

Breeding Behavior Effects for Yield, its Components and Fiber Quality Traits in Intraspecific Crosses of Cotton (*G. hirsutum* L.)

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Abstract: Six upland cotton (*G. hirsutum* L.) varieties were crossed in all possible combinations. The parents and F_1 were sown in a replicated experiment. Hayman's diallel cross analysis was employed to investigate the nature of gene action involved in the inheritance of number of sympodial branches per plant, number of bolls per plant, boll weight, yield, ginning out turn %, staple length, fiber fineness and fiber strength. The diallel analysis revealed that all the characters were polygenically inherited and exhibited partial dominance with additive gene action. The estimation of component of variation for these characters suggested that the (D) additive component was significant in all the traits under study and was lower than dominant components (H_1 and H_2) of variation except for number of sympodial branches per plant, number of bolls per plant and seed cotton yield per plant, where the dominant components were higher in magnitude than additive. The positive estimate of F indicated that dominant genes were in excess than recessive genes in the parents for all the traits except for ginning out turn percentage and fiber fineness. The ratio of $H_2/4H_1$ indicated largely asymmetry of positive and negative genes in parents for number of bolls per plant, seed cotton yield, staple length, fiber fineness and fiber strength, and symmetrical distribution of positive and negative genes in the parents was observed for number of sympodial branches per plant, boll weight and ginning out turn percentage. The h^2 value for number of number of sympodial branches per plant, number of bolls per plant, boll weight, seed cotton yield per plant, ginning out turn, staple length, fiber fineness, and fiber strength was positive and significant which indicated that hetrotic breeding was rewarding for these traits. The correlation between $W_r + V_r$ and Y_i indicated that dominant genes are mainly responsible for the expression of all traits. Mass selection will be an effective method for improving the boll weight and reciprocal recurrent selection method will be helpful for improving the sympodial branches per plant, number of bolls per plant, seed cotton yield, fiber fineness and fiber strength. The full sib or half sib family selection, pedigree, and progeny test would probably be necessary to achieve the genetic progress for GOT% and staple length.

Key words: Yield, fiber, cotton

Introduction

Cotton has been a major Pakistan crop since the invention of the cotton gin made mass production possible. Within the limit of accepted fiber quality, breeders and geneticist have selected for increased lint yield per unit land area in order to produce competitive varieties.

Afzal (1949) and Worley *et al.* (1974) suggested that number of bolls per plant or per unit area, the size of boll (boll weight) and percentage of lint are the physical features that determine the yield of seed cotton and the main characteristics of cotton fiber, which influence its end-user and its price, are fiber length, fiber strength and fineness. In 1975, Culp and Harrell reported that maintaining a high lint percentage was necessary to ensure high lint yield. Selection for boll size and seed size could positively influence lint yield, especially if the breeder selected for medium to small boll with the greatest possible number of small seeds boll and maintained high lint percentage. Green and Culp (1990) reported additive gene action for fiber length, fiber strength, fiber fineness and lint per unit land area. Tiwari *et al.* (1992) studied thirteen F_1 and F_2 inter-varietal crosses in cotton (*G. hirsutum* L.) for inheritance of seed cotton yield, boll number and boll weight, both additive and non-additive gene actions were found equally important in the expression of boll number and boll weight. They further reported that seed cotton yield showed non-additive gene action. The degree of dominance varied from cross to cross in each trait. Ikram *et al.* (1993) reported non-additive type of genetic behavior for yield, ginning out turn percentage, while boll number, boll weight, staple length and number of sympodial branches were predominantly controlled by additive gene action. Yingxin and Xiangming (1998) suggested that bolls per plant, seed cotton yield, lint percentage was controlled by additive and non-additive gene actions while fiber length, strength and fineness were mainly under the control of non-additive gene action. Non-additive gene effects mainly controlled Boll size. Rady *et al.* (1999) also reported non additive genetic effects in determining the performance of seed cotton yield, number of bolls per plant, boll weight, lint percentage and lint yield. Hendawy *et al.* (1999) suggested that the additive genetic variance (D) and dominance variance (H_1 and H_2) were highly significant for fiber length, strength and fiber fineness, but dominance genetic variance (H_1 and H_2) were greater in their magnitude than the corresponding additive genetic variances. Parental varieties carried more dominant genes than recessive genes for these traits. The average degree of dominance (H_1/D) was greater than unity, revealing the presence of over dominance in the inheritance of these traits. Subhan *et al.* (2001) observed significant differences among hybrids and their parents in upland cotton for quantitative traits and reported additive type of gene action for number of bolls per plant and lint percentage, while, over-dominance type of gene action for seed cotton yield per plant.

Materials and Methods

Ten varieties of upland cotton, representing a wide range of seed cotton yield and its components and fiber quality traits were grown in 1998 in a performance experiment at Cotton Research Station Multan. The purpose of this test was to survey varieties for suitable parental material for a genetic study. Out of these, six selected varieties viz; Reshmi, MNH-439, S-14, NIAB-78, DPL-54 and MNH-93 were crossed in all possible combinations. F_1 of each cross was raised in

three replications using Randomized Complete Block Design (RCBD). The data was recorded from the centrally ten guarded plants of each replication. Experimental plot was 4.6 meter long, single row with 30 cm plant to plant distance, while row to row distance was kept 75 cm. The data Number of sympodial branches per plant, number of bolls per plant, Boll weight (g), Yield of seed cotton (g), Ginning out turn (GOT %), Staple length (mm), Fiber fineness (micronaire) and Fiber strength (TPPSI).

The data was subjected to standard analysis of variance technique (Steel and Torrie 1980) was applied to determine significance of means. Only where significant genotype differences were found, data were further subjected to genetic analysis. The diallel cross technique developed by Hayman (1954a, 1954b and 1958), Jinks (1954 and 1956) and Jinks and Hayman (1953) was used for genetic analysis.

Results and Discussion

Number of sympodial branches per plant

The sympodial branches play an important role in yield of seed cotton as these branches bear fruit directly. Information concerning to the nature of gene action involved in number of sympodial branches per plant greatly helps in breeding new high yielding varieties bearing higher number of sympodial branches per plant.

The analysis of variance for this trait indicated that highly significant differences existed among genotypes under study (Table 1). These results are in conformity with the earlier findings of Ikram *et al.* (1993), Estimates of genetic components of variation (Table 2) revealed that both additive (D) and dominance effects (H_1 and H_2) were significant. However, dominance component ($H_1=54.20$ and $H_2=46.84$) was higher in magnitude than that of additive component. The positive estimate of F indicated that dominant alleles were in excess than recessive ones in the parents. The ratio of $(H_1/D)^{1/2} = (1.25)$ was greater than unity, thus showing higher degree of dominance. The ratio $H_2/4H_1$ indicated unequal distribution of positive and negative genes in the parental population. The ratio $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$ having value (1.81) more than one, indicated the preponderance of dominant genes in the parents.

Total number of bolls per plant

Number of bolls per plant plays an important role in yield of seed cotton. Boll setting is affected by the agronomic inputs, plant protection measures and genetic constitution of a genotype (Poehlman, 1986). Therefore to develop new genotypes with improved genetic constitution, the behaviour of this trait was included in the study. The analysis of variance for number of bolls per plant indicated that differences among genotypes were highly significant (Table 1).

The estimates of components of genetic variance (D, H_1 , H_2 , F) along with their standard errors (Table 2) showed that the additive component ($D=65.69$) and non-additive (dominance) component ($H_1=79.37$, $H_2=52.80$) were significantly different from zero. It was further observed that dominance genetic variance was larger than additive genetic variance. The value of H_1 is greater than H_2 , which indicated the occurrence of unequal gene frequencies at all

heterozygous loci. The positive and significant value of F (4.50) indicated that there were more dominant alleles than recessive alleles in the parents. This finding was further supported by the estimate of ratio $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$, as the value was higher than one. The degree of dominance was determined by computing the ratio $(H_1/D)^{1/2}$. Since its value was greater than 1.0, therefore it indicated the prevalence of dominance over additive effects. The value of $H_2/4H_1$ (0.17) indicated asymmetrical frequency of positive and negative effects of dominant genes. The estimate of h^2 (40.03) which measures the overall heterosis was positive and significant for this trait, thus suggested that the heterosis breeding for this trait might be rewarding. Correlation between the parental order of dominance ($W_r + V_r$) and parental mean performance (y_i) showed that this trait is controlled mainly by dominant genes. Similar findings were also observed by Yingxin and Xiangming (1998) and Subhan *et al.* (2001).

Table 1: Mean squares for various plant characters of cotton in F₁ generation of 6 × 6 diallel cross

Source of variation	d.f	No. of sympodial brancher	Total No. of bolls	Seed cotton yield	Boll weight	G.O.T (%)	Staple length	Fiber Strength	Fiber fineness
		plant ⁻¹	plant ⁻¹	plant ⁻¹					
Block	2	0.36	3.24	1.67	0.16	0.95	0.25	0.04	0.09*
Genotypes	35	57.08**	155.02**	2138.08**	0.27**	25.0**	17.45**	4.93**	0.40**
Error	70	4.95	4.13	2.153	0.04	0.12	1.20	0.06	0.01

*: P ≤ 0.05 ; ** : P ≤ 0.01

Table 2: Estimates the components of genetic variance for each character

Component	No. of sympodial brancher	Total No. of bolls	Boll weight	Seed cotton yield per plant	G.O.T (%)	Staple length	Fiber Strength	Fiber fineness
	per plant	per plant		plant				
D	34.79±5.95**	69.46±2.49*	0.14±0.01**	1041.4±127.3**	26.17±0.47**	7.17±0.65**	0.20±0.01**	4.46±0.17**
H ₁	54.20±15.11**	22.24±6.45*	0.01±0.01	1101.5±323.3**	1.89±0.47**	4.38±1.66**	0.19±0.03**	2.50±0.43**
H ₂	46.84±13.49**	0.47±5.76	-0.01±0.01	721.5±288.8**	1.78±0.42**	4.36±1.48**	0.09±0.03**	1.47±0.38**
h ²	17.02±9.08*	7.71±3.87**	0.02±0.08	641.2±194.3**	0.78±0.28	3.10±0.10**	1.35±0.02**	1.62±0.26**
F	25.05±14.53	8.69±6.20	0.04±0.04	202.8±311.1	-1.83±0.45	-4.11±1.60	0.05±0.03*	2.93±0.42**
E	1.48±2.25	6.52±7.34	0.016±0.01**	0.72±48.2	0.04±0.07	0.40±0.39	0.20±0.01**	0.02±0.06
(H ₁ /D) ^{1/2}	1.25	0.566	0.258	1.028	0.268	0.75	0.930	0.562
H ₂ /4H ₁	0.22	0.005	0.250	0.160	0.232	0.24	0.190	0.153
h ² /H ₂	0.36	16.38	2.000	0.880	0.443	0.92	15.07	1.101
(4DH ₁) ^{1/2} +	1.81	1.26	3.395	1.127	0.769	0.46	1.004	2.563
F/(4DH ₁) ^{1/2} -F								
r(Y _i and W _r +V _r)	0.05	0.78	-0.92	-0.78	-0.838	-0.45	-0.92	-0.92
Heritability _(b.s)	71.3	62.4	71.6	59.3	63.8	67.1	68.3	65.3
Heritability _(n.s)	54.6	45.1	5/.3	42.5	52.3	49.4	59.6	55.2

*: P ≤ 0.05; ** : P ≤ 0.01

Boll weight

Average boll weight is one of the major component of seed cotton yield in cotton (Poehlman, 1982). The analysis of variance for boll weight (Table 1) revealed that differences among genotypes were highly significant.

The estimates of component of genetic variance (D, H₁, H₂, F) along with their standard errors indicated that the additive component (D=0.135) was highly significant, while dominance component (H₁=0.012 and H₂=-0.012) were non-significant (Table 2). These values indicated that magnitude of additive component was higher than dominance component. The degree of dominance (H₁/D)^{1/2} having value 0.258 also indicated that greater part of genetic variation was additive as the ratio was less than one. The positive and non significant value of F (0.04) showed that dominant and recessive genes were higher in equal proportion in the parents, which was also supported by the value (3.395) of $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$ being positive. The allelic frequency of positive and negative effects of dominant genes (H₂/4H₁) was symmetrical as its value was 0.25. The estimate of h² which measures the over all heterosis was positive and significant, which suggested that heterosis breeding may be rewarding for this trait. The correlation (r) between the parental order of dominance (W_r+V_r) and the parental mean performance (Y_i) showed that the high expression of trait is controlled mainly by dominant genes as the value is negative (-0.919). It suggested that dominant genes should be fixed in early segregating generations as the trait is additive in nature to improve the boll weight. The results are in agreement with the earlier finding of Tiwari *et al.* (1992), Ikram *et al.* (1993) and Rady *et al.* (1999).

Seed cotton yield

The analysis of variances for this trait showed significant differences among the genotypes for seed cotton yield per plant (Table 1). The estimates of components of genetic variance (D, H₁, H₂, F) indicated that additive component (D=1041.4) and non-additive (dominance) component (H₁=1101.48, H₂=721.48) were significant (Table 2). It was further observed that dominance component was higher than additive component. As the H₁ was greater than H₂ occurrence of unequal gene frequencies at all loci was indicated. The positive value of F (202.8) indicated that there were more dominant genes than recessive genes in the parents, which is also supported by the estimate of ratio $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$ as its value is positive (0.827). The degree of dominance was exhibited by the ratio (H₁ / D)^{1/2}, having value greater than one (1.028), demonstrated that greater part of genetic variation was due to dominance gene action. The ratio of H₂/4H₁ having value 0.16 indicated asymmetrical allelic frequency of positive and negative effects of dominant genes. The estimate of h², which measures the overall heterosis was positive and significant for this trait, indicating heterosis breeding could be rewarding for this trait. The correlation (r) between (W_r + V_r) and (Y_i) showed that this trait is controlled by dominant genes as the value is negative. It suggested that dominant genes should fixed in early segregating generations as the trait is additive in nature to improve the seed cotton yield per plant. The results confirmed the earlier findings of Yingxin and Xiangming (1998), Ikram *et al.* (1993) and Rady *et al.* (1999).

Ginning out turn percentage (GOT %)

The ultimate objective of cotton cultivation is lint production. To increase the lint production, ginning out turn % of the genotypes has to be increased. As a rough estimate one percent increase in GOT would be about three percent increase of seed cotton yield. (Afzal and Ali, 1983) The analysis of variance for GOT % (Table 1) indicated that highly significant differences existed among the genotypes under study.

The estimate of components of genetic variance (D, H₁, H₂, F) showed that the additive component (D = 26.17) and non-additive component (dominance) (H₁ = 1.89, H₂ = 1.78) were highly significant (Table 2) and the additive component was larger than dominance component indicating the prevalence of additive gene action for this trait. As H₁ is nearly equal to H₂, the occurrence of equal gene frequencies at all heterozygous loci was indicated. The negative value (-1.83) of F indicated equal proportion of dominant and recessive genes in the parents, which is also supported by the ratio of $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$ as the value is less than one. The degree of dominance $(H_1/D)^{1/2}$ demonstrated that greater part of genetic variation was additive as the value was less than one. The allelic frequency of positive and negative effects of dominant genes $(H_2/4H_1)$ was symmetrical as the value is nearly 0.25. The estimate of h², which measured the overall magnitude of heterosis was positive and but non-significant thus suggested that heterosis breeding may not be rewarding. Correlation (r) between the parental order of dominance $(W_r + V_r)$ and parental mean performance (Y_i) showed that high expression of this trait was controlled mainly by dominant genes as the value is negative (-0.838). Earlier researchers like Yingxin and Xiangming (1998) and Subhan *et al.* (2001) also reported partial dominance with non-allelic interaction.

Staple length

Staple length of a variety is an important quality character, as it plays an important role in textile industry. Staple length is also called fiber length. Long fiber is a desirable trait for textile industry with reference to spinning. The analysis of variance for fiber length (Table 1) indicated that highly significant differences existed among the genotypes under study.

The estimates of components of genetic variance (D, H₁, H₂, F) indicated that the additive component (D=7.17) and non-additive (dominance) component (H₁=4.38, H₂=3.36) were highly significant but additive component was higher in magnitude than dominance (Table 2). The occurrence of equal gene frequencies at all heterozygous loci was indicated by nearly equal values of H₁ and H₂ estimates. The degree of dominance $(H_1/D)^{1/2}$ for this trait, demonstrated that greater part of genetic variation was additive as the ratio is less than one. The component F (-4.11) was non-significant and negative, indicating equal proportion of dominant and recessive genes in the parents. The allelic frequency of positive and negative effects of dominant genes $(H_2/4H_1)$ was symmetrical for this trait as the value is 0.21 which is supported by the estimate of ratio $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$, having value 0.46 which is less than 1.0. The estimate of h² (3.10), which measures the overall heterosis, was positive and significant for this trait suggesting that heterotic breeding may be rewarding for this trait. Correlation between the parental order of dominance $(W_r + V_r)$ and parental mean performance (Y_i) showed that high expression of this trait

was controlled mainly by dominant genes as the value is negative, suggesting that dominant genes can be accumulated in early segregating generations as the trait is additive in nature to staple length. Similar finding were also reported earlier by Hendawy *et al.* (1999) and Ikram *et al.* (1993).

Fiber fineness

Cotton fibers from some varieties feel soft and silky, fibers from other varieties feel coarse and harsh. The fineness or coarseness of the fibers determines the difference in the way they feel. Fiber fineness is associated with perimeter or diameter of the fiber and with the thickness of the fiber wall. The analysis of variance for fineness showed existence highly significant differences among the present genotypes (Table 1)

The estimates of components of genetic variance (D, H_1 , H_2 , F) showed that additive component ($D=0.204$) and non additive (dominance) component ($H_1=0.190$, $H_2=0.090$) were found highly significant but additive component was higher in magnitude than dominance component (Table 2). As H_1 is greater than H_2 , the occurrence of unequal gene frequencies at all heterozygous loci was evident. The degree of dominance $(H_1/D)^{1/2}$ for this trait, demonstrated that greater part of genetic variation was additive as the ratio is less than one. The F value (0.05) was positive and significant, indicating unequal proportion of dominant and recessive genes in the parents. The ratio of $(H_2/4H_1)$ having value 0.190 indicated that the allelic frequency of positive and negative effects of dominant of genes was not symmetrical for this trait, which is also supported by the unequal magnitude of H_1 and H_2 and ratio $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$ as value is more than one. The overall estimate of heterosis (h^2) was positive and non-significant for this trait suggesting that heterosis breeding may not be rewarding. Correlation (r) between the parental order of dominance ($W_r + V_r$) and parental mean performance (Y_1) showed that high expression of this trait was controlled mainly by dominant genes as the value was negative, thus for fineness recessive genes need to be accumulated and single plant selection in early segregating generations would be fruitful. The results are in accordance with the earlier findings of Hendawy *et al.* (1999).

Fiber strength

It is an important fiber character, which affects the spinning of the lint and quality of the spun yarn. High fiber strength is one of the most desirable character in cotton. The analysis of variance for fiber strength (Table 1) indicted that highly significant differences existed among the genotypes under study.

The estimates of components of genetic variance (D, H_1 , H_2 , F) showed that additive component ($D=4.46$) and non-additive (dominance) components ($H_1=2.50$, $H_2=1.48$) are highly significant but additive component was higher in magnitude than dominance components (Table 2). As H_1 is greater than H_2 , the occurrence of unequal gene frequencies at all heterozygous loci was evident. The estimate of F was positive and larger than its standard error, which indicated a preponderance of dominant alleles governing this character in the parents. The estimate of average degree of dominance $(H_1/D)^{1/2}$ is less than one (0.562) demonstrating the operation of partial dominance for this trait. A rough estimate of frequencies of non-additive loci

can be obtained from $H_2/4H_1$. The ratio (0.153) between the genes with positive and negative effects, being less than 0.25 indicated asymmetrical distribution of positive and negative alleles among the parents. The value of ratio $[(4DH_1)]^{1/2} + F / [(4DH_1)]^{1/2} - F$ is greater than one, thus indicated the excess of dominant genes for this trait in the parents. The positive and significant value of h^2 suggested that heterosis breeding may be rewarding for this trait. The correlation (r) between parental order of dominance ($W_r + V_r$) and parental mean performance (Y_i) was negative, indicating that higher expression of this trait was controlled by dominant alleles. Similar findings have also been reported earlier by Hendawy *et al.* (1999).

Breeding implication

The results obtained by using the analysis of diallel crosses as developed by Jinks and Hayman provided useful information about the genetic relationship among the parents and their hybrids. The analysis of diallel crosses provides information about the gene action in given population or set of parents and in selecting the favourable combinations. Results of present studies indicated that major portion of the variance exhibited by boll weight was additive and additive \times additive in nature (as D is significant, H_1 non significant, narrow sense heritability greater than 50%) suggested that using effective breeding method within this material for improving boll weight would be leading towards the production of varieties rather than commercial hybrids, and mass selection will be an effective breeding method for improving of these two traits within this material. On the other hand mass selection would be less effective for GOT % and staple length as D_1 , H_1 , H_2 were significant, F non-significant and narrow sense heritability moderate to high. Alternative methods such as half or full sib family selection, pedigree, and progeny tests would probably be necessary to achieve genetic progress for these traits in this material. The information obtained regarding D , H_1 and degree of dominance suggested that a substantial potential existed for obtaining improvement for above mentioned traits in this material through the use of breeding programs utilizing F_1 hybrids. The nature of inheritance of number of sympodial branches per plant, number of bolls per plant, seed cotton yield, fiber fineness and fiber strength revealed that in the current studies, the use of reciprocal recurrent selection which would permit simultaneous exploitation of both the additive and non additive genetic variances, should provide improvement in above mentioned traits, as the additive (D) and non additive (H_1 and H_2) components were significant, $H_2/4H_1$ value was less than 0.25.

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