Study of Gene Action for Yield and Yield Components in *Gossypium hirsutum* L.

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Abstract: A diallel cross experiment was conducted in Randomized Complete Block Design involving Stone-Ville-213, HG-6-1-N, Fregobract-83 and AG-hirsutum-87 upland cotton cultivars to ascertain the type of gene action for different quantitative traits. Data was collected on ginning out turn percentage, seed index and seed cotton yield/plant. The genotypes were highly (P< 0.01) significant. Results demonstrated that GOT% and seed index were controlled by over dominant type of gene action, whereas seed cotton yield/plant was governed by partial dominance type of gene action. The variety Stone-ville-213 is good general combiner for GOT% and seed cotton yield/plant whereas AG-hirsutum-87 is best general combiner for the character seed index. The crosses Stone-ville-213 x Fregobract-83, Stone-ville-213 x HG-6-1-N and Stone-ville-213 x AG-hirsutum-83 were the best specific combiner for GOT%, seed cotton yield/plant and seed index, respectively.

Key words: Gene action, combining ability, *Gossypium hirsutum* L.

Introduction

Pakistan is an agricultural country and cotton crop is the backbone for earning foreign exchange of the country. However, per acre production is low as compared to the other cotton growing countries. Now major dilemma faced by the cotton breeders is how to increase the declining yield level. This can be possible if existing scarce genetic sources are properly utilized. Therefore, it is a dire need to fix the desirable genes in such a manner that homoyzygous lines may be obtained to improve the cotton genotypes. Genetic improvement of cotton plant will ultimately lead to the enhanced productivity. Larik et al. (1999, 2000) have assessed the efficiency and effectiveness of selection for superior genotypes based on the estimation of gene action and other genetic parameters. Therefore, the research work was designed to determine gene action and relative performance with respect to general as well as specific combining ability for yield and yield components.

Materials and Methods

The experiment was conducted in Randomized Complete Block Design (RCBD) at the Department of Plant Breeding and Genetics, Agricultural University Faisalabad during 1998-99. The direct and reciprocal crosses were made of four upland cotton varieties viz. Stone-ville-213, HG-6-1-N, Fregobract-83 and AG-hirsutum-87. Data was collected for the characters, GOT%, Seed index and Seed cotton yield/plant, and was statistically analyzed through analysis of variance technique (Steel and Torrie, 1960) to determine the difference among F1 hybrids and parents. For further genetic analysis diallel cross technique developed by Jinks (1955, 1956) was used. The information on gene action was inferred by plotting the variance (Vr) of each array against its covariance (Wr).

Results and Discussion

The mean performance of parents and F1 hybrids is presented in Table 1 to 3. The mean square values of the characters are presented in Table 4, which showed that the differences between genotypes were highly (P< 0.01) significant indicating the existence of genetic variability among genotype for the traits studied.

Ginning out turn percentage: The analysis of variance for ginning out turn percentage (Table 4) indicated that the differences among the genotypes were significant. The values of variance and covariance graph shown in Fig. 1, also display that the regression line cuts the Wr axis below the origin. This signifies the over dominance type of gene action. As the regression line deviates significantly from a unit slope the expression appeared to be contaminated with non-allelic interaction. From the position of array points on the regression line it was shown that AG-hirsutum-87 being the most proximate to the origin had most dominant genes while the HG-6-1-N possesses the recessive genes for this character. It is clear from Table 1, that Stone-ville-213 displayed 35.66 ginning

![Fig. 1: Wr/Vr graph for ginning out turn percentage](image1)

![Fig. 2: Wr/Vr graph for seed index](image2)
Seed index: The analysis of variance for seed index is presented in Table 4, which indicates that the difference among the genotypes were significant. The variance and covariance graph for the character seed index is depicted in Fig. 2, which showed that the regression line intercepted the Wr axis below the origin, indicating the over dominance type of gene action. As the regression line deviates significantly from unit slope there appears some non-alleric interactions in this respect. The variety Fregobract is close to the origin which showed maximum dominant genes, whereas the Stone ville-213 have maximum recessive genes. In Table 2, the variety AG-hirsutum-87 showed the mean 6.1 g but in the array it carries the highest mean (7.30 g) value which showed that it is good general combiner for this trait. Within the array the cross of Stone ville-213 x AG-hirsutum-87 had the highest value (8.28g) suggesting that the cross is specific combiner in this respect. The results are in conformity with the results of Larik et al. (1997), whereas, the Singh et al. (1982) reported additive type of gene action.

Seed cotton yield/plant: The analysis of variance for seed cotton yield/ plant is presented in Table 4, indicates that the differences among the genotypes were highly significant. The Fig. 3 showed that the regression line passes the Wr axis above the origin which revealed the additive type of gene action with partial dominance. As the regression line deviates significantly from a unit slope there appears some interaction of nonallelic genes in this respect. The variety AG-hirsutum-87 is nearer to the origin indicating the presence of maximum dominant genes whereas, HG-6-1-N is far from the origin demonstrating that this variety has maximum recessive genes for this character. Results further (Table 3) showed that Stone ville-213 had highest array mean value (107.69) which suggested that Stone ville-213 is good general combiner for this trait and the cross. Stone ville-213 and HG-6-1-N had the highest value (127.07), thus it indicates that is better specific combiner as compared to other crosses. Azhar et al. (1963) and Nadir et al. (1984) have also reported similar results from their studies. However, Keerio et al. (1995) reported over dominance type of gene action.

References