Estimates of Combining Ability and Heterosis among Peanut Cultivars[1]

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ABSTRACT

Six parental peanut *(Arachis hypogaea* L.) cultivars, representing a wide range in genetic diversity, and 15 F_1 diallel hybrids were field evaluated for combining ability and heterosis. The parental cultivars included two spanish, two runner, and two virginia market types. Estimates of general and specific combining abilities were highly significant for all ten characters studied: partial biomass, harvest index, total pod weight, total pod number, total seed weight, total seed number, seed per pod, weight per seed, weight per pod, and meat content. Cultivars varied in relative general combining ability for different characteristics. Crosses of spanish x runner type parents showed the greatest specific combining ability and heterosis for partial biomass, total pod weight, total pod number, total seed weight, and total seed number. Small or negative heterosis was found for the other traits. Highly significant positive phenotypic correlations were detected among several of these ten traits. The largest significant correlations were between total pod vs seed weight, total pod vs seed number, and weight per pod vs seed. These data indicate the importance of parental evaluation for improving peanut yield and related characters.

Key Words: *Arachis hypogaea,* L., groundnut, general combining ability, specific combining ability, phenotypic correlations.

Traditionally in the U.S., there has been four peanut *(Arachis hypogaea* L.) market types: valencia, spanish, runner, and virginia. Each type imposes standard limitations in cultivar development; however, all four types are cross-compatible and represent potential sources for genetic variability. Spanish and valencia types represent *A. hypogaea* subspecies *fastigiata* var. *vulgaris* and *fastigiata,* respectively, whereas, runner and virginia types represent the other subspecies *hypogaea* var. *hypogaea* (6).

Peanut breeding programs throughout the world have been directing more and more emphasis towards hybridization followed by selection for increasing yield. The success of this type of breeding approach depends upon the proper choice of parents. Estimates of heterosis, general combining ability (GCA), and specific combining ability (SCA) may be very helpful in such parental selection. Unfortunately, simultaneous evaluation of only a limited number of genotypes can feasibly be assessed in peanut because of time and labor restrictions involved in hand-crossing and subsequent evaluation of hybrid progenies. Therefore, the breeder is constantly needing to determine the potential of additional germplasm as parents.

Stokes and Hull (15) studied F_1 hybrids from 11 different crosses and concluded that there was little hybrid vigor in peanut. Since then, significant heterosis has been reported for yield and related characters (1,3,7,8, 11,14,17,18). Other investigations have shown that GCA and SCA were both significant for yield and/or its components in peanut and that GCA was usually of greater magnitude than SCA (2,4,9,11,12,18).

These earlier studies suggest the importance of additive (GCA) and nonadditive (SCA and heterosis) genetic effects in evaluating hybrid yield performance among parental peanut lines. Thus, our primary objective was to identify superior parents and cross combinations from estimates of heterosis and combining ability among F_1 hybrids for ten yield-related traits.

Materials and Methods

Six parental peanut cultivars were selected to represent a range in genetic diversity, and were crossed in a half-diallel mating design. The cultivars included Dixie Spanish (DSH), Spancross (SCS), Southeastern Runner 56-15 (SER), Tifrun (TRN), Virginia Runner G26 (VRG), and Georgia 119-20 (G119) which represent two spanish, runner, and virginia market types, respectively.

The 15 F_1 hybrids and six parents were planted on May 18, 1984, at the Agronomy Farm, Coastal Plain Experiment Station, Tifton, Georgia. These 21 entries were replicated ten times in a randomized complete block design with borders. Individually pregerminated seeds were equidistantly spaced 1.8 m apart. Standard cultural practices were used throughout the growing season. Three harvesting dates were used according to the visual maturity of each entry.

Single plant measurements were made on the following ten characters: partial biomass (excluding roots), harvest index, total pod weight, total pod number, total seed weight, total seed number, seed per pod, weight per seed, weight per pod, and meat content (total seed weight ÷ total pod weight).

Data were analyzed using a DIALL computer program which performs general least squares analysis from diallel crosses (13). Combining ability estimates were determined according to Method II, Model I given by Griffing (5). GCA and SCA effects were t-tested for deviations from zero, and least significant differences (LSD) were used to compare estimates within GCA and SCA, respectively. Estimates of heterosis were obtained from calculated midparent values for each cross, and values are reported as a percent of the midparental means. Correlations among the ten characters measured in this study were computed using the means of the genotypes.

Results and Discussion

Highly significant differences (P less than 0.01) were observed among the means of 21 entries for the ten characteristics studied. Likewise, highly significant differences were found for GCA and SCA among each of the ten characters (Table 1). These results agree with those reported by Hammons (6) and Wynne and Coffelt (16).

Table 1. Mean squares from the combining ability analyses of variance and coefficient of variation among 21 genotypes for ten peanut characters.

| Character | Mean Square | | | CV |
	GCA	SCA	Error	(%)
Harvest index	0.2508**	0.0096**	0.0028	11.34
Partial biomass	1061538.04**	1236680.20**	110270.01	24.27
Total pod weight	612985.13**	211533.26**	22098.33	23.30
Total pod number	265824.83**	122602.93**	9810.33	19.93
Total seed weight	322474.54**	109754.67**	11406.45	22.77
Total seed number	828511.10**	361136.46**	34165.26	21.61
No. of seed/pod	0.1359**	0.0325**	0.0125	6.50
Weight/seed	0.8304**	0.0153**	0.0027	9.18
Weight/pod	4.1569**	0.1257**	0.0177	9.93
Meat content	0.0169**	0.0030**	0.0009	4.13

** Significant at the 0.01 probability level.

The relative GCA of the six parental cultivars varied for the different characters (Table 2). Spancross had a larger GCA effect for the number of seed per pod than Southeastern Runner 56-15, Virginia Runner G26, Georgia 119-20, or Dixie Spanish, while Southeastern Runner 56-15 had the highest GCA effect for total pod number and total seed number. For harvest index and meat content, Tifrun had the highest GCA effect, although not significantly different from Southeastern Runner 56-15 or Spancross for meat content. Virginia Runner G26 exhibited the largest GCA effects for partial biomass, total pod weight, and total seed weight, but Virginia Runner

G26 was not significantly different from Southeastern Runner 56-15 or Tifrun for total seed weight. Georgia 119-20 had the largest GCA effect for weight per seed and weight per pod.

Parents having the highest GCA frequently had the highest mean value for that character (Table 3). However, this does not imply that high mean performance is a general, reliable indicator of good combining parents. It also was interesting to note that parents (Virginia Runner G26, Tifrun, and Southeastern Runner 56-15) which had high GCA effect for total pod and seed weight (yield) possessed runner growth habits.

Table 3. Six parental peanut means for ten yield-related characters.

| Characters | Parents | | | | | |
| | Spanish | | Runner | | Virginia | |
	DSH	SCS	SER	TRN	VRG	G119
Harvest Index	0.34 c*	0.33 c	0.53 a	0.54 a	0.52 a	0.45 b
Partial Biomass (g)	943.6 c	628.2 d	1025.5 bc	936.7 c	1661.7 a	1359.8 a
Total Pod Weight (g)	315.5 c	208.8 c	538.5 b	496.8 b	813.8 a	617.5 b
Total Pod Number	304.1 d	287.1 d	587.9 a	406.3 c	497.2 b	310.6 d
Total Seed Weight (g)	222.5 c	159.2 c	410.2 b	377.0 b	561.0 a	433.6 b
Total Seed Number	552.9 c	533.7 c	1007.9 a	710.5 b	798.7 b	527.5 c
Number of Seed/Pod	1.82 ab	1.86 a	1.72 bc	1.73 bc	1.62 d	1.69 cd
Weight/Seed (g)	0.40 d	0.30 e	0.40 d	0.55 c	0.71 b	0.82 a
Weight/Pod (g)	1.05 d	0.73 f	0.91 e	1.22 c	1.69 b	1.98 a
Meat Content (%)	70.11 b	75.78 a	76.28 a	76.18 a	68.13 b	70.19 b

* Means within the same row followed by the same letter do not differ significantly at the 0.05 probability level as determined by Waller-Duncan Multiple Range Test.

In general, crosses within botanical types gave negative or low SCA effects (Table 4 and 5). The largest SCA effect for harvest index was found in the cross, DSH x TRN, but at the P = 0.05 level it was only better than SCS x G119, VRG x G119, and the other crosses that involved Dixie Spanish (Table 4).

The cross, DSH x SER, exhibited the highest SCA effect for partial biomass, total pod weight, total pod number, total seed weight, and total seed number (Table 4 and 5). However, DSH x SER was not significantly

Table 2. Estimates of general combining ability (GCA) effects for ten characters of six parental peanut cultivars.

| Parents | Harvest index | Partial biomass | Total pod weight | Total pod number | Total seed weight | Total seed number | Seed per pod | Weight per seed | Weight per pod | Meat content |
		(g)	(g)		(g)		(no.)	(g)	(g)	(%)
Dixie Spanish	-0.0788**	47.70	-81.35**	-9.33	-64.92**	-12.45	0.0154	-0.0855**	-0.1727**	-0.0112**
Spancross	-0.0565**	-141.46**	-117.47**	-12.38	-83.16**	1.54	0.0539**	-0.1227**	-0.2675**	0.0085**
Southeastern Runner 56-15	0.0402**	14.72	44.98**	103.02**	44.40**	172.67**	-0.0063	-0.0517**	-0.1479**	0.0154**
Tifrun	0.0648**	-83.52*	37.52*	-1.02	38.48**	19.49	0.0349**	0.0311**	0.0673**	0.0165**
Virginia Runner G26	0.0298**	158.81**	112.29**	9.53	69.25**	-5.96	-0.0421**	0.0890**	0.2086**	-0.0162**
Georgia 119-20	0.0006	3.75	4.03	-89.81**	-4.06	-175.29**	-0.0558**	0.1398**	0.3122**	-0.0130**
LSD ($\hat{g}i - \hat{g}j$)										
P < 0.05	0.0165	102.91	46.07	30.69	33.10	57.28	0.0347	0.0161	0.0412	0.0092
P < 0.01	0.0216	135.25	60.55	40.34	43.50	75.28	0.0456	0.0211	0.0541	0.0121

*, ** Significantly different from zero at the 0.05 and 0.01 probability levels, respectively.

Table 4. Specific combining ability estimates for harvest index, partial biomass, total pod weight, total pod number, and total seed weight among 15 F₁ peanut cross combinations.

Parent	Character	SCS	SER	Parent TRN	VRG	G119
DSH	Harvest index	-0.0096	-0.0478**	0.0416**	-0.0286	-0.0088
	Partial biomass(g)	-210.69*	734.52**	277.77**	397.53**	131.61
	Total pod weight(g)	-101.72*	228.63**	190.29**	89.02*	-76.12
	Total pod number	-37.69	187.91**	111.24**	107.49**	-16.07
	Total seed weight(g)	-62.24*	151.09**	135.02**	63.74*	-49.64
SCS	Harvest index		0.0111	0.0378*	0.0182	-0.0047
	Partial biomass(g)		452.08**	278.03**	108.19	314.05**
	Total pod weight(g)		192.75**	153.22**	48.04	106.70*
	Total pod number		154.36**	116.38**	79.74**	61.88*
	Total seed weight(g)		130.70**	121.65**	38.38	63.09*
SER	Harvest index			0.0161	0.0359*	0.0303*
	Partial biomass(g)			-60.56	-286.89**	-67.33
	Total pod weight(g)			8.47	-70.01	29.55
	Total pod number			-33.31	-79.45**	5.18
	Total seed weight(g)			6.19	-23.08	34.93
TRN	Harvest index				0.0040	0.0182
	Partial biomass(g)				36.96	24.22
	Total pod weight(g)				44.25	46.72
	Total pod number				-22.62	10.02
	Total seed weight(g)				43.74	35.95
VRN	Harvest index					-0.0056
	Partial biomass(g)					-80.02
	Total pod weight(g)					-39.26
	Total pod number					-43.03
	Total seed weight(g)					-25.12

	LSD($\hat{S}_{ij}-\hat{S}_{ik}$)		LSD ($\hat{S}_{ij}-\hat{S}_{kl}$)	
	P<0.05	P<0.01	P<0.05	P<0.01
Harvest index	0.0433	0.0569	0.0402	0.0528
Partial biomass(g)	272.26	357.83	252.08	331.30
Total pod weight(g)	121.89	160.20	112.84	148.30
Total pod number	81.20	106.72	75.19	98.82
Total seed weight(g)	87.57	115.10	81.07	106.54

*, ** Significantly different from zero at the 0.05 and 0.01 probability levels, respectively.

Table 5. Specific combining ability estimates for total seed number, number of seed per pod, weight per seed, weight per pod, and meat content among 15 F₁ peanut cross combinations.

Parent	Character	SCS	SER	Parent TRN	VRG	G119
DSH	Total seed number	-48.48	332.10**	192.87**	147.62**	-60.74
	No. of seed/pod	0.0342	0.0013	-0.0115	-0.0674*	-0.0985**
	Weight/seed(g)	-0.0232	0.0207	0.0328*	-0.0168	-0.0412**
	Weight/pod(g)	-0.0789*	0.0813*	0.0888*	-0.0821*	-0.1929**
	Meat content(%)	0.0292**	-0.0201*	-0.0011	-0.0004	0.0161
SCS	Total seed number		254.31**	230.29**	156.23**	65.37
	No. of seed/pod		-0.0370	0.0293	0.0131	-0.0960**
	Weight/seed(g)		0.0509**	0.0227	-0.0299*	0.0161
	Weight/pod(g)		0.0326**	0.0732*	-0.0505	0.0162
	Meat content(%)		-0.0192*	0.0069	-0.0043	-0.0236**
SER	Total seed number			-62.34	-142.89**	12.65
	No. of seed/pod			-0.0020	-0.0077	0.0196
	Weight/seed(g)			0.0244	0.0307*	-0.0219
	Weight/pod(g)			0.0662	-0.0092	-0.0733*
	Meat content(%)			-0.0051	-0.0355**	-0.0153
TRN	Total seed number				3.18	11.92
	No. of seed/pod				0.0927**	0.0097
	Weight/seed(g)				0.0333*	0.0369*
	Weight/pod(g)				0.1463**	0.0729
	Meat content(%)				0.0089	0.0032
VRG	Total seed number					-66.43
	No. of seed/pod					-0.0030
	Weight/seed(g)					0.0468**
	Weight/pod(g)					0.0743*
	Meat content(%)					0.0035

	LSD ($\hat{S}_{ij}-\hat{S}_{ik}$)		LSD ($\hat{S}_{ij}-\hat{S}_{kl}$)	
	P<0.05	P<0.01	P<0.05	P<0.01
Total seed number	151.55	199.18	140.32	184.42
No. of seed/pod	0.0917	0.1206	0.0849	0.1115
Weight/seed(g)	0.0425	0.0559	0.0394	0.0518
Weight/pod(g)	0.1092	0.1435	0.1009	0.1327
Meat content(%)	0.0247	0.0325	0.0227	0.0299

*,** Significantly different from zero at the 0.05 and 0.01 probability levels, respectively.

different from the other crosses between spanish and runner type cultivars for total pod weight, total pod number, total seed weight, and total seed number, or DSH x VRG for total pod number and total seed weight.

For number of seed per pod, the cross that performed best for SCA was TRN x VRG, but it was only significantly

different from DSH x SER, DSH x TRN, DSH x VRG, DSH x G119, SCS x SER, SCS x G119, SER x TRN, SER x VRG, and VRG x G119. Crosses with the highest SCA for weight per seed and weight per pod were SCS x SER and TRN x VRG, respectively. However, SCS x SER and TRN x VRG was only significantly different from DSH x SCS, DSH x VRG, DSH x G119, SCS x VRG, and SER x G119 for weight per seed or weight per pod, whereas TRN x VRG also differed from SCS x G119, SCS x SER, and SER x VRG for weight per pod.

More than one-half of the crosses showed negative SCA for meat content (Table 5). The highest SCA was exhibited by the cross, DSH x SCS, but it did not differ significantly from DSH x G119, SCS x TRN, or TRN x VRG.

Crosses exhibiting the most heterosis generally involved parents from different botanical types (Table 6). Crosses between spanish and runner parental lines showed approximately 100% heterosis for partial biomass, total pod weight, and total seed weight. Positive heterosis over the midparent was more common than negative heterosis for most of the characters studied, except number of seed per pod. The highest heterosis was found with the following characters: partial biomass, total pod weight, total pod number, total seed weight, and total seed number. Heterosis was not as high for harvest index (total pod weight ÷ partial biomass) as compared to total pod weight or partial biomass, respectively. Lesser amounts of heterosis were also observed for weight per seed and weight per pod.

Average heterosis values for number of seed per pod in crosses among types were found to be negative (Table 6). In the case of meat content, very little or negligible heterosis was observed. Layrisse et al. (10) also noted more negative than positive heterosis in the F₂ generation for meat content from the diallel cross of ten peanut lines, two from each of five centers of diversity in South America.

Highly significant positive phenotypic coefficients of correlation were found among eight of the ten characteristics, excluding seed per pod and meat content (Table 7). Total pod weight vs seed weight, total pod number vs seed number, and weight per seed vs pod exhibited the strongest correlations (r = 0.99). These associations might be expected because of the similarities between these particular seed and pod traits.

Total pod weight was also found to be highly correlated with harvest index, partial biomass, total pod number, total seed number, weight per seed, and weight per pod. Likewise, total seed weight was also highly correlated with harvest index, partial biomass, total pod number, and total seed number. Total pod and seed number were also highly correlated with partial biomass.

Significant positive but smaller correlations were detected between weight per seed and pod vs harvest index and total seed weight, while significant negative correlations were observed with seed per pod. Meat content was positively correlated with seed per pod and negatively correlated with weight per pod.

Among the six cultivars studied in this one environment, Virginia Runner G26, Southeastern Runner 56-15, and Tifrun exhibited the highest GCA, and cross combi-

Table 6. Percent heterosis from midparental means for ten characteristics of 15 F₁ crosses among and within botanical types of six peanut cultivars.

Cross	Harvest index	Partial biomass	Total pod weight	Total pod number	Total seed weight	Total seed number	No. seed /pod	Weight/ seed	Weight/ pod	Meat content
					Within type					
DSH X SCS	- 3	37	31	49	37	47	- 1	- 6	-12	4
SER X TRN	11	28	42	14	42	15	1	19	21	0
SER X VRG	10	- 4	7	- 2	16	- 2	2	13	5	7
SER X G119	10	12	25	15	30	13	- 2	2	- 3	3
TRN X VRG	7	17	26	7	33	16	8	14	19	3
TRN X G119	11	16	31	17	34	16	0	4	10	1
VRG X G119	2	- 1	- 1	- 7	3	8	- 2	10	4	-3
Mean	6.9	15.0	23.0	13.3	27.9	13.9	0.9	8.0	6.3	2.1
					Among types					
DSH X SER	-12	121	96	76	90	73	- 2	10	8	-2
DSH X TRN	13	73	94	69	93	68	- 1	13	14	1
DSH X VRG	- 8	55	33	51	38	46	- 6	- 1	- 8	2
DSH X G119	- 4	13	5	25	7	13	-10	- 6	-13	4
SCS X SER	8	106	104	70	98	67	- 3	25	25	-3
SCS X TRN	19	83	103	74	105	79	3	17	21	1
SCS X VRG	9	35	32	47	38	52	0	- 1	- 1	1
SCS X G119	4	57	54	53	51	42	- 9	6	1	-3
Mean	3.6	67.8	65.1	58.7	65.0	55.0	- 3.5	7.9	5.9	0.1

Table 7. Phenotypic correlation coefficients between ten characteristics of 21 peanut genotypes (6 parents + 15 F₁ hybrids).

Character	Partial biomass	Total pod wt.	Total pod no.	Total seed wt.	Total seed no.	No. seed per pod	Wt. per seed	Wt. per pod	Meat content
Harvest index	0.05	0.62**	0.23	0.68**	0.21	-0.15	0.55**	0.51*	0.34
Partial biomass		0.81**	0.70**	0.76**	0.64**	-0.41	0.27	0.29	-0.45
Total pod wt.			0.65**	0.99**	0.60**	-0.39	-0.56**	0.55**	-0.18
Total pod no.				0.68**	0.99**	-0.03	-0.23	-0.25	0.16
Total seed wt.					0.63**	-0.32	0.52*	0.51*	-0.05
Total seed no.						0.12	-0.30	-0.30	0.23
No. seed per pod							-0.57**	-0.49*	0.48*
Wt. per seed								0.99**	-0.37
Wt. per pod									-0.44**

*,** Significant at the 0.05 and 0.01 probability levels, respectively.

nations between spanish and runner market types showed the largest SCA for many yield components. However, none of these parents were superior in GCA for all ten characters evaluated. Thus, our findings suggest the continuing need for careful selection of parents for specific traits in the hybridization approach to peanut breeding.

Acknowledgments

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