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Behaviour of Some Polygenic Characters in Cotton (*Gossypium hirsutum* L.)

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Abstract: Six quantitative traits were studied by analyzing F₁ data derived from a 6 x 6 diallel cross. Two traits i.e., yield of seed cotton and number of bolls per plant showed complete adequacy of additive dominance model. Two characters lint percentage and seed index partially passed the assumption for diallel analysis. Both additive and dominance (non-additive) variations were observed in the diallel cross population for yield of seed cotton per plant, boll numbers per plant, lint percentage and seed index. The magnitude of non-additive genetic components were greater than additive for yield of seed cotton per plant and seed index, whereas the value of additive genetic components were higher than dominance for boll numbers per plant. The substantial contribution to dominance was due to heterogeneity of loci for the four traits analysed in this experiment. The recessive alleles were in excess in the parents for yield of seed cotton per plant, number of bolls per plant, lint percentage and seed index. The operation of over-dominance was estimated for yield of seed cotton per plant and seed index whereas partial dominance was observed for boll number per plant. The lint percentage possessed complete dominance in this set of diallel cross. The ratio of positive and negative alleles at the loci exhibiting dominance were in equal proportion in these parents for yield of seed cotton per plant and number of bolls per plant whereas asymmetrical distribution of negative and positive alleles among the parents was suggested for lint percentage and seed index. The level of dominance was not constant in all loci and it varied in some loci for yield of seed cotton per plant, number of bolls per plant and seed index. The level of dominance at all loci was almost constant for lint percentage. Dominant genes were responsible for the increase of yield of seed cotton per plant, number of bolls per plant, lint percentage and seed index in this material. S-12 had maximum number of dominant genes for yield of seed cotton per plant and lint percentage. The variety LRA-5166 had maximum number of recessive alleles for yield of seed cotton per plant and seed index. The variety CIM240 possessed maximum number of dominant alleles for number of bolls per plant and lint percentage. The genotype Albacala (69)11 have maximum concentration of recessive alleles for boll number per plant and seed index.

Key words: *Gossypium hirsutum* L., additive-dominance model, diallel, gene action, quantitative genetic analysis, Pakistan

Introduction

The genetic improvement of crop is an unending process due to one or other improvement programme. For the proper accomplishment of these programmes, genetic analysis is the pre-requisite for new plant breeding methods. These analysis not only provide the information about genetic architecture of the character that help formulating an appropriate selection programme but also predict progress through selection. Azhar *et al.* (1994) reported that ginning percentage and seed index controlled by gene with additive gene effect. For yield of seed cotton, Khan *et al.* (1995) observed additive with partial dominance and greater value of D than H₁ and H₂ for boll weight whereas over dominance for yield of seed cotton and boll numbers per plant. Iqbal and Khan (1996) suggested over dominance genetic control for lint index and partial dominance for seed index. Amin *et al.* (1997)

reported over dominance gene action for seed cotton yield per plant and number of bolls per plant. Esmail *et al.* (1999) and Kumaresan *et al.* (2000) observed both additive and dominant gene action for yield of seed cotton per plant whereas additive gene action was found by Saeed *et al.* (1996), Rady *et al.* (1999) and Baloch *et al.* (2000). Subhan *et al.* (2001) estimated over dominance for yield of seed cotton and additive with partial dominance for number of bolls per plant and lint percentage. Many scientists made studies based on diallel analysis to estimate gene effects in cotton. But the findings of these studies revealed that it is not possible to generalize particular type of gene action present for different attributes and hence need is obvious for studying genetic variance in the material that has specific concern to a breeder. Keeping in view, the present study was made to understand the inheritance of yield and its components,

which will be helpful in choosing proper breeding method and reshaping the selection fashion.

Materials and Methods

Six parent full diallel crosses including reciprocals were made at Cotton Research Sub-Station, Khanewal during the September 2000. These six parents including four local (viz. S-12, S-14, NIAB-78, S-14) and two exotic (viz. LRA-5166 and Albacala (69)-11) genotypes. All the six parents along with 30 F_1 s were grown at Cotton Research Sub-Station, Khanewal during the year 2001 in a randomized complete block design. The recommended agronomic and plant protection practices were adopted during the course of experiment equally to all the genotypes and replication. Fifteen competitive plants, excluding the border plants, were randomly selected per replication for each parents and F_1 for recording the data.

For the six characters i.e, yield of seed cotton per plant (g), boll number per plant, boll weight (g), lint percentage, seed index and lint index. The data recorded were subjected to analysis of variance suggested by Steel and Torrie (1980) for knowing variability for further analysis. The genotypic variance was partitioned with male and female and interaction of male and female as described by Mather and Jinks (1977).

Diallel assumptions and test for their validity

The diallel analysis was carried out on the following assumption.

- Diploid segregation.
- No reciprocal effect.
- Homozygous parents.
- No epistasis.
- No multiple allelism.
- Independent genes distribution among parents.

Though *Gossypium hirsutum* L. is an amphidiploid between the species of A and D genome but it segregates in diploid manner. Endrizzi (1962) and Kimber (1961), so the research material fulfil the first assumption. For removing reciprocal differences the entries in the off diagonal cells of the diallel table were replaced by their means of cross and reciprocal prior to analysis. To maintain true to type, the parental lines were selfed for three generations.

For 4, 5 and 6th assumption, the data were subjected to two tests. Failure of any one or any combination of these tests invalidates the additive dominance model. For those parameters, which showed complete inadequacy of additive dominance model, their further analysis was stopped. However the genetic analysis was extended for those traits having sufficient variability and their W_r - V_r

does not vary significantly from array at 0.01 probability level. But according to Hayman (1957) the estimates were less reliable than, when all the assumptions have been fulfilled. The direct and derived genetic components were computed according to Hayman (1954) and used by Singh and Chaudhry (1985). Heritabilities in narrow and broad sense were worked out following Mather and Jinks (1977).

Results and Discussion

The results pertaining the analysis of variance for six characters under study were presented in Table 1. The mean squares due to genotypes were highly significant for all the characters indicated that there was considerable genetic variability in the material for study. Male, female and interaction of male and female mean squares were significant ($P < 0.01$) for all the character except boll number per plant. This signified the presence of boll additive and non-additive genetic variation for yield of seed cotton per plant, boll weight, lint percentage, seed index and lint index in this material. The non-significant interaction of male and female for boll numbers per plant may revealed the importance of additive genetic effect or may be due to maternal effect as male ($P < 0.01$) and female ($P < 0.05$) parents were not contributed equally to the progeny, however further analysis will clarified it.

Adequacy of additive-dominance model: Results revealed that W_r - V_r differed highly significantly ($P < 0.01$) for boll weight and lint index whereas lint percentage and seed index showed non significant differences at this probability level and were significant at $P < 0.05$ (Table 2). This highly significant difference ($P < 0.01$) invalidated the additive dominance model for boll weight and lint index. Although for boll weight the regression values deviated significantly from zero but not from unity i.e. validate the model but W_r - V_r analysis provided considerably more vigorous test of fitness of the data hence further analysis of boll weight and lint index will be stopped. For lint percentage and seed index W_r - V_r between array varied at 0.05 probability level (non-significant at $P < 0.01$) and regression analysis permitted the fitness of data hence the analysis of these two parameters were continued keeping in view that they were partially fulfilled the all diallel assumption.

Both consistency of W_r - V_r and significantly deviation of regression value from zero but not from one fully validated the data for additive-dominance model for yield of seed cotton and number of bolls per plant.

Characters showed complete adequacy of model

Yield of seed cotton per plant: The estimates of components genetic analysis revealed that both additive

Table 1: Mean squares for replication, genotypes (male + female + interaction) male, female, male X female interaction and error for different characters

| Source of Variance | df | Yield of seed cotton plant ⁻¹ | Boll No. plant ⁻¹ | Boll weight | Lint % | Seed index | Lint index |
|---------------------------|----|--|------------------------------|-------------|-----------|------------|------------|
| Replications | 2 | 96.75 NS | 8.5368 NS | 0.064 ** | 5.1962 ** | 0.4401 ** | 0.0732 NS |
| Genotypes | 35 | 878.598 ** | 44.9840** | 0.6450** | 34.6031** | 2.6012** | 2.5642** |
| Male | 5 | 1976.63** | 134.1932** | 1.5587** | 98.159** | 7.0364** | 5.2769** |
| Female | 5 | 1706.239** | 93.4283* | 1.6631** | 97.0715** | 4.6610** | 4.1951** |
| Male X Female interaction | 25 | 493.461** | 17.4533 NS | 0.2539** | 9.3882** | 1.3022** | 1.6955** |
| Error | 70 | 80.207 | 9.0573 | 0.0092 | 0.4456 | 0.0511 | 0.0956 |

* significant at P=0.05 ** significant at P=0.01 NS non-significant.

Table 2: Tests of goodness of fit of the data to the additive dominance model

| Traits | Mean square for Wr-Vr Between array b-o (SE _{b(o)}) | Departure of regression coefficient from zero 1-b/(SE _{b(o)}) | Departure of regression coefficient from unity 1-b/SE _{b(o)} | Remarks |
|--|---|---|---|---|
| Yield of seed cotton plant ⁻¹ | 409.039NS | 26.2966** | 0.94184NS | The Wr-Vr and regression analyses validate the additive dominance model. |
| Boll number plant ⁻¹ | 13.468NS | 14.6079** | 2.4998NS | Both Wr-Vr and regression analysis validate the additive dominance model |
| Boll weight | 0.0011 ** | 11.2926** | 0.317NS | Wr-Vr analysis invalidates the additive dominance model at 0.01 probability level. There further analysis waived. |
| Lint percentage | 4.875* | 6.8526** | 0.4022NS | Wr-Vr analysis invalidates the model at 0.05 probability level but not at 0.01 level. The regression analyses validate the model. Further analysis will be performed. |
| Seed Index | 0.0375* | 5.0851** | 0.5195NS | Wr-Vr analysis invalidates the model at 0.05 probability level but not at 0.01 level. The regression analyses validate the model. Further analysis will be performed. |
| Lint index | 0.1454** | -0.4979 NS | 4.7727 * | Both the tests invalidate the additive dominance model. There further analysis stopped |

* Significant at P=0.05 ** significant at P=0.01 NS non-significant.

Table 3: Components of variance of various genetic estimates for yield of seed cotton, boll number per plant, lint percentage and seed index in *Gossypium hirsutum* L.

| Status Statistic | Characters showing complete adequacy of additive dominance model | | Characters showing partial adequacy of additive dominance model. | |
|---|--|---------------------------|--|----------------|
| | Yield of seed cotton per plant | Number of bolls per plant | Lint percentage | Seed index |
| Estimates of observational components of variance | | | | |
| VoLo | 352.284 | 20.987 | 10.917 | 0.666 |
| VoL ₁ | 100.945 | 6.137 | 5.419 | 0.322 |
| WoLo ₁ | 188.495 | 11.509 | 7.545 | 0.433 |
| V ₁ L ₁ | 234.412 | 10.755 | 8.006 | 0.672 |
| (ML ₁ -MLo) ² | 461.772 | 7.024 | 7.261 | 0.878 |
| Estimates of genetic components of variances and their standard error | | | | |
| D | 329.39± 7.292* | 17.973± 0.866* | 10.725± 0.904* | 0.645± 0.109* |
| H ₁ | 464.25±18.513* | 9.935±2.199* | 12.251±2.294* | 1.569±0.278* |
| H ₂ | 480.09±16.538* | 12.446±1.964* | 9.965±2.05* | 1.362±0.248* |
| h ² | 1832.15±11.31* | 26.421±1.322* | 28.939±1.38* | 3.503±0.167* |
| F | -85.26±17.815* | -8.08±2.116* | -8.601±2.208* | 0.427 ±0.273NS |
| E | 26.89±2.756* | 3.014±0.463* | 0.1925±0.342NS | 0.021 ±0.041NS |
| Other derived statistics | | | | |
| (H ₁ /D) ^{1/2} | 1.194 | 0.553 | 1.068 | 1.559 |
| H ₂ /4H ₁ | 0.258 | 0.313 | 0.203 | 0.217 |
| H ₁ - H ₂ | -15.842 | -2.51 | 2.286 | 0.209 |
| (4DH ₁) ^{1/2} +F | 0.802 | 0.536 | 0.454 | <u>0.65</u> |
| (4DH ₁) ^{1/2} -F | | | | |
| 1/2F/[D(H ₁ -H ₂)] ^{1/2} | 0.594 | 0.601 | 0.868 | <u>0.584</u> |
| h ² /H _E | 3.816 | 2.123 | 2.904 | 2.232 |
| Y _D | 678.368 | 23.485 | 36.769 | 8.507 |
| Y _R | 156.946 | 56.663 | 59.061 | 9.037 |
| r: = correlation b/w Wr + Vr and parental value | -0.959* | -0.634 | -0.921* | -0.982* |
| h ² NS = (heritability narrow sense) | 0.573 | 0.658 | <u>0.801</u> | <u>0.639</u> |
| h ² b = (heritability broad sense) | 0.922 | 0.831 | <u>0.985</u> | <u>0.979</u> |

The under line statistics are less reliable due to non significant of their derivatives

Table 4: Relative frequencies of dominant to recessive alleles in parents (Fr) for yield of seed cotton per plant, boll numbers per plant, lint percentage and seed index in 6X6 diallel crosses *Gossypium hirsutum* L.

| Genotype | Yield of seed cotton plant ⁻¹ | Number of bolls plant ⁻¹ | Lint percentage | Seed index |
|----------------|--|-------------------------------------|-----------------|------------|
| S-12 | 401.627 | 8.444 | 19.242 | -1.463 |
| NIAB-78 | 281.028 | 13.098 | -8.131 | 0.056 |
| CIM240 | 256.367 | 13.201 | -26.576 | -0.757 |
| S-14 | -240.834 | -16.181 | -6.261 | 0.561 |
| LRA-5166 | -597.325 | -31.099 | -10.838 | -2.595 |
| Albacala(69)11 | -621.479 | -35.099 | -19.041 | 1.637 |

Values are arranged in descending order of yield of seed cotton plant⁻¹.

(D) and dominance (H_1 , H_2 and h^2) values were significant hence suggested that both additive and non-additive effects were responsible for the variation observed in the diallel cross population (Table 3). However the magnitude of H_1 and H_2 were higher than D indicated that largely non-additive genetic effects governed this trait. The measurement of net dominance (h^2) over all loci in heterozygous phase in all the crosses was significant and positive indicated direction of dominance was toward greater yield. The negative significant F component revealed excess of recessive alleles in the parents for yield of seed cotton per plant. This excess of recessive alleles as compare to dominant was confirmed from the $(4DH_1)^{1/2}+F/(4DH_1)^{1/2}-F$ value that was less than unity. The component E was significant. The estimate of average degree of dominance $(H_1/D)^{1/2}$ was more than one devoted the operation of over-dominance for this character. Khan *et al.* (1995), Amin *et al.* (1997) and Subhan *et al.* (2001) also observed over-dominance gene action so these findings are quite resemblance with these earlier research workers. A crude estimate of frequencies at non-additive loci can be obtained from $H_2/4H_1$. This ratio between the genes with positive and negative effects, was somewhat close to 0.25, indicated symmetry of positive and negative homozygotes among the six parents for yield of seed cotton per plant. The further proof of this equal distribution of alleles over loci was obtained from negative value of H_1-H_2 , which indicated that $U=V$ at all loci. In this context, U refers to frequency of alleles, which increases the mean expression of the character and are situated at loci, which exhibited dominance on the other hand V correspond to the frequency of alleles at loci that decreases the expression of this character and was recessive. These estimates permit a determination as to which type of alleles occurs more frequently. As stated above the estimate of ratio $(4DH_1)^{1/2}+F/(4DH_1)^{1/2}-F$ permitted the determination of type of alleles, which were more frequent. This ratio measured the total number of dominant to recessive alleles in all parents was 0.802. Thus it can be assumed that the six parents used for this study carried more recessive than dominant alleles for

yield of seed cotton per plant. The value of ratio $1/2F/[D(H_1-H_2)]^{1/2}$ was less than unity. This implied that dominance level is not constant in all loci and it varied in some loci. The number of genes that control the yield of seed cotton per plant and exhibited dominance (h^2/H_2) was 3.82. This indicated that there were at least four groups of genes, governed this trait. Correlation between parental means (Y_r) and the parental order of dominance (W_r+V_r) provided a meaningful estimate of the direction of dominance. This value was significant and negative for yield of seed cotton per plant, which suggested that the dominant genes were responsible for the increase of yield in this material. Because of the high dominance variation (H_1 and H_2) found in this trait, a large difference between the narrow and broad sense heritabilities was found. The relative low value of the narrow sense heritability and high dominance level of yield per plant reduce the efficiency of selection for higher yield of seed cotton per plant in the early segregating generation.

The Fr values indicated that S-12 had maximum number of dominant genes and LRA-5166 had maximum number of recessive alleles for yield of seed cotton per plant (Table 4). The Table 4 also elucidated that the complete homozygous parent had $YD=678.368$ and completely recessive parent had $Yr=156.946$.

Number of bolls per plant: The data given in Table 3 divulged that the additive genetic variance (D) and the three components of dominance (H_1 , H_2 , h^2) were significant and indicated that both additive and non-additive gene action were important in the inheritance of this character. However, the magnitude of D was higher than H_1 and H_2 indicated that this trait was governed largely by additive gene effect. The positive significant value of h^2 showed that direction of dominance trend toward positive side and substantial contribution to dominance was due to heterogeneity of loci. The excess of recessive alleles in the parents for boll number per plant was indicated by negative significant F value and the value of $(4DH_1)^{1/2}+F/(4DH_1)^{1/2}-F$ that was less than unity. The component $(H_1/D)^{1/2}$ estimated partial dominance. Khan *et al.* (1995) and Amin *et al.* (1997) observed over-dominance for this trait. This difference may be due to different material used under different climatic conditions. The $H_2/4H_1$, which estimated $U=V$ indicated that the positive and negative alleles at the loci exhibiting dominance were in equal proportion in these parents. The negative determinant of H_1-H_2 proofs this symmetrically distribution of negative and positive alleles exhibited dominance. However the dominance level was not constant over all loci ($1/2F/[D(H_1-H_2)]^{1/2}=0.601$) and there were at least two group of genes exhibiting

dominance governed this trait. The correlation coefficient was non-significant suggested bi-directional dominance, however its negative sign indicated that genes increased the number of boll were dominant. The narrow sense heritability was 65.8% and the broad sense heritability was 83.1%. High estimates might be expected since the genetic system controlling the inheritance of boll number per plant had been shown to be inherited by basically additive genetic effects. As boll number per plant is one of the secondary yield components hence the selection for this component character will definitely contribute for the improvement of yield. The additive gene action and high heritabilities suggested both pedigree breeding and recurrent selection programme for its improvement.

The Fr values presented in Table 4 revealed that CIM240 and NIAB-78 possessed maximum number of dominant alleles and Albacala (69)11 had maximum number of recessive alleles for this trait. Table 4 also showed that the value of completely dominant parent was 23.485 and completely recessive parent was 56.663. In fact these YD and YR are the predictions of the possible limits of selection for amongst the genes exhibiting dominance (Hayman 1954).

Character showed partial adequacy of model

Lint percentage: The data presented in Table 3 contain the component analysis which revealed that both additive (D) and dominance (H_1 , H_2 and h^2) value were significant suggested that both additive and non-additive effects were responsible for the variation observed in diallel cross population of lint percentage. The positive, significant h^2 indicated substantial contribution to dominance was due to heterogeneity of loci and direction of dominance was positive for this trait. An excess of recessive genes was found in the parents for lint percentage, as value of F was negative and significant. The component $(4DH_1)^2 + F / (4DH_1)^2 - F$ less than unity for this trait confirm this finding. The environmental component E was non-significant. The mean degree of dominance over all loci was close to unity i.e., 1.068 suggested the presence of complete dominance in this set of diallel cross. Subhan *et al.* (2001) found partial dominance for this trait. This might be due to different material used under different climatic condition. The $H_2/4H_1$ deviated from 0.25; hence positive and negative alleles were unequal in their proportion in the parents for this trait. The positive value of $H_1 - H_2$ confirmed the asymmetrical distribution of negative and positive alleles among the parents for this trait. The larger estimate 0.868 from $\{1/2F/[D(H_1-H_2)]^2\}$ suggested that level of dominance at all loci was almost constant. The ratio h^2/H_2 suggested the involvement of three groups of gene having dominance at these stages for lint

percentage. Table 3 also showed a negative correlation between parental order of dominance and parental measurement indicated that the dominant genes were associated with high lint percentage. As the component E was non-significant and it is one of the relevant component in computation of narrow and broad sense heritabilities, hence it is less reliable than when all its relevant components were significant. However, high heritabilities value for lint percentage indicated that it can be improved by simple selection and followed by careful progeny testing.

Perusal of Table 4 indicated that S-12 carried maximum number of dominant alleles and CIM240 possessed maximum number of recessive alleles for lint percentage.

Seed index: The estimated genetic components of variation and their derived statistics presented in Table 3. Additive (D) and three components of dominance (H_1 , H_2 and h^2) were significant thus suggested the presence of both additive and non-additive genetic variation among these material for seed index. However preponderance of dominance as compare to additive genetic effects as dominance components were higher than additive component. The positive significant estimate of h^2 showed that dominance occurred toward the parent exhibited higher seed index and a substantial contribution to dominance was due to heterogeneity of loci. As h^2 value was greater than H_1 and H_2 , hence suggested bi-directional dominance for seed index in this material. The component F was non-significant and equal to zero indicated almost equal distribution of dominant and recessive genes among the parents. The non-significant of F component also indicated that all its derived components were less reliable, so they were underline in the Table 4. The environmental component of variance was also non-significant, which may be due to partial failure of diallel assumptions. The average degree of dominance estimated from $(H_1/D)^2$ was over dominance. Iqbal and Khan (1996) reported partial dominance for this character, which may be due to different material used under different climatic condition. Gene frequency asymmetry was shown to exist ($H_2 < H_1$) but relatively unimportant ($H_2/4H_1 = 0.217$) for seed index. The recessive alleles were more frequent than dominant alleles for this trait as suggested by the $(4DH_1)^2 + F / (4DH_1)^2 - F$. The value of estimate $\{1/2F/[D(H_1-H_2)]^2\}$ less than unity indicated dominance level for this character varied from one loci to another in this material. The ration h^2/H_2 suggested the involvement of three groups of genes having dominance at these stages for this character. The negative significant correlation between $W_r + V_r$ and parental values suggested dominant alleles were

associated with the increase of seed index. The preponderance of dominance effect also reflected in the difference of heritabilities hence pedigree-breeding method is suggested for seed index improvement in this material.

The data showed maximum concentration of dominants alleles for seed index was in parent Albacala (69)11 and maximum concentration of recessive alleles were in LRA 5166 (Table 4).

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