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

Muhammad Babar and Iftikhar Ahmad Khan
University College of Agriculture, B.Z. University, Multan
Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan

Abstract
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 here 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 dominent 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 demanded 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 seed 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 genetic analysis of four cotton cultivars using Hayman (1954) and Jinks (1955) technique was adopted.

Materials and Methods
Assess the genetic architecture in upland cotton present study was under taken at the University of Agriculture Faisalab during 1992-93. Three exotic lines i.e. Allepo-40, 546 and Coker-304 and one local line i.e. Express of Gossypium hirsutum L. was crossed in a diallel fashion. 12F1 progenies along with parents were grown in a randomized Complete Block Design with three replications. Each 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 cotyledonal 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 croses were arranged into arrays in the form of diallel tables and two statistics, the variance (Vr) of family mean with in an array and the covariance (Wr) 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 (Wr) of each array against its variance (Vr). The slope and the position of regression line fitted to the array points within the limited parabola (Wr = Vpx Vr) indicated the degree of dominance and the presence or absence of gene interaction.

The limiting parabola was constructed on the basis of general formula, Wp = Vpx Vr, i.e. by plotting Vr (Vx Vp) points. The corresponding values for Wr for all observed Vr values were calculated as (Vx Vp), where Vp = variance of the parents. The different arrays (Cultivars) were fitted with in 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.
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, therefore, 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 Alepp-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 wr/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 Alepp-40 possesses maximum dominant genes, being nearest to the origin while LB-546 has maximum recessive genes due to 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 the 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 form 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 clear 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 Azhar et al. (1992), Aftab (1993) and Rehman et al. (1996).

Fibre Fineness: The regression line intercepted 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 for this trait. From the position of the array points it can be seen that Alepp-40 has maximum dominant genes while LB-546 has maximum recessive genes due to its farthest position.
Babar and Khan: Genetic analysis of cotton.

Table 1. Mean squares of various plant characters

<table>
<thead>
<tr>
<th>Replication</th>
<th>D.F.</th>
<th>Plant</th>
<th>No. of out turn branches</th>
<th>Seed index height</th>
<th>Fibre Sympodial</th>
<th>Fibre Fineness</th>
<th>Lint Length</th>
<th>Percentage</th>
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<td>2</td>
<td>15</td>
<td>15</td>
<td>30</td>
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<td>1.91</td>
<td>0.066</td>
<td>0.074</td>
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<td>5.0873**</td>
<td>5.15*</td>
<td>0.2265*</td>
<td>0.348**</td>
<td>0.4186**</td>
<td>1.7722*</td>
<td>0.378**</td>
<td>9.421**</td>
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<td>528.38*</td>
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</tbody>
</table>

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

(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. D: Vr/Wr graph for Fibre fineness

Fig. E: Vr/Wr graph for Fiber length

In regression line it revealed that LB-546 being nearest to the line possessed maximum dominant genes while Allepo-40 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.,

Fig. F: Vr/Wr graph for Lint Index

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


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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), Tanig(1992) and Shah et al. (1993). However, the genetic analysis made by Khan et al. (1991), Afzal (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 form 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 clear that Aleppo-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.

Allelo-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 do not have any dominant genes.

The characters with additive type of gene action with all the involvement of any sort of epistatic effects provide better chance to a breeder improving his crop through simple selection procedure. Over dominance means when 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.

References


