

Full Length Research Paper

Genetic dissection of yield and its components in upland cotton (*Gossypium hirsutum* L.)

Ghulam Sarwar¹, Muhammad Baber^{2*}, Nazim Hussain³, Iftikhar Ahmed Khan¹, Muhammad Naeem⁴, Muhammad Aman ullah⁵ and Azhar Ali Khan⁶

¹Department of Plant Breeding and Genetic, University of Agriculture, Faisalabad, Pakistan.

²Institute of Biotechnology, B.Z. University, Multan, Pakistan.

³Department of Agronomy, University College of Agriculture, B.Z. University, Multan, Pakistan.

⁴Institute of Pure and Applied Biology, B. Z. University, Multan, Pakistan.

⁵Department of Statistic, B.Z. University, Multan, Pakistan.

⁶Pakistan Agricultural Research Center, University College of Agriculture, B. Z. University, Multan, Pakistan.

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A 4x4 diallel cross experiment involving three exotic lines that is DPL-775, 71-821 Bulk-OP and Coker-100/A-2 and one local line that is MNH-53, was conducted for genetic analysis of yield and its components in upland cotton, to evaluate the gene action for different agronomic and fiber characters in upland cotton. Additive gene action with partial dominance appeared to control plant height, number of sympodial branches, number of bolls, yield of seed cotton, boll weight and lint percentage, where as over dominance type of gene action was noted for number of seeds per boll, seed index, lint index, staple length, fiber fineness. On over all basis 71-82 Bulk-OP has maximum dominant genes for number of sympodial branches, yield of seed cotton, seed index, lint index and fiber fineness while dominant genes for number of seeds per boll, boll weight, lint percentage and staple length are present in Coker-100/A-2. MNH-53 has maximum dominant genes for plant height and number of bolls while DPL-775 did not possess and dominant genes for any character.

Key words: Gene action, diallel cross agronomic traits, cotton.

INTRODUCTION

Cotton is ready cash crop of Pakistan and grown widely in areas of Punjab and Sindh. The roll of cotton plant in generating foreign exchange and as a source of providing raw material to textile and agro-based industries is very much obvious. Therefore, the cotton breeders attended the plant with great devotion in order to increase acre-yield and improve quality characteristics of lint. During the past two decades, a galaxy of cotton cultivars were developed which responded well to varying climate conditions of the cotton belt of the country. As a result of wider adoption of high yielding varieties from total national production had increased significantly compared to that harvested in the early days of Pakistan. However, acre yield is still lower and needs to be exploited in order to keep pace with the changing circumstances in the

country. Therefore, researchers are obliged to study the plant more extensively than ever before. Before embarking upon a plant improvement program through selection and breeding, the breeders are required to collect information about the existence of variation in different plant characters, the patterns of their inheritance and the extent to which the trait variability is transmitted to the next generation. With this objective in mind, the present genetic experiment was conducted in the department by using diallel cross techniques (Hayman, 1954; Jinks, 1955). The information derived from these investigations would be useful to the workers engaged in cotton improvement program. There are ample evidence reported on the genetic control of variation in *Gossypium hirsutum* characters. Here are brief review of some of the studies is given.

Khan et al. (1990) found that nature of gene for yield of seed cotton, boll weight, number of boll, staple length appeared to be over dominant. Whereas, genes for lint percentage were commutative in their effects showing

non-allelic interaction. Rehman and Khan (1933) studied 4x4 diallel cross character like number of days taken to first bud, first flower and number of bolls per plant were controlled by additive type of gene action with partial dominance and height of main stem, boll weight and seed cotton yield were controlled by over dominance type of gene action. Non allelic interaction was observed for number of bolls per plant. Khan et al. (1995) analyzed six varieties of *G. hirsutum* L. In a diallel cross experiment to study gene action, component of variation, heritability and heterosis. Plant height and boll weight were controlled by additive type of gene action with partial dominance. While over dominance was found to be operative for number of bolls per plant and seed cotton yield. Epistasis influenced the phenotypic manifestation of all these traits. Carvalho et al. (1995) studied six *G. hirsutum* L. Varieties and their hybrids obtained from complete diallel set of crosses. The result of analysis showed that additive genetic effects were significant for yield, boll weight and earliness. Additive genetic effect pre-dominated for number of bolls per plant, plant height and fiber maturity.

MATERIALS AND METHODS

To assess the genetic architecture in upland cotton present study was carried out. Three exotic that is DPL-775, 71-821 Bulk-OP and Coker-100/A-2 and one local line that is MNH-53, of *G. 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 m long row. The middle six plants leaving two plants on each side of the line were selected for the collection of data.

The heights of plants were recorded in centimeter when epical growth of the main stem ceased. The measurement was done with a measuring rod from the first cotyledonary node to epical bud. The number of sympodial branches on individual plants was counted and recorded when picking was over 100 seed were weighed in grams to calculate seed index. Fibre fineness was determined with help of Sheffield microneaire in microgram/inch, similarly length was measurement in millimeter by using Tuft method. The seed cotton from each plant was ginned separately lint thus obtained was weighed and ginning out turn percentage was calculated. Lint index or weighed of lint obtained from 100 seed in grams was also calculated.

The data for number of bolls per plant and yield of seed cotton were recorded from 6 selected plants in each plot. Similarly, boll weight was recorded by dividing the yield of seed of a particular plant by the total number of bolls picked from that every plant. The total number of seeds was counted for each boll, the average number of seeds per boll was calculated for all the families.

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 Jimks (1955), was used for genetic analysis. All the crosses were arranged into arrays in the form of dialled tables and two statistics, the covariance (v_r) of family mean with in 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 ($w_r^2 = v_r x v_r$) indicated the degree of dominance and the presence of absence of gene interaction. The limiting parabola was constructed on the basis of formula, $w_r^2 = v_r x v_r$, that is by plotting v_r ($v_r x v_r$) 05 points. The corresponding values for w_r for all observed v_r values were calculated as $(v_r x v_r)^{0.5}$, where v_p = 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 lid 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. The results obtained from the diallel analysis are discussed as under.

Plant height

The regression line intercepted the w_r -axis above the origin there by, indicating additive type of gene action with partial dominance. As the regression line does deviate significantly from the unit slop, 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 MNH_53 being nearest to the origin possessed maximum dominant genes while DPL-775 had maximum recessive genes due its farthest position. These results got support from the finding 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 observation because they observed 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 v_r/w_r graph showed that the regression line passed through w_r -axis above the origin signifying additive type of gene action with partial dominance. There is no evidence non-allelic interaction because regression line does deviate significantly from the unit slop. The position of array along the regression line revealed that 71-821 Bulk-OP possessed maximum dominant genes, being nearest to the origin, DPL-775 has maximum recessive genes due to its farthest position. These results are in agreement with those of Hussain (1991), Aftab (1993) and Khan and Khan (1993) who reported additive type of gene action.

Number of bolls

The regression line intercepted the wr -axis above the origin there by, indicating additive type of gene action with partial dominance. 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 is revealed that MNH-53 being nearest to the origin possessed maximum dominant genes while Coker 100/A-2 had maximum recessive genes due to its farthest position. These results got support from the finding of Shah et. al. (1992), Khan and Khan (1993) and Shah et al. (1993), who reported additive type of gene action with partial dominance, while Saleem (1990), Tariq et al. (1992) and Haq and Khan (1993), reported over dominance type of gene action for this trait. These deviations from the above finding results may be due to different environmental conditions.

Number of seeds per boll

The regression line intercepted wr -axis below the origin there by, indicating over dominance type of gene action. The regression line does not deviate from the unit slope, there appears no non-allelic interaction. As for as dominance relationship of the array point is concerned it is observed that Cocker 100/A-2 secure maximum dominant genes while DPL-775 had maximum recessive genes due to their closest and farthest position from origin respectively. Over dominance type of gene action for this trait has been reported by Saleem (1990), while additive type of gene action with partial dominance was reported by Gururajan and Henry (1995). These deviations from the above finding results may be due to different environmental conditions.

Boll weight

A study of graphic presentation of variance (vr) and covariance (wr) for boll weight indicate that the regression line with a unit slope intercepted the wr -axis just above the origin signifying additive type of gene action with partial dominance type of gene. 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 Cocker 100/A-2 possessed the maximum dominant genes due to its nearest position to the origin where as 71-821 Bulk-OP have recessive alleles, being away from the origin. The results of Saleem (1990) and Shah et al. (1992) also reported additive type of gene action with partial dominance for this trait, while Hussain (1991), Tariq et al. (1992), Haq and Khan (1993), indicated over dominance type of gene action for this

trait, these deviations from the above finding results may be due to different environmental conditions.

Yield of seed cotton

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. 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 71-821 Bulk-OP possessed maximum dominant genes, being nearest to the origin, while Cocker 100/A-2 has maximum recessive genes due to its farthest position. These results are in agreement with those of Shah et al. (1992), Murtaza et al. (1992), Saeed et al. (1996) and Hussain (1991), who reported additive type of gene action, while Saleem (1990), Tariq et al., (1992) and Haq and Khan (1993) reported over dominance type of gene action for this trait. These deviations from the above finding results may be due to different environmental conditions.

Seed index

A study of graphic presentation of variance (Vr) and covariance (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. As regression line does not deviate significantly from unit slope, therefore, there is no kind of non allelic interaction involved. From the position of array point along the regression line, it is clear that LB-546 possessed the maximum dominant genes due to its nearest position to the origin where as Cocker-304 had most of the recessive allele, being away from the origin. Additive type of gene action controlling the inheritance of seed index has also been reported by Tariq et al. (1992), Aftab (1993) and Rehman et al. (1994).

Ginning out turn percentage

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. There is no evidence of non-allelic interaction because regression does not deviate significantly from the unit slope. The position of array along regression line revealed that Coker-100/A-2 possessed maximum dominant genes, being nearest to the origin, while DPL-775 has maximum recessive genes due to its farthest position. Additive type of gene action has been reported by Rehman et al. (1991). While over dominance type of gene action controlling the inheritance of ginning out turn

percentage has also been reported by Aftab (1993) and Haq and Khan (1993) while 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 (V_r) covariance (W_r) for lint index indicated that the regression line with a unit slope intercepted the w_r -axis below the origin signifying over dominance type of gene action. As regression does deviate significantly from a unit slope, therefore, there is no kind of non-allelic action involved. From the position of array points along the regression, it is clear that 71-821 Bulk-OP possessed the maximum dominant genes due to its nearest position to the origin where Coker 100/A-2 had most of the recessive allele being away from the origin. Aftab (1993) and Rehman et al. (1993) observed this trait to be inherited by over dominance type of gene action. Whereas, additive type of gene action controlling the inheritance link index has also been reported by Rehman et al. (1991). This difference may be due to different genotype.

Fiber fineness

The regression line intercepted w_r axis below the origin there by, indicating over dominance type of gene action. As the regression line does not deviate significantly from unit slope therefore, there is no evidence of non-allelic action of this trait. From the position of the array point along the regression line it revealed 71-821 Bulk-OP being nearest to the origin possessed maximum dominant gene while DPL-775 had maximum recessive gene due to its farthest position. The genetic analysis Hussain (1991), Khan et al. (1991) and Rehman (1993) also found over dominance type of gene action. Additive type of gene action with partial dominance for this trait has been reported by Aftab (1993) disagree with the above results, the differences may be due to different genotypes studied in different ecological zones.

Fiber length

The study of v_r/w_r graph showed that the regression line passed through w_r -axis below the origin signifying over dominance type of gene action. There is no evidence of non-allele interaction because the regression line does not deviate significantly from the unit slope. The position of array along the regression line revealed that coker-100/A-2 possessed maximum dominant gene, being nearest to origin, while DPL-775 has maximum recessive genes due to its farthest position. These results got support from the findings of Babar et al. (1999), Khan et al. (1991), Aftab (1993) and Rehman et al. (1993).

However, the genetic analysis made by Hussain (1991), Tariq (1992) and Shah et al. (1993) disagree with above result because they additive type of gene action for this trait the difference of the result might attributed to different genetic stock and ecology of the breeding place.

On over all basis additive gene action with partial dominance appeared to control plant height, number of sympodial branches, number of bolls, yield of seed cotton, boll weight and lint percentage, where as over dominance type of gene action was noted for number of seeds per boll, seed index, lint index, staple length, fiber fineness. As a whole 71-821 Bulk-OP possess maximum dominant genes for number of sympodial branches, yield of seed cotton, seed index, lint index and fiber fineness while dominant genes for number of seeds per boll, boll weight, lint percentage and staple length are present in Coker-100/A-2. MNH-53 has maximum dominant genes for plant height and number of bolls while DPL-775 did not possess any dominant genes for any character.

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 in their phenotypic expression could be useful for identifying and selecting better performing progenies/hybrids to be exploited in any program leading to hybrid cotton. With out the involvement of any sort of epistatic effects, the characters with additive type of gene action provides better chance to a breeder improving his crop through simple selection procedure.

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