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# Genetics of Some Polygenic Traits of Upland Cotton

### Muhammad Naeem,<sup>\*</sup> Sadaf Ijaz, Muhammad Iqbal, Sami Ul-Allah, Zaitoon Shareef and Maryam Rana

Department of Plant Breeding and Genetics, UCA&ES, The Islamia University of Bahawalpur

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## ABSTRACT

Present study was conducted to investigate the genetics of some polygenic traits of cotton. The experiment was conducted involving four upland cotton (*Gossypium hirsutum* L.) genotypes i.e. IUB-222, IUB-52, MM-58 and FH-113 and their  $F_1$  hybrids in a RCBD with three replications. The data were collected for number of monopodial branches per plant, number of bolls per plant, boll weight, seed index, ginning outturn, fiber length, fiber fineness and seed cotton yield per plant. Analysis of variance (ANOVA) revealed significant genotypic differences for all above mentioned traits. The variance (Vr) and covariance (Wr) graphical representation depicted additive type of gene action along with partial dominance for all the traits studied. It is further concluded that early selection may be useful for the improving the cotton traits.

KEY WORDS: Gossypium hirsutum L, diallel analysis, gene action, morphological traits

# **1 INTRODUCTION**

Cotton being the most important fiber crop worldwide and contributes in foreign exchange earning of Pakistan. It provides raw material for textile industry and cotton seed is a vital source of edible oil. As the textile industry is expanding so the need for cotton is also increasing day by day and it is only possible if the yield and production of cotton is increased. A good variety has always been an important factor for yield improvement in any crop, so by utilizing different genetic manipulation and breeding approaches cotton breeders managed to produce varieties with high yield. Consequently significant achievements attained in this connection [1]. For the purpose to develop cotton genotypes with high yield potential, the information on genetics of different polygenic characters may be helpful for the breeders in improving and maintaining higher crop production standard [2, 3, 4]. For this purpose, the utility of pre-existing genetic variation in the breeding material as well as, the development of new variation having understanding of genetic constitution is very important in a breeding program. In order to evaluate the genetic variability, diallel crossing methods have been widely utilized by the plant breeder [5, 6, 7, 8, 9]. The aim of this study was to investigate the mechanism of genetic control in some polygenic traits of cotton.

## 2. MATERIALS AND METHODS

Four upland cotton genotypes IUB-222, IUB-52, MM-58 and FH-113 along with their direct and reciprocal crosses were sown during the year 2013 in the experimental area of Plant Breeding and Genetics Department, UCA & ES, The Islamia University of Bahawalpur in a triplicated randomized complete block design (RCBD). Row to row distance was maintained 75 cm and plant to plant 30 cm. Identical cultural and management practices including irrigation, fertilizer, hoeing and thinning were applied to all genotypes throughout the growing season. Data was recorded from ten guarded from each genotype per replication. Traits recorded were monopodia per plant, no. of bolls per plant, boll weight, seed index, fiber length, fiber strength, fiber fineness and seed cotton yield per plant. While GOT % was calculated by following formula given by [9]; Ginning out-turn (%) = lint weight (g)/ seed cotton Weight (g)  $\times$  100. Data of each trait was subjected to analysis of variance to test the difference among mean of each genotype (10). Traits showing the significant genotypic differences were analyzed by diallel analysis technique as devised by [11, 12].

## 3. RESULTS AND DISCUSSIONS

The results from analysis of variance (Table 1) and join regression analysis for all traits showed that the significant differences exist among genotypes and the data is fit for additive-dominance model. The Vr/Wr graph indicated additive type of gene action along with partial dominance for number of monopodial branches per plant, no. of bolls per plant, boll weight, seed index, GOT percentage, fibre length, fibre strength, fibre fineness, seed cotton yield par plant as regression line cut the Wr-axis above the origin (Fig 1-9). As the regression line didnt deviate from the unit slop hence, non-allelic interactions were not present so the trait can be improved through selection.

<sup>\*</sup> Corresponding Author: Muhammad Naeem, Department of Plant Breeding and Genetics, UCA&ES, The Islamia University of Bahawalpur. mniub@iub.edu.pk

Position of array points on regression line indicated that the genotype IUB222 owing to its nearest position near the origin possessed more dominant genes for bolls per plant, boll weight, seed index, fibre length (Fig 2,3,4,6) while FH13 possessed maximum dominant genes for monopodial branches per plant, fibre strength and for seed cotton yield per plant (Fig 1,7,9) MM58 possessed maximum dominant genes seed cotton yield per plant (Fig 9). Genotype IUB52 possessed least number of dominant genes for bolls per plant, seed index, fibre strength and seed cotton yield per plant (Fig 2,4,7,9), while FH113 possessed least dominant genes for boll weight, GOT and fibre fineness (Fig 3,5,8) respectively. Among all, MM58 possessed intermediate amount of dominant genes for boll weight, seed index, fibre strength and fibre fineness (Fig 3,7,8). There were no evidences of epistasis for all of the traits because regression line did not deviate from unit slop and such findings suggest that the trait can be improved by making selection in early segregating population. For no. of monopodial branches per plant our results are in accordance with findings of [13] who also confirmed the additive type of gene action with partial dominance for monopodial branches per plant. For number of bolls per plant [2, 6] also found additive type of gene action along with partial dominance as detected in present study. In case of Boll weight our results are in consistent with findings of [13, 14]. Seed index is crucial yield component and our results are in accordance with findings of [15, 16]. For Ginning out turn percentage earlier researchers [2, 13] presented similar results as observed by us in present study. For Fiber length and strength similar results were observed by [16, 17] while for Fiber fineness earlier researchers [8, 13] also observed additive gene action accompanied with partial dominance. Seed cotton yield per plant was also found to be governed by additive type of gene action with partial dominance was observed by [6, 18, 19].

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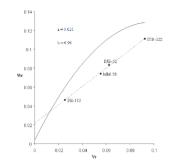
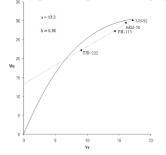
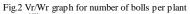


Fig.1 Vr/Wr graph for monopodial branches per plant





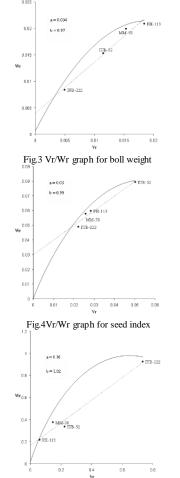


Fig.5 Vr/Wr graph for ginning out turn percentage

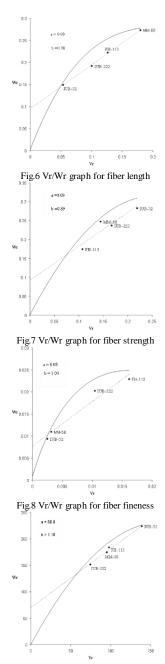


Fig.9. Vr/Wr graph for seed cotton yield per plant Table.1 Mean squares values of different traits of cotton studied in a 4×4 diallel cross

| Sr.  | Traits                           | <b>DF(t-1)</b> | MS       |
|--|----------------------------------|----------------|----------|
| 1  | No. of monopodial branches/plant | 15             | 0.42*    |
| 2  | Bolls/plant                      | 15             | 99.00**  |
| 3  | Boll weight                      | 15             | 0.11**   |
| 4  | Seed index                       | 15             | 0.16**   |
| 5  | G.O.T percentage                 | 15             | 1.288*   |
| 6  | Fiber length                     | 15             | 0.82*    |
| 7  | Fiber strength                   | 15             | 0.91*    |
| 8  | Fiber fineness                   | 15             | 0.05*    |
| 9  | Seed cotton yield/plant          | 15             | 565.63** |
| *,** Significant at 5% & 1% level of probability |                                  |                |          |