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Comparison of the Gene Action Controlling Metric Characters in Upland Cotton (*Gossypium hirsutum* L.)

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Abstract: Significant differences among hybrids and their parents were noted. The boll weight and staple length reflected additive type of gene action while in seed index and lint index, over-dominance gene action was observed. The non-significant deviation of regression line from unit slope indicates the absence of non-allelic interaction in staple length showing absence of epistasis providing positive lines for isolating superior genotypes. Boll weight and lint index shows the significant deviation from unit slope which surely indicates the presence of epistasis.

Keywords: Gene action, metric characteristics

Introduction

Since independence, research work on cotton crop for its genetic improvement has been undertaken and as a consequence a large number of varieties possessing rich combinations of germ plasm for various characteristics like higher yield, higher ginning out turn, better quality along with the adaptation to the local ecological and agronomic conditions have been evolved. In this way a startling improvement in its production on unit area basis has been obtained. The success of cotton breeding programme and knowledge of the heredity mechanism of various characters such as yield and its components are indispensable. Amin *et al.* (1989) and Mahmood *et al.* (1989) reported the over dominance type of gene action for plant height and yield of seed cotton. While Mahmood *et al.* (1989) recorded additive type of gene action for the number of bolls and boll weight. The present study was thus arranged to get information about the heredity pattern in some important cultivars of cotton under the environmental conditions of D.I.Khan.

Materials and Methods

The germ plasm of eight varieties of cotton (*Gossypium hirsutum* L), viz, AUH-50, CIM-70, NIAB-78, CIM-240, CYTO-21/91, CYTO-14/87, MNH-410, MNH-156, and their F₃-seed of all possible combinations obtained from the Department of Plant Breeding and Genetics, Faculty of Agriculture, Gomal University, Dera Ismail Khan. The above stated F₃ material along with their parents were sown in the Experimental area of the Faculty of Agriculture during the crop season 1998. The experiment was arranged in Randomized Complete Block Design with dibbling method. The experimental plot was kept as 48 x 3.60 m² with 30 cm plant to plant distance. While row to row distance was set as 75 cm. The number of plants per genotype were 12. The data of the following parameters were recorded from central 10 plants in each treatment.

1. Boll Weight (g)
2. Seed Index
3. Lint Index
4. Staple Length (mm)

Statistical Analysis: The data regarding different plant characters were averaged and subjected to statistical manipulation for the analysis of variance technique to establish the level of variability among F₃ hybrids and their

parental lines. Further analysis for the diallel cross technique developed by Jinks (1956) and as applied by Whitehouse *et al.* (1958) was adopted for genetic analysis. All the crosses were arranged into arrays in the form of diallel tables and two statistics, the variance (Vr) of the family mean within an array and the covariance (Wr) of these means with the non-recurrent parental values were calculated from each diallel table by the following methods.

Estimation of Variances and Covariances:

a. Variance was calculated by the following formula.

$$Vr = \frac{\sum X^2i - (\sum Xi)^2/n}{n-1}$$

b. Covariance (Wr) was calculated by the following formula.

$$Wr = \frac{\sum Xi Yi - (\sum Xi)(\sum Yi)/n}{n}$$

Calculation of Limiting Parabola: 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 the regression line fitted to the array points within the limiting parabola ($Wr^2 = Vp \cdot Vr$) indicated the degree of dominance and the presence or absence of gene interaction. The limiting parabola was constructed on the basis of formula, $Wr^2 = VrxVp$ by plotting $Vr, VrxVp$ points. The corresponding values of Wr for all observed Vr values were calculated as $(VrxVp)^{1/2}$, where Vp = variance of the parents. The different arrays (varieties) were fitted within the limits of the parabola using the individual variance and covariance as their limiting point. Array nearest to the point of origin possessed most of the dominant genes, while the array that lay the farthest from the origin possessed the most recessive genes and the intermediate position signified the presence of both dominant and recessive genes in the array. The standard error for the regression line slope was estimated according to Snedecor (1962).

Results and Discussion

Boll weight: An examination of Table 1 and Fig. 1, shows that the regression line cuts the Wr axis above the origin there by signifies an additive type of gene action with partial dominance for boll weight as the line makes a tangent with parabola. From the position of array points along the regression line it becomes disclosed that CYTO-21/91 keeps the maximum dominant genes because of its

Table 1: 8 x 8 Diallel table for average boll weight per plant

Varieties	AUH-50	CIM-70	NIAB-78	CIM-240	CYTO 21/91	CYTO 14/87	MNH-410	MNH-410	Vr	Wr
AUH-50	3.17	3.70	3.69	3.44	3.56	3.59	3.51	3.36	0.03	0.01
CIM-70	3.70	3.28	3.78	3.61	3.58	3.49	3.69	3.46	0.03	0.007
NIAB-78	3.69	3.78	3.48	3.86	3.80	3.69	3.56	3.57	0.02	0.00
CIM-240	3.44	3.61	3.86	3.27	3.62	3.45	3.44	3.37	0.03	0.02
CYTO 21/91	3.56	3.58	3.80	3.62	3.44	3.59	3.46	3.50	0.01	0.004
CYTO 14/87	3.59	3.49	3.69	3.45	3.59	3.17	3.42	3.46	0.02	0.01
MNH-410	3.51	3.69	3.56	3.44	3.46	3.42	3.26	3.30	0.02	0.007
MNH-156	3.36	3.46	3.57	3.37	3.50	3.46	3.30	3.16	0.02	0.01
Total	28.02	28.59	29.43	28.06	28.55	27.86	27.64	27.18	0.18	0.07
Mean	3.50	3.57	3.68	3.51	3.57	3.48	3.46	3.40	0.02	0.0088

Table 2: 8 x 8 Diallel table for seed index

Varieties	AUH-50	CIM-70	NIAB-78	CIM-240	CYTO 21/91	CYTO 14/87	MNH-410	MNH-410	Vr	Wr
AUH-50	6.00	7.56	7.55	6.61	6.37	7.19	7.21	7.41	0.88	0.33
CIM-70	7.56	6.40	7.15	7.62	7.00	6.73	6.95	7.43	0.18	0.04
NIAB-78	7.55	7.15	6.75	8.00	7.72	7.55	7.95	7.35	0.17	0.03
CIM-240	6.61	7.62	8.00	7.15	6.60	7.43	7.93	7.71	0.30	0.09
CYTO 21/91	6.37	7.00	7.72	6.60	6.30	7.49	6.45	6.95	0.28	0.03
CYTO 14/87	7.19	6.73	7.55	7.43	7.49	6.37	7.55	6.71	0.21	0.05
MNH-410	7.21	6.95	7.95	7.93	6.45	7.55	6.75	6.95	0.30	0.09
MNH-156	7.41	7.43	7.35	7.71	6.95	6.71	6.95	6.65	0.15	0.03
Total	55.63	56.84	60.02	59.05	54.88	57.02	57.74	57.16	2.47	0.69
Mean	6.95	7.11	7.50	7.38	6.86	7.13	7.22	7.15	0.31	0.086

Table 3: 8 x 8 Diallel table for lint index

Varieties	AUH-50	CIM-70	NIAB-78	CIM-240	CYTO 21/91	CYTO 14/87	MNH-410	MNH-410	Vr	Wr
AUH-50	3.00	4.11	4.21	3.45	3.48	3.85	3.96	3.98	0.17	0.05
CIM-70	4.11	3.35	4.00	4.15	3.83	3.62	3.85	4.00	0.17	0.01
NIAB-78	4.21	4.00	3.65	4.54	4.43	4.28	4.56	4.11	0.09	-0.004
CIM-240	3.45	4.15	4.54	3.76	3.69	4.11	4.29	4.23	0.13	0.05
CYTO 21/91	3.48	3.83	4.43	3.69	3.23	4.10	3.65	3.74	0.13	0.05
CYTO 14/87	3.85	3.62	4.28	4.11	4.10	3.36	4.34	3.57	0.13	0.03
MNH-410	3.96	3.85	4.56	4.29	3.65	4.34	3.46	3.65	0.15	0.04
MNH-156	3.98	4.00	4.11	4.23	3.74	3.57	3.65	3.43	0.08	0.02
Total	30.04	30.91	33.78	32.22	30.15	31.23	31.76	30.71	0.95	0.25
Mean	3.76	3.86	4.22	4.03	3.77	3.90	3.97	3.84	0.12	0.03

Table 4: 8 x 8 Diallel table for staple length

Varieties	AUH-50	CIM-70	NIAB-78	CIM-240	CYTO 21/91	CYTO 14/87	MNH-410	MNH-410	Vr	Wr
AUH-50	26.85	27.75	28.10	28.15	28.17	28.19	28.75	28.25	0.30	0.07
CIM-70	27.75	28.00	28.65	28.55	28.00	27.85	28.65	28.45	0.14	0.01
NIAB-78	28.10	28.65	26.55	27.87	28.00	28.15	27.65	28.11	0.37	0.19
CIM-240	28.15	28.55	27.87	27.13	27.65	27.79	27.65	27.95	0.17	0.06
CYTO 21/91	28.17	28.00	28.00	27.65	27.55	28.25	28.15	28.45	0.09	0.01
CYTO-14/87	28.19	27.85	28.15	27.79	28.25	26.65	27.45	27.85	0.28	0.05
MNH-410	28.75	28.65	27.65	27.65	28.15	27.45	27.63	28.55	0.28	0.13
MNH-156	28.25	28.45	28.11	27.95	28.45	27.85	28.55	27.67	0.10	0.07
Total	224.21	225.90	223.08	222.74	224.22	222.18	224.48	225.28	1.73	0.57
Mean	28.03	28.24	27.89	27.84	28.03	27.77	27.95	28.06	0.22	0.07

nearest position to the lower interception of line and parabola. While AUH-50, CIM-70 and CIM-240 receives the most recessive genes for boll weight being away from the origin. The regression line deviates significantly from the unit slope, so there is non-allelic interaction present. The genetic mechanism of the control of boll weight is of additive type and thus these observations are in conformity with those already expressed by research workers like Gill and Kalsy (1981), Mirza and Khan (1986) who were of the view that boll weight was additively controlled. But on the other hand observations of Kassem *et al.* (1986) and Khan *et al.* (1991b) exposed the genetic mechanism of control of boll weight that of over dominance type which is the direct reflection of heterotic effects in F_1 progenies. Contradictions for the manifestations of this character might be due to progenies of different generations and due

to different breeding materials of their parents utilized in the conduct of experiment.

Seed Index: A contemplation to Table-2 and Fig. 2, indicate that the regression line intercepts the covariance axis below the origin and hence signifies an over dominance type of gene action for the character like seed index. It is clear from the position of array points along the regression line that MNH-156, being nearest to the origin contains the most dominant genes for seed index. While CIM-240 being farthest from the origin possesses the most recessive genes for seed index. The regression line does not deviate significantly from the unit slope so there is no non-allelic interaction present. The results are in accordance with those already reported by Khan *et al.* (1987) and Rehman *et al.* (1988). However, White (1986) and Virk *et al.* (1984)

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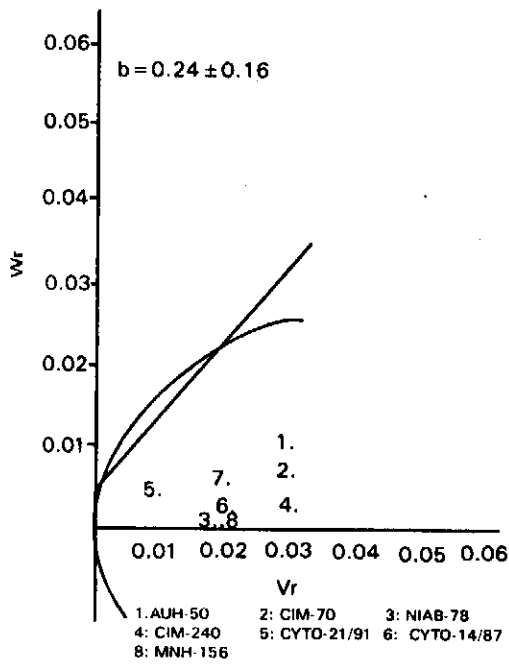


Fig. 1: Vr/Wr graph for Boll Weight per Plant

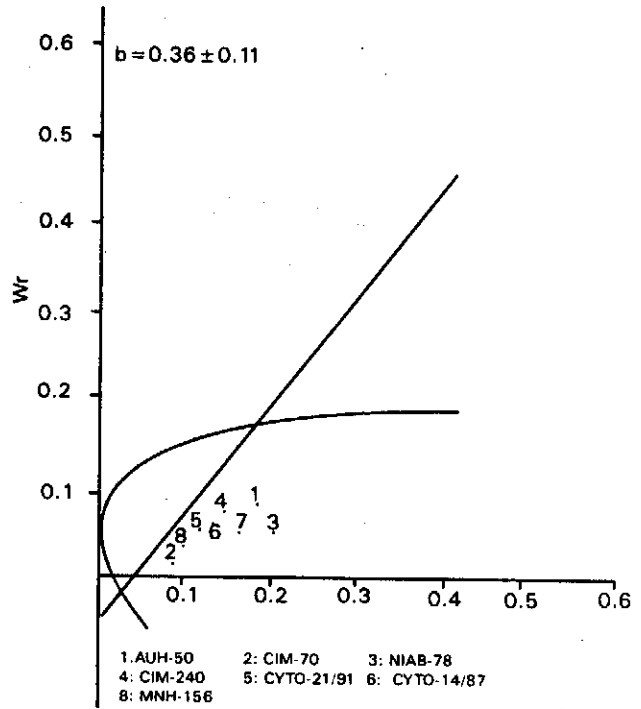


Fig. 3: Vr/Wr graph for Lint Index

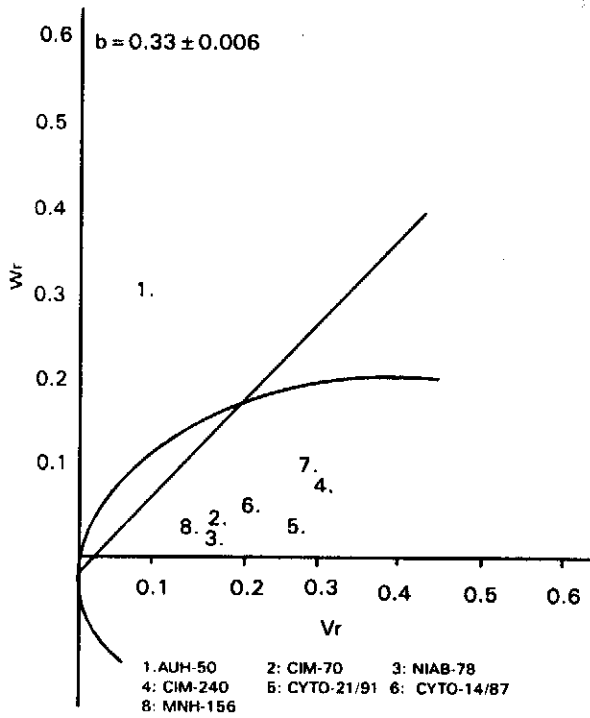


Fig. 2: Vr/Wr graph for Seed Index

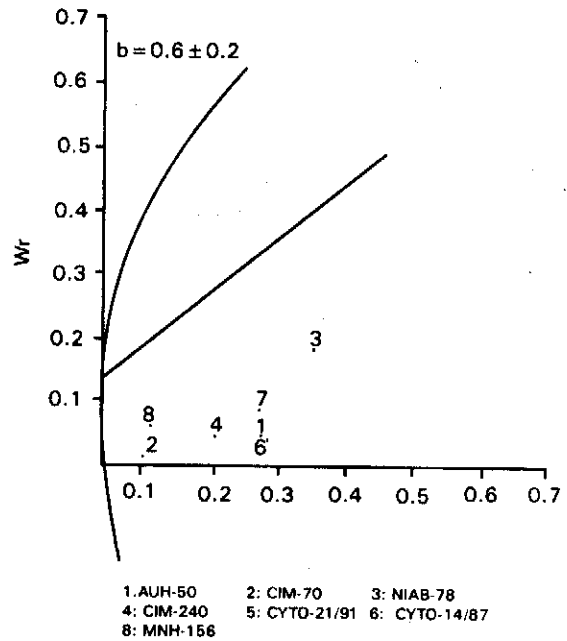


Fig. 4: Vr/Wr graph for Staple Length

were not in line with these observations. These differences might be due to different sources of germplasm used under different agro-climatic conditions.

Lint Index: A reference to Table 3 and Fig. 3, indicates that the regression line intercepts the covariance axis below the origin and hence signifies an over dominance type of gene action. It is evident from the position of array points along the regression line that CIM-70, being nearest to the origin contains the most dominant genes for lint index. While NIAB-78, being lying farthest from the origin possesses the most recessive genes for lint index. The regression line is deviating significantly from the unit slope, hence pointing for non-allelic interaction.

In support of these observations the experimental evidences of Khan *et al.* (1987), are enough to confirm the present findings. However, there are also some differences of opinion in regard to this parameter presented by Dahoon and Singh (1983) who are of the view that lint index has a type of gene action of additive type and with partial dominance. These deviations might be due to different germplasm used under different environments.

Staple Length: A reference to Table 4 and Fig.4, indicates that the regression line intercepts the covariance axis above the origin. This situation signifies additive type of gene action for the manifestation of staple length. An examination of the position of array points along the regression line indicates that CIM-70 being nearest to the origin contains the most dominant genes for staple length. While NIAB-78 receives the most recessive genes for staple length being away from the origin. The non-significant deviation of regression line from unit slope indicates the absence of non-allelic interaction for the manifestation of staple length per plant. These observations are in conformity with those already expressed by Duhoon and Singh (1983), Khan (1984), Nawaz (1984) and Latif *et al.* (1988). But on the other hand research workers like Khan (1986) and Khan *et al.* (1987), reported over-dominance type of gene action in the manifestation of this character. Contradictions for the manifestation of this character might be due to different breeding germplasm utilized in the conduct of this experiment.

The conclusion of the results of the analysis of variance shown that the mean genotypic differences between hybrids and their parents in F_2 generation were highly significant for the characters boll weight per plant. In case of seed and lint indices the analysis of variance revealed that the differences among genotypes were only significant except staple length for which the level reduced to non significant only. (Appendix)

The estimates of Variance (V_r) and Covariance (W_r) are represented by diallel Tables (1 to 4). It can be determined easily from V_r and W_r graphic presentation that the varieties possessing the most dominant genes are Cyto-21/91, Niab-78, Niab-78, CIM-70. The character, staple length was controlled by additive type of gene action which provides outlines for reasonable expectation for success in isolating the superior genotypes.

Whereas, over dominance type of gene action was predominant for seed and lint indices. The non-significant deviation of regression line from unit slope indicates the absence of non-allelic interaction which was present for the

traits under study like, seed index and staple length. It is the type of gene interaction leading towards absence of epistasis which is necessary for isolating superior genotypes. But the characters like, boll weight per plant, lint index showing the significant deviation from unit slope which surely shown the presence of epistasis, that is, selection of such genotypes is undesirable.

Keeping in view the results of the genetic analysis study it is, therefore, strongly suggested that the number of bolls per plant, yield of seed cotton, seeds per boll and staple length may be made the criteria for selecting high yielding genotypes of cotton under the limits of this experiment.

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