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ESTIMATION OF GENETIC PARAMETERS THROUGH GENERATION MEAN ANALYSIS FOR FIBER QUALITY TRAITS IN UPLAND COTTON

B. SRINIVAS and D. BHADRU

Department of Genetics and Plant Breeding, College of Agriculture, Acharya N.G. Ranga Agricultural University,
Rajendranagar, Hyderabad-500030, India
*Corresponding author's email: srinu.bdd@gmail.com
Email address of co-author: badri002gpb@yahoo.co.in

SUMMARY

Gene effects for 5 fiber quality traits were estimated from 6 upland cotton crosses through generation mean analysis from 6 generations (P1, P2, F1, F2, BC1 and BC2). Results revealed that dominant genes played major role for the traits 2.5% span length (CPD 420 × 4084 and NA 1325 × LK 861), uniformity ratio (NA 1325 × 4084), micronaire value (BC 68-2 × 4084) and bundle strength (CPD 420 × 4084 and BC 68-2 × 4084) whereas, additive gene effects [d] were found to be important for the traits 2.5% span length (NA 1325 × 4084 and BC 68-2 × 4084) and micronaire value (NA 1325 × LK 861). The traits, ginning percentage (CPD 420 × 4084), 2.5% span length (NA 1325 × LK 861 and NA 1325 × 4084), uniformity ratio (NA 1325 × 4084), micronaire value (CPD 420 × 4084, NA 1325 × LK 861, BC 68-2 × LK 861 and BC 68-2 × 4084) and bundle strength (CPD 420 × 4084) were possessing opposite sign of [h] and [l] indicating the role of duplicate gene action controlling the traits which will pose hindrance to a plant breeder while attempting selection in long run. Therefore, heterosis breeding would be advantageous and none of studied traits were found to be controlled by the complementary type of interaction. Epistatic gene interactions additive × additive (i), additive × dominance (j) and dominance × dominance (l) also showed significant role in inheritance of all fiber characters in one or other cross, whereas linkage or higher order interactions were observed for the inheritance of ginning percentage, micronaire value and bundle strength in cross CPD 420 × 4084 and ginning percentage in NA 1325 × 4084.

Key words: Cotton, gene action, epistasis, fiber quality and generation mean

Key findings: Apart from the yield, fiber quality is the key area need to be focused much in cotton. The present study indicates, breeders should draw the attention on breeding methodologies like biparental mating, recurrent selection and diallel selective mating system to improve fiber quality parameters of cotton.

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INTRODUCTION

Cotton popularly known as "white gold" is an important fiber crop of global importance, cultivated in tropical and sub-tropical regions of about 80 countries. Despite the inroads made by the artificial fibers, cotton continues to remain established as most widely used textile fiber in the world due to its natural qualities such as softness, durability and versatility. Due to highest consumption in textile mills, cotton is known as queen of the fiber plants. In cotton breeding, improvement of lint yield is not the objective rather quality traits particularly strength, length and 'micronaire' a measure of fiber fineness and maturity are critical in maximizing price returns to growers and accessing premium markets. Cotton has been a subject of interest for geneticists and breeders throughout the world because of its economic importance and a wider range of adaptability. Plant breeders have played significant role in improving fiber quality characters which are quantitatively inherited. The information about the nature and magnitude of gene action prevailing in the breeding material is necessary to choose the type of breeding procedure to be followed to achieve desired genetic improvement in any crop. Genetic analysis using generation mean analysis has been used in cotton breeding to determine the type of gene action controlling the fiber quality traits which are quantitatively inherited. Generation mean analysis is a quantitative genetic method used to estimate components of mean (additive, dominance and interaction effects and heterosis) of individual traits (Mather and Jinks, 1982). In cotton, magnitude of additive as well as non-additive gene effects for fiber quality traits have reported by several workers *viz.,* Bhatti *et al.* (2006), Nidagundi *et al.* (2012) and Srinivasan *et al.* (2013). Mather (1949) introduced tests for epistasis through scaling test, which were further elaborated by Cavalli (1952). Hayman (1958) described the procedure for partitioning of generation mean in to 6 parameters *viz.,* mean (m), additive [d], dominance [h], additive × additive [i], additive × dominance [j] and dominance × dominance [l] gene effects. Gamble (1962) proposed a model partitioning the estimation of additive, dominance and epistasis effects from 6 generations *viz.,* P_1, P_2, F_1, F_2, BC_1 and BC_2 of a cross. This model is considered to be perfect fit and is not materially different from the one proposed by Hayman and Mather (1955). Pathak (1975) used 6 populations (P_1 P_2, F_1, F_2, BC_1 and BC_2) of 5 upland cotton crosses to evaluate genetic effects for fiber traits in cotton. Scaling tests and joint scaling tests are established mechanisms used by conventional breeders to understand allelic and non-allelic gene actions, nature and magnitude of genetic variance of genotypes in specific combinations.

The information on the gene effects for various fiber quality traits is needed for formulation of an efficient breeding program to achieve desired genetic improvement in fiber quality characters. Hence, the present investigation has been carried out to investigate the gene effects in 6 crosses of upland cotton for various fiber quality traits.

MATERIALS AND METHODS

The present experiment was carried out during 2006, 2007 and 2008 *kharif* seasons in college farm, College of Agriculture, Rajendranagar, Hyderabad. In *kharif* 2006, 5 genotypes (CPD-420, NA 1325, BC 68-2, LK-861 and 4084) were involved in development of 6 crosses *viz.,* CPD 420 × LK 861 (cross 1), CPD 420 × 4084 (cross 2), NA 1325 × LK 861 (cross 3), NA 1325 × 4084 (cross 4), BC 68-2 × LK 861 (cross 5) and BC 68-2 × 4084 (cross 6) and to produce F_1 seed. During *kharif* 2007, these 6 crosses were selfed and backcrossed with their respective parents to obtain the F_2 and backcross (BC_1 and BC_2) generations respectively. Selfed seed was also obtained for all the parents. Thus, 6 basic generations, P_1, P_2, F_1, F_2, BC_1 and BC_2 were developed for each of the 6 crosses. In *kharif* 2008, evaluation of P_1, P_2, F_1, F_2, BC_1 and BC_2 generations was undertaken in Randomized Block Design with 3 replications to understand the genetic nature of fiber quality characters through generation mean analysis. The F_2's were sown in 6 rows and backcrosses in 3 rows, whereas parents and hybrids were sown in 2 rows each. Rows were 5 meter long and spacing adopted was 90 cm between the rows and 60 cm between the plants. The recommended packages of practices were followed to raise a good crop. Data were recorded on 40 plants for F_2, 20 plants for each BC_1 and BC_2 and 5 plants for each F_1, P_1 and P_2 generations in each replication for ginning percentage, 2.5% span length, uniformity ratio, micronaire value and bundle strength and mean was taken into consideration for statistical analysis.

Statistical analysis

The means were computed for each generation of P_1, P_2, F_1, F_2, BC_1 and BC_2 for each cross over 3 replications. The variance and corresponding standard errors of the means were computed from the deviations of the individual values from the pooled mean for each of the generation in each cross. To determine the presence or absence of non-allelic interactions 4 scaling tests (A, B, C and D) were used as described by Mather (1949) and Hayman and Mather (1955). The standard error of A, B, C, and D were worked out by taking square root of respective variances. The t- values were calculated by dividing the effects of A, B, C and D by respective standard errors and compared with 't' table values at 5% and 1% level of significance. Significance of at least one of the tests indicates the presence of epistatic interactions.

The mean values over replications were used for the estimation of the gene effects. Owing to presence of 6 generations in each cross, 6 parameter model (Hayman, 1958) ((m), additive gene effects (d), dominance gene effects (h) and 3 types of non-allelic gene interactions *viz.,* additive × additive (i), additive × dominance (j) and dominance × dominance (l)) was followed to estimate gene effects including epistatic interactions.

Standard error of these parameters and calculated 't' values were estimated according to Gamble (1962) and Singh and Chaudhary (1985) in a similar manner done as in case of scaling tests. The data on all the traits were analyzed with the help of joint scaling test (Cavalli, 1952 and Mather and Jinks, 1982) of 3 and 6 parameter models (to know non-significant parameters) where sequential model fit scheme was employed and the best model fit scheme was searched. The parameters m, [d] and [h] estimated from the observed mean of the available generations were compared with expected values derived from the estimates of these 3 parameters. Further, the mean of various generations were not known with equal precision and hence, the generation means and their expectations were weighed.

The adequacy of the additive-dominance model was tested by determining the expected values of 6 different generations with the help of estimates obtained from m, [d] and [h] and following the comparison between observed and expected means of these generations. Six deviations between the observed and expected values of each generation were obtained and by squaring each of these deviations and multiplying them by their corresponding weights tested the goodness of fit. After confirmation of presence of epistasis, joint scaling test of 6 parameter model significance estimates of m, [d], [h], [i], [j] and [l] was applied. The presence of the non-significant parameters in additive, dominance, additive × additive, additive × dominance and dominance × dominance model was investigated and subsequently those were eliminated. Through sequential model fit scheme after eliminating the non-significant parameters of 6 parameter model best fit scheme was traced and tested through $\chi 2$.

RESULTS AND DISCUSSION

The results of analysis of variance (Table 1) revealed significant differences for generations for all the characters studied indicating the presence of genetic variability except for ginning percentage in cross 1 and 5, 2.5% span length in cross 5, uniformity ratio in cross 3 and 5 and for bundle strength in crosses 1, 3, 4 and 5. Mean data (Table 2) on various characters recorded on 6 generations *viz.,* P1, P2, F_1, F_2, BC_1 and BC_2 for 6 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 6 crosses. As all the 5 characters studied exhibited lack of good fit for simple additive-dominance model, the data were subjected to 6 parameter model of joint scaling test to know the non-significant parameters and the appropriate sequential fit model was sought. The estimates of different genetic components of generation mean in terms of best fit model for 5 characters of 6 crosses are furnished in Table 4.

Search was made for best sequential model fit scheme. Five parameter sequential fit model was observed for 2.5% span length (cross 1, 2, 3, 4, and 6), uniformity ratio (cross 2 and 4) and micronaire value (cross 3 and 5).

Table 1. Analysis of variance for fiber quality traits in 6 upland cotton crosses.

Character	Source	d.f	Mean squares					
			Cross 1	Cross 2	Cross 3	Cross 4	Cross 5	Cross 6
Ginning percentage	Replications	2	2.65	0.86	6.89	0.51	0.08	0.19
	Generations	5	NS	6.42**	NS	16.75**	NS	7.03*
	Error	10	7.39	1.02	2.73	2.45	2.38	2
2.5 % span length	Replications	2	0.09	0.57	0.53	0.55	0.66	1.03
	Generations	5	4.71**	16.50**	11.96**	2.82*	NS	8.23**
	Error	10	0.75	1.26	0.9	0.83	3.32	0.63
Uniformity ratio	Replications	2	1.49	0.67	22.04	9.98	1.62	0.15
	Generations	5	5.03*	14.76*	NS	13.24*	NS	12.51*
	Error	10	1.07	3.28	1.05	3.9	2.73	2.88
Micronaire value	Replications	2	0.42**	0.22*	0.03	0.02	0.14	0.19
	Generations	5	0.10*	0.53**	0.24*	0.34*	0.32*	0.45*
	Error	10	0.03	0.05	0.05	0.07	0.09	0.11
Bundle strength	Replications	2	0.49	0.57	1.22	3.3	1.84	0.25
	Generations	5	NS	4.97**	NS	NS	NS	2.42*
	Error	10	1.62	0.82	1.01	1.34	2.24	0.64

** At 1 % LOS, * At 5 % LOS

Best fit 4 parameter sequential model was observed for ginning percentage (cross 6), uniformity ratio (cross 1 and 6), micronaire value (cross 1, 4 and 6) and bundle strength (cross 6).

In case of ginning percentage only in cross 6, sequential 4 parameter model showed good fit wherein m, [d], [i] and [j] genetic components were important. Whereas under sequential 5 parameter model in cross 2 and 4 parameter model in cross 4 higher order interactions were predicted.

For 2.5% span length, the joint scaling test of sequential 5 parameter model was found to be adequate in 5 crosses (cross 1, 2, 3, 4 and 6) with relatively greater magnitude of additive × dominance [j] component. The genetic components m, [d], [i], [j] and [l] were found to be important for the crosses 1 and 6. While m, [d], [h], [j] and [l] genetic parameters were significant in crosses 3 and 4 possessing the opposite sign for [h] and [l] components indicating the presence of duplicate type of epistasis which will pose hindrance to a plant breeder while attempting selections in long run. In the cross 2 the genetic parameters m, [d], [h], [i] and [j] were found to be important. Two crosses (cross 2 and 4) were found to be best fit for sequential 5 parameter model and crosses 1 and 6 for 4 parameter model for the trait uniformity ratio. The genetic components m, [d], [h], [i] and [j] have played significant role in cross 2, while m, [d], [h], [j] and [l] genetic components were found to be important in cross 4, where, the genetic components [h] and [l] recorded relatively greater values with opposite sign indicating the prevalence of duplicate epistasis. Under sequential 4 parameter model the genetic components m, [d], [h] and [i] for cross 1 and m, [i], [j] and [l] components for cross 6 were observed to be important. For the trait micronaire value, the crosses 3 and 5 exhibited best fit for sequential 5 parameter model, while the crosses 1, 4 and 6 were found to be best fit for 4 parameter model. Under 5 parameter model the genetic components m, [d], [h], [i] and [l] for cross 3 and m, [h], [i], [j] and [l] for cross 5 were found to be important, and both the crosses exhibited duplicate type of epistasis which was evident from possessing the opposite sign by [h] and [l] components.

Table 2. Mean performance of parents, F1, F2 and back cross generations of 6 cotton crosses for fiber quality characters.

Character	Cross	P1	P2	F1	F2	BC1	BC2
Ginning percentage (%)	CPD 420 × LK 861	33.36±0.72	31.19±0.26	28.59±1.03	32.59±0.17	32.44±0.22	30.56±0.13
	CPD 420 × 4084	33.14±0.26	36.41±0.18	33.87±0.2	36.56±0.11	33.63±0.01	34.5±0.21
	NA 1325 × LK 861	29.53±0.46	32.03±0.42	31.17±0.41	32.8±0.26	33.24±0.14	32.4±0.22
	NA 1325 × 4084	31.12±0.45	35.18±0.21	37.76±0.3	37.36±0.04	35.76±0.27	35.15±0.24
	BC 68-2 × LK 861	30.7±0.23	31.52±0.43	31.55±0.31	30.33±0.09	30.03±0.1	30.31±0.3
	BC 68-2 × 4084	30.95±0.5	34.2±0.15	33.64±0.41	34.05±0.09	32.47±0.2	34.84±0.16
2.5 % span length (mm)	CPD 420 × LK 861	27.66±0.29	30.13±0.11	29.52±0.11	31.14±0.06	30.85±0.06	30.34±0.16
	CPD 420 × 4084	23.66±0.46	22.63±0.14	28.46±0.16	25.25±0.09	27.59±0.08	23.72±0.1
	NA 1325 × LK 861	25.16±0.23	29.51±0.12	29.4±0.15	30.12±0.18	30.12±0.05	30.54±0.04
	NA 1325 × 4084	26.39±0.14	25.92±0.19	25.23±0.09	25.14±0.13	26.19±0.08	23.96±0.24
	BC 68-2 × LK 861	27.23±0.27	29.13±0.24	28.29±0.6	27.48±0.12	27.01±0.32	29.29±0.18
	BC 68-2 × 4084	26.97±0.18	26.1±0.21	25.24±0.22	23.57±0.03	26.26±0.1	22.75±0.17
Uniformity ratio	CPD 420 × LK 861	44.73±0.18	46.93±0.1	45.53±0.29	48.03±0.15	46.63±0.29	47.17±0.12
	CPD 420 × 4084	49.23±0.37	53.77±0.1	48.83±0.53	50.73±0.09	48.3±0.32	52.67±0.26
	NA 1325 × LK 861	48.5±0.36	47.07±0.33	46.3±0.59	47.63±0.29	46.8±0.3	46.87±0.28
	NA 1325 × 4084	46.93±0.61	49.03±0.37	50.1±0.6	51.57±0.24	50.17±0.37	52.57±0.3
	BC 68-2 × LK 861	49.57±0.16	46.03±0.43	48.7±0.23	48.27±0.2	48.23±0.34	46.5±0.16
	BC 68-2 × 4084	49.5±0.38	49.43±0.52	50.43±0.33	53.73±0.11	50.57±0.23	53.93±0.01
Micronaire value	CPD 420 × LK 861	3.44±0.07	3.57±0.04	3.52±0.07	3.83±0.05	3.91±0.03	3.55±0.05
	CPD 420 × 4084	3.85±0.05	5±0.04	4.25±0.09	4.5±0.02	3.95±0.04	4.13±0.04
	NA 1325 × LK 861	3.89±0.05	3.39±0.09	3.88±0.07	3.4±0.03	3.75±0.02	3.57±0.04
	NA 1325 × 4084	3.92±0.13	4.14±0.03	4.15±0.08	4.43±0.03	4.16±0.02	4.56±0.08
	BC 68-2 × LK 861	4.05±0.12	3.86±0.05	3.46±0.03	4.02±0.02	3.79±0.02	3.23±0.07
	BC 68-2 × 4084	3.44±0.03	4.47±0.1	3.98±0.08	4.25±0.05	4.08±0.05	4.5±0.04
Bundle strength (g/tex)	CPD 420 × LK 861	22.07±0.25	22.63±0.39	22.77±0.1	22.63±0.03	21.23±0.12	23.63±0.27
	CPD 420 × 4084	23.03±0.16	19.73±0.24	22.77±0.17	20.7±0.09	22.33±0.19	21.37±0.04
	NA 1325 × LK 861	21.27±0.2	23.03±0.07	22±0.28	21.47±0.12	23.17±0.06	22.47±0.23
	NA 1325 × 4084	22.87±0.1	21.17±0.11	21.23±0.16	21.33±0.14	21.73±0.33	22.1±0.24
	BC 68-2 × LK 861	22.17±0.35	22.97±0.1	22.3±0.38	22.83±0.13	22.13±0.15	23.47±0.33
	BC 68-2 × 4084	22.13±0	22.27±0.09	22.6±0.22	21.73±0.1	23.5±0.03	21.07±0.23

Table 3. Estimates of scaling tests for fiber quality traits in 6 upland cotton crosses.

Trait	Cross	A	B	C	D
Ginning percentage (%)	CPD 420 × LK 861	2.21**±1.33	1.23±1.09	3.76±2.29**	5.11±0.42**
	CPD 420 × 4084	0.73±0.33	-2.56±0.51*	13.49±0.66**	16.61±0.30**
	NA 1325 × LK 861	8.55±0.68**	2.19±0.73*	5.02±1.45**	-0.08±0.58
	NA 1325 × 4084	3.48±0.76**	-4.35±0.61**	9.66±0.79**	10.32±0.37**
	BC 68-2 × LK 861	-5.03±0.43**	-3.05±0.80**	-4.57±0.87**	0.90±0.36
	BC 68-2 × 4084	0.45±0.76	3.43±0.54**	3.64±1.04**	2.55±0.31*
2.5 % span length (mm)	CPD 420 × LK 861	13.69±0.33**	2.88±0.36**	17.29±0.45**	5.12±0.21**
	CPD 420 × 4084	5.92±0.52**	-12.38±0.29**	-3.25±0.68**	-3.71±0.22**
	NA 1325 × LK 861	19.64±0.29**	10.14±0.21**	8.35±0.84**	-1.12±0.37
	NA 1325 × 4084	3.27±0.23**	-6.11±0.53**	-3.66±0.61**	0.36±0.37
	BC 68-2 × LK 861	-1.64±0.91	1.57±0.74	-2.26±1.34*	-3.09±0.44**
	BC 68-2 × 4084	0.93±0.34	-13.02±0.45**	-17.43±0.53**	-9.50±0.2**
Uniformity ratio	CPD 420 × LK 861	4.48±0.67**	4.78±0.39**	11.07±0.85**	5.26±0.43**
	CPD 420 × 4084	-1.62±0.91	3.64±0.75**	1.92±1.18	1.12±0.45
	NA 1325 × LK 861	-1.30±0.92	0.42±0.88	1.37±1.73	2.23±0.72*
	NA 1325 × 4084	2.90±1.14**	6.46±0.93**	5.96±1.70**	0.59±0.68
	BC 68-2 × LK 861	-2.44±0.74*	-2.96±0.59**	0.07±1.03	3.28±0.55**
	BC 68-2 × 4084	1.75±0.69	12.87±0.62**	14.73±1.03**	9.34±0.32**
Micronaire value	CPD 420 × LK 861	7.69±0.11**	0.03±0.13	5.22±0.24**	1.93±0.11
	CPD 420 × 4084	-1.43±0.14	-8.08±0.12**	3.00±0.22**	12.81±0.07**
	NA 1325 × LK 861	-2.67±0.10**	-0.96±0.14	4.63±0.21**	9.92±0.07**
	NA 1325 × 4084	1.62±0.16	4.63±0.18**	5.74±0.24**	1.45±0.1
	BC 68-2 × LK 861	0.49±0.13	-5.92±0.15**	7.77±0.16**	13.42±0.08**
	BC 68-2 × 4084	5.30±0.14**	3.74±0.15**	4.10±0.28**	-0.62±0.12
Bundle strength (g/tex)	CPD 420 × LK 861	-6.71±0.35**	2.75±0.68**	0.58±0.52	1.33±0.3
	CPD 420 × 4084	-2.57±0.44**	0.79±0.30	-9.56±0.58**	-8.60±0.27**
	NA 1325 × LK 861	8.35±0.37**	-0.18±0.55	-3.18±0.77**	-8.12±0.33**
	NA 1325 × 4084	-0.93±0.68	3.43±0.52**	-1.74±0.67	-2.36±0.5*
	BC 68-2 × LK 861	-0.33±0.60	2.15±0.78*	1.63±0.98	0.15±0.44
	BC 68-2 × 4084	9.44±0.24*	-5.31±0.52**	-4.42±0.60**	-3.64±0.3**

** At 1 % LOS, * At 5 % LOS

In case of 4 parameter model the genetic components m, [i], [j] and [l] for cross 1 and 4 and m, [d], [h], and [l] for cross 6 were found to be significantly important. Under sequential 5 parameter model, higher order interactions were predicted for cross 2. In case of bundle strength, only one cross (cross 6) exhibited sequential best fit model of 4 parameter model wherein, the genetic components m, [h], [i] and [j] were found to be important. Higher order interactions were found to play role in cross 2 under 5 parameter model.

It was observed that in majority of the characters, higher magnitude of significant dominance estimates implicate a much larger role of dominance compared to that of additive gene effects in the inheritance of traits which suggested the selection of high yielding genotypes need to be postponed till later generations when the dominance effect would have diminished. These results are in line with the reports by Refaey and Razek (2013) and Srinivasan *et al.* (2013). Apart from the magnitude of [h] its sign also plays important role. Positive sign of [h] suggests its enhancing effects on the performance of traits.

Table 4. Estimates of components of generation mean analysis for fiber quality traits in 6 cotton crosses.

Trait	Cross	m	d	H	i	j	l	χ2
Ginning percentage (%)	CPD 420 × LK 861	-	-	-	-	-	-	-
	CPD 420 × 4084	43.87 ± 0.54**	-1.36 ± 0.13**	-19.25 ± 1.33**	-8.99 ± 0.49**	-	9.26 ± 0.89**	8.25 **
	NA 1325 × LK 861	-	-	-	-	-	-	-
	NA 1325 × 4084	37.26 ± 0.11**	-2.25 ±0.24**	-	-4.46 ± 0.26**	6.07 ± 0.86**	-	21.39 **
	BC 68-2 × LK 861	-	-	-	-	-	-	-
	BC 68-2 × 4084	34.19 ± 0.18**	-1.61 ± 0.25**	-	-1.61 ± 0.31**	-1.52 ± 0.67*	-	0.95 NS
2.5% span length (mm)	CPD 420 × LK 861	31.73 ± 0.09**	-1.17 ± 0.15**	-	-2.75 ± 0.18**	3.67 ± 0.45**	-2.19 ± 0.16**	2.05 NS
	CPD 420 × 4084	22.05 ± 0.24**	0.66 ± 0.21**	6.48 ± 0.37**	1.26 ± 0.32**	6.46 ± 0.51**	-	1.54 NS
	NA 1325 × LK 861	27.33 ± 0.13**	-2.18 ± 0.13**	9.88 ± 0.43**	-	3.51 ± 12.20**	-7.81 ± 0.42**	1.26 NS
	NA 1325 × 4084	26.16 ± 0.12**	0.24 ± 0.12*	-3.27 ± 0.51**	-	3.89 ± 0.48**	2.34 ± 0.47**	0.13 NS
	BC 68-2 × LK 861	-	-	-	-	-	-	-
	BC 68-2 × 4084	23.01 ±0.08**	0.43 ± 0.14**	-	3.55 ± 0.15**	6.27 ± 0.43**	2.26 ± 0.30**	0.28 NS
Uniformity ratio	CPD 420 × LK 861	50.53 ± 0.41**	-1.10 ± 0.10**	-4.98 ± 0.64**	-4.70 ± 0.42**	-	-	3.80 NS
	CPD 420 × 4084	52.60 ± 0.50**	-2.26 ± 0.19**	-3.73 ± 0.94**	-1.10 ± 0.52*	-4.23 ± 0.89**	-	0.02 NS
	NA 1325 × LK 861	-	-	-	-	-	-	-
	NA 1325 × 4084	47.98 ± 0.36**	-1.05 ± 0.36**	11.82± 1.41**	-	-2.62 ± 1.19*	-9.70 ± 1.55**	0.35 NS
	BC 68-2 × LK 861	-	-	-	-	-	-	-
	BC 68-2 × 4084	55.41 ± 0.71**	-	-	-5.93 ± 0.64**	-6.7 ± 0.46**	-3.25 ± 1.37*	0.83 NS
Micronaire value	CPD 420 × LK 861	3.94 ± 0.05**	-	-	-0.43 ± 0.07**	0.85 ± 0.13**	-0.42 ± 0.11**	2.73 NS
	CPD 420 × 4084	6.39 ± 0.15**	-0.47 ± 0.03**	-5.41 ± 0.40**	-1.93 ± 0.14**	-	3.27 ± 0.31**	40.13 **
	NA 1325 × LK 861	5.03 ± 0.14**	0.21 ± 0.04**	-2.98 ± 0.35**	-1.37 ± 0.13**	-	1.83 ± 0.25**	0.87 NS
	NA 1325 × 4084	4.54 ± 0.05**	-	-	-0.49 ± 0.20**	-0.49 ± 0.20**	-0.38 ± 0.11**	2.90 NS
	BC 68-2 × LK 861	5.94 ± 0.16**	-	-5.20** ± 0.46	-2.05** ± 0.15	1.11** ± 0.14	2.72** ±0.31	2.14 NS
	BC 68-2 × 4084	3.96** ± 0.05	-0.51 ± 0.05**	1.27 ± 0.20**	-	-	-1.24 ± 0.22**	1.43 NS
Bundle strength (g/tex)	CPD 420 × LK 861	-	-	-	-	-	-	-
	CPD 420 × 4084	16.06 ± 0.49**	1.41 ± 0.12**	11.86 ± 1.23**	5.42 ±0.45**	-	-5.15 ± 0.82**	8.09 **
	NA 1325 × LK 861	-	-	-	-	-	-	-
	NA 1325 × 4084	-	-	-	-	-	-	-
	BC 68-2 × LK 861	-	-	-	-	-	-	-
	BC 68-2 × 4084	19.98 ± 0.61**	-	4.38 ± 1.61**	2.20 ± 0.61**	4.87 ± 0.46**	-	3.93 NS

** At 1 % LOS, * At 5 % LOS

Dominant gene effect appeared to be more important for 2.5% span length (cross 2 and 3), uniformity ratio (cross 4), micronaire value (cross 6) and bundle strength (cross 2 and 6). The contribution of the parent to dominance effects varies according to trait. The sign for dominance effects is a function of the F_1 mean value in relation to the mid parental value and indicates which parent is contributing to the dominance effect (Cukadar and Miller, 1997). 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 (Haleem *et al.,* 2010). Whereas additive gene effects [d] were found to be important for the traits 2.5% span length (cross 4 and 6) and micronaire value (cross 3). Jagtap (1986) 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.* (2013), Refaey and Razek (2013) and Esmail (2007) for one or other fiber quality traits. Even though, the traits 2.5% span length and bundle 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, ginning percentage (cross 2), 2.5% span length (cross 3 and 4), uniformity ratio (cross 4), micronaire value (cross 2, 3, 5 and 6) and bundle strength (cross 2) 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 (1999) for 2.5% span length and Bhatti *et al.* (2006) and Refaey and Razek (2013) and Srinivasan *et al.* (2013) 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 none of the signs of [h] were similar to the [l] type of epistasis, it was concluded that no complementary type of interaction was present in the genetic control of the studied traits. Similar findings were reported by Rajendrakumar and Raveendran (1999) and Refaey and Razek (2013). Recent evidences suggest that dispersion of favorable alleles coupled with complementary epistasis are major components of heterosis. It is for this reason, Jinks and Jones (1958) suggested that heterosis is likely to be expressed with greater magnitude in crosses where complementary type of interaction was observed. The type of gene action is the intrinsic property of genes and no simple breeding methodology developed so far can convert duplicate epistasis into complementary epistasis (Chahal *et al.,* 1991).

The possibility that epistasis accounts for a significant proportion of the genetic variance of quantitatively inherited traits has been investigated extensively. Besides the main genetic component [d] and [h], epistatic components have also contributed to genetic variation for the most characters studied. Additive × additive [i] type of interaction was responsible in the majority of crosses for the expression of ginning percentage (cross 2, 4 and 6), 2.5% span length and uniformity ratio (cross 1, 2 and 6), micronaire value (cross 1, 2, 3, 4 and 5) and bundle strength (cross 2 and 6) which would improve the isolation of superior recombinants from the segregating generations from these crosses. Significant contribution of additive × dominance [j] gene effects were found to be in increasing direction in certain crosses for ginning percentage (cross 4 and 6), 2.5% span length (cross 1, 2, 3, 4 and 6), uniformity ratio (cross 2, 4 and 6), micronaire value (cross 1, 4 and 5) and bundle strength (cross 6). Preponderance of additive × dominance gene effects (higher magnitude) for a character suggests that, delayed selection and inter-mating the segregants followed by recurrent selection may improve that trait (Ramalingam and Sivasamy, 2002). Whereas, significant dominance × dominance [l] type of gene interaction was observed for ginning percentage (cross 2), 2.5% span length (cross 1, 3, 4 and 6), uniformity ratio (cross 4 and 6), micronaire value (cross 1, 2, 3, 4, 5 and 6) and bundle strength (cross 2). Srinivasan *et al.* (2013), Refaey and Razek (2013) and Sajid and Tanwar (2008) and Esmail (2007) also reported the importance of epistatic gene interactions ([i],

[j] and [l]) for fiber quality traits. The preponderance of [h] and [l] type of gene effects in the present study reveals that the expression of these traits was largely controlled by many genes having small effects and also dominant in their action.

From the present study, it could be concluded that dominance gene effects played major role in controlling the genetic variance in most of studied traits. However, additive gene effects also found to be important for inheritance of some studied fiber quality traits. Biparental mating, recurrent selection and diallel selective mating system might be profitable in exploiting both additive and non-additive gene actions to obtain desirable recombinants. The characters for which additive and dominance gene actions were observed reciprocal breeding techniques may be appropriate. Presence of epistatic gene interactions in the inheritance of some of studied characters reveals that some alleles showing interactions are present in some populations so, during breeding for traits under study selection of plants in early generations would not be effective as they would not reproduce progeny with the same magnitude of the trait due to recombination. Selection in later generations would be more feasible. However, when dominance and epistatic effects are significant, the possibility of obtaining desirable segregants through intermating in each segregation by breaking undesirable linkage could be available or it is suggested to adopt recurrent selection for handling these crosses for rapid improvement. With regard to the negative values observed in most cases either with main effects [d] and [h] or epistatic interaction effects ([i], [j] and [l]), these might indicate that preponderance was towards the reducer trait and alleles responsible for less value of traits were over dominant over the alleles controlling high values.

REFERENCES

Bhatti MA, Azhar FM, Alvi AW (2006). Estimation of additive, dominance and epistatic components of genetic variation in fiber quality characters of upland cotton grown in salinized conditions. *Int. J. Agric. Biol.* 8(6): 824-827.

Cavalli LL (1952). An analysis of linkages in quantitative inheritance In: ECR Reevee and CH Waddington, eds., Quantitative inheritance, HMSO, London, pp. 135-144.

Chahal GS, Singh TH, Virk DS (1991). Measurement and utilization of non-allelic interactions in plant breeding. *The Crop Improvement Society of India,* Ludhiana. pp. 59.

Cukadar OB, Miller JF (1997). Inheritance of the stay green trait in sunflower. *Crop. Sci.* 37: 150-153.

Esmail RM (2007). Genetic analysis of yield and its contributing traits in two intra-specific cotton crosses. *J. Appl. Sci. Res.* 3(12): 2075-2080.

Gamble EE (1962). Gene effects in corn I: Separation and relative importance of gene effects for yield. *Canadian J. Plant. Sci.* 15: 77-78.

Haleem SHM, Metwali MR, Felaly MM (2010). Genetic analysis of yield and its components of some Egyptian cotton (*Gossypium barbadense* L.) varieties. *World J. Agric. Sci.* 6 (5): 615-621.

Hayman BI (1958). The separation of epistatic from additive and dominance variation in generation means. *Heredity.* 12: 371-390.

Hayman BI, Mather K (1955). The description of genic interaction in continuous variation. *Biometrics.* II: 69-82.

Jagtap DR (1986). Combining ability in upland cotton. *Indian J. Agric. Sci.* 56: 833-840.

Jinks JL, Jones M (1958). Estimation of the components of heterosis. *Genetics.* 43(2): 223-234.

Mather K (1949). Biometrical genetics. Methuen and Co. London.

Mather K, Jinks JL (1982). Biometrical Genetics, 3rd edition, Chapman and Hall, London.

Nidagundi JM, Patil SS, Salimath PM, Kajjidoni ST, Patil BC, Hegde MG (2012). Genetic analysis of seed cotton yield and its component traits in *Gossypium hirsutum* L. *Karnataka J. Agric. Sci.* 25(2): 260-261.

Pathak RS (1975). Gene effects for fiber properties in upland cotton (*Gossypium hirsutum* L.). *Theor. Appl. Genet.* 46(3): 129–33.

Rajendrakumar P, Raveendran TS (1999). Genetic analysis of yield and quality traits in upland cotton (*Gossypium hirsutum* L.) through generation mean analysis. *Indian J. Agric. Sci.* 69(7): 538-540.

Ramalingam A, Sivasamy N (2002). Genetics and order effects of seed cotton yield in upland cotton (*Gossypium hirsutum* L.) triallel analysis. *Indian J. Genet. Pl. Br.* 62(4): 359-360.

Refaey RA, Razek UA (2013). Generation mean analysis for yield, its components and quality characteristics in four crosses of

Egyptian cotton (*Gossypium barbadense* L.). *Asian J. Crop Sci.* 5(2): 153-156.

Sajid UR, Tanwar AM (2008). Genetic analysis of fiber traits in cotton. *Int. J. Agric. Biol.* 10(2): 209–212.

Singh RK, Chaudhary BD (1985) Biometrical methods in quantitative genetic analysis. Kalyani Publishers, Ludhiana. pp. 205-214.

Srinivasan K, Rajashekaran R, Mahalingam G (2013). Genetic analysis for quantitative and quality characters in three single crosses of upland cotton. *Not. Sci. Biol.* 5(4): 450-453.