

Effectiveness of Stratified Mass Selection for Yield in Intrasubspecific and Intersubspecific Crosses of Peanut¹

R. N. Holley and J. C. Wynne*²

ABSTRACT

Methods of broadening the genetic base of the peanut (*Arachis hypogaea* L.) generally involve crosses of exotic germplasm with locally adapted cultivars. Broadening the genetic base effectively requires the evaluation of a large number of crosses and lines within crosses. Mass selection within a cross in early generation, as opposed to single seed descent or bulk breeding methods, eliminates many undesirable segregates from crosses of exotic with adapted germplasm. In this study five plant introductions, representing different levels of diversity, were crossed with an adapted virginia (ssp. *hypogaea* var. *hypogaea*) breeding line. Twelve high and 12 low yielding plants in the F₂ generation of each cross were selected with a high and low selection being made from among 10 plants grown in sixteen 12-plant rows. The selected material was increased and evaluated in F₄ generation yield trials at two locations. Stratified mass selection for higher seed yield was effective for both intersubspecific crosses but was only effective for one of the three intrasubspecific crosses. Confounding effects of meat content with seed yield and the small number of F₂ plants evaluated may be partially responsible for the lack of effective selection for two of the intrasubspecific crosses. Selection for higher seed yield separated the F₂ plants into two groups for meat content with the selections for high seed yield having higher meat content. However, the high and low selections, when evaluated in the F₄ generation, were not different for meat content except for one intrasubspecific cross.

Key Words: *Arachis hypogaea*, groundnut, exotic germplasm.

The genetic vulnerability of peanut (*Arachis hypogaea* L.) cultivars grown in the United States to disease and insect attack (1, 7) has stimulated studies to determine methods for expanding the current germplasm base. Introductions of cultivated peanut represent a readily usable source of germplasm for the improvement of a

number of traits including pest resistance and yield. This germplasm, although representing a wide range of diversity, is generally not adapted to the specialized USA market. To expand the germplasm base efficiently, a large number of crosses and lines within crosses must be utilized. Mass selection within a cross in early generations, as opposed to single seed descent or bulk methods, could eliminate many undesirable segregates from crosses of exotic with adapted germplasm. The use of mass selection has increased since Gardner (3) demonstrated its effectiveness in increasing the yield of corn. The use of grid units (microenvironments) for making selections within a larger field greatly reduces selection bias due to environment and increases realized heritability for yield. In recent years mass selection has proven effective in a number of self-pollinated crops, including selection for leaf yield in tobacco (11), oil and protein content in soybean (8,13) and plant height in oats (12). Bulk selection has been effective in peanuts for some of the highly heritable characters like fruit size and quality, but little previous work has been published in peanuts using stratified mass selection for yield (6,14).

Heritability estimates for yield for early generation progeny of peanuts derived from diverse sets of parents ranged from a broad-sense estimate of .54 (2) to a narrow-sense estimate of .79 (4). In general, populations produced from intersubspecific crosses yield much less than those produced from intrasubspecific crosses of virginia x virginia, but the presence of transgressive segregates suggests that selection should be effective in isolating desired genotypes from both types of crosses (9, 15, 16). However, heritability in the narrow sense under a single plant selection scheme in the early generations of a cross in a self-pollinated crop is dependent upon the predominance of additive genetic variance for the character being selected.

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²Graduate Research Assistant and Professor of Crop Science, North Carolina State University, Raleigh, NC 27695. The investigation was submitted by the senior author as partial fulfillment of the Master of Science degree in Crop Science.

An earlier study using a six-parent half-diallel of diverse peanut lines indicated a significant amount of epistasis involved in the expression of yield (from the F₁ through the F₅ generations) that would greatly reduce the effectiveness of early generation selection of individual plants (10). Estimates of specific combining ability for the same material were large, suggesting that early generation selection for yield would be ineffective in both intersubspecific and intrasubspecific crosses (16). In contrast, a study by Gibori *et al.* (4) using a diverse set of cultivars as parents in a 9 x 9 diallel cross found a narrow-sense heritability estimate of .79 for pod yield per plant. In addition, a study using 27 exotic lines crossed to a common, locally adapted virginia cultivar indicated that dominance or epistasis effects on yield are primarily associated with intersubspecific crosses and should not be considered to be important for yield among progeny derived from intrasubspecific crosses (9).

In this study the effectiveness of stratified mass selection for seed yield in five peanut populations was examined by selecting high and low yielding individual F₂ plants followed by yield trials of F₂ families in the F₄ generation. If successful, mass selection could be used to reduce the number of F₂ plants of a cross and could be followed by single seed descent or a pedigree breeding scheme for isolating pure lines before recombination of selected materials. The objectives of this study were to (a) determine if stratified mass selection for yield is effective in peanuts, (b) investigate the relationship between parental diversity level and selection response and (c) determine the effect of mass selection for yield on meat content, fruit length, seed weight, and number of seed per pod.

Materials and Methods

A locally adapted virginia-type peanut breeding line selected from the cross of Florigiant and Florunner and designated NC Ac 18000 was used as the female parent in crosses with five plant introductions. The five plant introductions represent a range of diversity from the adapted line as shown by Isleib and Wynne (9). The lines included one representative from both the *fastigiata* (PI 275699) and *vulgaris* (PI 155245) botanical varieties of the subspecies *fastigiata*, in addition to three representatives (PI 262113, PI 268906, PI 158850) from the subspecies *hypogaea* (5). The three virginia lines represent different levels of diversity from the common parent within the subspecies. PI 262113 is from Bolivia and is the line most closely related to the common parent. PI 268906 is from Africa and is intermediate among the three in relative diversity from the common parent, while PI 158850 from China represents the most diverse male parent within the *hypogaea* subspecies.

Selection was conducted at the Peanut Belt Research Station at Lewiston, NC. Seeds from F₁ plants within a cross were bulked for testing the F₂ generation. The F₂ generation (192 plants from each cross) was grown in blocks of 16 rows with 12 plants each, 91 cm between rows and 25 cm between plants during 1980. Each row represented a unit for selection as referred to by Gardner (3). To remove bias due to unequal plant competition, all border row and intra-row unbordered plants were excluded from selection. The remaining plants were hand-harvested and fruit (pod and seed) weights were recorded for each plant. Within each row the highest and lowest yielding plants were selected on the basis of seed weight. Seeds from selected plants were planted in F₃ generation progeny rows in 1981.

Progeny in F₄ generation arising from the selected F₂ plants were grown in yield trials with three replications at two locations, the Peanut Belt Research Station and the Upper Coastal Plain Research Station, Rocky Mount, NC in 1982. The number of selections for each cross was reduced to a consistent number so that each cross was represented by 24

entries, 12 high and 12 low selections. The entries were grown in a split plot design at each location with crosses assigned to whole plots and entries assigned to subplots. Plots consisted of two 6.1 m rows with 25 plants per row and .91 m between rows. The plots were mechanically harvested on 4 October at both locations. After drying, fruit weight per plot was determined. A random sample of 20 fruits was used to determine the percent meat content (ratio of seed weight to fruit weight x 100), fruit length, and number of seed per fruit.

In the analysis of variance, location, cross, and entry were considered as fixed effects and replication, nested in location, was considered a random effect. For yield per plot, a regression model with stand count as a covariant was used to compute the sums of squares for the analysis of variance. For each cross the entry sums of squares was partitioned into sums of squares due to selection, among high selection and among low selection with 1, 11, and 11 degrees of freedom, respectively.

Results

Selection for seed yield per plant in the F₂ generation separated the F₂ plants into two very distinct groups for all five crosses. Means of plants selected as high or low for yield differed by approximately two standard deviations for all crosses (Table 1). In addition, the mean for percent meat content for the high selections was 7 to 16% higher than the corresponding mean for the low selections. The mean difference between the high and low selections for meat content decreased as the level of diversity of the parents of the cross increased. The large difference in percent meat content between the high and low selections suggests that selection for seed yield in the F₂ generation also indirectly selects for earlier maturing genotypes. Since all plants were harvested at the same time, high yielding, but late maturing, plants would be considered as low yielding.

Table 1. Means and standard deviations of F₂ populations and selected individuals for seed yield and meat content.

Identity	Cross	No. plants evaluated	Seed wt of F ₂ plants		Seed wt of F ₂ selections		Meat content of selections ^a					
			Mean	S.D.	High	Low	High	Low	High	Low		
			(g)		(g)		(%)		(%)			
NC Ac 18000												
x PI 155245 (spanish)	I	78	50.66	27.14	87.63	22.82	24.49	8.47	66.81	7.94	57.46	11.01
x PI 275699 (valencia)	II	72	41.99	32.09	73.89	27.57	17.70	7.84	58.41	7.29	51.74	9.34
x PI 262113 (virginia)	III	60	43.41	28.02	66.47	30.86	20.97	12.97	62.07	9.81	46.40	10.18
x PI 268906 (virginia)	IV	89	53.20	28.44	91.56	30.69	27.38	10.63	65.39	3.59	52.57	11.50
x PI 158850 (virginia)	V	84	42.24	23.84	74.62	18.51	19.78	9.06	65.71	3.52	56.75	8.82

^a% meat content = seed weight/fruit weight x 100.

The difference between the high and low yielding selections was statistically significant in three of the five crosses in the F₄ generation (Table 2). There was very little genotype by location (environment) interaction, with the exception of yield per plot and fruit length in cross IV and average weight per seed in cross II. Within the intrasubspecific crosses, selection for yield in the F₂ produced highly significant differences among the F₄ progenies for cross III but no differences for crosses IV and V. However, selection for high yield significantly shortened fruit length for cross IV and significantly increased the percent meat content and seed weight in cross V. A significant amount of genetic variation for yield within the high selections was retained for all three intrasubspecific crosses, but the mean yield of the high selections was much less in the progeny from the most diverse cross (cross V) as opposed to the progeny from the more

closely related crosses (III and IV). Within the interspecific crosses, selection was effective in both crosses, but the mean yield of the high selections was much less than that of the two highest yielding intraspecific crosses. Significant genetic variation remained among the high selections from cross II but not among the high selections for cross I (Table 2). Selection for high yield in the virginia x spanish cross (cross I) reduced fruit length and seed weight and increased the number of seed per fruit. Selection for high yield in the virginia x valencia cross (cross II) increased fruit length and slightly increased the number of seed per fruit.

Table 2. Means of high and low F₂ generation selections in F₄ generation for yield and fruit characters.

Cross	Selection	Yield/	Yield/	Meat content	Length	Avg	Seed/
		plot	plant	(Seed wt/ fruit wt)			
		(kg)	(g)	(%)	(cm)	(g)	(no.)
I	High	3.04 a	79.0 a	72.6 a	62.9 a	.56 a	2.24 a
	Low	2.67 b	70.9 b	71.4 a	65.5 b	.63 b	2.04 b
II	High	3.27 a	86.0 a	70.9 a	64.8 a	.60 a	2.00 a
	Low	2.85 b	76.7 b	70.7 a	62.9 b	.60 a	1.93 b
III	High	5.00 a	131.5 a	72.9 a	65.9 a	.84 a	1.95 a
	Low	4.80 b	116.0 b	72.1 a	66.2 a	.84 a	1.92 a
IV	High	4.43 a	115.4 a	72.8 a	64.7 a	.74 a	1.93 a
	Low	4.50 a	112.0 a	74.0 a	66.0 b	.74 a	1.94 a
V	High	3.47 a	77.4 a	72.6 a	64.9 a	.64 a	2.00 a
	Low	3.21 a	73.6 a	70.9 b	64.7 a	.60 b	1.97 a

^aMeans within a cross with different letters are significantly different at $p = 0.05$ according to F-test.

Discussion

Stratified mass selection for yield among individual F₂ plants was effective for both interspecific and one of the three intraspecific crosses. The crosses used in this study were previously evaluated for heterosis and genetic variance (9). Dominance and epistatic effects increased in magnitude as the genetic diversity between parents of the crosses increased. Dominance, the predominant source of nonadditive genetic variance, was large enough that the authors concluded that early generation selection for yield would be ineffective (9). The observed selection response in this study was opposite that expected based on the estimates of additive and nonadditive genetic effects for the five crosses. Selection for seed yield was effective for the crosses with large estimates of nonadditive effects in the F₂ generation. Interspecific crosses, which give significant estimates for nonadditive effects, generally segregate for a few genes which produce low yielding F₂ plants. This may explain why expectations based on additive effects are not realized when selecting in these crosses.

Selection for fruit yield may have been effective for the interspecific crosses but not for the intraspecific crosses because of differences in percent meat content which is thought to partially reflect differences in maturation. The correlation of percent meat content between the F₂ and F₄ generations for the interspecific crosses was significant ($r = .54$ and $.44$ for crosses I and II, respectively), while there was no significant correlation for meat content between the F₂ and

F₄ generations for the intraspecific crosses. The consistent response for meat content over generations for the interspecific crosses suggests that indirect selection for maturity may have contributed to the effectiveness of selection for the interspecific crosses.

The effectiveness of stratified mass selection for seed yield of interspecific crosses in peanuts suggests that mass selection can be used to select higher yielding F₂ plants from crosses of local by exotic germplasm. Selection for a few highly heritable traits like fruit size and shape could also be practiced among the F₂ plants of an interspecific cross. Mass selection in the F₂ generation of interspecific crosses could be followed by single seed descent of desired selections. However, some caution is needed in selecting for high yield in the early generations of interspecific crosses as indicated by the significant shortening of maturity and of fruit lengths, lowering of weight per seed, and increasing number of seed per fruit in the cross with PI 155245, as changes in these characters may be opposite to that desired for cultivar development.

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