

Gene Action and Heritability Studies in Cotton (*Gossypium hirsutum* L.)

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Abstract: Mode of gene action and heritability were estimated for ginning out-turn, staple length, fibre maturity, fibre fineness, fibre strength and yield of cotton. Six genotypes B-557, Culture 728-4, MNH156, B-1850 (ne), Culture-604-4 and MNH147 were crossed in all possible combinations in diallel fashion. The results from scaling tests for the adequacy of additive-dominance model indicated that ginning out-turn, fibre fineness and fibre strength were found full adequate, whereas staple length, fibre maturity and seed cotton yield were partially adequate for further genetic analysis. Ginning out-turn, fibre fineness, fibre strength and yield were controlled by additive genes, whereas over-dominance was prevalent in staple length and fibre maturity. High narrow sense heritability for ginning out-turn and fibre strength suggested that these parameters could effectively be improved through selection in the early segregating generations, whereas chances of improvement for fibre fineness and seed cotton yield would be moderate as heritability estimates for these parameters were medium ($h^2_{NS} = 0.608$ and 0.702% respectively, but poor for staple length).

Key words: Fibre traits, yield, additive, over-dominance, cotton

Introduction

Mode of inheritance of economic traits is a pre-requisite for enhanced progress in breeding new varieties of cotton. The diallel analysis technique (Mather and Jinks, 1982) is a useful tool to obtain precise information about the type of gene action involved for the expression of various yield and fibre characters and to predict the performance of the progenies in the latter segregating generations.

Various studies pertaining to genetic analysis of cotton have been carried out by different research workers. For instance, additive and dominant effects of genes (Esmail *et al.*, 1999; Kumaresan *et al.*, 2000), additive gene action (Saeed *et al.*, 1996; Rady *et al.*, 1999; Baloch *et al.*, 2000) and over-dominance (Subhan *et al.*, 2001) for seed cotton yield have been reported in different studies. Medium narrow sense heritability for the same character was estimated by Yingxin and Xiangming (1998). Ginning out turn percentage was found under the control of additive effects of genes with partial dominance (Shah *et al.*, 1992; Hussain *et al.* (1999) in *G. hirsutum* L. Contrasting to this additive type of gene action for ginning out-turn (Hendway *et al.*, 1999; Kalwar and Babar, 1999; Rady *et al.*, 1999) and staple length (Kalwar and Babar, 1999) have also been investigated in cotton. Jagtap and Mehtari (1998) working on *G. hirsutum* L. calculated

high narrow sense heritability estimates for ginning out turn, whereas both broad and narrow sense heritability estimates for ginning out-turn were high in the findings of Esmail *et al.* (1999). In the studies of Ahmad *et al.* (1997), over dominance prevailed for control of staple length and fibre fineness in cotton (*G. hirsutum* L.). In another study, Hussain *et al.* (1999) estimated over-dominance for staple length in a diallel cross of cotton (*G. hirsutum* L.). Hendway *et al.* (1999) studied inheritance of fiber strength and fiber fineness in inter specific crosses (*G. barbadense* x *G. hirsutum*) and concluded that additive type of gene action were of greater importance in the inheritance of the studied traits

The above review indicates that much work needs to be done for genetic analysis of different parameters of cotton. The present studies were aimed to investigate the genetic basis for some economic cotton traits, e.g., ginning out-turn, staple length, fibre maturity, fibre fineness, fibre strength and seed cotton yield per plant to lay basis for the development of varieties with high yield potential and better fibre traits.

Materials and Methods

Six parental genotypes of cotton, i.e., B-557, MNH-147, MNH-156 (local) Culture-728-4, B-1580 (ne) and Culture 604-4 (exotic) were used to produce F₁ seed.

The parental material was grown in normal soil under natural field conditions during the month of June, 2000. At flowering, during August-September, the parental lines were crossed in a complete diallel fashion to generate 30 F₁ crosses. At maturity, crossed bolls were picked and seed cotton was ginned with roller ginning machine. Six parents and their F₁ hybrids were grown in four replications at Cotton Research Station, Multan with plant to plant distance of 1.25 ft. and row to row distance of 2.5 ft. At maturity, data were recorded for monopodia per plant, sympodia per plant, plant height, bolls per plant, seed oil content and seed cotton yield. Diallel technique (Mather and Jinks, 1982) was applied for determination of gene action of different traits. Genetic components of variation were obtained using the procedures described by Hayman (1954a) and Mather and Jinks (1982) and adopted by Singh and Chaudhry (1985).

Results

The results of different characteristics from progeny plants are presented as under:

Ginning out turn

The analysis of variance (Table 1) indicated highly significant differences ($P \leq 0.01$) among genotypes. Tests for the validity of the additive-dominance model (Table 2) showed adequacy of data. The estimates for genetic components of variation (Table) showed significant additive and dominant effects of genes. The higher value of D than H₁ expressed incomplete or partial dominance, which was in accordance with a result of $(H_1/D)^{1/2} = 0.259$. The unequal value of H₁ and H₂ signified the asymmetrical gene distribution, which was supported by $H_2 / 4 H_1 = 0.298$. The negative F value (-1.648) indicated pre-dominance of recessive alleles. This was well supplemented by $4DH_1 - F / 4DH_1 + F = 0.587$. The h^2 (1.102) was significant which revealed that over all dominance was due to heterozygous loci. The external effect ($E = 0.407$) was significant for the expression of trait

under consideration. Narrow sense heritability (0.946) was high, indicating rapid progress for this trait in the early segregating generation. This corresponds to the findings of Jagtap and Mehtari (1998). The positive intercept of regression line in W_r/V_r graph (Fig. 1) expressed additive gene action, which is in accordance with the previous results of studies in cotton (Hendway *et al.*, 1999; Kalwar and Babar, 1999; Rady *et al.*, 1999). The position of array points (Fig. 1) pointed out that except B-1580 (NE), all the other genotypes showed the trend towards recessive genes.

Staple length (mm)

Significant differences were found among genotypes (Table 1) for the trait under consideration. Genetic analysis was possible because the data partially fulfilled the assumption of additive-dominance model (Table 2). The computation of genetic components of variation (Table 3) revealed the importance of both additive and dominant components of variation. Asymmetrical distribution of genes, among the parents was present due to $H_1=H_2$ and the value of $H_2/4H_1$ (0.186). The frequency of dominant genes was high as indicated by the positive value of F (0.828). These results were further verified by $(4DH_1)^{1/2}+F/(4DH_1)^{1/2}-F=0.719$ (Table 3). The environment had an important effect for the expression of character under study. Low narrow sense heritability (0.160) (Table 3) indicates chances of better progress of individual plant selection for the improvement of this character. Lower value of H_1 or H_2 than h^2 indicated that directional dominance was due to heterozygous loci. The regression line in W_r/V_r graph (Fig. 2) suggested over-dominant gene action, which corresponds to findings Ahmad *et al.* (1997) and Hussain *et al.* (1999).

Fibre Maturity

Highly genotypic differences for fibre maturity allowed for testing the adequacy of additive-dominance model. The data were found partially adequate (Table 2) for genetic analysis. The estimates for genetic components (Table 3) indicated significant role of both additive and dominant genes for the expression of trait under consideration. Lesser value of D (4.89) than H_1 (6.78) revealed over dominance, which was confirmed by average degree of dominant (1.17). Un equal values of H_1 and H_2 and the ratio of $H_2/4H_1$ depicted un-balanced distribution of genes among the parents. Dominant genes were more than the recessive because of positive value of F (4.20). The positive value of h^2 (1.74) pointed out substantial contribution of heterozygous loci. The greater contribution of additive variance could produce better results for commercial hybrid seed programme. The environment did not play any significant role for the expression of the trait. W_r/V_r graph (Fig. 3) reflected over dominance gene action. The position of array points denoted that B-1580 (ne), C-604-4, MNH147 and MNH156 contained maximum dominant genes while C728-4 had maximum recessive genes for fibre maturity.

Fibre fineness

The genotypes differed significantly (Table 1). Three scaling tests employed for the adequacy of additive dominant model suggested the data to be fully adequate (Table 2) for further genetic analysis. The estimates of genetic components of variation (Table 3) depicted additive as well as

Table 1: Mean squares for various traits in 36 crosses including selfs

Source	df	GOT	Staple length	Maturity	Fineness	Fibre Strength	Cotton seed yield
Replication	3	0.27	1.42	0.36	0.03	1.05	482.92
Genotypes	35	26.97**	2.72**	13.42**	0.09**	18.44**	1378.06**
Error	105	1.66	0.64	0.82	0.01	1.24	274.97
Total	143						

** Significant at 0.01% level of significant

dominant gene action because of significant values of D and H_1 . Asymmetrical gene distribution was indicated by the unequal H_1 and H_2 , which was confirmed by the value of $H_2/4H_1$ (0.136). The positive value of F (0.032) and proportion of dominant to recessive genes (2.931) expressed more frequency of dominant genes (Table 3). The value of $(H_1/D)^{1/2}$ (0.714) showed incomplete and partial dominant. The environmental effects were non-significant. The heritability estimates (0.608) suggested some effectiveness of individual plant selection in segregating population. The graphical presentation of the data (Fig. 4) indicated positive intercept thus revealing additive gene action. These results are in agreement with the previous studies of Hendway *et al.* (1999), who also found additive gene action for fibre fineness in cotton. The location of array points indicated that B1580 (ne) possessed maximum recessive whereas MNH147 and MNH156 contained maximum dominant genes. C728-4 and C604-4 had both dominant and recessive genes.

Fibre strength

After obtaining highly significant genotypic differences (Table 1) and full adequacy of the additive dominance model (Table 2) diallel analysis was carried out to assess the gene action. The estimates of genetic components of variation (Table 3) indicated significant role of additive and dominant genetic effects. The greater value of D than H_1 and mean degree of dominance of (0.742) depicted additive gene action. Asymmetrical gene distribution ($H_1 \neq H_2$) of was confirmed by the value of $H_2/4H_1$ (0.162). The F value (1.292) represented more frequency of recessive alleles which was also supported by the value of $(4DH_1)^{1/2} + F - (4DH_1)^{1/2} - F = 0.689$. The effect of environment (0.309) was non-significant. High narrow sense heritability (0.862) signified additive genetic variance suggesting rapid progress in early generation through selection. The location of array points along the regression line (Fig. 5) expressed that C-728-4 and C604-4 had maximum dominant genes, whereas MNH147, MNH156 and B-180(ne) possessed more recessive genes. The positive intercept of regression lines showed additive gene action for fibre strength. Hendway *et al.* (1999) also reported similar results for the character under study.

Seed cotton yield

Analysis of variance (Table 1) showed highly significant ($P \leq 0.01$) genotypic differences. Tests for the validity of the additive-dominance model (Table 2) showed partial adequacy of data. The estimates for genetic components of variation for seed cotton yield are given in Table 3. The positive and significant values of D and H suggested control of both the additive and dominant gene effects, which corresponds to the findings of (Esmail *et al.*, 1999; Kumaresan *et al.*, 2000). The lesser value of D than H_1 indicated over dominance. Unequal values of H_1 and H_2 signified

Table 2: Tests of adequacy of additive-dominance model for 6x6 diallel of cotton

Characters	Joint regression	Test for b=0	Test for b=1	test for t ²	Wr + Vr	Wr - Vr	Remarks
Ginning outturn	b=-0.899±0.159	5.668*	0.633 ^{ns}	0.081 ^{ns}	0.159 ^{ns}	0.183 ^{ns}	Full adequacy of additive-dominance model
Staple length	b=0.432±0.167	0.2589 ^{ns}	3.409 [*]	4.439 ^{ns}	3.292*	1.008 ^{ns}	Partial adequacy of additive-dominance model
Fibre maturity	b=1.028±0.137	7.515 [*]	-0.205 ^{ns}	0.232 ^{ns}	18.327 ^{**}	8.261 ^{**}	Partial adequacy of additive-dominance model
Fibre fineness	b=1.035±0.313	3.308 [*]	-0.112 ^{ns}	0.547 ^{ns}	1.485 ^{ns}	1.549 [*]	Full adequacy of additive-dominance model
Fibre strength	b=0.775±0.140	5.542 ^{**}	1.607 ^{ns}	1.314 ^{ns}	2.582 ^{ns}	1.744 ^{ns}	Full adequacy of additive-dominance model
Seed cotton	b=0.774± 0.052	14.994 ^{**}	4.384 ^{ns}	1.121 ^{ns}	5.475 ^{**}	2.681 ^{**}	Partial adequacy of additive-dominance model

Table 3: Estimates of variation for ginning out turn, staple length, fibre maturity, fibre fineness, fibre strength and seed cotton yield

Components	Ginning out turn	Staple length	Fibre maturity	Fibre fineness	Fibre strength	Cotton seed yield
D	12.207±0.212 ^{**}	0.403±0.40ns	4.894±0.386 ^{**}	0.046±0.003 ^{**}	4.736±0.341 ^{**}	297.848±40.226 ^{**}
H ₁	0.820±0.539ns	2.58±1.02 ^{**}	6.781±0.979 ^{**}	0.023±0.007 ^{**}	2.611±0.865 ^{**}	322.26±102.113 ^{**}
H ₂	0.976±0.481 ^{**}	1.922±0.93 ^{**}	4.013±0.875 ^{**}	0.013±0.006 ^{**}	1.691±0.772 ^{**}	310.984±91.211 ^{**}
h ²	1.102±0.324 ^{**}	5.299±0.62 ^{**}	1.747±0.589 ^{**}	0.001±0.004ns	0.422±0.520ns	-34.688±61.412ns
F	-1.648±0.518ns	0.818±1.00ns	4.205±0.942 ^{**}	0.032±0.007 ^{**}	-1.292±0.832ns	-166.957±98.237ns
E	0.407±0.018ns	0.168±0.15ns	0.204±0.147ns	0.005±0.001 ^{**}	0.309±0.130 ^{**}	70.185±15.35 ^{**}
(H ₁ /D) ^{1/2}	0.259	2.533	1.177	0.714	0.742	1.040
H ₂ /4H ₁	0.298	0.186	0.148	0.136	0.162	0.241
[(4DH ₁) ^{1/2} +F]/[(4DH ₂) ^{1/2} -F]	0.587	2.337	2.150	2.931	0.689	0.575
h ² /H ₂	1.129	2.757	0.435	0.104	0.249	-0.111
h ² _{NS} , h ² _{BS}	0.913, 0.946	0.160, 0.783	0.589, 0.930	0.608, 0.767	0.826, 0.926	0.712, 0.818

Table 4: List of some outstanding cross combinations

Crosses	Ginning out turn(%)	Staple length (mm)	Fibre maturity (%)	Fibre fineness (µg/inch)	Fibre strength (tppsi)	Cotton seed yield per plant (g)
B557XMNH156	36.00	26.50	86.80	4.32	99.3	96.57
C728XMNH156	37.00	26.25	87.92	4.42	100.27	94.85
C604XMNH147	37.45	25.00	86.80	4.67	97.72	60.40
C604XMNH156	42.95	24.90	86.50	4.30	98.10	61.42
B1580XB557	33.35	26.62	81.17	4.55	101.42	76.20
MNH156XMNH147	39.75	26.00	85.75	4.35	97.35	70.50
MNH147XB1580	35.50	26.87	83.80	4.45	102.30	59.70
MNH147XC728	35.15	27.00	84.75	4.55	97.50	66.45

47

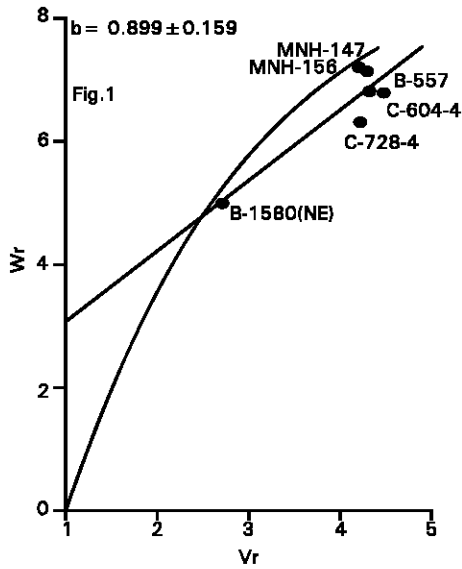


Fig. 1: Ginning outturn

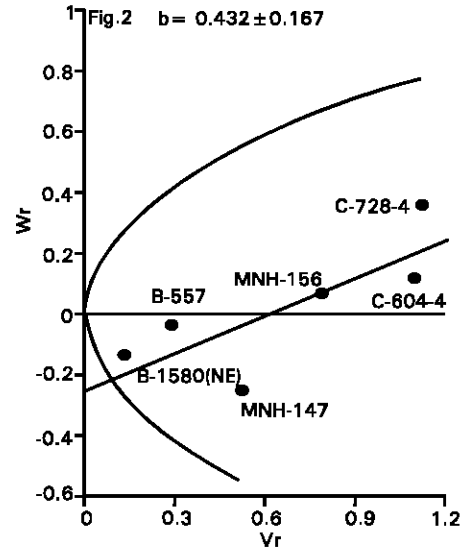


Fig. 2: Staple length

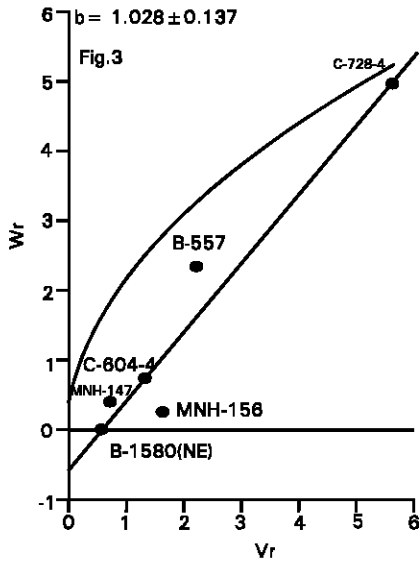


Fig. 3: Fibre maturity

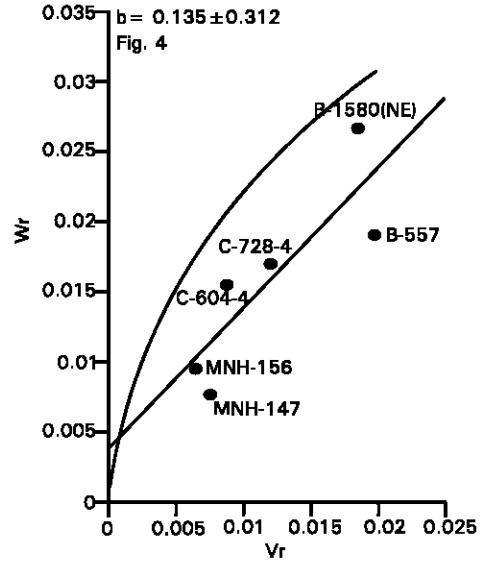


Fig. 4: Fibre fitness

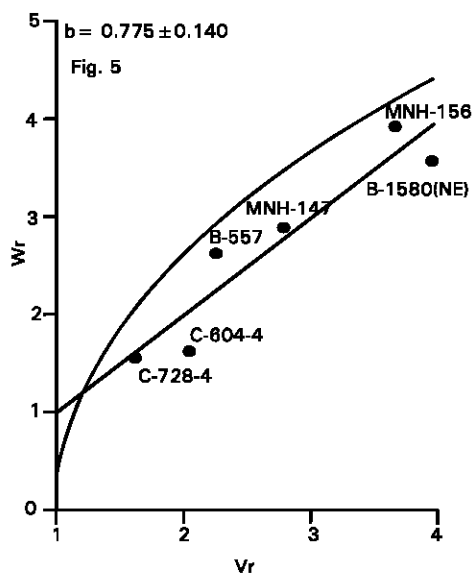


Fig. 5: Fibre strength

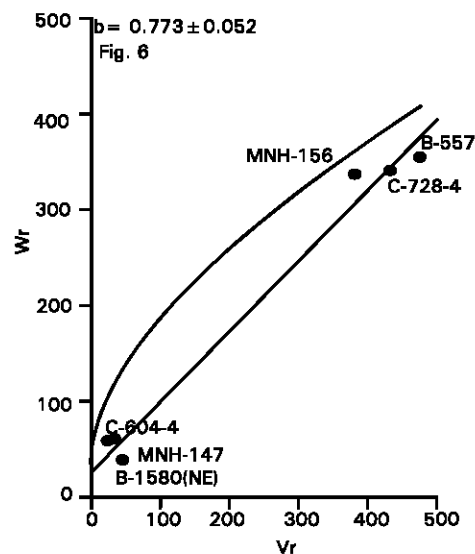


Fig. 6: Seed cotton yield

asymmetrical distribution of positive and negative alleles. The negative value of F showed excess of recessive genes for the expression of the character under study. The greater values of H_1 and H_2 over h^2 suggested the absence of directional dominance non-significance of h^2 showed absence of overall dominant effects due to heterozygous loci. The environmental influence was significant. The positive intercept of W_r/V_r regression line (Fig. 5) reflected additive gene action. Similar results have been obtained by Saeed *et al.* 1996; Rady *et al.*, 1999 and Baloch *et al.* 2000. Saeed *et al.* (1996), Esmail *et al.* (1999), Shanti and Raveendran (1999) and Kumaresan *et al.* (2000). Narrow sense heritability (0.617) suggested that selection based on individual plant will give better progress for the character under study. Yingxin and Xiangming (1998), Esmail *et al.* (1999) and Kumaresan *et al.* (2000) also reported high heritability for seed cotton yield.

Some top potential combinations are given in Table 4. On the basis of 6 characteristics, B557xMNH156, C728-4xMNH156, B-1580xB557 and MNH156 x MNH147 are the crosses which could culminate in the form of good varieties. Besides these combinations can be reconstituted for commercial production of hybrid cotton.

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