

Genetic Study of Yield of Seed Cotton and Plant Height in Cotton Genotypes

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ABSTRACT

A genetic study involving diallel crossing scheme in eight upland cotton cultivars having some particular attribute for repelling the cotton insect pests was used to investigate the inheritance of number of bolls per plant, yield of seed cotton per plant and height of the main stem. Average dominance over all the loci across all the parents was within the range of incomplete dominance. The estimates of genetic components indicated both additive (d) as well as dominance estimates (H_1 & H_2) affect the variation in the material, because $H_1 > D$, the effect of genes with dominance properties appeared to be more pronounced. These additive and non additive genetic components can be utilized by adopting biparental mating in early generations among the selected lines or diallel selective mating in breeding programs for the improvement of the yield character in the crosses of these cotton cultivars.

Key Words: Cotton; Gene action; Inheritance; Genetics

INTRODUCTION

Almost all plant species are consumed by herbivorous animals. Among these, insects are especially conspicuous in all the communities (Futuyma, 2000). Insect herbivory is often detrimental to plants and causes a significant loss of plant growth, survival and, therefore, a reduction in plant fitness (Lehtila & Strauss, 1999). Evolutionary interactions between herbivores and plants have resulted in an impressive variety of adaptations and herbivory pressure has led to the evolution of chemical, mechanical and phenological defenses in plants. Empirical studies have demonstrated that there is a wide range of characters involved in plant defense. In cotton plant, these include, gossypol glands, red leaves, nectariless, fregobtracts, okra type leaves and hairy ness.

In this study, we selected eight varieties of upland cotton belonging to same species (*Gossypium hirsutum* L.), which were the same in life form, but with different origins. We used diallel crosses, which help in parental selection, supplying data on parental genotypic values and mainly on their ability to combine in hybrids that produce promising segregant populations. Diallel analysis also allows understanding genetic control of the trait, which helps the breeder to advance and select the segregant populations. Diallel crossing technique in cotton has been used by other cotton breeders also to get the genetic information about different characters (Deshmukh *et al.*, 1999; Baloch, 2002; Basal & Ismail, 2003; Chandio *et al.*, 2003; Deshpande *et al.*, 2003; Mehetre *et al.*, 2003).

The method proposed by Jinks and Hayman (Hayman, 1954a; Jinks, 1954) for diallel analysis allows a quick and

general estimate of the genetic relationship among the parents involved in a diallel cross. The objectives of this work were to assess the inheritance pattern of yield and other quantitative characters and their genetic components in the parents belonging to *Gossypium hirsutum* and to obtain data on the allelic interaction among the parents involved in crosses within this species.

MATERIALS AND METHODS

This study was conducted on a field at the department of Plant Breeding and Genetics, University College of Agriculture, Bahauddin Zakaryia University, Multan, (30.2°N, 71.4°E) Pakistan. The eight varieties of cotton were chosen based on comparable maturity duration and presence of one or more non-preference traits for insect pests (Table I).

Glasshouse cultivation. Seeds of the parental cultivars were grown in 30 x 30 cm earthen pots containing a mixture of equivalent volumes of sand, soil and farm yard manure from mid November 2000 to mid March 2001 in the greenhouse. Temperature in the glasshouse was maintained at 30°C during the day and 25°C at night by using steam as well as electric heaters. The plants were exposed to natural sunlight and supplemented with artificial lighting, a photoperiod of 16 h. Seedlings were thinned to one plant per pot after two weeks of planting and after every 14 days 0.25 g of Urea (46% Nitrogen) was added to each pot, plants were watered daily. Crosses were attempted among eight parental cultivars to obtain 56 F_1 (direct & reciprocal) crosses. Parental cultivars were maintained through self pollination.

Table I. Particular attributes of cotton cultivars

Sr. No.	Cultivar	Distinctive feature
1	Laokra 5.5	Okra type leaf (L°L°)
2	DPL - 7340-424	Nectariless (ne ₁ ne ₂ ne ₃)
3	Fregobract	Fregobracts
4	Glandless 4195-220	Glandless
5	SA100	Red leaves (R ₁ R ₁)
6	Stoneville-857	Nectariless (ne ₁ ne ₂ ne ₃)
7	S-12	High yield cultivar
8	B-557	Obsolete local cultivar

Field evaluation. The eight varieties of cotton along with their 56 hybrids were planted on a clay loam soil on June 1, 2001. The experimental design was a triplicate randomized complete block design. The growth protocol was identical for all the genotypes. The experimental plot was a 3.3 m single row with intra and inter row distances of 30 and 75 cm, respectively. The F₁ hybrid and parents were self-pollinated to raise F₂ progeny. F₂ progeny was sown in the same field also in a triplicate randomized complete block design (RCBD) on first of June 2002. The plot size for each cross in each replication was 3.3 x 6 m. Ten plants in F₁ generation in each replication were randomly selected for data recording. Sample size for F₂ generation was sixty competitive plants in each replication. The matured bolls were hand picked after every two weeks as soon as bolls started to open F₁ and F₂ for both the generations 150 days after planting (DAP) for three harvests and seed cotton was collected in Kraft paper bags. Picking was done when the dew had evaporated.

Bolls number per plant. The number of matured bolls from all the three picks was counted and cumulative record was maintained for each plant separately. Then the average number of bolls per plant for each genotype per replication was computed.

Yield of seed cotton per plant (grams). The matured bolls were hand picked after every two weeks as soon as bolls started to open F₁ and F₂ for both the generations 150 days after planting (DAP) for three harvests and seed cotton was collected in Kraft paper bags. Picking was done when the dew had evaporated. The harvest was weighed on electronic balance (Mettler PE 360) and the average yield of seed cotton per plant for each genotype in each replication was then calculated and recorded.

Height of the main stem (cm). When apical growth of the main stem had ceased, the final height of the plants were recorded in centimeters. The measurement was done with a measuring rod from the 1st Cotyledonary node to the apical bud. Average height per plant for each family was worked out for statistical analysis.

Statistical analysis. Mean squares estimates were calculated following Fisher's analysis of variance (Steel & Torrie 1980). Simple additive – dominance model approach of (Hayman, 1954a, b; Jinks, 1954; Singh & Chaudhary, 1979) as modified by Mather and Jinks (1982) was followed for genetic analysis and for the estimation of components of genetic variation. The estimates of the components of

variation and related genetic parameters were estimated for those characters, which showed complete or partial adequacy of additive dominance mode. The significance of components of variation in F₁ generation was tested (Jinks, 1956; Hayman, 1958; Mather & Jinks, 1971). When the value of a parameter divided by its standard error exceeds 1.96 then it was significant, while for F₂ generation the significance of the various statistics were tested by 't' test at n-2 degree of freedom as: $t = \text{parameter} / S - E \text{ of parameter}$

RESULTS AND DISCUSSION

Bolls numbers/plant. The mean sum of squares and appropriate degrees of freedom for analysis of variance are given in Table II. The 'F' test indicated that the difference among sixty four genotypes were highly significant at 0.01% probability level in both F₁ and F₂ generations. The significant differences indicated that the parents were diverse for the characters studied and that this diversity could be transmitted to, the offspring's and it validated the genetic analysis of the data.

The diallel analysis of variance (Table III) contains the significance levels of the components. The significance of component (a) shows that additive effects are present. The significance of (b) shows that dominance is also present, while highly significant (b₁) in F₁ generation shows that it is largely unidirectional and it is non-significant in F₂ generation showing absence of directional dominance effects. The (b₂) item is non significant for both the generations so asymmetry is present at loci exhibiting dominance. The (b₃) portion of the (b) item is significant in F₁ generation therefore showing presence of specific gene effects, while it is non-significant in F₂ generation thus absence of specific gene effects. The significant differences between reciprocal families (c) in F₁ generation are an unfortunate systematic effect due to faulty layout, so that the use of mean reciprocals in all other computations was justified. It is now significant so (a) was retested by (c). After retesting, the item (a) is again significant it means that additive effects are not affected by maternal effects. However, in F₂ generation (c) is non-significant so (a) item is not retested against (c). Reciprocal effects are not present as (d) item was non-significant in both the generations so we cannot retest b, b₁ and b₃ against it.

The regression analysis of F₁ generation (Table IV) regarding number of bolls per plant indicated that the regression coefficient ($b = 0.48 \pm 0.20$) depart significantly from unity but not from zero, which indicated, non-additive variation included epistasis or multiple allelism and correlated genes distribution among the parents. Therefore, the data did not fulfill the diallel assumptions; hence, additive dominance model was partially inadequate. The regression analysis of F₂ generation (Table IV) regarding number of bolls per plant indicated that the regression coefficient ($b = 1.22 \pm 0.27$) depart significantly from zero and not from unity, suggesting no non-allelic interaction and

Table II. Estimates of mean square for boll number, yield of seed cotton and height of stem

Parameters	Mean Squares	
	Genotypic	Error
Boll number		
F ₁	110.00**	54.00
F ₂	30.00**	4.00
Yield of seed cotton		
F ₁	1661.00**	1013
F ₂	386.20**	33.00
Height of Main stem		
F ₁	854.64**	1.07
F ₂	701.79**	18.07

* = Indicate significant differences at P < 0.05 probability level.

** = Indicate significant differences at P < 0.01 probability level.

NS = Non significant at P < 0.05 probability level.

an independence of genes distribution among the parents for number of bolls per plant. Thus, the additive-dominance model did provide fair basis for interpreting the results.

The diallel data with variance and covariance for F₁ generation are presented in Table V. This table elaborated that there was no evidence of dominance effects as the mean square between arrays for Wr + Vr was non-significant, while the mean square between arrays for Wr - Vr was also non-significant, thus emphasizing partial adequacy of additive dominance hypothesis. The analysis of variance of Wr + Vr and Wr - Vr (Table V) revealed that Wr + Vr varies significantly from array to array, where as Wr - Vr did not vary in F₂ generation. There was, therefore, clear evidence of non-independence in effect of non-allelic genes. This means that not only was there no evidence of interaction between non-allelic genes in producing their effects, but also that there was no evidence of the genes being associated in a non-random way in their distribution between the parents (Mather & Jinks, 1977). Evidently, the additive dominance model was adequate to account for the behavior of this diallel. The additive-dominance model was shown to be adequate by both the tests for number of bolls per plant in F₂ generation. Similar findings were also reported by Amin *et al.* (1989), Khan *et al.* (1990) and Murtaza *et al.* (1995), who advocated the presence of over dominance type of genetic mechanism for number of bolls per plant.

The estimates of the components of variation for these characters are presented in Table VI. These estimates indicated that both additive (d) as well as dominance

estimates (H₁ & H₂) affect the variation in the material, because H₁ > D, the effect of genes with dominance properties appeared to be more pronounced. The dominance ratio (H₁/D)^{0.5} exceeded 1.0, which would arise when dominance was complete and offered a quantification of the level of "over dominance" this was for number of bolls per plants (F₂). The values of H₁ and H₂ for boll numbers were higher than those of D and were significant and positive, which indicated the predominance of non-additive genetic variance to control the character under study.

The H₂ component was smaller than the H₁, indicating the un-equal proportion of positive (u) and negative (v) alleles in the loci governing the character. The asymmetrical distribution of genes in the parents were further evidenced by the value of H₂/4 H₁ (Table VI), which were below the maximum value of 0.25, which arises when, u = v = 0.5 over all loci. The positive F value also indicated gene asymmetry, i.e. there were more dominant than recessive alleles in the parents for this character. This was further confirmed by the proportion of dominant and recessive alleles, which was more than one for boll number, proving that dominant alleles were in excess as compared to recessive alleles.

Net dominance effect obtained by (h²) estimate expressed as algebraic sum over all loci in heterozygous condition in all the crosses were non-significant for boll number (Table VI), and suggested that substantial contribution of dominance was not due to heterogeneity of loci in this parameter. The non-significance of environmental component of variation (E₂) indicated that environment did not play any role in the phenotypic expression of this character. The number of gene groups exhibiting dominance to some degree, estimated on h²/H₂ was not near unity for number of boll character. However, this estimate provides no information about groups of genes exhibiting little or no dominance.

High estimates of heritability in narrow sense were obtained for number of bolls per plant (F₂), which represents fixable, additive heritable variation, indicates that response to selection should be rapid. This offers a lot of scope for improvement of this character through individual plant selection.

Yield of seed cotton. The results pertaining to analysis of variance are presented in Table II for F₁ and F₂ revealed that the genotypic differences among sixty four genotypes were

Table III. Diallel analysis of variance for boll number, yield of seed cotton and height of stem

Parameters Item	d.f F ₁ & F ₂	Boll number Mean Squares		Yield of seed cotton Mean Squares		Height of stem Mean Square	
		F ₁	F ₂	F ₁	F ₂	F ₁	F ₂
a	7	1161.00**	294.89**	1589.0*	3746.0**	6143**	5355.4**
b	28	252.01**	71.00**	3572.3**	993.9**	2571**	1542.9**
b ₁	1	1088.00**	29.88 ^{NS}	1048.8*	4602.0*	3528*	8909.3*
b ₂	7	230.00 ^{NS}	101.00 ^{NS}	3422.9**	957.0 ^{NS}	2018 ^{NS}	2202 ^{NS}
b ₃	20	216.95*	61.93 ^{NS}	32.79 ^{NS}	827.0 ^{NS}	1110 ^{NS}	943.8 ^{NS}
c	7	313.90*	58.90 ^{NS}	4414.0**	518.0 ^{NS}	2079 ^{NS}	1459 ^{NS}
d	21	160.95 ^{NS}	51.94 ^{NS}	3411.0**	719.9 ^{NS}	1523 ^{NS}	1987 ^{NS}
e	63	111.92	50.91	1297.0	705.0	1600	1367

Table IV. Test of regression coefficient for boll number, yield of seed cotton and height of stem

Parameters	Regression Coefficient (b)	Standard Error of regression SE (b)	t value for b-0	t value for 1-b
Boll number				
F ₁	0.48	0.20	2.40 ^{NS}	2.70 [*]
F ₂	1.22	0.27	4.50 [*]	-0.80 ^{NS}
Yield of seed cotton				
F ₁	0.24	0.18	1.35 ^{NS}	4.29 [*]
F ₂	0.76	0.23	3.24 [*]	1.05 ^{NS}
Height of stem				
F ₁	0.93	0.17	5.60 [*]	0.44 ^{NS}
F ₂	1.04	0.23	4.54 [*]	-0.16 ^{NS}

significant at 0.05 and 0.01% level of significance, respectively in both the generations, hence it permits to proceed for further genetic analysis.

The analysis of variance (Table III) for yield of seed cotton in both the generations showed that (a) and (b) items were highly significant, so they showed presence of additive and dominance effects. The significance of item (b₁) in both the generations showed the presence of directional dominance effects. The (b₂) was significant in F₁ generation indicating symmetrical distribution of genes, while it was non significant in F₂ generation showing asymmetrical distribution of genes. The (b₃) item was also significant in F₁ generation showed presence of specific gene effects, while it was non-significant in F₂ generation, which indicated that specific gene effects were absent. The (c) and (d) items both were non-significant in F₂ generation showed the absence of maternal and reciprocal effects, while they were significant in F₁ generation so we retested (a) by (c) and b, b₁, b₂ and b₃ by (d). After retesting (a) become non-significant, which means that additive effects were masked by the presence of maternal effects. Similarly after retesting b, b₁, b₂ and b₃ were also become non-significant, which indicated that dominance effects had been suppressed due to the reciprocal effects.

The analysis of Vr and Wr regression (Table IV) showed that regression coefficient depart significantly at 0.01% level of significance from unity but not from zero ($b = 0.24 \pm 0.18$) in F₁ generation, Which indicated that non-additive variation included epistasis, multiple allelism and correlated genes distribution among the parents were present. Therefore, the data did not fulfill the diallel assumptions hence additive dominance model was partially inadequate.

The diallel data with variance and covariance for F₁ generation are presented in Table V. This table elaborated that there was no evidence of dominance effects as the mean square between arrays for Wr + Vr was non significant, while the mean square between arrays for Wr - Vr was also non-significant, in F₁ generation for yield of seed cotton per plant, thus emphasizing partial adequacy of additive-dominance hypothesis. These findings were in agreement with earlier scientists, who also observed additive with partial dominance in their material for yield of seed cotton

as we have seen in our material, (Tyagi, 1988; Murtaza *et al.*, 1992).

The results presented in Table IV showed regression coefficient of ($b = 0.76 \pm 0.23$) F₂ generation for yield of seed cotton per plant which differed significantly at 0.05% level of significance from zero but not from unity, which indicated the adequacy of additive-dominance model. The analysis of variance of arrays presented in Table V indicated that for F₂ generation mean square between array of Wr + Vr and Wr - Vr were also significant at 0.01% level of significance. The significant Wr - Vr mean squares between arrays due to the presence of non-allelic interaction hence invalidate the model and did not permit further analysis.

The estimates of the components of variation analysis are given in Table VI, which showed that additive genetic component (D) were non-significant and indicated the predominance of non-additive genetic variance in the inheritance of this character in F₁ generation. However, F₂ generation showed that additive genetic effects were predominant due to significance of (D).

Dominance (H₁ & H₂) components of genetic variation exceeded the additive component (D) supporting "over dominance" for yield of seed cotton (F₂); while dominance components were non significant for yield of seed cotton (F₁).

The existence of unequal gene frequencies in the parents were suggested by (H₁ & H₂) as H₂ component was smaller than H₁. The asymmetrical distribution of genes in the parents were further evidenced by the value of H₂/4 H₁, which were found to be less than maximum value of 0.25 for this character in both the generations, which arises when $u = v = 0.5$ over all loci.

The positive "F" value also indicates gene asymmetry i.e. there were more dominant than recessive alleles in the parents for this character. This was further confirmed by the proportion of dominant and recessive alleles, which were more than one for this character, proving that dominant alleles were in excess as compared to recessive alleles. Net dominance effects obtained by (h²) estimate expressed as algebraic sum over all loci in heterozygous condition in all of the crosses were significant, which suggested substantial contribution of dominance was due to heterogeneity of loci in this parameter.

The significant value of environmental component of variation (E₂) indicated that environment play an important role in the phenotypic expression of, yield of seed cotton (F₁), where it did not play any role in the phenotypic expression in F₂. The over all degree of dominance ratio (H₁/D)^{0.5} were more than unity. This indicated the operation of over dominance in this character.

The number of gene groups exhibiting dominance to some degree, estimated on h₂/H₂ was above unity. Narrow sense heritability is a reflection of the amount of additive, fixable, heritable variation. The low additive effect decreases heritability values, while high additive effects increase it. Yield of seed cotton showed moderate or high h²

Table V. Heterogeneity test for (Wr + Vr) and (Wr - Vr) estimates

Parameters	d.f	Boll number		Yield of seed cotton Mean Squares		Height of stem Mean Squares	
		Mean Squares		F ₁	F ₂	F ₁	F ₂
		F ₁	F ₂				
Wr + Vr between arrays	7	30.31 ^{NS}	2.31*	3.09 ^{NS}	0.28**	2.23**	1.29**
Wr + Vr within arrays	16	24.0	0.71	5.80	0.07	0.15	0.02
Wr - Vr between arrays	7	5.60 ^{NS}	0.20 ^{NS}	1.61 ^{NS}	0.03**	0.08**	0.09**
Wr - Vr within arrays	16	3.12	0.09	2.23	0.008	0.02	0.005

Table VI. Genetic parameters for boll number, yield of seed cotton and height of stem

Components of Variation	Boll number		Yield of seed cotton		Height of stem	
	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂
D	6.99 ^{NS} ± 7.91	18.0 ^{NS} ± 1.77	-126 ^{NS} ± 90.0	186.9 [*] ± 24.0	543 [*] ± 42.3	504 [*] ± 41.47
H ₁	24.00 ^{NS} ± 18.1	73.6 [*] ± 16.50	106 ^{NS} ± 207	1005 [*] ± 219.0	679 [*] ± 97.1	1997 [*] ± 3.81
H ₂	18.80 ^{NS} ± 16.0	45.1 [*] ± 14.40	86.0 ^{NS} ± 180	730 [*] ± 191.0	524 [*] ± 84.5	1287 [*] ± 332
H ²	44.81 [*] ± 10.62	-11.9 ^{NS} ± 9.62	355 [*] ± 121	741.1 [*] ± 628.0	1704 [*] ± 56.7	1648 [*] ± 223
F	-15.3 ^{NS} ± 18.8	35.4 [*] ± 8.51	-459 ^{NS} ± 213	315.0 [*] ± 113	534.0 [*] ± 99	1078 [*] ± 196
E ₂	18.54 [*] ± 2.63	1.28 ^{NS} ± 0.61	359 [*] ± 30.0	10.9 ^{NS} ± 7.90	23.7 ^{NS} ± 14.1	6.02 ^{NS} ± 13.8
(H ₁ /D) ^{0.5}	1.85	1.02	-0.42	1.16	1.12	1.00
(H ₂ /4H ₁)	0.20	0.15	0.20	0.18	0.19	0.16
K _D /K _R	0.26	65.34	1.19	6.31	2.57	-27.40
K=h ² /H ₂	2.40	-0.26	4.12	1.02	3.25	1.28
H ² (ns)	0.37	0.75	0.50	0.57	0.35	0.99

(n.s). According to Hayman (1957), epistasis can decrease or increase degree of dominance, which also effect on heritability estimates.

The results of diallel analysis showed that additive type of gene action with partial dominance was operative in the inheritance Yield of seed cotton. The estimates of the genetic components also indicated that both additive and non additive genetic components were important in governing the various yield and yield components, biparental mating in early generation among the selected lines or diallel selective mating can be adopted in breeding programs for the improvement of the yield character in these cotton cultivars crosses.

Height of the main stem. The mean sums of square for analysis of variance and appropriate degrees of freedom are given in Table II. The "F" test indicated that the mean sum of squares of families were highly significant for both the generations thus permitting the data for further analysis.

A perusal of Table III revealed the significance of (a) and (b) components in both the generations, which showed that additive and dominance effects were present. The significance of (b₁) in both F₁ and F₂ generations showed the presence of directional dominance effects. The asymmetrical distributions of genes along with absence of specific gene effects were evident from the non-significance of the (b₂) and (b₃) components. The absence of maternal effects along with absence of reciprocal effects was clear from the non-significance of both (c) and (d) components in both the generations for height of the main stem.

The regression analysis of F₁ generation (Table IV) regarding height of the main stem indicated that the regression coefficient (b = 0.93 ± 0.17) depart significantly from zero and not from unity, suggesting no non-allelic interaction and an independence of genes distribution

among the parents for height of the main stem. Thus, the additive dominance model did provide fair basis for interpreting the results.

The analysis of variance of Wr + Vr and Wr - Vr for F₁ generation (Table V) revealed that Wr + Vr and Wr - Vr varies significantly from array to array. The significant variance ratio for Wr - Vr invalidates the additive-dominance model. Therefore, it was difficult to get a clear picture about the inheritance of this character in F₁ generation due to the failure of diallel assumptions, i.e. no epistasis, no multiple allelism and genes were not independently distributed among the parents.

The regression analysis of F₂ generation (Table IV) indicated that the regression coefficient (b = 1.04 ± 0.23) did not depart significantly at 0.05% level of significance from unity. There was, thus, evidence of dominance but no evidence of non-allelic interaction and non-random distribution of genes among the parents. The analysis of arrays for Wr + Vr and Wr - Vr for F₂ generation, revealed that Wr + Vr and Wr - Vr varies significantly from array to array. The significant variance ratio for Wr - Vr invalidates the additive-dominance model. Therefore, there was no clear picture about the inheritance of this character and it did not permit for further analysis. This being the case, it was not legitimate to produce graphs of Wr on Vr.

Kalsy and Gary (1988) and Khan and Khan (1993) also found that Wr - Vr varies significantly from array to array and observed the involvement of epistasis in the inheritance of height of the main stem in cotton.

Both additive (D) and dominance (H₁ & H₂) components were involved in the control of plant height (Table VI), confirming the conclusion from (Wr + Vr) and (Wr - Vr) values. The value of (H₁/D)^{1/2} was found to be 1.00 it also indicated additive with dominance type of gene

action. H_1 and H_2 were not similar, indicating that positive (u) and negative (v) allele frequencies were not equal. The positive value of 'F' indicated that the number of dominant alleles were greater than the recessive alleles. The ratio of $\frac{1}{4}(H_2/H_1)$ was less than 0.25 it also indicated that positive and negative alleles frequencies over all loci were un-equal. The value of the quantity $(4 DH_1)^{1/2} + F/(4 DH_1)^{1/2} - F$ was also more than one, which also showed that dominant genes were greater than recessive genes as proved by positive value of F. The ratio of h^2/H_2 indicated that at least 2 - 3 alleles were responsible for plant height. Moderate to high heritability (ns) was observed. Since both additive and non additive genetic components were important in governing the plant height, reciprocal recurrent selection as a breeding procedure may be very useful for getting smaller plants.

CONCLUSION

The inheritance pattern of variation for different quantitative characters in these eight genotypes of (*Gossypium hirsutum* L.), having non-preference traits for insect pests, revealed by the diallel data appeared to be complex. Although genetic variation for the characters appeared to be influenced predominantly by genes with additive or dominance effects, the presence of a significant additive component is encouraging. Based on narrow sense heritability and expected genetic gain because of selection, a potentially useful advance in high yielding with short stature cultivars seems possible to achieve by selecting individual plants showing better qualities.

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