INHERITANCE OF QUANTITATIVE TRAITS IN COTTON (G. HIRSUTUM L.). II. LINT INDEX AND FIBRE QUALITY COMPONENTS

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Four varieties of cotton (G. hirsutum L.) were genetically analysed in a complete set of diallel crosses to study the gene action involved in the phenotypic manifestation of their lint index, staple length, fibre fineness and fibre maturity percentage. Additive type of gene action with partial dominance complicated with some non-allelic interactions was observed to be involved in the inheritance pattern of all the characters. Non-significance of parents vs crosses mean squares for the traits indicated no heterosis.

INTRODUCTION

The fibre traits such as staple length, fibre fineness, fibre strength and fibre maturity go a long way in determining the demand of a cotton variety in the textile industry, because the quality of the fabrics depends upon the quality of its fibre (Afzal and Khan, 1961).

To improve such characters in prevailing cotton cultivars, the breeding procedures are determined by the action, interaction and linkage relationship of the genes controlling these traits (Gururaja Rao, 1975; Khan et al., 1982; Green and Culp, 1990 and Khan et al., 1991).

It is, therefore, imperative to have such information before a breeder starts a programme for adjusting his crops according to his needs. The present studies were conducted to have an information about the gene action involved in the phenotypic ex-

pression of some fibre quality traits in upland cotton.

MATERIALS AND METHODS

Four varieties of cotton (NIAB 78, AU 59, Genetic cotton and Coker 201) were crossed in a diallel fashion to obtain twelve F₁ crosses including reciprocals. The F₁ crosses and their parents were sown during 1987-88 in a randomized complete block design with four replications at Postgraduate Agricultural Research Station (PARS), University of Agriculture, Faisalabad. Each genotype, comprised of ten plants spaced 30 cm apart, keeping 75 cm distance from row to row.

Lint index, staple length, fibre fineness and fibre maturity percentage were analysed statistically (Steel and Torrie, 1980). Information regarding the gene action expressed as the phenotypic manifestation of the characters was then studied following Hayman (1954) and Jinks (1954).

recessive, being the nearest and the farthest from the origin, respectively. These results

Table 1. Mean squares from the analysis of variance of lint index and fibre quality components in a 4 x 4 diallel cross of G. hirsutum L.

Source of variance	Df	Lint index	Fibre length (mm)	Fibre fineness (µg inch ⁻¹)	Fibre maturity percentage
Replications	3	0.77**	0.61	0.08	11.80**
Genotypes	15	0.38**	2.91**	0.43**	5.45**
Parents (P)	3	0.69*	4.10**	0.37**	4.38**
Crosses (C)	11	0.42**	2.28**	0.14**	6.13**
Pvs C	1	0.37	6.20	0.01	1.19
Error	45	0.13	0.51	0.05	1.74
Reps. x Parents	9	0.11	0.46	0.05	0.64
Reps. x Crosses	33	0.11	0.45	0.02	2.10
Reps. x Pvs C	3	0.29	1.35	0.07	3.16

^{*, ** =} Significantly different at 0.05 and 0.01 probability levels, respectively.

RESULTS AND DISCUSSION

Analysis of variance (Table 1) showed that statistically significant differences existed among genotypes, parents and crosses for all the traits under study. Non-significant differences of parents vs crosses mean squares for the traits indicated no heterosis.

A study of Figure 1 for lint index indicated that regression line passed through covariance (Wr) axis above the origin, signifying additive type of gene action with partial dominance. As the regression line deviated significantly from a unit slope, some non-allelic interaction appeared affecting the phenotypic manifestation of this trait. From the position of the array points on the regression line "Genetic Cotton" behaved as dominant and NIAB 78 as

are in close agreement with the findings of Gururaja Rao (1975) and Green and Culp (1990) who reported additive type of gene action with partial dominance in the inheritance of this character.

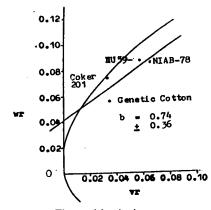


Fig. 1. Lint index.

The Vr/Wr graph plotted in Figure 2 for staple length indicated the regression line passing through the Wr axis above the origin. Therefore, the gene action controlling the inheritance of staple length was of additive type. As the line deviated significantly from a unit slope, there appeared some interaction of genes affecting the phenotypic manifestation of this trait. Position of the array points on the regression line indicated that "Coker 201" possessed maximum dominant genes, while Genetic Cotton had recessive genes. These results could be compared with the findings of Khan et al. (1982) who also advocated additive type of gene action in the phenotypic manifestation of this character.

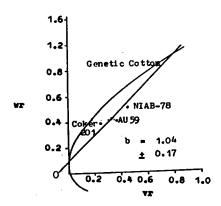


Fig. 2. Staple length.

The phenotypic expression of the fibre fineness also involved additive type of gene action complicated by some epistatic effects as the regression line deviated significantly from a unit slope intercepted the Wr axis above the origin (Fig. 3). The array of "AU 59" scored the maximum dominant genes while Coker 201 had the recessive ones due to their nearest and distal positions from the origin, respectively. These findings substan-

tiated the results reported by Khan et al. (1991).

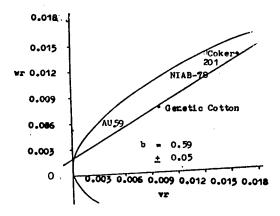


Fig. 3. Fibre fineness

Fibre maturity percentage was also found to be controlled by additive type of gene action with partial dominance as the regression line (Fig. 4) intercepted Wr axis above the origin. The deviation of the line from a unit slope indicated some non-allelic interactions involved in the expression of this character. From the position of the array points on the regression line "AU 59" seemed to have maximum dominant and Coker 201 maximum recessive genes for this character.

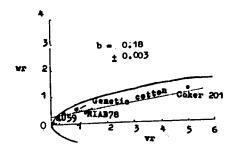


Fig. 4. Fibre maturity.

From the above mentioned results, it is clear that gene action involved in the expression of all the characters was of additive type. With additive gene action, the phenotype faithfully reflects the genotype, assuming no environmental effects. This means that the selection for a particular genotype is accurate within the limits imposed by environmental effects but in the present studies the involvement of non-allelic interactions in the phenotypic reflection of the characters makes the situation a bit complicated. Therefore, the simple selection procedures for the improvement of these plant characters may be misleading unless type of gene interactions are investigated and well understood.

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