



Studies on Gene Effects in Intervarietal Crosses of *Hirsutum* Cotton

M. Paramjit Singh, V.P. Mittal and K.S. Brar

Punjab Agricultural University
Regional Research Station, Bathinda, Punjab - 151 001

Basic sets of six generations of two varietal crosses of cotton were studied to estimate nature and magnitude of gene effects operative in the inheritance of yield components and fibres quality traits. Scaling tests as well as joint scaling test detected the presence of epistasis for seed cotton yield, bolls per plant, boll weight and 2.5% span length in cross LH900 x Senegal and for boll weight, ginning outturn and 2.5% span length in cross LH900 x LRA 5166. Additive-dominance model was sufficient to explain variation in generation means for the remaining traits. Inheritance pattern of various traits differed in the two crosses and additive as well as non-additive gene effects were found to be important. Keeping in view the importance of both additive and non-additive gene effects, it was suggested that sophisticated selection procedures as recurrent selection and population improvement might be followed for simultaneous improvement of yield and fibre characters.

Key words: Cotton, gene effects, yield, fibre quality, generation mean analysis, epistasis.

Cotton, a well-known fibre crop, plays a key role in the textile industry. However cotton productivity in India is the lowest among major cotton growing nations of the world. To meet requirement of ever growing population of the country with limited land resources, future cotton breeding programs should be aimed at increasing its productivity. Genetic variability in a crop is the basis for improvement. The progress in the improvement of a trait would depend upon the nature and magnitude of heritable variation in the population. Further the estimates of gene effects have a direct bearing upon the choice of selection procedure and breeding methodology to be adopted for improvement of quantitative characters. The additive gene effect is primarily useful in developing pure line varieties while dominance and epistatic gene effects can be valuable for the exploitation of hybrid vigour. The genetic control of quantitative characters often reflects the combined action of a number of genes. Although individual effect of such genes cannot be determined, yet biometric models are available for the separation of epistatic from additive and dominance variation in generation means. The involvement of both additive and non-additive gene effects in the inheritance of different quantitative characters in upland cotton has been reported by many workers (Singh and Chahal, 2004; Chandio *et.al.*, 2003). The present study was planned to gather information about the nature and magnitude of gene effects for yield and fiber characters in two varietal crosses of *hirsutum* cotton. The genetic information so obtained will be useful in formulating

an efficient breeding methodology for the development of improved genotypes of cotton.

Materials and Methods

The experimental material consisting of a basic set of six generations i.e. P₁, P₂, F₁, F₂, B₁ and B₂ derived from two varietal crosses viz., LH900 x Senegal and LH900 x LRA5166 were studied in the experimental area of Punjab Agricultural University, Ludhiana. Each cross was grown in a separate experiment in a randomized block design with three replications. The plants were spaced 67.5 cm between the rows and 30 cm within rows. All the recommended cultural practices were adopted to raise a healthy crop. The data were recorded on individual plant basis in each row for seed-cotton yield (g), bolls per plant, boll weight (g), ginning out-turn (%) and 2.5% span length (mm). The generation means were calculated by taking the average over all the replications for each generation. To test the adequacy of the additive -dominance model the individual scaling tests given by Mather (1949) as well as joint scaling test by Cavalli (1952) were applied. First, simple additive - dominance model consisting of mean [m], additive [d] and dominance [h] gene effects was tried and the adequacy of the model was tested by the chi-square test. When this model failed to explain variation among generation means, successively non-allelic interaction parameters i.e. additive x additive [i], additive x dominance [j] and dominance x dominance [l] were included in this model. Thus, all possible models with different combinations of epistatic parameters were tried to identify the best fit model with minimum/

*Corresponding author email: paramjit1967@yahoo.co.in

non-significant value of chi-square with maximum number of significant parameters as suggested by Mather and Jinks (1982).

Results and Discussion

The estimates of scaling tests and joint scaling test along with standard errors for different traits of two varietal crosses viz, LH900 x Senegal (cross-1) and LH900 x LRA5166 (cross-2) are presented in table-1. Scaling tests as well as joint scaling test detected the presence of epistasis for seed cotton

yield, bolls per plant, boll weight and 2.5% span length in cross-1 and for boll weight, ginning outturn and 2.5% span length in cross-2. The significance of additive and/or dominance components detected for these characters could not be relied upon due to inadequacy of the model as shown by significant chi-square values. Scaling tests and joint scaling test indicated that additive-dominance model was sufficient to explain variation in generation means for ginning outturn in cross-1 and for seed-cotton yield and bolls per plant in cross-2. Additive gene

Table 1. Estimates of scaling tests and joint scaling test for crosses LH 900 x Senegal (C1) and LH 900 X LRA 5166 (C2).

Parameter	Seed-cotton yield		Bolls per plant		Boll weight		Ginning outturn		2.5% span length	
	C1	C2	C1	C2	C1	C2	C1	C2	C1	C2
Scaling test										
A	-12.33±6.00	2.33±11.94	-5.99±2.66	-0.33±3.17	1.11**±0.34	0.42**±0.11	-0.72±0.60	-3.46±2.46	0.20±0.41	2.00*±0.92
B	13.22*±6.28	-13.28±11.34	0.01±2.07	1.66±3.13	1.27**±0.24	-1.38**±0.11	-2.59±2.97	-3.98*±1.71	2.80**±0.27	-4.90**±0.36
C	35.56±19.76	-17.40±29.09	2.89±4.73	-4.22±6.85	1.88**±0.62	0.39±0.86	3.22±2.82	4.63±3.06	1.00*±0.42	0.70±1.08
Joint scaling test										
m	32.42±1.02	29.38±2.00	9.65±0.50	9.18±0.52	3.59±0.06	3.14**±0.04	34.23±0.12	34.73±0.19	26.75±0.09	27.29±0.14
[d]	0.92±0.94	6.95**±1.87	1.13**±0.43	1.85**±0.42	-0.37**±0.06	0.44**±0.03	0.60**±0.12	0.36±0.19	-1.53**±0.10	-1.65**±0.14
[h]	13.16**±2.74	34.24**±5.29	3.87**±1.07	10.71**±1.20	-0.26**±0.07	0.19*±0.08	-0.33±0.56	-4.04**±0.70	1.72**±0.16	2.38**±0.19
X ²	31.58**	3.69	11.49**	3.49	44.18**	227.51**	4.32	16.70**	106.81**	196.96**

*,** Significant at 5 and 1% levels respectively

effects were found to be operative in the inheritance of ginning outturn in cross-1 which might be fixed in pure lines. Both additive and dominance gene effects were found to be important for seed-cotton yield and bolls per plant in cross-2. For exploiting both types of gene effects, selection in the segregating populations should be delayed to later generations when dominance gene effects would have diminished.

The inferences about the type of gene effects were drawn from the best fit model where epistasis was identified by scaling tests and joint scaling test. The estimates of parameters along with standard errors for such traits are given in table-2. In cross-1, model having m, [d], [h] and [j] components was

found to be adequate for seed cotton yield with all the three parameters to be significant while for bolls per plant, model with m,[d], [h],[i] and [j] was adequate, but only [d] component was significant. For boll weight, best fit model identified additive, dominance and dominance x dominance gene effects in cross1, while dominance x dominance gene effects in cross-2. The negative sign of [d] in cross-1 indicated more contribution by dispersed pairs of genes than by associated pairs while opposite signs of [h] and [i] implied the role of duplicate epistasis in the genetic control of this trait. For ginning outturn dominance, additive x additive and dominance x dominance components were found to be important in cross-2. The negative sign of [h] indicated decreaser alleles to be dominant

Table 2. Estimates of genetic components in the best fit model for crosses LH 900 x Senegal (C1) and LH 900 X LRA 5166 (C2).

Parameter	Seed-cotton yield		Bolls per plant		Boll weight		Ginning outturn		2.5% span length	
	C1	C2	C1	C2	C1	C2	C1	C2	C1	C2
Scaling test										
m	32.72±1.02	-----	12.81±2.22	-----	2.85±0.70	3.41±0.06	-----	47.07±3.04	24.60±0.47	27.55±0.15
[d]	3.23**±1.04	-----	1.63**±0.52	-----	-0.26**±0.06	-0.26±0.06	-----	0.31±0.19	-1.30**±0.14	-2.25**±0.15
[h]	14.24**±2.74	-----	-1.84±3.57	-----	3.42*±1.62	-0.80±0.19	-----	-36.01**±7.93	8.50**±1.31	1.30±0.83
[i]	-----	-----	-3.26±2.25	-----	0.56±0.69	-----	-----	-12.32**±3.03	2.00**±0.45	-----
[j]	-25.92**±4.94	-----	-3.60±1.84	-----	-----	1.80±0.13	-----	-----	-2.60**±0.48	8.19**±0.84
[l]	-----	-----	-----	-----	-2.99**±0.94	0.95**±0.18	-----	20.00**±5.37	-5.00**±0.87	1.25±0.78
X ²	4.03	-----	6.27	-----	0.16	2.55	-----	0.04	-----	6.94

*,** Significant at 5 and 1% levels respectively

over increaser alleles. For 2.5% span length, all the fitted parameters viz., additive, dominance, additive x additive, additive x dominance and dominance x dominance were significant in cross-1 while only additive and additive x dominance components in cross- 2 while in cross-1, the adequacy of the fitted

model could not be tested as no degree of freedom was left for the chi-square test. So the role of higher order interactions and linkages between the interacting genes in the inheritance of this trait could not be ruled out.

In the present study, epistasis was detected for different traits except ginning outturn in cross1 and for seed cotton yield and bolls per plant in cross2. Besides digenic epistasis, higher order interactions might be involved in the inheritance of 2.5% span length in cross1. It demonstrated that estimation of only additive-dominance gene effects by models neglecting epistasis might provide biased information and designing breeding strategies presuming absence of epistasis in the inheritance of different traits would be misleading. It was further revealed that nature and magnitude of gene effects differed in two crosses and showed the importance of additive as well as non-additive gene effects in the inheritance of characters studied which was also reported by different workers (Ahmed and Mehra, 2000; Singh and Singh, 2001; Patel *et al.*, 2007; Singh *et al.*, 2008 and Singh, 2010). In view of the parallel role of additive and non-additive gene effects in the inheritance of different characters in the two crosses, sophisticated selection procedures as recurrent selection and population improvement programs should be followed for the simultaneous improvement of yield and fiber characters. However, additive gene effects may be fixed in pure lines for some specific traits as bolls per plant and ginning outturn in cross 1.

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