

## ESTIMATION OF GENETIC EFFECTS AND HERITABILITY FOR EARLY MATURITY AND AGRONOMIC TRAITS IN PEANUT (*ARACHIS HYPOGAEA* L.)

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### Abstract

Studies were carried out to determine the inheritance and heritability of early maturity and yield traits where 2 high yielding virginia types (No. 334 and 'NC 9') were crossed with an early maturing spanish type (ICGSE-4) of peanut (*Arachis hypogaea* L.). A field trial with eight generations per cross ( $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_{11}$ ,  $BC_{12}$ ,  $BC_{11}S$ ,  $BC_{12}S$ ) was conducted at two locations in North Carolina during 1989. Analysis of generation means indicated that additive genetic effects were important for yield per plant, maturity index and seed weight in both crosses. Dominance effects were also important for yield per plant, maturity index, seed number and shelling percentage in cross 1 but only for maturity index in cross 2. Epistasis was not important for the desired traits in either population. Significant additive effects suggest that effective selection for early maturity, seed weight and yield is possible. Selection for seed weight could be accomplished in the  $F_2$  generation in both crosses. Selection for early maturity would be more effective in later generations. Narrow sense heritability ( $h^2$ ) was estimated using variance components in  $F_2$  generation and two backcrosses. Narrow sense heritability estimates were fairly high for seed number (0.83) and pod length (0.43) in cross 1 and for all the traits except yield/plant in cross 2. The results suggested that selection for seed number, pod length and seed weight is possible in early segregating generations in both the crosses while for early maturity it is possible in cross 2 only. For yield selection would be more effective in later generations. Correlations of maturity with seed number and shelling percentage were positive and highly significant in both the crosses. Maturity was negatively correlated with pod length and seed weight in cross 2. Positive and highly significant correlations for yield per plant with seed number, seed weight and shelling percentage indicated that selection based on any of these traits could indirectly increase yield.

### Introduction

Early maturing and high yielding cultivars of peanut (*Arachis hypogaea* L.) are desired for many peanut growing countries including Pakistan and North Carolina. To combine different quantitative traits it is important to understand the type of gene action involved in the inheritance of the desired traits in order to choose the most effective and efficient breeding procedure. Wynne & Gregory (1981) stated that improving traits in peanuts require sufficient variability, an understanding of genetic control, techniques for measuring desired traits, and a breeding strategy for effective use of variability. Several genetic models have been proposed to estimate the type of gene action. Most of these models were developed to estimate the relative importance of additive and dominance gene effects (Comstock & Robinson, 1948; Mather, 1949; & Jinks, 1954).

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Epistatic gene effects were assumed to be negligible. Since that time several studies have shown the importance of epistasis for quantitative traits in plants like soybean (Brim & Cockerham, 1961) and corn (Gamble, 1962).

Epistatic gene action for pod yield, number of pods per plant and plant dry weight has also been reported in peanuts by Sandhu & Khera, (1976) and Isleib *et al.*, 1978. Isleib & Wynne (1983) partitioned the heterotic responses and indicated that dominance was more important for pod length, pod yield and seed yield, whereas epistasis was important for pod number, seed number and meat content. Sanun (1988) indicated that additive effects, dominance, and epistasis were all important for agronomic traits and leafspot resistance in peanut. Significant additive x dominance interaction has been shown for maturity in six and five parameter models in a cross of spanish and virginia type peanuts (Rachmeler, 1988). He further reported high heritability for fruit length, early maturity and fatty acid composition in Virginia x Virginia cross. Mohammed *et al.*, (1978) indicated that only additive effects were significant for maturity in peanuts. Narrow sense heritability estimates for maturity, fruit size and yield were 0.35, 0.27, 0.21, respectively. Genotypic correlation was positive and significant between maturity and yield. Coffelt & Hammons (1974) reported high broad-sense heritability estimates (0.71-0.90) for 100 seed weight, pod length, pod breadth and pod length-breadth ratio. Abraham (1990) also reported positively significant correlations between kernel yield and pods/plant, kernels/plant, shelling %age and 100 kernel wt. Ali & Wynne (1994) and Ali *et al.*, (1998) reported fairly high heritability estimates for seed weight, maturity index and pod yield in Virginia x Spanish crosses of peanut. They further indicated positive and significant correlations between maturity and shelling percentage, pod length and seed weight. Few studies have been performed to determine the genetic control for early maturity. The present study was conducted to estimate the genetic variance components and heritability for early maturity and agronomic traits in two crosses of peanut (*Arachis hypogaea* L.).

## Materials and Methods

Two crosses were made to study the inheritance of early maturity and agronomic traits. Two high yielding virginia type (*A. hypogaea* ssp. *hypogaea* var. *hypogaea*) parents, No. 334 and NC 9 were crossed with ICGSE-4, an early spanish line (*A. hypogaea* ssp. *fastigiata* Waldron var. *vulgaris* Harz) for a source of early maturity. F<sub>1</sub> plants of each cross were grown in the greenhouse to produce F<sub>2</sub> seeds. F<sub>1</sub> plants were also backcrossed with female and male parents to generate two (BC<sub>11</sub>) and two (BC<sub>12</sub>) generations, respectively. Five plants each of BC<sub>11</sub> and BC<sub>12</sub> were selfed to generate BC<sub>11</sub>S and BC<sub>12</sub>S, respectively. The following eight generations were evaluated in a field trial in 1989.

IDENTITY	GENERATION	IDENTITY
Cross 1		Cross 2
No. 334	P <sub>1</sub>	NC 9
ICGSE-4	P <sub>2</sub>	ICGSE-4
No. 334 X ICGSE-4	F <sub>1</sub> <sup>1</sup>	NC 9 X ICGSE-4
(No. 334 X ICGSE-4) selfed	F <sub>2</sub> <sup>1</sup>	(NC 9 X ICGSE-4) selfed
(No. 334 X ICGSE-4) X No. 334	BC <sub>11</sub>	(NC 9 X ICGSE-4) X NC 9
(No. 334 X ICGSE-4) X ICGSE-4	BC <sub>12</sub> <sup>11</sup>	(NC 9 X ICGSE-4) X ICGSE-4
[(No. 334 X ICGSE-4) X No. 334] selfed	BC <sub>11</sub> <sup>12</sup> S	[(NC 9 X ICGSE-4) X NC 9] selfed
[(No. 334 X ICGSE-4) X ICGSE-4] selfed	BC <sub>12</sub> <sup>12</sup> S	[(NC 9 X ICGSE-4) X ICGSE-4] selfed

The 16 entries were planted at the Peanut Belt Research Station, Lewiston, North Carolina (NC), and the Central Crops Research Station, Clayton, NC, USA, respectively. A randomized complete block design with four replications was used at each location. Plot size varied by generation. Each plot was a single five-plant row for the P<sub>1</sub>, P<sub>2</sub> and F<sub>1</sub> generations, two five-plant rows for the BC<sub>11</sub>, BC<sub>12</sub>, BC<sub>11</sub>S and BC<sub>12</sub>S, and three five-plant rows for F<sub>2</sub> generations. Standard cultural practices were followed during the growing season. Individual plants were harvested by hand 125 days after planting. Pods were picked from each plant separately and dried in the dryer for one week. The traits measured were: yield per plant (g), length of 20 pods (cm), weight of 50 pods (g), number of seeds in 50 pods, weight of seeds in 50 pods and number of pods in each of five maturity classes (MC) based upon inner hull color ranging from white to black (white = MC1, yellow = MC2, light brown = MC3, dark brown = MC4, and black = MC5).

A sample of 50 pods were shelled and rated for maturity. From the recorded data the following variables were calculated.

$$a) \text{ Seed weight (g/100 seeds)} = \frac{\text{weight of seeds in 50 pods}}{\text{number of seeds in 50 pods}} \times 100$$

$$b) \text{ Shelling percentage} = \frac{\text{weight of seeds in 50 pods}}{\text{weight of 50 pods}} \times 100$$

$$c) \text{ Maturity index} = (MC1*1)+(MC2*2)+(MC3*3)+(MC4*4)+(MC5*5)$$

For maturity index, pods in each class were multiplied with its class number and summed. The higher values of the maturity index reflect earlier maturity.

**Statistical Analysis**

a) **Generation Means:** A preliminary univariate analysis was performed for each cross to determine if the experimental error was normally distributed. A square root transformation was required to normalize distribution for seed weight (g/100 seeds) in both crosses. The means of maturity yield per plant, pod length, seed number, seed

weight, and shelling percentage for each generation in each cross were used to estimate parameters in the genetic model. Locations were considered random. Analysis of variance was performed on the means of each trait and a Waller-Duncan multiple range test was used to determine the significant differences among the means of various generations. The generation means analysis proposed by Mather & Jinks (1982) was followed. Gamble's (1962) notation was used to define the genetic parameters in the model.

M	=	Mid parent value
A	=	Pooled additive effects
D	=	Pooled dominance effects
AA	=	Pooled additive x additive effects
AD	=	Pooled additive x dominance effects
DD	=	Pooled dominance x dominance effects

The expectations of the generation means according to Mather & Jinks (1982) are:

$$\begin{aligned}
 P_1 &= M + A + AA \\
 P_2 &= M - A + AA \\
 F_1 &= M + D + DD \\
 F_2 &= M + 0.5 D + 0.25 DD \\
 BC_{11} &= M + 0.5 A + 0.50 D + 0.25 AA + 0.25 AD + 0.25 DD \\
 BC_{12} &= M - 0.5 A + 0.50 D + 0.25 AA + 0.25 AD + 0.25 DD \\
 BC_{11}^S &= M + 0.5 A + 0.25 D + 0.25 AA + 0.125 AD + 0.0625 DD \\
 BC_{12}^S &= M - 0.5 A + 0.25 D + 0.25 AA + 0.125 AD + 0.0625 DD
 \end{aligned}$$

A general linear model procedure (Anon., 1985) was used to estimate the genetic effects from the generation means of each cross at each location and combined over locations. A full model including all genetic effects was fit to the data. F-test of the sequential sum of squares for genetic effects was used to reduce the model. In the selected model, genetic parameters having significant effects were included and all the nonsignificant parameters were removed. When any high order effect was significant the lower order effects were also included in the model, even if they were nonsignificant.

b) **Heritability:** An estimate of narrow sense heritability ( $h^2$ ) was computed from the variance components in  $F_2$  generation and the two backcrosses as described by Allard (1960).

$$\begin{aligned}
 2V_{F_2} &= 2V_A + 2V_D + 2V_E \\
 V_{BC11} + V_{BC12} &= V_A + 2V_D + 2V_E \\
 V_{h^2} &= 2V_{F_2} - V_{BC11} - V_{BC12} \\
 h^2 &= \frac{V_{F_2}}{V_{F_2}}
 \end{aligned}$$

where: $V_{F_2}$	=	Variance of $F_2$ generation
$V_A$	=	Additive variance
$V_D$	=	Dominance variance
$V_E$	=	Environmental variance
$V_{BC11}, V_{BC12}$	=	Variance of the two back crosses
$h^2$	=	Estimate of narrow sense heritability

Location effects were highly significant for most of the traits. Therefore, the heritability estimates were also computed from variance components, described above, after removing the location effects. Correlations among traits were computed on the basis of generation means in both the crosses.

## Results and Discussion

### A. Generation Means:

Cross 1 (No. 334/ICGSE-4): Parents differed significantly for yield per plant, maturity and seed weight but not for pod length, seed number and shelling percentage (Table 1). The early parent, ICGSE-4, had the earliest average maturity (MI = 183.1). For seed weight and yield per plant No. 334 was the high parent. Pooled  $F_1$  means for yield per plant were equal to the better parent and seed weight was equal to the midparental value. For the maturity index, the  $F_1$  mean was close to the late parent. The  $BC_{11}$  ( $F_1$ /No.334) means of 194.0 and 6.85 for yield per plant and seed weight exceeded their higher parents, but the differences were nonsignificant. The  $BC_{12}$  ( $F_1$ /ICGSE-4) means for maturity index and seed weight were close to midparental values (Table 1).

**Table 1. Generation means for selected variables in two crosses over two locations, 1989.**

Generation	Yield per plant (g)	Pod length (cm/20 pods)	Maturity index	Seed no (50 pods)	Seed weight <sup>a</sup> (g/100 seeds)	Shelling %
<b>Cross 1 (No.334/ICGSE-4)</b>						
$P_1$ (No.334)	178.5ab*	55.1ab	126.5d	91.2	6.77ab (46.1)	74.3a
$P_2$ (ICGSE-4)	146.8c	55.9ab	183.1a	90.3	6.42c (41.6)	74.7a
$F_1$	189.4ab	56.2a	129.2cd	86.5	6.68ab (44.7)	69.6b
$F_2$	161.0bc	55.0ab	135.2bcd	86.2	6.58abc (43.9)	72.3ab
$BC_{11}$	194.0a	56.7a	133.6cd	89.7	6.85a (47.5)	74.0a
$BC_{12}$	171.7abc	53.3bc	148.8b	89.4	6.47bc (42.2)	74.0a
$BC_{11}S$	187.8ab	54.5abc	134.4cd	88.7	6.71ab (45.6)	71.7ab
$BC_{12}S$	165.3bc	52.3c	142.6bc	87.2	6.35c (40.8)	73.5ab
<b>Cross 2 (NC 9/ICGSE-4)</b>						
$P_1$ (NC9)	231.8a	69.4a	105.5d	92.0	8.57a (73.8)	72.0d
$P_2$ (ICGSE-4)	154.9b	53.1f	171.5a	91.9	6.14e (37.9)	76.6a
$F_1$	224.6a	59.9cd	122.1c	90.2	7.21c (52.2)	72.3cd
$F_2$	181.5b	58.4d	137.2bc	89.9	7.02c (50.0)	73.7bcd
$BC_{11}$	236.9a	62.3b	121.3cd	90.6	8.04b (65.2)	75.3ab
$BC_{12}$	188.0b	54.5ef	150.7b	90.6	6.67d (44.8)	75.1abc
$BC_{11}S$	194.6b	60.5c	131.6c	88.7	7.89b (63.0)	74.4abc
$BC_{12}S$	166.4b	55.7e	152.3ab	91.5	6.62d (44.5)	74.8abc

<sup>a</sup>Means are based on square root transformed data. Nontransformed values are shown in parentheses.

\*Means with same letters are not significantly different according to Waller-Duncan multiple range test (K ratio = 100).

**Table 2. Mean squares for maturity and agronomic traits for cross 1 (No.334/ICGSE-4) over two locations-1989.**

Source of Variation	df	Yield per plant (20 pods)	Pod length	Maturity index (100 seeds)	Seed no (50 pods)	Seed weight <sup>a</sup>	Shelling %
Location (Loc)	1	1113231.81**	7.41	7393.69**	517.49**	2.93**	268.02**
Rep (Loc)	6	864.95	5.46	62.43	28.36	0.07	16.06
Generations (Gen)	7	2308.63*	16.92	2302.04*	27.53	0.28	24.15**
Additive (A)	1	9330.43**	10.98	10757.51**	11.01	1.53*	4.57
Dominance (D)	1	3668.42*	7.29	2920.04*	82.92*	0.14	85.91**
AA	1	0.59	39.58	784.31	52.81	0.07	3.92
AD	1	236.94	50.39	834.81	0.20	0.12	1.75
DD	1	316.65	1.31	259.06	35.29	0.07	66.97**
Residual	2	1303.69	4.45	279.27	5.23	0.02	2.98
Loc x Gen	7	492.12	9.59	519.20*	10.78	0.13	3.34
A*Loc	1	906.22	13.47	3073.53**	29.70	0.00	0.00
D*Loc	1	1038.74	42.25**	193.72	0.13	0.76**	10.26
AA*Loc	1	39.86	8.54	64.21	32.24	0.00	3.15
AD*Loc	1	752.98	1.18	42.15	6.76	0.02	0.71
DD*Loc	1	533.28	1.26	28.43	0.28	0.00	1.75
Residual	2	97.38	0.23	116.18	3.17	0.05	3.74
Error	42	650.97	4.82	211.59	24.92	0.07	9.54
CV (%)		14.80	4.00	10.33	5.64	4.07	4.24

<sup>a</sup>Based on square root transformed data.

\*\*Significant at 5 and 1% levels, respectively.

Generation means analysis indicated that additive mean squares were significant for yield per plant, maturity index and seed weight (Table 2). Dominance mean squares were also significant for yield per plant, maturity index, seed number and shelling percentage. Epistasis mean squares were nonsignificant for all traits except shelling percentage, which had significant dominance x dominance epistasis in this cross. Additive x location interaction was significant for maturity index and dominance x location interaction for pod length and seed weight indicating that the genetic estimates for these traits are not consistent over locations. These results suggest that evaluation for early maturity should be practiced in different environments. Sanun (1988) reported similar results for agronomic traits in peanuts.

Non significant parameters were removed from the full model to get the better estimates of the significant components. In the reduced model, additive effects were significantly different from zero for yield per plant, maturity index and seed weight (Table 3). Dominance effects were also significant for maturity index, yield per plant, seed number and shelling percentage. The magnitude of dominance effects was high for yield per plant, seed number and shelling percentage. For the maturity index,

Table 3. Estimates of genetic effects in reduced model for maturity and agronomic traits in two crosses.

Parameter	Yield per plant (g)	Pod length (cm/20 pods)	Maturity index	Seed no (50 pods)	Seed weight <sup>a</sup> (g/100 seeds)	Shelling %
Cross 1 (No.334/ICGSE-4)						
M	162.18** ± 4.52 <sup>b</sup>	---	148.96** ± 4.42	89.75** ± 0.78	6.59** ± 0.04	67.37** ± 1.87
A	19.74** ± 4.53	---	-21.19** ± 4.65	0.86 ± 0.67	0.26* ± 0.07	-0.18 ± 0.45
D	26.52* ± 9.06	---	-21.73* ± 9.12	-3.44* ± 1.34	---	17.18* ± 0.45
AA	---	---	---	---	---	6.91** ± 1.85
AD	---	---	---	---	---	-0.92 ± 1.95
DD	---	---	---	---	---	-14.94* ± 3.64
R <sup>2</sup> (%)	95.37(95.75) <sup>c</sup>	---	77.58 (84.65)	77.33 (88.08)	76.44 (83.57)	92.42 (92.42)
Cross 2 (NC 9/ICGSE-4)						
M	195.85** ± 7.34	55.80** ± 1.46	141.87** ± 2.71	---	7.26** ± 0.04	---
A	38.91* ± 12.95	7.57** ± 0.60	-30.04** ± 2.65	---	1.25** ± 0.06	---
D	---	3.70 ± 2.08	-15.18* ± 5.30	---	---	---
AA	---	5.25* ± 1.70	---	---	---	---
AD	---	---	---	---	---	---
DD	---	---	---	---	---	---
R <sup>2</sup> (%)	83.08 (91.11)	93.49 (94.16)	92.17 (94.75)	---	96.40 (97.75)	---

<sup>a</sup>Based on square root transformed data.

<sup>b</sup> ± = Standard error.

<sup>c</sup>Values in parentheses are R<sup>2</sup> for full model.

... Significant at 5 and 1% levels, respectively.

dominance was almost equal to additive effects indicating complete dominance. Epistasis was negligible for all traits except shelling percentage where additive x additive and dominance x dominance type of epistasis were significant. Signs of estimates for additive effects were a function of which parent was assigned as  $P_1$  or  $P_2$ . A negative sign of additive effects indicated that  $P_2$  (ICGSE-4) is the source of early maturity in this cross. Positive signs of additive effects for yield per plant and seed weight indicated that No. 334 was the major contributor for high yield and larger seed size. A positive sign of dominance effects indicated that dominance is in the direction of high yield. Negative sign for maturity index indicated that dominance is in the direction of late maturity.

These results indicated that additive effects were important for yield, maturity and seed weight. Dominance effects were also important for yield per plant and maturity index. Epistasis was not important for these desired traits in this cross. These results agree with the findings of Isleib & Wynne (1983) who indicated that dominance was more important for pod and seed yield. Mohammed *et al.*, (1978) reported that for maturity only additive effects were important. The presence of significant additive effects indicated that selection for high yielding, early maturing lines with large seed size is possible from this cross. These results suggested that selection for larger seed size could be practiced in early generations but the presence of significant dominance effect suggests that selection for high yield and early maturity should be practiced in later generations. Significant additive x location interaction suggested that for early maturity this population should be evaluated at different environments.

Cross 2 (NC 9/ICGSE-4): In this cross also the parents differed significantly for all the traits except seed number. Parent ICGSE-4 was the early parent with highest maturity index of 171.5 (Table 1). For yield per plant pod length, and seed weight NC 9 was the favorable parent. Pooled  $F_1$  means were close to the better parent for yield per plant and mid parent for pod length. For the maturity index  $F_1$  means were less than the midparental value. The  $F_2$  mean for the maturity index was close to the midparent. Backcrossing of the  $F_1$  with the earlier parent, ICGSE-4, increased earliness and with NC 9 increased the mean yield per plant, pod length and seed weight.

Generation means analysis indicated that additive mean squares were significant for yield per plant, pod length, maturity index and seed weight. Dominance was significant only for maturity index (Table 4). Epistasis mean squares were nonsignificant for all traits except pod length where additive x additive type of epistasis was significant. These results indicated that additive effects were important for the desirable traits. The estimates of additive effects were consistent over locations for all traits, but dominance estimates were not consistent over locations for yield per plant, seed number and shelling percentage as the interaction with location was significant for these traits. For the maturity index and seed weight none of the parameters showed interaction with location.

After removing the nonsignificant parameters from the model the  $R^2$  was still high indicating that the parameters removed made little contribution for the variation. The results from the reduced model indicated that additive effects were significant and much higher in magnitude than dominance effects for pod length and the maturity index. Dominance effects were significant only for maturity index. Additive x additive



**Table 4. Mean squares for maturity and agronomic traits for cross 2 (NC.9/ICGSE-4) over two locations-1989.**

Source of Variation	df	Yield per plant	Pod length (20 pods)	Maturity index	Seed no (50 pods)	Seed weight <sup>a</sup> (100 seeds)	Shelling %
Loc	1	180393.47**	14.54	3458.95*	552.92**	2.82**	191.45**
Rep (Loc)	6	328.24	4.86	303.86	8.31	0.06	6.20
Generations (Gen)	7	8050.29	219.53**	3378.91**	8.08	5.37**	19.86
Additive (A)	1	31204.87*	1386.67**	21384.69**	2.32	36.72**	60.88
Dominance (D)	1	10675.97	14.57	1068.73*	5.79	0.11	11.71
AA	1	11541.58	87.48*	646.88	27.38	0.23	3.88
AD	1	724.76	6.00	176.63	1.68	0.11	30.42
DD	1	586.57	5.47	18.70	0.01	0.12	21.55
Residual	2	809.14	18.45	178.38	9.69	0.14	5.30
Loc x Gen	7	4023.16*	8.64	168.33	19.14	0.09	12.85
A* Loc	1	587.87	5.81	477.34	6.49	0.09	2.13
D* Loc	1	20484.76**	9.87	111.19	78.57*	0.00	44.64**
AA* Loc	1	1248.10	30.26*	79.71	2.63	0.14	1.04
AD* Loc	1	3872.47	0.94	357.50	2.78	0.15	9.63
DD* Loc	1	80.47	0.26	0.15	40.88	0.05	19.71
Residual	2	944.21	6.66	76.20	1.32	0.10	6.40
Error	42	1299.83	4.22	361.45	13.29	0.07	5.85
CV (%)		18.27	3.47	13.99	4.03	3.71	3.26

<sup>a</sup>Based on square root transformed data

\*\* Significant at 5 and 1% levels, respectively.

epistatic effects were significant for pod length (Table 3). Epistasis was negligible for all other traits. The negative sign of additive effects for the maturity index indicated that ICGSE-4 is source of early maturity as expected because it was chosen as the early parent. The positive sign for yield per plant, pod length and seed weight indicated that NC 9 is contributing genes for higher yield and larger seed size. The negative sign of the dominance effects for maturity indicated that dominance is in the direction of late maturity.

These results indicated that additive effects were important for yield per plant pod length, the maturity index and seed weight. Dominance effects were important only for the maturity index, but the magnitude of dominance effects was lower than additive effects. For pod length additive x additive epistasis was important indicating that transgressive segregants for pod length could be selected from this population. These results indicate that selection for high yield, early maturity and large seed size is possible in this cross. It is suggested that selection for yield, pod length and seed weight should be practiced in F<sub>2</sub> generation. For the maturity index nonadditive effects were also important suggesting selection for early maturity in later generations.

Results from the generation means analysis indicates that additive effects are important for yield per plant, the maturity index and seed weight in both the crosses studied. Dominance effects were important for yield in cross 1 (No. 334/ICGSE-4) and for the maturity index in both crosses. Dominance was in the direction of high yield and late maturity. Epistatic effects were also important for the shelling percentage in cross 1 and pod length in cross 2. For all other traits epistatic effects were negligible. Isleib & Wynne, (1983) also indicated significant dominance effects for pod and seed yield in peanuts. Isleib *et al.*, (1978) reported significant epistasis effects for yield per plot, pod length and extra large kernels. The results did not agree with Rachmeler (1988) who reported significant epistasis for maturity index. The results are in agreement with Mohammed *et al.*, (1978) who indicated significant additive effects for maturity. In cross NC 9/ ICGSE-4 only additive x additive epistasis was significant for pod length. Similar epistatic effects have been reported for pod length in peanuts (Sanun, 1988). It would suggest that additive and dominance effects were important for all the desired traits except seed weight, in which only additive gene effects were important. Epistasis was negligible for all the desirable traits such as yield, early maturity and seed weight in both crosses. The presence of significant and large additive effects indicate that improvement for yield, early maturity and large seed size is possible in these crosses. Selection for seed weight could be accomplished in  $F_2$  generation in both populations. Selection for yield per plant in cross 2 could also be practiced in early generations. Selection for early maturity should be more effective in later generations. The results further suggested that the evaluation for early maturity should be done in different environments because of significant additive x location effects.

#### B. Heritability and Correlation:

Cross 1 (No. 334/ICGSE-4): Narrow sense heritability ( $h^2$ ) estimates from variance components in the  $F_2$ ,  $BC_{11}$ , and  $BC_{12}$  ranged from 0.0-0.83 (Table 5). A high heritability estimate of 0.83 was obtained for seed number, while  $h^2$  was intermediate for pod length (0.43). For seed weight and yield per plant heritabilities were 0.23 and 0.08, respectively. Mohammad *et al.*, (1978) reported similar results showing low to intermediate narrow sense heritability for fruit size and pod yield. Narrow sense heritability estimates computed from variance components were negative for the maturity index and shelling percentage because of negative estimates of additive variances. This occurred when the sum of  $BC_{11}$  and  $BC_{12}$  variances exceeded twice the variance of  $F_2$ . Therefore, heritability for these traits are considered zero. Chow & Wynne (1983) also obtained negative genetic variance for maturity indicating zero heritability for this trait. As location effects were highly significant, the narrow sense heritability estimates were also computed after excluding these effects to see if there is a location effect on variance estimates. The estimates were almost similar for yield per plant, pod length, maturity index and seed number indicating that locations did not effect the variance estimates for these traits. For seed weight and shelling percentage the estimates were a little higher indicating the effect of location interaction with the genotypes of segregating generations. However, these results indicated that selection for seed number, pod length and seed weight is possible in early generations. For yield the selection would be effective in later generation.

**Table 5. Narrow-sense heritability ( $h^2$ ) estimate for maturity and agronomic traits in two crosses on the basis of variance components**

Trait	Cross 1 (No.334/ICGSE-4)		Cross 2 (NC9/ICGSE-4)	
	Including all effects	Excluding loc effects	Including all effects	Excluding loc effects
Yield/plant (g)	0.08	0.07	b	0.32
Pod length (cm/20 pods)	0.43	0.43	0.90	0.91
Maturity index	b	b	0.87	0.86
Seed no (50 pods)	0.83	0.80	0.69	0.52
Seed wt (g/100 seeds) <sup>a</sup>	0.23	0.37	0.58	0.62
Shelling %	b	0.27	0.58	0.27

<sup>a</sup>Based on square root transformed data.

$b = V_{BC11} + V_{BC12} > 2V_{F2}$  expected  $h^2$  for these traits equal to zero.

Phenotypic correlations of maturity with seed number, shelling percentage, yield per plant and pod length were positive and significant (Table 6). Though these phenotypic correlations were significant but none was high. Nonsignificant correlation between maturity index and seed weight ( $r = 0.156$ ) indicated that selection for early maturing and large seeded recombinant are possible from these progenies. Yield per plant showed a considerable positive correlation with seed weight ( $r = 0.645$ ), seed number ( $r = 0.575$ ) and shelling percentage ( $r = 0.482$ ). It suggests that selection based upon any of these traits could indirectly increase yield. The results confirm that findings of Abraham (1990) who found positive and significant correlations of yield with kernel weight, kernels/plant and shelling percentage.

**Cross 2 (NC 9/ICGSE-4):** The magnitudes of narrow sense heritability ( $h^2$ ) estimates from variance components were higher than from cross 1 and ranged from 0.0-0.90 (Table 5). Heritability estimates of 0.90, 0.87, 0.69, 0.58, and 0.58 were obtained for pod length, maturity index, seed number, seed weight and shelling percentage, respectively. The high heritability estimates indicated that early generation selection for early maturity, large seed size and fruit length would be effective in this population. High heritability estimates for these traits has also been reported by Coffelt & Hammons (1974) and Ali & Wynne (1994). For yield per plant, heritability was considered zero due to a negative estimate of additive variance. Heritability estimates, after excluding location effects were not much different for pod length, maturity index and seed weight. There were considerable differences for yield per plant, seed number and shelling percentage indicating biased estimates due to genotype x location interaction. It is evident from these results that effective selection for desirable traits is possible in early generation in this cross.

Positive and highly significant correlations were obtained between maturity index and seed number ( $r = 0.35$ ), and maturity index and shelling percentage ( $r = 0.50$ ) (Table 6). Significant negative correlations of maturity index with pod length and seed

**Table 6. Correlation coefficients among selected traits for two crosses.**

Trait	Pod length (20 pods)	Maturity index	Seed no. (50 pods)	Seed weight <sup>a</sup> (100 seeds) (g)	Shelling %
Cross 1 (No.334/ICGSE-4)					
Yield/plant (g)	0.234	0.265*	0.575**	0.645**	0.482**
Pod length (cm/20 pods)		0.263*	0.332**	0.558*	0.143
Maturity index			0.460**	0.156	0.452**
Seed no (50 pods)				0.375**	0.707**
Seed wt. (g/100 seeds) <sup>a</sup>					0.469**
Cross 2 (NC 9/ICGSE-4)					
Yield/plant (g)	0.347**	-0.008	0.590**	0.505**	0.416**
Pod length (cm/20 pods)		-0.582**	0.105	0.885**	-0.281*
Maturity index			0.351**	-0.496**	0.501**
Seed no (50 pods)				0.171	0.651**
Seed wt. (g/100 seeds) <sup>a</sup>					-0.002

<sup>a</sup>Based on square root transformed data

\*\*Significant at 5 and 1% levels, respectively.

weight indicate that selection of early maturing lines could reduce the pod length and seed size. The maturity index also showed a negative but nonsignificant correlation with yield per plant, which indicates that early maturing and high yielding recombinant can probably be selected in the segregating population of this cross. Rachmeler (1988) and Ali & Wynne (1994) also reported negative correlations of early maturity with pod length and seed weight. Positive and highly significant correlations were observed between pod length, seed weight and yield per plant. These results suggested that phenotypic selection for long pods and heavier seeds could result in higher seed yield. These results agree with Coffelt & Hammons (1974), Chiow & Wynne (1983) and Ali *et al.*, (1998) who reported highly significant correlation between fruit length and seed weight.

The present studies showed that narrow sense heritability estimates from variance components ranged from low to high in both crosses. Selection in early generation should be effective for pod length, seed number and seed weight in both populations. Selection for yield would be more effective in later generations. Low phenotypic correlations of yield and maturity suggested that selection for favourable recombinant from among the progeny lines could be possible.

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