations, and
r = No. of replications per year and location.

Results and Discussion

The interactions in which a plant breeder is most interested are the predictable ones. Allard and Bradshaw (1) have stated that if there is a large predictable interaction, a breeding program could develop cultivars adapted to those predictable environments. The predictable interactions in this study are σ^2_{GW} and $\sigma^2_{GL(W)}$.

Estimates for the variance components expressed as percentages are given in Table 4. The predictable interactions for all the traits are small relative to σ^2_G, indicating that the relative performance of genotypes is similar when grown using different water-management systems and also at different regions within a water-management system. Thus, there would be little possibility for selecting cultivars with superior performance for those traits to be grown in a specific region or for a specific water-management system.

Table 4. Estimated variance components expressed as percentages.

Variance components	% SS	% OK	% TSMK	Pod yield	Gross return
G	10.80	11.48	15.76	20.25	8.83
G X Y	10.07	14.62	8.71	8.21	5.75
G X W	0.00	1.58	6.61	0.70	0.13
G X Y X W	0.00	0.00	0.00	6.29	9.56
G X L(W)	2.58	0.00	5.45	0.39	4.91
G X Y X L(W)	19.96	12.80	18.14	7.12	0.00
Error	56.59	59.52	45.33	57.04	70.82

Table 5 demonstrates that, for % TSMK, pod yield, and gross return, at least two locations must be used in the testing program to obtain variances comparable to those obtained with the present testing system of three years, three locations, and two replications. When testing for gross return, the performance testing program could be changed from the present testing system to two years, three locations, and five replications while maintaining approximately the same level of accuracy and simultaneously reducing by one year the time necessary to evaluate genotypes. This suggesiton would increase the number of plots per genotype per year from 6 to 15 and increase the total number of test plots required for evaluation from 18 to 30. Thus, the advantage of reducing the time necessary to evaluate genotypes must be compared with the disadvantage of an increase in the cost of evaluation.

Table 5. Estimated variances [$\bar{Y}$ genotype$_1$ - $\bar{Y}$ genotype$_2$] for % TSMK, pod yield, and gross return as years, locations, and replications are changed in a peanut performance testing program.†

Trait	Years	Locations	Replications no. 1	2	3	4	5	6
% TSMK	1	1	84.2	61.6	54.0	50.2	48.0	46.5
		2	46.5	35.1	31.4	29.5	28.3	27.6
		3	35.0	27.4	24.9	23.7	22.9	22.4
		4	29.2	23.6	21.7	20.7	20.2	19.6
		5	25.8	21.3	19.8	19.0	18.5	18.2
		6	23.5	19.7	18.5	17.8	17.5	17.2
	2	1	46.2	36.8	33.0	31.2	30.0	29.3
		2	26.3	20.6	18.7	17.8	17.2	16.8
		3	20.1	16.3	15.0	14.4	14.0	13.8
		4	17.0	14.1	13.2	12.7	12.4	12.2
		5	15.1	12.6	12.1	11.7	11.6	11.4
		6	13.9	12.0	11.3	11.0	10.8	10.7
	3	1	36.1	28.6	26.0	24.8	24.0	23.5
		2	19.5	15.7	14.5	13.8	13.5	13.2
		3	15.1	12.6	11.7	11.3	11.0	10.9
		4	12.5	11.0	10.3	10.0	9.8	9.7
		5	11.6	10.0	9.5	9.2	9.1	9.0
		6	10.6	9.4	8.9	8.8	8.6	8.5

Trait	Years	Locations	Replications 1	2	3	4	5	6
POD YIELD	1	1	79.8	51.2	41.7	37.0	34.1	32.2
		2	44.0	29.7	25.0	22.8	21.2	20.2
		3	33.2	23.7	20.5	19.0	18.0	17.4
		4	27.8	20.7	18.3	17.1	16.4	16.0
		5	24.6	18.9	17.0	16.1	15.5	15.1
		6	22.5	17.7	16.1	15.3	14.9	14.5
	2	1	40.4	26.2	21.4	19.0	17.6	16.7
		2	22.3	15.1	12.8	11.6	10.9	10.4
		3	16.9	12.1	10.5	9.7	9.2	8.9
		4	14.1	10.6	9.4	8.8	8.4	8.2
		5	12.5	9.7	8.7	8.2	8.0	7.8
		6	11.4	9.1	8.3	7.9	7.6	7.6
	3	1	27.3	17.6	14.6	13.1	12.1	11.5
		2	15.0	10.3	8.7	7.9	7.4	7.1
		3	11.4	8.2	7.2	6.6	6.3	6.1
		4	9.6	7.2	6.4	6.0	5.8	5.6
		5	8.5	6.6	6.0	5.6	5.4	5.3
		6	7.8	6.2	5.7	5.4	5.2	5.1

Trait	Years	Locations	Replications 1	2	3	4	5	6
GROSS RETURN	1	1	91.2	55.8	44.0	38.1	34.5	32.2
		2	48.5	30.8	24.9	21.9	20.1	19.0
		3	35.8	24.0	20.1	18.1	17.0	16.2
		4	29.5	20.7	17.7	16.2	15.4	14.8
		5	25.7	18.7	16.3	15.1	14.4	13.9
		6	23.2	17.3	15.3	14.4	13.8	13.4
	2	1	48.1	30.4	24.5	21.5	19.8	18.6
		2	25.5	16.6	13.7	12.2	11.3	10.7
		3	18.8	12.9	10.9	9.9	9.3	8.8
		4	15.4	11.0	9.5	8.6	8.3	8.0
		5	13.4	9.9	8.7	8.1	7.7	7.5
		6	12.1	9.1	8.1	7.6	7.3	7.1
	3	1	33.8	21.9	18.0	16.0	14.9	14.1
		2	17.8	11.9	10.0	9.0	8.4	8.0
		3	13.1	9.1	7.8	7.2	6.8	6.5
		4	10.7	7.8	6.8	6.3	6.0	5.8
		5	9.3	6.9	6.1	5.7	5.5	5.3
		6	8.3	6.6	5.7	5.4	5.2	5.0

† When locations are two or more, it is assumed that two water-management systems are involved:

▒ represents the present testing system;

▨ indicates that variance is smaller than the variance for the present testing system; and

▩ indicates the variance is not more than 10% greater than the present testing system

Table 5 indicates that the testing program becomes more accurate as years and locations increase. This was expected because as years and locations increase so does the total number of test plots. To clarify the importance of years and locations in a testing program, Fig. 1 was constructed holding the number of plots constant at 18. Fig. 1 indicates that both the number of years and locations in a

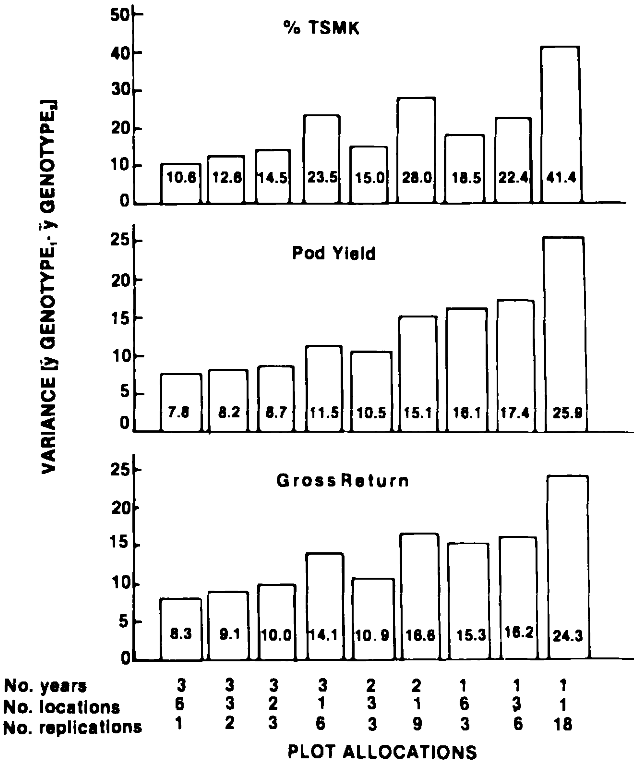

Fig. 1. Effect of number of years, locations and replications on the variance [$\bar{Y}$ genotype$_1$ - $\bar{Y}$ genotype$_2$] of % TSMK, pod yield, and gross return when number of plots is held constant at 18. When locations are two or more, it is assumed that two water-management systems are involved.

testing program have an effect on the accuracy of estimates for % TSMK, pod yield, and gross return.

For all three traits, a large increase in variance is obtained when only one location is used in the testing program. It was unclear whether this increase in variance was caused by reduction in the number of locations or by reduction from two to one water-management system. To clarify this point, Fig. 2 was constructed. This demonstrates that variance increases when the number of water-management systems is reduced from two to one. Thus, it is important to include at least one irrigated and one dryland location in the testing program.

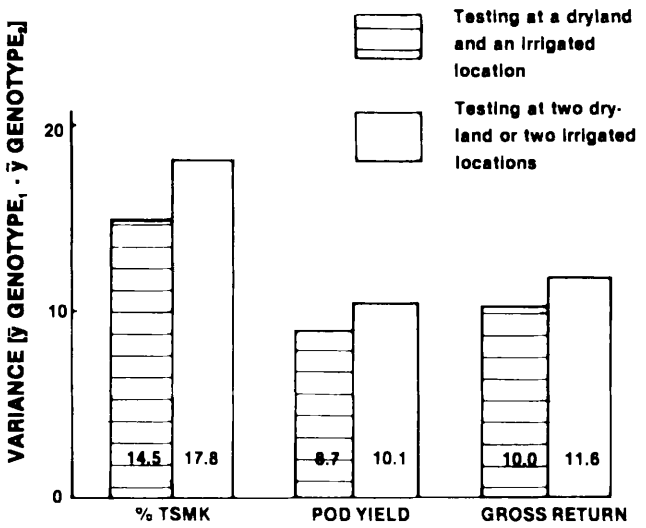

Fig. 2. Effect of number of water-management systems on the variance [$\bar{Y}$ genotype$_1$ - $\bar{Y}$ genotype$_2$] of % TSMK, pod yield, and gross return when a testing program of 3 years, 2 locations, and 3 replications is used.

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