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Generation Mean Analysis of 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 fibre quality traits in three 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 with respect to some specific traits such as micronair value and fibre strength.

Keywords: Generation mean; Scaling tests; Recurrent selection

Introduction

Cotton, which has been reputed as "Queen of the fibre plants" is an important fibre crop in India Cotton is an important fibre crop being used in the textile industry. Over 90% of cotton grown in the world is *Gossypium hirsutum* L. or upland cotton. 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 [1,2]. In the present study, additive, dominance and epistatic gene effects were estimated by Generation Mean analysis for fibre quality traits in three crosses of upland cotton (*Gossypium hirsutum* L).

Materials and Methods

The experimental material comprised of three hybrids namely BN-1 × AC-738 (NHH-44), NH-615 × NH-625 (NHH-206), AK-32 × DHY 286-1 (AKH HY2). The three hybrids *viz.*, NHH-44, NHH-206 and AKH HY-2 were selfed and backcrossed to their parents to get seeds of F2 and backcross generations viz., BC1 and BC2. Thus, six generations (P1, P2, F1, F2, BC1 and BC2) were developed for each of these three cross combination during *kharif* 2013-14. Each cross was grown in a separate experiment in a randomized block design with three replications during *kharif*, 2014-15 at experimental farm of Department of Agriculture Botany, VNMKV, Parbhani. The plants were spaced 90 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 F1s, 20 plants from BC1 and BC2 generations and 50 plants from F2 populations in each replication were randomly selected for recording data for upper half mean length (mm), ginning (%), micronaire value, fibre strength, uniformity index and fibre maturity coefficient. The scaling test (A, B and C) were calculated for each trait to detect adequacy of additive-dominance model or presence of non-allelic interaction according to Hayman and Mather [3]. The adequacy of additive-dominance model was tested by joint scaling test of Cavalli [4]. The six parameters (m, d, h, i, j and l) were computed according to Hayman [5].

Result and Discussion

The analysis of variance for all characters studied in three crosses of cotton is presented in Table 1. The analysis of variance revealed that the mean square due to crosses were significant for all the traits except for fibre maturity coefficient in all three crosses. The character which failed to show significant variation among the generation in respective crosses was not subjected to further genetic analysis of generation means. Mean data (Table 2) on various characters recorded on 6 generations *viz.*, P1, P2, F1, F2, BC1 and BC2 for 3 cross combinations were subjected to scaling test and joint scaling test. Significance of at least one of the scaling tests (Table 3) revealed the presence of non-allelic interactions for all the traits in 3 crosses.

For upper half mean length (mm), the A, B, C, scaling tests were significant for all the crosses except C scale in C1 cross. The chi square values were significant for the all the crosses. The additive (d) gene effects were negatively significant in all crosses except C1. The dominance (h) gene effects were negatively significant in crosses C1 and C3. As regards, digenic interaction all the components recorded significant effect (except (j) component in C1 cross) with higher magnitude of values for (l) components. The dominance (h) and dominance × dominance (l)

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Character	Source of variation	d.f.	NHH-44	NHHH-206	AKH HY-2
Upper half mean length (mm)	Replication	1	0.77	0.09	0.07
	generation	5	2.52*	4.18**	6.85**
	Error	5	0.44	0.09	0.31
Ginning (%)	Replication	1	0.538	0.080	0.0919
	generation	5	0.885*	1.209*	1.092*
	Error	5	0.163	0.117	0.206
Micronair value	Replication	1	0.006	0.007	0.007
	generation	5	0.059*	0.071*	0.093**
	Error	5	0.005	0.012	0.008
Fibre strength	Replication	1	0.48	1.76	0.21
	generation	5	5.84**	9.08**	6.28*
	Error	5	0.34	0.38	0.68
Uniformity index	Replication	1	0.27	1.92	0.05
	generation	5	3.72**	12.31**	9.58**
	Error	5	0.21	0.85	0.16
Fibre maturity coefficient	Replication	1	0.00013	0.00013	0.00021
	generation	5	0.00021^{NS}	0.00016^{NS}	0.00011^{NS}
	Error	5	0.00013	0.00021	0.00011

* and ** significant at 5% and 1% respectively.

Table 1: Analysis of variance for crosses and generations for different characters in cotton.

Character	Cross	P1	P2	F1	F2	BC1	BC2	SE±	CD (5%)
Upper half mean length (mm)	NHH-44	22.24	22.11	24.57	23.42	21.67	21.88	0.66	1.70
	NHH-206	23.88	20.51	23.46	21.44	20.78	21.05	0.31	0.79
	AKH HY-2	23.74	23.26	25.74	24.15	20.23	22.38	0.56	1.43
Ginning (%)	NHH-44	33.43	34.15	35.29	34.17	34.77	34.92	0.404	1.039
	NHH-206	38.43	39.34	40.08	38.09	39.21	39.84	0.342	0.879
	AKH HY-2	33.92	33.57	35.28	33.31	34.05	34.74	0.454	1.166
Micronair value	NHH-44	3.24	3.29	3.72	3.51	3.42	3.45	0.068	0.174
	NHH-206	3.54	3.62	3.89	3.44	3.34	3.61	0.108	0.278
	AKH HY-2	3.79	3.64	4.2	3.66	3.94	3.7	0.088	0.226
Fibre strength	NHH-44	21.20	20.10	23.60	23.20	20.50	19.40	0.59	1.51
	NHH-206	24.60	21.70	25.50	23.80	19.60	23.10	0.62	1.58
	AKH HY-2	23.40	21.10	26.20	24.10	22.40	22.30	0.82	2.12
Uniformity index	NHH-44	75.50	73.70	75.30	76.30	72.90	73.40	0.45	1.17
	NHH-206	71.20	71.90	77.20	73.60	70.70	71.00	0.92	2.37
	AKH HY-2	73.20	75.30	77.10	76.10	71.40	72.80	0.40	1.02

* and ** significant at 5% and 1% respectively.

Table 2: Mean performance of parents, F1, F2 and back cross generations of three cotton crosses for fiber quality characters.

Parameter		C1 (NHH44)	C2 (NHH206)	C3 (AKH Hy- 2)
Scaling test	A	-3.470** ± 0.351	-5.780** ± 0.150	-9.020** ± 0.082
	B	-2.920** ± 0.166	-1.870** ± 0.196	-4.240** ± 0.284
	C	0.190 ± 0.390	-5.550** ± 0.306	-1.880** ± 0.291
Joint scaling test	X^2	1171.53**	17178.60**	10775.80**
Digenic model	m	23.420** ± 0.207	21.440** ± 0.145	24.150** ± 0.185
	d	-0.210 ± 0.190	-0.270** ± 0.012	-2.150** ± 0.138
	h	-4.185** ± 0.610	-0.835 ± 0.433	-9.140** ± 0.530
	I	-6.580** ± 0.082	-2.100** ± 0.144	-11.380** ± 0.123
	J	-0.275 ± 0.385	-1.955** ± 0.129	-2.390** ± 0.293
	l	12.970** ± 0.408	9.750** ± 0.398	24.640** ± 0.351
Type of epitasis		Duplicate	Duplicate	Duplicate

* and ** significant at 5% and 1% respectively.

Table 3: Scaling test, joint scaling test and estimation of gene effects by digenic model in respect of Upper half mean length (UHML).

components were in the opposite direction in all the crosses in dicated duplicate type of epistasis (Table 3). The ginning % indicated that the A, B, C scaling tests and chi-square values were significant in all the crosses. As regards main gene components, additive (d) component recorded significantly negative effect in all the crosses while dominance (h) component recorded positive significant effect in all the crosses. As regards digenic gene interaction, all the components exhibited significant effects with additive x additive (i) component exhibiting the positive direction and in considerable magnitude in all the crosses. The dominance (h) and dominance × dominance (l) components were in the opposite direction in all the crosses indicated duplicate type of epistasis (Table 4).

The chi- square values were significant for all the crosses under study for micronair value. All crosses have significant individual scaling tests (except C scale in C1 cross). The main effect and digenic interaction effects were also significant for all the crosses under study except (i) in C2 cross, (j) component in C1 cross and (i) component in C3 cross. The additive (d) and dominance (h) effects were in positive direction with magnitude of later was higher than former component in cross C3. The additive (d) effects were in negative direction and significant in cross C1 and C2 while in dominance (h) effect had higher magnitude and positive significant in cross C1 and C2. As regards to digenic interaction, additive × additive (i) component had positive effect in cross C2 and C3 except C1 crosses. The C1 and C2 crosses exhibited negative additive × dominance (j) effect. The dominance × dominance (l) components had positive significant effect in crosses C1 and C2 showed complimentary epistasis except C3 (Table 5). The chi-square values were significant in all the three crosses with significant A, B, and C scaling tests for fibre strength. The additive effects (d) were significant in cross C1 and C2 while dominance effect (h) were negatively significant in crosses C1 and C2. Among the epistasis gene interaction, additive × additive (i) components were negatively significant in all the three crosses. The interaction additive × dominance (j) effects were negatively significant in cross C2 and C3. The dominance × dominance (l) components was positively significant in all the crosses under study. The dominance (h) and dominance x dominance (l) components were in the opposite direction in all the crosses indicated duplicate type of epistasis (Table 6). Uniformity index recoded the scaling tests A, B, C and chi-square values significant an all the three crosses. The additive (d) effect and dominance (h) effects were in negative direction and significant in all the crosses except cross C2. Among the epistasis interaction additive x additive (i) component negatively significant in all three crosses. The (j) component negatively significant in cross C1 and had little I magnitude than other components. The dominance x dominance (l) component had higher magnitude while found to be positively significant in all the crosses. The (h) and (l) components were in the opposite direction in all the crosses indicated duplicate type of epistasis (Table 7).

Dominant gene effect appeared to be more important for upper half mean length (mm) (cross 2 and 3), ginning (%) (cross 1, 2 and 3), micronair value (cross 3), fibre strength (cross 1 and2) and uniformity index (cross 1, 2 and 3). The contribution of the parent to dominance effects varies according to trait. The sign for dominance effects is a function of the F1 mean value in relation to the mid parental value and indicates which parent is contributing to the dominance effect [6]. Whereas, absence of significant values for [h]component signifies no dominance genetic differences or presence of bi-directional dominance between 2 parents and the dominant effects seemed to be not important in the genetic control of these crosses [7]. Whereas additive gene effects [d] were found to be important for the traits fibre strength (cross 1). Jagtap [8] stated that when additive effects are larger than non-additive ones, selection in early segregating generations would be effective. For exploiting these characters pedigree selection may also be suitable. Similar conclusions were drawn by Srinivasan et al. [9], Refaey and

Parameter		C1 (NHH44)	C2 (NHH206)	C3 (AKH Hy- 2)
Scaling test	A	0.320* ± 0.148	-0.090 ± 0.138	-1.100** ± 0.180
	B	0.400* ± 0.179	0.260* ± 0.140	0.630** ± 0.169
	C	-1.980** ± 0.345	-5.570** ± 0.278	-4.810** ± 0.516
Joint scaling test	X^2	141.28**	806.82**	1886.59**
Digenic model	m	34.170** ± 0.394	38.090** ± 0.267	33.310** ± 0.530
	d	-0.150** ± 0.030	-0.630** ± 0.044	-0.690** ± 0.042
	h	3.950** ± 0.926	6.935** ± 0.634	5.875** ± 1.163
	I	2.700** ± 0.392	5.740** ± 0.263	4.340** ± 0.528
	J	-0.040 ± 0.223	-0.175 ± 0.168	-0.865** ± 0.223
	I	-3.420** ± 0.552	-5.910** ± 0.399	-3.870** ± 0.661
Type of epitasis		Duplicate	Duplicate	Duplicate

* and ** significant at 5% and 1% respectively.

Table 4: Scaling test, joint Scaling test and estimation of gene effects by digenic model in respect of ginning percentage.

Parameter		C1 (NHH44)	C2 (NHH206)	C3 (AKH Hy- 2)
Scaling test	A	-0.120** ± 0.036	-0.750** ± 0.072	-0.110** ± 0.038
	B	-0.110* ± 0.048	-0.290** ± 0.068	-0.440** ± 0.039
	C	0.070 ± 0.053	-1.180** ± 0.053	-1.190** ± 0.070
Joint scaling test	X^2	5265.09**	2583.88**	988.50**
Digenic model	m	3.510** ± 0.047	3.440** ± 0.091	3.660** ± 0.044
	d	-0.030** ± 0.008	-0.270** ± 0.014	0.240** ± 0.017
	h	0.155 ± 0.142	0.450 ± 0.273	1.125** ± 0.112
	I	-0.300** ± 0.046	0.140 ± 0.090	0.640** ± 0.041
	J	-0.005 ± 0.048	-0.230** ± 0.093	0.165** ± 0.041
	I	0.530** ± 0.106	0.900* ± 0.187	-0.090 ± 0.083
Type of epitasis		Complimentary	Complimentary	Duplicate

* and ** significant at 5% and 1% respectively.

Table 5: Scaling test, joint scaling test and estimation of gene effects by digenic model in respect of micronair value.

Parameter		C1 (NHH44)	C2 (NHH206)	C3 (AKH Hy- 2)
Scaling test	A	-3.800** ± 0.576	-10.900** ± 0.341	-4.800** ± 0.374
	B	-4.900** ± 0.190	-1.000** ± 0.311	-2.700** ± 0.336
	C	4.300** ± 0.198	-2.100** ± 0.666	-0.500** ± 0.566
Joint scaling test	X^2	817.63**	1329.26**	660.72**
Digenic model	m	23.200** ± 0.590	23.800** ± 0.608	24.100** ± 0.686
	d	1.100** ± 0.071	-3.500** ± 0.101	0.100 ± 0.106
	h	-10.050** ± 1.767	-7.450** ± 1.437	-3.050 ± 1.715
	I	-13.000** ± 0.586	-9.800** ± 0.599	-7.000** ± 0.678
	J	0.550 ± 0.600	-4.950** ± 0.375	-1.050* ± 0.495
	I	21.700** ± 1.183	21.700** ± 0.919	14.500** ± 1.058
Type of epitasis		Duplicate	Duplicate	Duplicate

* and** significant at 5% and 1% respectively.

Table 6: Scaling test, joint scaling test and estimation of gene effects by digenic model in respect of fiber strength.

Parameter		C1 (NHH44)	C2 (NHH206)	C3 (AKH Hy- 2)
Scaling test	A	-5.000** ± 0.077	-7.000** ± 0.405	-7.500** ± 0.212
	B	-2.200** ± 0.161	-7.100** ± 0.342	-6.800** ± 0.205
	C	5.400** ± 0.413	-3.100** ± 0.870	1.700** ± 0.343
Joint scaling test	X^2	2053.30**	1093.78**	1051.79**
Digenic model	m	76.300** ± 0.423	73.600** ± 0.675	76.100** ± 0.215
	d	-0.500** ± 0.050	-0.300 ± 0.168	-1.400** ± 0.035
	h	-11.900** ± 0.911	-5.350** ± 1.492	-13.150** ± 0.613
	I	-12.600** ± 0.420	-11.000** ± 0.654	-16.000** ± 0.212
	J	-1.400** ± 0.173	0.050 ± 0.391	-0.350 ± 0.192
	I	19.800** ± 0.501	25.100** ± 0.957	30.300** ± 0.496
Type of epitasis		Duplicate	Duplicate	Duplicate

* and** significant at 5% and 1% respectively.

Table 7: Scaling test, joint scaling test and estimation of gene effects by digenic model in respect of uniformity index.

Razek [10] and Esmail [11] for one or other fiber quality traits. Even though, the traits upper half mean length (mm) and fibre strength (cross 2) were found to be influenced by additive and dominance gene actions, magnitude of [h] reveals the importance of dominance gene action in inheritance of these traits.

The traits, upper half mean length (mm) (cross 1, 2 and 3), ginning percentage (cross 1, 2 and 3), micronaire value (cross 3), fibre strength (cross 1, 2 and 3) and uniformity index (cross 1, 2 and 3), were possessing opposite sign of [h] and [l] indicating the role of duplicate gene action controlling these traits. Similar results were obtained by Rajendrakumar and Raveendran [12] for 2.5% span length and Bhatti et al. [13] and Refaey and Razek [10] and Srinivasan et al. [9] for 2.5% span length, bundle strength, uniformity raito and micronaire value. Such type of duplicate type of gene action would limit the range of variability and thus slow down the pace of progress. In such situations, heterosis breeding would be advantageous. Since only two crosses for micronaire value (cross 1 and 2), the signs of [h] were similar to the [l] type of epistasis, it was concluded that complementary type of interaction was present. These variations can be exploited by simple pedigree selection. Mass selection for several early generation aimed at the improvement of heterozygous population by modifying the frequencies of desirable gene followed by single plant selection in the resulting material would be cheapest and quickest procedure. However, the presence of non-fixable (h, j and l) component together with duplicate type of epistasis may cause delay in the improvement in this trait through selection in early generations.

It is clear from the result that epistasis cannot be ignored when establishing a new breeding programme to improve cotton population for economic traits. The inheritance of all the traits studied was controlled by additive and non-additive genetic effects, with greater value of dominance gene effect than the additive one in most cases. Among the non-additive effect, the other fixable component, i.e., additive × additive (i) type of interaction was also significant and constitutes a major portion of gene effects; therefore it may be possible to exploit it. The conclusion drawn in the present investigation can be compared with those reported in cotton by other workers. Jagtap [8] stated that when additive effects are larger than non-additive ones, selection in early generation would be effective, while if the non-additive portions are larger than additive one, the improvement of the character need intensive selection through later generation. The evidence of non-allelic interaction was reported by Refaey and Razek [10] for fibre traits.

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