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## Genetic Analysis of Some Agronomic & Fibre Characters in Upland Cotton (*Gossypium hirsutum* L.)

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### Abstract

A 4 X 4 diallel cross experiment involving three exotic lines i.e. Allepo 40, LB-546 and Coker-304 and one local line i.e. Express, was conducted to evaluate the gene action for different Agronomic & Fibre characters in upland cotton. Additive gene action with partial dominance appeared to control plant height, seed index, fibre fineness, fibre length & lint index where as over dominance type of gene action was noted for ginning out turn percentage and number of sympodial branches. On over all basis Allepo-40 has maximum dominant genes for number of sympodial branches and lint index while dominant genes for plant height, seed index and fibre fineness are present in LB-546. Coker-304 has maximum dominant genes for fibre length and ginning out turn percentage while Express did not have any dominant genes.

### Introduction

Improvement of cotton plant for its yield and quality is a never ending process, for the reason of ever changing needs and preference of the society. Cotton, the most important cash crop of Pakistan, has been under concerted effort of the breeder for its improvement through breeding. Consequently, high yielding varieties were evolved and recommended for general cultivation from time to time in the cotton belt of Pakistan. Although these varieties contributed a lot in increasing total production and considerably in the foreign exchange earning but they seem not well adapted to the prevailing environmental conditions of Pakistan. Moreover the onslaught of cotton leaf curl virus disease for the last few years is also putting our cotton production under strain. This situation implies the importance of evolution of new cotton varieties through the breeding process under our local environmental conditions. The main objective of this research is to study the type of gene action controlling the heredity of various plant characters. For a systematic and successful program of genetic improvement in cotton, it is necessary to measure the nature and relative magnitude of different gene action governing various quantitative traits. Therefore a program of genetic analysis of four cotton cultivars using Hayman (1954) and Jinks (1955) technique was adopted.

### Materials and Methods

To assess the genetic architecture in upland cotton present study was under taken at the University of Agriculture Faisalabad during 1992-93. Three exotic lines i.e. Allepo-40, LB-546 and Coker-304 and one local line i.e. Express of *Gossypium hirsutum* L. was crossed in a diallel fashion. The 12F1 progenies along with parents were grown in a randomized Complete Block Design with three replications. The plant to plant and row to row distance was kept at 30 and 75 cm respectively. Every genotype consisted of 10 plants in a 3-meter long row. The middle six plants leaving two plants on each side of the line were selected for the collection of data. The height of plants were recorded in centimeters (cm) when apical growth of the main stem

ceased. The measurement was done with a measuring rod from the first cotyledonary node to the apical bud. The number of sympodial branches on individual plant was counted and recorded when picking was over. 100 seeds were weighed in grams to calculate seed index. Fibre fineness was determined with the help of Sheffield micronaire in microgram per inch, similarly, length was measured in millimeter by using tuft method. The seed cotton from each plant was ginned separately and lint thus obtained was weighed and ginning out turn percentage was calculated. Lint index or weight of lint obtained from 100 seeds in grams was also calculated.

The data were subjected to analysis of variance techniques (Steel and Torrie, 1980) to determine the significance of differences among F1 hybrids and their respective parents. The diallel cross technique developed by Hayman (1954), and Jinks (1955), was used for genetic analysis. All the crosses were arranged into arrays in the form of diallel tables and two statistics, the variance ( $V_r$ ) of family mean within an array and the covariance ( $W_r$ ) of these means with the non-recurrent parental values were calculated from each diallel table. The information on gene action was inferred by plotting the covariance ( $W_r$ ) of each array against its variance ( $V_r$ ). The slope and the position of regression line fitted to the array points within the limited parabola ( $W_r^2 = V_p x V_r$ ) indicated the degree of dominance and the presence or absence of gene interaction.

The limiting parabola was constructed on the basis of formula,  $W_r^2 = V_p x V_r$ , i.e. by plotting  $V_r$  ( $V_r x V_p$ )<sup>0.5</sup> points. The corresponding values for  $W_r$  for all observed  $V_r$  values were calculated as  $(V_r x V_p)$ <sup>0.5</sup>, where  $V_p$  = variance of the parents. The different arrays (Cultivars) were fitted within the limits for the parabola using the individual variance and covariance as their limiting points. Array nearest to the point of origin possessed most of the dominant genes, while the array that laid the farthest possessed most recessive genes, and the intermediate position signified the presence of both dominant and recessive genes in the array.

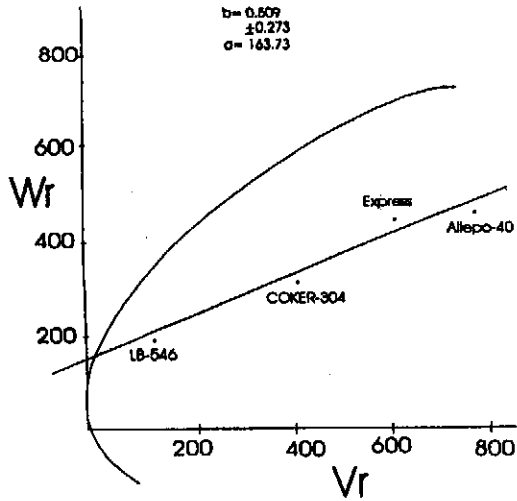


Fig. A: Vr/Wr graph for Plant height.

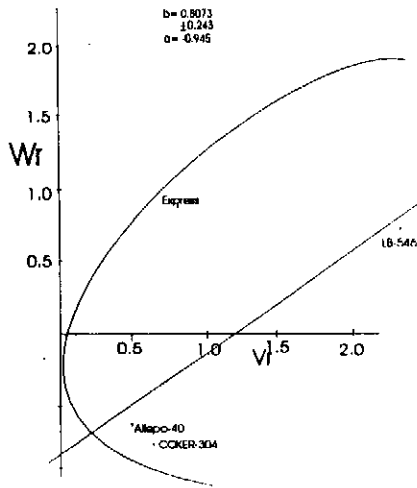


Fig. B: Vr/Wr graph for Number of Sympodial branches

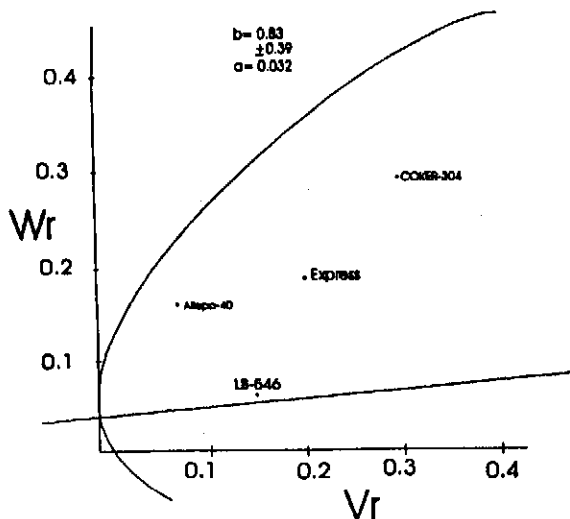


Fig. C: Vr/Wr graph for Seed Index

## Results and Discussion

Analysis of variance showed significant genotypic variation in all the characters (Table 1). The results obtained from the diallel analysis are discussed as under.

**Plant Height:** The regression line intercepted the  $wr$ -axis above the origin there by, indicating additive type of gene action with partial dominance, (Fig. A). As the regression line does not deviate significantly from the unit slope, there fore, there is no evidence of non allelic interaction of this trait. From the position of the array points along the regression line it revealed that LB-546 being nearest to the origin possessed maximum dominant genes while Allepo-40 had maximum recessive genes due to its farthest position. These results got support from the findings of Hussain (1991), Haq and Khan(1993), Khan and Khan(1993) and Shah *et al.* (1993) who reported additive type of gene action with partial dominance, while Rehman and Khan(1993) differ from present observations because they observe over dominance type of gene action for this trait. This difference in the phenotypic manifestation could be due to different varieties tested under different environmental conditions.

**Number of Sympodial Branches:** The study of  $vr/wr$  graph showed that the regression line passed through  $wr$ -axis below the origin signifying over dominance type of gene action (Fig. B). There is no evidence of non allelic interaction because the regression line does not deviate significantly from the unit slope. The position of array points along the regression line revealed that Allepo-40 possess maximum dominant genes, being nearest to the origin while LB-546 has maximum recessive genes due to its farthest position. These results are in agreement with those of Hussain (1991), Aftab (1993), Khan and Khan (1993) and Azhar *et al.* (1994) who reported additive type of gene action.

**Seed Index:** A study of graphic presentation of variance and Co-variance ( $Wr$ ) for seed index indicated that regression line with a unit slope intercepted the  $wr$ -axis above the origin signifying additive type of gene action with partial dominance (Fig. C). As regression line does not deviate significantly from a unit slope, there fore, there is no kind of non-allelic interaction involved. From the position of array points along the regression line, it is revealed that LB-546 possessed the maximum dominant genes to its nearest position to the origin where as Coker had most of the recessive alleles, being away from the origin. Additive type of gene action controlling inheritance of seed index has also been reported by Hussain *et al.* (1992), Aftab (1993) and Rehman *et al.* (1994).

**Fibre Fineness:** The regression line intercepted the  $wr$ -axis above the origin there by, indicating additive type of gene action with partial dominance, (Fig. D). As the regression line does not deviate significantly from the unit slope, therefore, there is no evidence of non allelic interaction of this trait. From the position of the array point along

Table 1. Mean Squares of various plant characters

O.V.	D.F.	plant	No. of out turn branches	Seed index height	Fibre Sympodial	Fibre Fineness	Lint Length
Replication	2	528.38*	5.0873 <sup>NS</sup>	0.2265*	0.0443*	0.8125*	2.69125*
Genotypes	15	1391.09**	5.15*	0.348**	0.4186**	1.7722*	9.421**
Error	30	207.76	1.91	0.066	0.074	0.834	1.8872

\* and \*\* significant at 5% and 1% probability level respectively.

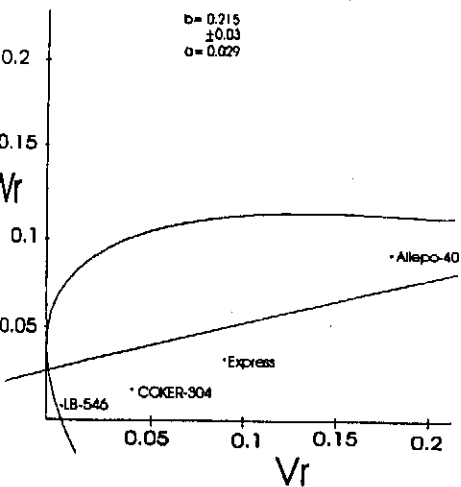


Fig. D: Vr/Wr graph for Fibre fineness

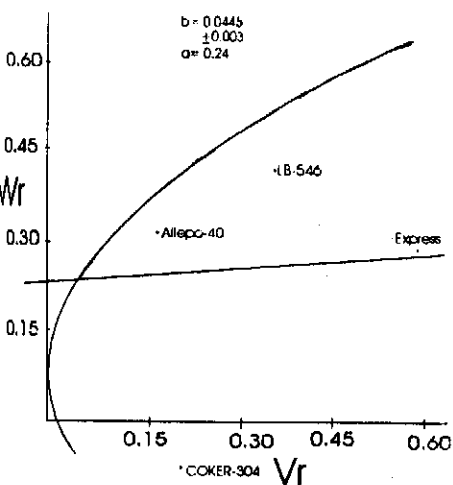


Fig. E: Vr/Wr graph for Fiber length

Regression line it revealed that LB-546 being nearest to the origin possessed maximum dominant genes while Allepo-40 possessed maximum recessive genes due to its farthest position. Additive type of gene action with partial dominance for this trait has been reported by Aftab(1993). However, the genetic analysis made by Hussain (1991), Khan *et al.*

(1991) and Rehman *et al.*(1993) disagree with the above results because they found over dominance type of gene action. The differences may be due to different genotypes studied in different ecological zones.

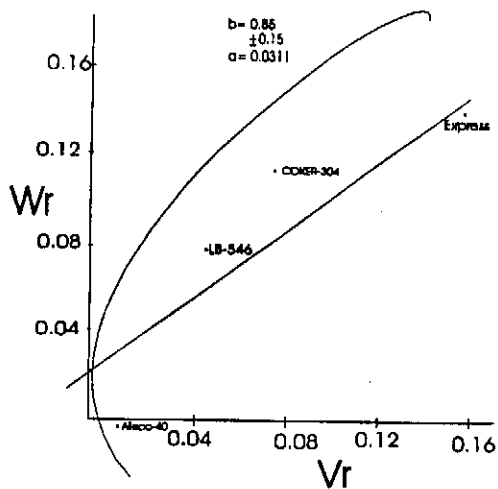


Fig. F: Vr/Wr graph for Lint Index

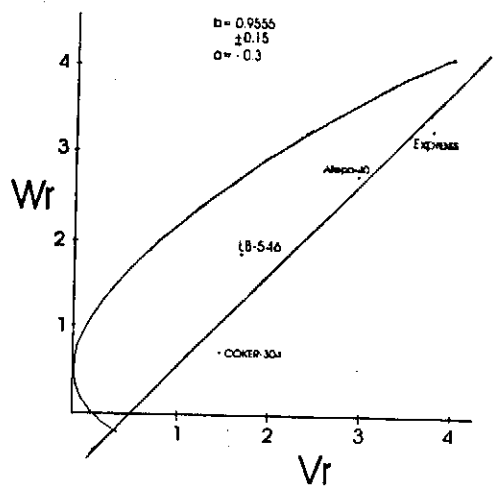


Fig. G: Vr/Wr graph for Ginning out turn percentage

**Fibre Length:** The study of *vr/wr* graph showed that the regression line passed through *wr*-axis above the origin signifying additive type of gene action with partial dominance (fig. E). There is no evidence of non allelic interaction because the regression line does not deviate significantly from the unit slope. The position of array along the regression line revealed that Coker-304 possessed maximum dominant genes, being nearest to the origin, while Express has maximum recessive genes due to its farthest position. These results got support from the findings of Hussain(1991), Tariq(1992) and Shah *et al.* (1993). However, the genetic analysis made by Khan *et al.* (1991), Aftab (1993) and Rehman *et al.* (1993) disagree with above results because they found over dominance type of gene action for this trait. The difference of the results might be attributed to different genetic stock and ecology of the breeding place.

**Lint Index:** A study of graphic presentation of variance (*Vr*) and Co-variance (*Wr*) for lint Index indicated that the regression line with a unit slope intercepted the *wr*-axis above the origin signifying additive type of gene action with partial dominance (Fig. F). As regression line does not deviate significantly from a unit slope, therefore, there is no kind of non-allelic interaction involved. From the position of array points along the regression line, it is clear that Allepo-40 possessed the maximum dominant genes due to its nearest position to the origin where as Express had most of the recessive alleles, being away from the origin. Additive type of gene action controlling the inheritance of lint index has also been reported by Rahman *et al.* (1991) and Azhar *et al.* (1994) where as Aftab (1993) and Rehman *et al.* (1993) observed this trait to be inherited by over-dominance type of gene action. This difference may be due to different genotypes.

**Ginning Out turn Percentage:** The study of *vr/wr* graph showed that the regression line passed through *wr*-axis below the origin signifying over dominance type of gene action (fig. G). There is no evidence of non allelic interaction because the regression line does not deviate significantly from the unit slope. The position of array along the regression line revealed that Coker-304 possessed maximum dominant genes, being nearest to the origin, while Express has maximum recessive genes due to its farthest position. Over dominance type of gene action controlling the inheritance of Ginning out turn percentage has also been reported by Aftab (1993) and Haq & Khan (1993) while Additive type of gene action has been reported by Azhar *et al.* (1994). The difference of the results might be attributed to different genetic stock and ecology of the breeding place.

On an over all basis gene action involved in the phenotypic expression of the characters like plant height, seed index, fibre fineness, fibre length, and lint index was observed to be additive with partial dominance, however over dominance type of gene action was observed in case of number of sympodial branches and ginning out turn percentage.

Allepo-40 has maximum dominant genes for number of sympodial branches and lint index while dominant genes for plant height, seed index and fibre fineness are present in

LB-546.Coker-304 has maximum dominant genes for fibre length and ginning out turn percentage while Express did not have any dominant genes.

The characters with additive type of gene action with out the involvement of any sort of epistatic effects provides better chance to a breeder improving his crop through simple selection procedure. Over dominance means where the progenies score more than their parents which in other words means heterosis or hybrid vigour. Therefore the information regarding the characters involving over dominance type of gene action in their phenotypic expression could be useful for identifying and selecting the better performing progenies/hybrids to be exploited in a program leading to hybrid cotton.

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