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Genetic analysis of yield components and fibre quality characters in upland cotton (*Gossypium hirsutum* L.)

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Abstract

Generation mean analysis was carried out to estimate the nature and magnitude of gene effects for yield components and fibre quality traits in four crosses of upland cotton (*Gossypium hirsutum* L). The presence of epistasis was reflected by scaling tests and inadequacy of simple additive-dominance model for most of the characters studied. The results obtained revealed that the nature and magnitude of gene effects differed in different crosses and showed importance of additive as well as non additive gene effects in the inheritance of different characters. In view of the parallel role of additive and non additive gene effects in the inheritance of different characters, selection in the segregating generations should be delayed when dominance gene effects would have diminished or sophisticated selection procedures as recurrent selection and population improvement programmes may be followed. However, additive gene effects may be fixed in the pure lines with respect to some specific traits such as boll weight in cross 1 and 4 while for 2.5% span length in cross 2.

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

Introduction

Cotton is an important fibre crop being used in the textile industry. It plays a key role in the national economy by way of its contribution in trade, industry, employment and foreign exchange earnings. The average productivity of cotton in India is the lowest among cotton growing nations of the world. In order to increase the yield potential, it is desirable to efficiently utilize the available genetic variability. Genetic analysis of quantitative traits further helps to elucidate the nature and magnitude of genetic variation present in the population. The estimates of gene effects in a plant improvement programme have a direct bearing upon the choice of breeding procedure to be followed. Additive gene effects are useful in the development of pure lines whereas dominance and epistatic effects can be used to exploit hybrid vigour. In upland cotton, various studies have been conducted to study the nature and magnitude of gene effects in the inheritance of different quantitative characters and involvement of both additive and non-additive gene effects have been reported by many workers (Phogat and Singh, 2000; Patel *et al*., 2007). In the present study, additive, dominance and epistatic gene effects were estimated by Generation Mean analysis for yield and fibre quality traits in four varietal crosses of upland cotton (*Gossypium hirsutum* L).

Materials and methods

Four diverse genotypes of upland cotton (Table 1) were selected to provide basic material in the study. The experimental material consisting of a basic set of six generations i.e. P_1, P_2, F_1, F_2, B_1 and B_2 derived from four varietal crosses *viz*., LH 1832 x RS 992, LH 900x CNH1012, LH 900 x RS 992 and LH 1832 x CNH 1012 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. Ten plants from each of parents and F_1s, 20 plants from B_1 and B_2 generations and 50 plants from F_2 populations in each replication were randomly selected for recording data for seed-cotton yield (g), number of 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

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Table 1. Mean values of different characters for parental genotypes

Sr. No.	Genotype	Seed cotton yield (g)	Boll number	Boll weight (g)	Ginning out-turn (%)	2.5% span length (mm)
1.	LH 900	35.89	11.44	3.15	35.06	25.30
2.	LH 1832	51.00	14.45	3.57	30.33	29.13
3.	RS 992	38.12	12.61	3.19	33.64	25.72
4.	CNH 1012	34.45	10.56	3.27	35.11	26.22

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

Results and discussion

The results obtained from scaling tests, joint scaling test and best fit model for the four varietal crosses *viz.*, LH 1832 x RS 992 (cross 1), LH 900x CNH 1012 (cross 2), LH 900 x RS 992 (cross 3) and LH 1832 x CNH 1012 (cross 4) with respect to seed cotton yield, number of bolls per plant, boll weight, ginning out turn and 2.5% span length are presented in tables 2 to 5, respectively. In cross-1, the scaling tests detected the presence of epistasis for all the five characters whereas joint scaling test detected epistasis only for boll number and 2.5% span length. Three parameter model identified [h] component for seed cotton yield and [d] component for boll weight whereas both [d] as well as [h] components for ginning out turn. Significance of different components detected by three parameter model for boll number and 2.5% span length is of little value due to inadequacy of the model. The best fit model identified [d], [h] and [j] parameters to be significant for boll number. For 2.5% span length, the model involving m, [d], [h], [j] and [l] with all parameters significant was found to be adequate and opposite signs of [h] and [l] indicated the presence of duplicate type of epistasis for this character.

In cross 2, scaling tests as well as joint scaling test detected the presence of epistasis for seed cotton yield, boll number, ginning out turn and 2.5% span length whereas three parameter model was adequate to explain the variation for boll weight for which dominance gene effects were found to be important. The best fit model consisting of m, [d], [h], [i] and [l] with all significant parameters was found to be adequate for seed cotton yield and for boll number, the best fit model showed [h], [i] and [l] components to be significant. The opposite signs of [h] and [l] for seed cotton yield and boll number indicated the involvement of duplicate type of interaction, while negative sign of [h] indicated that decreaser alleles were dominant in the inheritance of both the traits. For ginning out turn, the dominance, additive x additive and dominance x dominance components while for 2.5% span length, additive and additive x additive components were found to be significant by the best-fit model.

In cross 3, additive-dominance model was sufficient to explain the variation in generation means for boll number and ginning out turn for which neither the individual scaling test nor the joint scaling test detected epistasis whereas for seed cotton yield, boll weight and 2.5% span length scaling tests as well as joint scaling test detected epistasis. The negative sign of significant [h] component for ginning out turn indicated decreaser alleles to be dominant in the inheritance of this trait. In sequential model fitting, the best fit model indicated the presence of dominance and dominance x dominance gene effects for seed cotton yield and boll weight whereas additive, dominance, additive x additive and additive x dominance gene effects were significant for 2.5% span length. The opposite signs of [h] and [l] for seed cotton yield and boll weight showed the role of duplicate type of gene inter action in the inheritance of these traits.

In cross 4, scaling tests as well as joint scaling test indicated the adequacy of additive-dominance model for boll weight and identified the importance of additive gene effects whereas these tests showed epistasis for other characters. When models including non-allelic interaction components in all possible combinations were applied, the best-fit model revealed the presence of additive, dominance, additive x additive

Table 2. Estimates of different scaling tests, joint scaling test and genetic components in the best fit model for different characters in the cross LH-1832 x RS-992

Parameter	Seed cotton yield	Boll number	Boll weight	Ginning out-turn	2.5% span length
Scaling test					
A	–30.11±15.10*	–8.28±2.36**	–0.39±0.32	2.40±1.48	–0.60±0.67
B	12.21±10.75	6.72±2.81*	–0.52±0.26*	–3.32±1.68*	3.53±0.73**
C	–13.34±12.92	-6.34±5.04	0.44±0.95	–2.70±5.51	2.27±1.411
Joint scaling test					
m	40.53±2.71**	11.62±0.71**	3.48±0.92**	32.25±0.29**	28.12±0.9**
[d]	4.48±2.97	–0.31±0.68	1.10±0.88*	–1.54±0.29**	0.87±0.09**
[h]	21.75±3.63**	5.39±1.39**	0.19±0.17	2.34±0.36**	–1.80±0.20**
X^2	6.02	23.12**	5.42	6.92	127.96**
Best fit model					
m	-	9.81±2.27**	-	-	27.33±0.12**
[d]	-	1.80±0.81*	-	-	1.80±0.12**
[h]	-	8.96±3.15**	-	-	1.64±0.78*
[i]	-	2.93±2.46	-	-	-
[j]	-	–14.69±3.17**	-	-	–4.05±0.36**
[l]	-	-	-	-	–2.77±1.35*
X^2	-	0.18	-	-	1.45

*,**P $\leq$ 0.05 and 0.01, respectively.

Table 3. Estimates of different scaling tests, joint scaling test and genetic components in the best fit model for different characters in the cross LH-900 x CNH-1012

Parameter	Seed cotton yield	Boll number	Boll weight	Ginning out-turn	2.5% span length
Scaling test					
A	–19.06±4.11**	–6.72±1.70**	–0.36±0.35	–3.17±1.30*	1.60±0.59**
B	–21.50±4.66**	–6.28±1.38**	–0.17±0.29*	–2.71±1.19*	1.20±0.37**
C	2.66±5.69	0.03±0.16	0.14±0.48	–2.57±1.40	5.20±0.94**
Joint scaling test					
m	32.59±0.84**	10.48±3.62**	3.19±0.37**	33.77±2.81**	26.09±0.13**
[d]	1.29±0.87	0.67±0.38	–0.03±0.04	0.21±0.28	0.25±0.13
[h]	10.19±1.30**	1.59±0.69**	0.45±0.11**	–2..42±0.57**	3.44±0.21**
X^2	43.97**	44.59**	1.74	9.14*	37.42**
Best fit model					
m	76.81±7.69**	23.64±2.01**	-	38.32±1.43**	28.35±0.40**
[d]	2.69±0.88*	0.68±0.40	-	–0.07±0.30	–0.40±0.15**
[h]	–115.81±20.13**	–36.87±5.81**	-	14.02±4.29**	0.76±0.49
[i]	–42.82±7.62**	–12.95±1.98**	-	–3.20±1.36*	–2.65±0.44**
[j]	-	-	-	-	0.34±0.62
[l]	83.06±12.77**	25.84±3.96**	-	9.03±3.07**	-
X^2	0.16	0.05	-	0.09	0.07

*,** P $\leq$ 0.05 and 0.01, respectively.

Table 4. Estimates of different scaling tests, joint scaling test and genetic components in the best fit model for different characters in the cross LH-900 x RS-992

Parameter	Seed cotton yield	Boll number	Boll weight	Ginning out-turn	2.5% span length
Scaling test					
A	22.94±8.59**	4.50±3.49	0.39±0.27	0.44±2.25	0.01±0.49
B	12.05±8.80	–1.50±2.44	1.09±0.52*	1.83±1.57	–2.13±0.30**
C	–0.78±23.38	–5.00±5.80	0.81±0.31**	0.72±2.59	–2.60±0.55**
Joint scaling test					
m	37.86±1.87**	12.72±0.62**	3.23±0.06**	34.50±0.35**	25.35±0.11**
[d]	–1.17±1.56	–1.06±0.60	–0.03±0.07	0.57±0.36	–0.45±0.11**
[h]	20.43±4.82**	0.72±1.45	0.22±0.12	–1.39±0.45**	3.23±0.13**
X^2	10.02**	3.83	9.64**	1.39	70.77**
Best fit model					
m	38.34±2.63**	-	3.14±0.70**	-	24.17±0.22**
[d]	–2.44±2.63	-	0.02±0.06	-	–0.34±0.13**
[h]	38.99±11.53**	-	0.93±0.28**	-	4.52±0.25**
[i]	-	-	-	-	1.38±0.27**
[j]	8.82±6.84	-	-	-	2.44±0.54**
[l]	–32.82±15.92*	-	–0.83±0.30**	-	-
X^2	3.85	-	1.84	-	2.09

*,** $P \leq 0.05$ and 0.01, respectively.

Table 5. Estimates of different scaling tests, joint scaling test and genetic components in the best fit model for different characters in the cross LH-1832 x CNH -1012

Parameter	Seed cotton yield	Boll number	Boll weight	Ginning out-turn	2.5% span length
Scaling test					
A	15.33±14.40	7.22±2.02**	–0.65±0.42	5.67±2.20*	–4.27±0.28**
B	36.77±5.83**	12.78±2.56**	–0.19±0.27	0.57±1.85	–0.67±0.37
C	–31.23±8.82**	–6.23±4.37	–0.37±0.77	–11.43±4.02**	1.40±0.96**
Joint scaling test					
m	34.68±2.11**	14.01±0.55**	3.43±0.04**	32.65±0.46**	27.67±0.05**
[d]	–3.71±2.22	2.62±0.55**	0.13±0.04**	–2.12±0.45**	1.21±0.05**
[h]	30.46±3.73**	4.74±0.98**	0.33±0.06	1.04±0.99	0.26±0.15
X^2	82.42**	44.14**	2.99	20.92**	311.22**
Best fit model					
m	–54.35±10.28**	–11.60±4.69*	-	16.32±4.02**	36.67±0.95**
[d]	5.42±2.71*	1.10±0.62	-	–1.98±0.45**	1.40±0.06**
[h]	284.93±29.72**	71.56±11.12**	-	38.71±9.55**	–21.20±2.08**
[i]	96.90±10.81**	23.95±4.58**	-	16.29±3.99**	–8.94±0.95**
[j]	-	-	-	-	–3.60±0.38**
[l]	–165.36±20.15**	–42.52±6.73**	-	–21.36±5.96**	13.87±1.20**
X^2	2.02	3.23	-	4.20	-

*,** $P \leq 0.05$ and 0.01, respectively.

and dominance x dominance gene effects for seed cotton yield as well as ginning out turn. Dominance, additive x additive and dominance x dominance gene effect were found to be important for boll number whereas all the five parameters were significant for 2.5% span length. Opposite signs of [h] and [l] for seed cotton yield, boll number, ginning out turn and 2.5% span length suggested duplicate type of gene interaction to be operative in the genetic control of these traits. Negative sign of [i] for 2.5 % span length implied that sum of the contributions made to this type of interaction by dispersed pairs of genes was more than by associated pairs.

The results obtained in the present set of materials revealed that the nature and magnitude of gene effects differ in different crosses and showed importance of both additive and non additive gene effects in the inheritance of characters studied which were also reported by different workers (Ahuja, Tuteja and Singh, 1999; Ahmed and Mehra, 2000; Singh and Singh, 2001; Patel *et al.*, 2007). Hence, specific breeding strategy has to be adopted for a particular cross to get improvement in different characters of economic importance. The digenic epistasis was invariably detected for most of the characters in all the four crosses studied (i.e. 13 out of total 20 cases). This demonstrated that importance of epistasis in the inheritance of various characters couldn't be ignored and genetic models neglecting epistasis may provide biased information. Therefore, it is concluded that the estimation of only additive-dominance gene effects and formulating breeding procedures presuming absence of epistasis in the inheritance of different traits will be misleading. In view of the parallel role of additive and non additive gene effects in the inheritance of different characters in four crosses, selection in the segregating generations should be delayed when dominance gene effects would have diminished or sophisticated selection procedures as recurrent selection and population improvement programmes should be followed for the improvement of these characters. However, additive gene effects may be fixed in the pure lines with respect to some specific traits such as boll weight in cross 1 and cross 4 and 2.5% span length in cross 2.

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