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HERITABILITY ESTIMATES AND CORRELATION STUDIES OF EARLY MATURITY AND OTHER AGRONOMIC TRAITS IN TWO CROSSES OF PEANUT (*ARACHIS HYPOGAEA* L.)

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Abstract

Knowledge of heritability and correlation among traits is important in determining the effectiveness of direct and indirect selection. The objective of this study was to determine the potential effectiveness of selection for early maturity, and seed size, in two peanut crosses (NC 7/Chico and 73-30/Chico) by estimating the heritability for each trait and the correlations among the traits. Both narrow sense heritability and broad sense heritability estimates were fairly high for seed weight, maturity index, and pod length in both the crosses. Broad-sense heritability estimates were much greater than parent-offspring regressions and were biased upward due to nonadditive genetic effects and genotype x environment interaction. The results suggested that selection for early maturity, seed weight, and pod length could be practiced in early segregating generations. Correlations of maturity with shelling percentage were positive and highly significant in both crosses but correlation between maturity and seed number was positive and significant in cross 1 (NC 7/Chico). Maturity was negatively correlated with pod length and seed weight in cross 2. The highest positive and significant correlation was found between pod length and seed weight.

Introduction

Estimates of heritability from segregating populations are useful in understanding the genetic consequences of hybridization and inbreeding. They can help the breeder in selecting and utilizing superior individuals from a population. In peanut (*Arachis hypogaea* L.) many studies have been performed to estimate both broad-sense and narrow sense heritabilities for different traits of economic importance and to measure the correlations among these traits. Low estimates of broad-sense heritability for all traits of economic importance were shown in segregating population of crosses of virginia, valencia, and spanish types (Syakudo & Kawabata, 1965). Gupton & Emery (1970) measured heritability of maturity (based upon the percent light transmission through oil) in virginia type peanut families. High heritability estimates of 0.95 and 0.94 were obtained using variance components and parent-offspring regressions, respectively in the late pegging group.

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. Low heritability estimates were obtained for number of pods, pod weight, number of seeds, and seed weight. Positive and significant correlation was shown among the yield components: number of pods, pod weight, number of seeds, and seed weight. High heritability for fruit size has also been shown by Wynne *et al.*, (1975). Gibori *et al.*, (1978) reported a high heritability of 0.79 for pod yield. They suggested that phenotypic selection of the promising plants in large F_2 populations

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followed by careful progeny testing would increase productivity. A positive but low genetic correlation between fruit size and yield indicated that selection for both large pods and high yield is possible.

Narrow sense heritability estimates for maturity, fruit size, and yield were 0.35, 0.27, 0.21 in a cross of NC 6/R 22 and 0.20, 0.18, 0.16 in a cross of NC 6/922, respectively (Mohammed *et al.*, 1978). Broad- sense heritability estimates based on intraplot variance were biased upward by nonadditive genetic variances and genotype x environment interaction. Narrow-sense heritability estimates calculated by parent-offspring regression were less biased and more useful predictors of selection response. Genotypic correlation was positive and significant between maturity and yield, while correlation between maturity and fruit size was negative but nonsignificant. Rachmeler (1988) evaluated two crosses for early maturity and fatty acid composition using parent-offspring regression. Narrow sense heritability was high for fruit length, early maturity and fatty acid composition in virginia x virginia cross relative to a virginia x spanish cross, indicating that early generation selection was possible in the former. Early maturity was positively correlated with seed to hull ratio, but correlation was negative with fruit length. High heritability estimates for plant height, yield /plant and pegs/ plant have been found in groundnut (Kale & Dhoble, 1988). Halbrook *et al.*, (1989) reported high heritability for maturity while studying F_1 & F_2 plants of reciprocal crosses involving Chico (very early maturing) and PI 383421 (late maturing) groundnut lines. Positive correlation between pod yield and number of developed pods ($r = 0.41$) and pod yield and number of primary branches ($r = 0.34$) have been indicated by Nadaf & Habib (1989). In F_2 hybrids of two Virginia x Spanish crosses heritability estimates were high for pod and seed length and width (Tsaur *et al.*, 1989). They also indicated positive and significant correlations among all pod and seed traits. Abraham (1990) also reported positively significant correlations between kernel yield and pods/plant, kernels/plant, shelling % age and 100 kernel wt. The present report describes the heritability estimates and correlation studies of early maturity and other agronomic traits in two crosses of peanut.

Materials and Methods

Mekontchou (1987) studied the inheritance and combining ability for early maturity and seed dormancy in 28 crosses between three virginia and five spanish type parents. On the basis of F_1 results two crosses NC 7/Chico and 73-30/Chico were selected for heritability estimates for early maturity and other agronomic traits. The F_2 generations of these two crosses were planted along with their respective parents. Experiments were conducted in a randomized complete block design with four replications each at the Peanut Belt Research Station at Lewiston, NC, on May 13, 1987 and the Upper Coastal Plains Research Station at Rocky Mount, NC, on May 19, 1987. Each plot comprised two rows spaced 91 cm apart with 14 seeds planted at 25 cm spacing. Normal cultural practices were followed throughout the growing season. At 130 days after planting, 10 single plants were harvested randomly from each parental plot and 16 from each F_2 plot. The pods of these single plants were air dried for 2 weeks.

A random sample of 30 pods was taken from each single plant and the data recorded from these samples were: 20 pod length (cm), weight of 30 pods (g), number of seeds in 30 pods, weight of seeds in 30 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 30 pods were shelled and rated for maturity. From the recorded data the following variables were created.

a) Seed weight (g/100 seeds)

$$= \frac{\text{weight of seeds in 30 pods}}{\text{number of seeds in 30 pods}} \times 100$$

b) Shelling percentage

$$= \frac{\text{weight of seeds in 30 pods}}{\text{weight of 30 pods}} \times 100$$

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

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

Progenies of 120 F_2 derived families in each cross were evaluated during 1988. Families were divided into three sets having 40 families per set and parents were included as check in each set. Experiment was laid out in a randomized complete block design with two replications at the Peanut Belt Research Station, Lewiston, NC, on May 23, 1988. Each plot comprised two rows 91 cm apart with 14 seeds per row at 25 cm spacing. Standard cultural practices were followed during the growing season. The experiment was harvested 130 days after planting. Two to three pods from each plant within each plot were picked at random and bulked to make one sample per plot. Data for maturity and agronomic traits were collected from this sample as described for the F_2 generation.

In the F_2 generation 60 single plants per cross were evaluated at Lewiston and another 60 single plants at Rocky Mount in 1987. The progenies of all 120 single plants per cross were evaluated at Lewiston only in 1988. Therefore, parent-offspring regressions were estimated separately for progenies derived from two locations.

An analysis of variance was performed on F_3 field trial and from the variance components, a broad-sense heritability (H) was estimated on entry mean basis using the following formula.

H = Genotypic variance/phenotypic variance where,

Genotypic variance = (progeny mean square - error mean square)/r

Phenotypic variance = (Error mean square/r) + Genotypic variance

Narrow sense heritability (h^2) was estimated using parent- offspring regression (Smith & Kinman, 1965). Correlation coefficients were used to estimate narrow sense heritability (h^2) in standard units (Frey & Horner, 1957).

Table 1. Mean squares of maturity and agronomic traits of two crosses in F_3 generation at Lewiston (1988).

Source	df	Pod length (20 pods)	Maturity index	Seed no. (30 pods)	Seed weight (100 seeds)	Shelling %
			Cross 1 (NC 7/Chico)			
Set	2	433.58**	523.10	65.15*	504.80**	6.18
Rep (Set)	3	27.67*	332.04	37.79	22.46	27.12
Entry	121	133.20**	575.88**	52.87**	368.68**	17.82**
Error	125	8.60	175.53	15.84	9.60	10.79
CV (%)		5.76	12.88	7.24	7.26	4.48
			Cross 2 (73-30/Chico)			
Set	2	11.44	434.53*	20.55*	72.32*	13.18*
Rep (Set)	3	14.23*	363.99*	4.59	27.59**	8.09*
Entry	121	28.77**	698.01**	11.58**	90.01**	13.10**
Error	125	4.25	122.18	5.82	3.06	2.95
CV (%)		4.17	9.50	4.29	5.13	2.36

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

Results and Discussion

Highly significant differences among the F3 progenies were observed for all traits, indicating that substantial variability existed for these traits (Table 1). Because the F3 progenies were evaluated at only one location in one year, the genotype x environment interaction could have biased the estimates of among family variance. Broad-sense heritability estimates (H) were calculated from variance components of F3 progenies only. Narrow sense heritability (h^2) was estimated from parent-offspring regressions. Means of F3 progenies were regressed on F2 plants and the correction factor suggested by Smith & Kinman (1965) was used. Because parents and offspring were evaluated in different years, the parent-offspring regression estimates may be somewhat biased due to changes in genetic variance from year to year due to genotype x environment interaction. To reduce this effect a narrow sense heritability was also estimated in standard units (Frey & Horner, 1957). Correlation coefficients were used for heritability estimates, which is identical to parent-offspring regression in standard units.

Cross 1 (NC 7/CHICO): Narrow sense heritability estimates obtained by parent-offspring regression, when evaluated at the same location, were high for seed weight (0.71) and pod length (0.52), intermediate for maturity index (0.44) and seed number (0.31), while for shelling percentage was low (Table 2). Estimates of heritability computed by parent-offspring regression at different locations were lower for most of the traits. The differences were considerable for seed weight, maturity index, and shelling percentage indicating that the regression coefficients for the F2 plants grown at Lewiston were biased upward due to covariance of location effects on F2 plants and F2.3 families. When heritabilities were computed in standard units, high and medium

Table 2. Heritability estimates for maturity and agronomic traits in two crosses.

	Cross 1 (NC 7/Chico)					Cross 2 (73-30/Chico)				
	h^2_p		h^2_s			h^2_p		h^2_s		
Parameter	A	B	A	B	H	A	B	A	B	H
Pod length (cm/20 pods)	0.52	0.55	0.55	0.57	0.94	0.28	0.42	0.35	0.49	0.85
Maturity index	0.44	0.33	0.47	0.37	0.70	0.42	0.45	0.51	0.40	0.83
Seed no. (30 pods)	0.31	0.32	0.38	0.38	0.70	0.09	0.02	0.16	0.05	0.50
Seed weight (g/100 seeds)	0.71	0.47	0.59	0.55	0.97	0.64	0.55	0.50	0.59	0.97
Shelling %	0.23	0.10	0.33	0.16	0.39	0.22	0.19	0.43	0.35	0.77

h^2_p = narrow-sense heritability calculated using parent offspring regression, h^2_s = narrow- sense heritability calculated using parent offspring correlation (standard units), H = broad-sense heritability calculated from variance components of F_3 generation (one year and one location), A = parents and progenies tested at same location, and B = parents and progenies tested at different locations.

heritability estimates were not much changed. However shelling percentage showed medium heritability using standard units as compared to low heritability using parent-offspring regression (Table 2). The magnitude of standard unit heritabilities were little higher for all traits except seed weight. Covariance of location effects was important for maturity index and shelling percentage in standard unit estimates. Frey & Horner (1957) stated that differences in the ranges and variances between the F2 and F3 generations within a cross is responsible for higher heritability estimates in this method. They further stated that standard unit heritability corrects for a particular type of genotype- environment interaction which tends to cause expansion or contraction of the scale.

Broad-sense heritability estimates from variance components in F2.3 progenies were much higher in magnitude than parent offspring regression and standard unit methods (Table 2). These progenies were evaluated at one location in one year, so heritability estimates were biased upward due to the contribution of nonadditive genetic variances and genotype x environment interaction to the variance among $F_{2.3}$ families. Mohammad *et al.*, (1978) and Chiow & Wynne (1983) also reported much lower estimates of heritability from parent-offspring regression compared to estimates from variance components using F_2, F_3 and F_5, F_6 generations, respectively. They further reported that higher estimates of heritability from variances most likely resulted from within-plot competition and genotype x environment interaction. Relatively high estimates of narrow sense heritabilities for seed weight, maturity index, and pod length indicated that selection for these traits could be effective in early generations.

Maturity index was positively and highly significantly correlated with seed number and shelling percentage in F_3 progenies. Correlation between maturity index and seed weight was negligible "r = 0.094" (Table 3). Pod length was highly correlated with seed weight, but correlation with maturity was non significant. This indicated that selection for larger fruit and heavier seed could result in higher seed yield but may not favour early maturity.

Table 3. Phenotypic correlation coefficients of selected traits in F_3 generation of two crosses.

Trait	Maturity index	Seed no. (50 pods)	Seed weight (100 seeds) (g)	Shelling %
		Cross 1 (NC 7/Chico)		
Pod length (cm/20 pods)	0.082	0.017	0.815^{**}	-0.207^{*}
Maturity index		0.394^{**}	0.094	0.447^{**}
Seed no. (30 pods)			-0.072	0.478^{**}
Seed wt (g/100 seeds)				-0.051
		Cross 2 (73-30/Chico)		
Pod length (cm/20 pods)	-0.649^{**}	0.1410	0.841^{**}	-0.554^{**}
Maturity index		0.025	-0.771^{**}	0.660^{**}
Seed no. (30 pods)			0.060	0.181^{*}
Seed wt (g/100 seeds)				-0.457^{**}

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

Cross 2 (73-30/CHICO): Narrow-sense heritability estimates were lower in this population than in cross 1 for all traits. When F2.3 progenies were regressed on F2 plants grown at Lewiston, the narrow sense heritability was high for seed weight (0.64), medium for maturity index (0.42), and low for pod length, seed number, and shelling percentage (Table 2). Heritability estimates based on regression of F2.3 families on F2 plants at Rocky Mount were not much different for any trait except pod length and seed weight. As in cross 1, narrow sense heritability estimates in standard units were little higher than those obtained from unstandardized values. The covariances of location effects were not much important in this population.

Broad-sense heritability estimates were 0.97, 0.85, 0.83, and 0.77 for seed weight, pod length, maturity index and shelling percentage, respectively. The magnitude of H was much greater than parent-offspring regression and standard unit methods. These higher estimates were biased due to non additive genetic variances and genotype x environment effects. Narrow sense heritability estimates are less biased by genotype x environment interaction and are more useful predictors of selection response. High narrow sense heritability for seed weight and maturity index suggested that selection for these traits could be effective in early generations, whereas pod length selection in later generation would be more effective. The results agree with the findings of Coffelt & Hammons (1974), Wynne *et al.*, (1975) and Gibori *et al.*, (1978), Kale & Dhoble (1988), Tsaur *et al.*, (1989) who reported high heritability for pod yield, fruit size and seed weight. Results also agree with the results of Gupton & Emery (1970), Rachmeler (1988) and Mohammed *et al.*, (1978) who found relatively high narrow sense heritability for early maturity in peanuts. Halbrook (1989) also found high broad sense heritability for maturity in hybrid material of groundnut. Phenotypic correlations of maturity index with pod length and seed weight were negative and significant, while correlation with shelling percentage was positive and highly significant (Table 3). High and negative correlation suggests that the improvement for seed weight and pod length could result in a correlated response toward later maturity. Correlation between seed weight and pod length was positive and highly significant. The results agree with the findings of Tsaür *et. al.*, (1989) and Abraham (1990) who reported positive correlations between pod and seed traits. Nadaf & Habib (1989) found positive correlation between pod yield and number of pods and number of primary branches.

Narrow sense heritability estimates ranged from low to high in both the crosses. Fairly high estimates of heritability for seed weight, maturity index, and pod length suggested that selection for these traits could be effective in early generations in both crosses. Broad-sense heritability estimates were high for all traits. These estimates were inflated upward due to genotype x environment interaction because the variance components were estimated from a single environment data. Therefore, the broad-sense heritability estimates may not be useful criteria in predicting genetic gain from selection. Narrow sense heritability estimates were less biased by genotype x environment interaction. Among these methods, estimates of heritability in standard units is more reliable, because it is less biased by genotype x environment interaction and considers the change in scale due to these interactions. Phenotypic correlations between maturity and shelling percentage were highly significant in both the populations, whereas correlation between maturity and seed number were significant in cross 1 (NC 7/Chico). Correlation of maturity with pod length and seed weight were highly significant but negative in cross 2, while in cross 1 these correlations were positive but low indicating the possibility of desirable recombinants in this population.

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