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Research Article

Estimation of genetic parameters through generation mean analysis for yield and its components in four upland (*Gossypium hirsutum* L.) cotton crosses

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Abstract

The present study was conducted to evaluate genetic and epistatic effects governing the inheritance of seed cotton yield and yield components using the four crosses viz., CPD 420 x LK 861, CPD 420 x 4084, NA 1325 x LK 861 and NA 1325 x 4084 and their F2, parents and back cross generations for seven characters. Estimates of gene effects through joint scaling test of three, six parameter and sequential fit model revealed that simple additive dominance model exhibited lack of good fit for all the traits indicating the role of non-allelic interactions. Differential model schemes for same trait in different crosses were noticed in the present investigation which was due to different parents involved with variable gene frequency with opposing and reinforcing gene effects. The magnitude of [d] was relatively small to that of other gene effects indicating its minor role in the inheritance of these traits. All the traits exhibited the three types of epistatic interactions viz., add x add (i), add x dom (j) and dom x dom and duplicate type of interaction in one or other cross and none of the traits showed complementary type of interaction. Linkage or higher order interactions were also observed in all the crosses which were evidenced by the significance of all the tested parameters and $\chi2$ value.

Key words: Cotton, Gene action, Additive, Dominance, Epistasis, Generation mean

Introduction

Cotton is the one of the most important commercial crops of India. Over 90 per cent of the cotton grown in the world is the upland cotton or *Gossypium hirsutum* L. Seed cotton yield and yield components are governed by large number of genes in cotton. The phenotypic expression of these traits mainly depends upon the type of gene action i.e., additive and dominance. But the important role of non allelic interaction also observed in the inheritance of quantitative characters in cotton. True knowledge of these gene actions for the traits helps in making decision with regard to appropriate breeding system to be adopted. Expression of the quantitative traits not only governed by large number of genes which in turn affected by the so many environmental factors. Different types of gene action governs the traits in different type of crosses, so the breeding strategy should be based on the gene action involved in that particular cross to get desirable genotype. Favourable combinations of yield contributing characters may improve yielding capacity. Sufficient understanding of the inheritance of yield contributing traits and information about inheritance of seed cotton yield is essential to develop an efficient breeding strategy. Generation mean analysis is a biometrical method based on measurements of phenotypic performance of certain quantitative traits on as many as possible individuals in basic experimental breeding generations (parental, back cross, filial and segregating generations). It is a useful technique in plant breeding for estimating main genetic effects (additive and dominance) and their digenic (additive x additive, additive x dominance and dominance x dominance) interactions responsible for inheritance of quantitative traits (Kearsey and Pooni, 1996). It helps us in understanding performance of parents used in crosses and potential of crosses to be used either for exploitation of heterosis or pedigree selection. Genetic analysis using generation means have been used in cotton breeding programme to estimate type of gene action controlling the quantitative traits.

The present study was undertaken to estimate the main genetic effects including inter allelic interactions controlling yield and its component traits.

Materials and Methods

The experiment reported herein was carried out during 2006, 2007 and 2008 *kharif* seasons in college farm, college of Agriculture, Rajendranagar, Hyderabad. In *kharif* 2006, four genotypes (CPD-420, LK-861, NA 1325 and 4084) were sown and four crosses (CPD 420 x LK 861 (cross 1), CPD 420 x 4084 (cross 2), NA 1325 x LK 861 (cross 3) and NA 1325 x 4084 (cross 4)) were made to produce F1 hybrid seed. During *kharif* 2007, the material for generation mean studies was generated. For this, the four 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, six basic generations, P_1, P_2, F_1, F_2, BC_1 and BC_2 were developed for each of the four crosses. In 2008 *Kharif,* evaluation of P_1, P_2, F_1, F_2, BC_1 and BC_2 generations of the four crosses was undertaken under Randomized Block Design in three replications to understand the genetic nature of yield and yield contributing characters through generation mean analysis. The F_2's were sown in six rows and backcrosses in three rows, whereas parents and hybrids were sown in two rows each. Rows were 5 metre long and spacing adopted was 90 cm between the rows and 60 cm between the plants. The recommended package of practices was adopted all over the crop growing seasons. 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 days to 50% flowering, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight, number of seeds per boll and seed cotton yield per plant and mean was taken into consideration for statistical analysis. The mean values, variances and corresponding standard errors of means of different generations of each cross were subjected to weighed least square analysis using the scaling test (Mather, 1949) to determine the presence or absence of epistasis. After confirmation of presence of epistasis, joint scaling test (Cavalli, 1952; Hayman, 1958; Mather and Jinks, 1982) of six parameter model was applied. The presence of the non-significant parameters in additive, dominance, additive × additive, additive × dominance and dominance × dominance model was searched and subsequently those were eliminated. Through sequential model fit scheme after eliminating the non-significant parameters of six parameter model best fit scheme was traced and tested through $\chi 2$. The significance of the scales and gene effects were tested by using t- test (Singh and Chaudhary, 1985).

Results and Discussion

Analysis of variance (Table 1) revealed significant differences among the generations for all the crosses and characters under study expect for number of monopodia per plant and number of bolls per plant in cross 3 and number of seeds per boll in crosses 2 and 4. Mean data (Table 2) on various characters recorded on different generations *viz.*, P_1, P_2, F_1, F_2, BC_1 and BC_2 for four cross combinations were subjected to scaling test and joint scaling test. Significance of at least one of the scales (Table 3) in the four crosses for all the traits under study reveals the presence of non allelic interactions. The estimates of different genetic components of generation mean in terms of sequential best fit model for seven characters of four crosses are furnished in Table 4 and the results are elaborated below.

For days to 50 % flowering the joint scaling test of five parameter model exhibiting best fit in two crosses (crosses 1 and 4). The genetic parameters *viz.*, m, [d], [h], [i] and [l] in cross 1 and m, [d], [h], [j] and [l] in cross 4 recorded significant importance. In the above two crosses, dominance [h] and dominance x dominance [l] gene effects expressed opposite sign indicating duplicate type of epistasis, whereas sequential fit 4 parameter model (m, [d], [j] and [l]) was observed in cross 2. Under sequential fit five parameter model in cross 3 the $\chi 2$ values were found to be significant indicating the presence of epistasis or linkage.

Regarding number of monopodia per plant, non-allelic interactions were observed in crosses 2 and 4. These two crosses exhibited best fit for the sequential 5 parameter model, where the genetic components m, [d], [i], [j] and [l] were important in cross 2 and m, [h], [i], [j] and [l] components were found to be significant in cross 4. In case of cross 4 duplicate type of epistasis was observed which was evident from possessing the [h] and [l] components opposite sign. When sequential fit five parameter model was applied to cross 1, evidence of higher order of epistasis or linkage was predicted.

For the trait number of sympodia per plant sequential five parameter model was best fit for cross 2 and 3, whereas three parameter model was found to be important in cross 4. Under five parameter model, m, [d], [i], [j] and [l] for cross 2 and m, [d], [h], [j] and [l] for cross 3 were important, whereas 3 parameters *viz.*, m, [j] and [l] were found to be significant in cross 4. Cross 3 exhibited relatively higher magnitude of [h] and [l] components which also possessed opposite sign indicating the prevalence of duplicate type of epistasis. Under five parameter model, in cross 1 epistasis or higher order interactions were observed.

Cross 2 was found to be best fit for sequential 5 parameter model for the trait number of bolls per plant. Dominance [h], additive x additive [i], additive x dominance [j] and dominance x dominance [l] components were important for cross 2. In this cross dominance component [h] exhibited greater magnitude and possessed opposite sign to that of dominance x dominance [l] component indicating the prevalence of duplicate type of epistasis. Two crosses *viz.*, cross 1 and 4 exhibited significant χ2 values under sequential models which indicated the occurrence of higher order interactions of epistasis or linkage.

In case of boll weight, the cross 4 exhibited best fit for sequential 5 parameter model wherein genetic parameters m, [d], [h], [j] and [l] were important. Dominance [h] and dominance x dominance [l] parameters possessed opposite sign indicating the role of duplicate type of epistasis. For the crosses 1, 2 and 3 evidence of higher order of epistasis or linkage was predicted.

All the tested parameters and χ2 value were found significant in crosses 1 and 3 for number of seeds per boll and 1, 2, 3 and 4 for seed cotton yield per plant which suggests the involvement of higher order interactions or linkage or both in the inheritance of these traits.

Several workers have reported on the partitioning of gene effects in cotton. Further, most of these studies on gene action, researchers were used either the diallel or line x tester analysis which may account for the absence of epistasis in most of the cases. The presence of epistasis in cotton has been reported for days to 50 % flowering (Esmail, 2007), number of monopodia per plant (Ahmmed and Mehra, 2000), number of sympodia per plant (Rajendrakumar and Raveendran, 1999; Iqbal and Nadeem, 2003), number of bolls per plant and boll weight (Singh *et al.*, 2005) and seed cotton yield per plant (Pillai and Amirthadevarathinam, 1997; Ahmmed and Mehra, 2000; Iqbal and Nadeem, 2003; Singh *et al.*, 2005; Esmail, 2007).

In the present study, magnitude of [d] was relatively small to that of other gene effects. This indicates that additive gene is playing a minor contribution to the inheritance of these traits. The material used in present investigation was derived from single cross. It may be that, as material used becomes more selected in genetic background, additive gene effect is reduced (Gamble, 1962). In majority of the characters, the dominance gene action is playing a major role as compared to additive gene action. It suggests that selection of high yielding genotypes would be postponed till later generations when the dominance effect would have diminished. The importance of dominance gene effects was indicated not only by its significance and relative magnitude but also by its sign. Positive dominance gene effects suggest its enhancing effects on the performance of different traits and major role in controlling the genetic variation in the characters studied (Haleem *et al.*, 2010). However, for days to 50 % flowering in crosses 1 and 4 dominance gene effects possessed negative sign, indicating that dominance was in direction of early maturity. Negative sign of dominance effect indicates that alleles responsible for less value of traits were over dominant over the alleles controlling high value (Haleem *et al.*, 2010). In comparison to additive gene effect, dominant gene effect appeared to be more important for number of monopodia per plant (crosses 1 and 4), number of sympodia per plant (cross 1), number of bolls per plant (crosses 1, 2 and 4), boll weight (crosses 1, 2, 3 and 4), number of seeds per boll (crosses 1 and 3) and seed cotton yield per plant (crosses 1, 2 and 4). Refaey and Razek (2013) have also drawn the same conclusions for number of bolls per plant, boll weight and seed cotton yield per plant.

Considering the significance of epistatic interaction it was revealed that the characters *viz.*, days to 50 % flowering (crosses 1, 2, 3 and 4), number of monopodia per plant (crosses 1, 2 and 4), number of sympodia per plant (crosses 1, 2, 3 and 4), number of bolls per plant (crosses 1, 2 and 4), boll weight (crosses 1, 2, 3 and 4), number of seeds per boll (cross 3) and seed cotton yield per plant (cross 1, 2, 3 and 4) were influenced by dominance x dominance [l] type of gene interaction in one cross or other. Besides additive, epistatic component of additive x additive [i] significance indicates the preponderance of additivity over non-additivity. In such cases, in a particular cross to improve the trait pedigree method will be rewarding. Such interactions were noticed in certain crosses for various traits in the present study *viz.*, days to 50 % flowering and number of seeds per boll (crosses 1 and 3), number of monopodia per plant (crosses 1, 2 and 4), number of sympodia per plant (crosses 1 and 2), number of bolls per plant (crosses 1, 2 and 4), boll weight (crosses 1 and 2) and seed cotton yield per plant (crosses 1, 2, 3 and 4) and these interactions would enhance the isolation of superior recombinations from the segregating generations from these crosses. The epistatic component of additive x dominance [j] gene effects were found to be of considerable importance for days to 50 % flowering in crosses 2, 3 and 4, number of monopodia in crosses 1, 2 and 4, number of sympodia in crosses 1, 2, 3 and 4, number of bolls per plant in cross 2, boll weight and seed cotton yield per plant in crosses 1, 2, 3 and 4 and number of seeds per boll in cross 1 indicates the improvement for these characters through direct selection is not easy, therefore, postponement of selections to later generations through pedigree breeding programme and inter-mating the segregants followed by recurrent selection may improve these traits.

The traits, days to 50 % flowering (crosses 1, 3 and 4), number of monopodia per plant (crosses 1 and 4), number of sympodia per plant (crosses 1 and 3), number of bolls per plant (crosses 1, 2 and 4), boll weight (crosses 1, 2, 3 and 4), number of seeds per boll (cross 3) and seed cotton yield per plant (crosses 1, 2 and 4) were possessing opposite sign of [h] and [l] indicating the role of duplicate gene action controlling the traits. Similar results were reported by Haleem *et al.* (2010) for days to 50% flowering, Iqbal and Nadeem (2003) for number of sympodia per plant, Refaey and Razek (2013) for number of bolls per plant, boll weight and seed cotton yield per plant. Such type of duplicate type of gene action will pose hindrance to a plant breeder while attempting selection in long run.

In the complementary type of gene interaction particularly [h] and [l] reinforce the effect of dominance, while in the duplicate type of interaction, they oppose the effect of the dominance component. It is for this reason, heterosis is likely to be expressed with greater magnitude in crosses where complementary type of interaction was observed, while it may not be observed at all in crosses showing duplicate type of interaction (Jinks and Jones 1958). In the present investigation none of the characters of four crosses exhibited complementary type of epistasis the results of which are in agreement with the findings of Rajendrakumar and Raveendran (1999), Iqbal and Nadeem (2003) and Refaey and Razek (2013). Contrarily, complementary type of interaction for days to 50 % flowering, number of bolls per plant, boll weight and seed cotton yield per plant was reported by Ismail (2007).

In the present investigation rare cases of occurrence of significance of common genetic parameters was observed in two or more crosses for the same trait. A considerable variation in the relative magnitude of different genetic parameters *viz.,* m, [d], [h], [i], [j] and [l] was observed from cross to cross for the same character in the present study, it may be ascribed to the presence of variable frequency of genes with opposing and reinforcing effects in the parents involved in the crosses **(**Gamble, 1962; Hallauer and Mirinda, 1989)

To summarize, it was found that, sequential model schemes were found to be best fit for all characters studied in all the crosses which have two important advantages. Firstly it increases the precision with which the remaining parameters are estimated after the elimination of non-significant components and secondly it provides more degrees of freedom for $\chi2$ test (Mather and Jinks, 1982). The overall perusal of generation mean analysis results indicated that, epistasis is the integral part of genetic architecture of the present material used in the investigation and breeder cannot ignore it. Genetic models assuring negligible epistasis may be somewhat biased. The six genetic parameters estimated provide a test for different type of gene action and are useful in giving information for the improvement of these traits. However, these genetic effects cannot be interpreted based on relative genetic variances. Also estimates obtained from each cross may be unique in varying degrees and may not be applicable to its parental population (Sprague, 1966). The presence of dominance and epistatic effects for different traits in all the crosses would slow down the progress of selection. Hence, suggested the use of intermating of selector followed by visual selection in early segregating generations, which would simultaneously exploit both types of gene effects. Further, this approach is likely to break some undesirable linkages resulting in the establishment of rare useful recombinations.

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Table 1: Analysis of variance for various characters under study in four cotton crosses

S.No.	**Source**	**d.f**	**Mean squares**			
			Cross 1	**Cross 2**	**Cross 3**	**Cross 4**
1	Days to 50 % flowering					
	Replications	2	1.39	1.72	1.72	2.39
	Generations	5	20.76**	23.69**	20.48**	14.89**
	Error	10	1.59	2.32	0.72	1.32
2	Number of monopodia per plant					
	Replications	2	0.04	0.03	0.05	0.60*
	Generations	5	0.42*	0.78**	NS	0.35*
	Error	10	0.13	0.09	0.24	0.09
3	Number of sympodia per plant					
	Replications	2	0.85	0.53	2.85*	0.46
	Generations	5	3.73**	2.50*	6.44**	4.50*
	Error	10	0.42	0.52	0.46	1.13
4	Number of bolls per plant					
	Replications	2	2.44	6.34	12.38	20.91
	Generations	5	118.40**	19.41*	NS	124.99**
	Error	10	9.11	4.83	18.77	14.14
5	Boll weight					
	Replications	2	0.01	0.37	0.18	0.77**
	Generations	5	0.49**	1.56*	1.30*	1.18**
	Error	10	0.03	0.39	0.28	0.08
6	Number of seeds per boll					
	Replications	2	14.24	10.09	8.19	0.7
	Generations	5	34.34*	NS	45.86*	NS
	Error	10	9.99	7.24	12.82	11.2
7	Seed cotton yield per plant					
	Replications	2	25.01	42.64	206.77	485.85
	Generations	5	7925.80**	1844.79**	1158.28**	2567.16**
	Error	10	264.05	185.85	186.53	182.09

*Significant at 5% level, **Significant at 1% level

Table 2: Mean performance of parents, F_1, F_2 and back cross generations in four cotton crosses for characters under study

Character	Cross	P1	P2	F1	F2	BC1	BC2
Days to 50% flowering	CPD 420 X LK 861	57.67±0.13	56.67±0.13	63.67±0.33	59.00±0.21	57.33±0.18	57.00±0.00
	CPD420 X 4084	56.33±1.13	61.67±0.33	53.00±0.22	57.67±0.16	56.67±0.38	58.00±0.15
	NA 1325 X LK 861	60.33±0.13	57.33±0.25	58.33±0.13	58.33±0.12	57.00±0.152	64.00±0.15
	NA 1325 X 4084	61.67±0.33	62.67±0.13	58.00±0.22	58.33±0.06	59.00±0.00	57.00±0.30
No. Of monopodia per plant	CPD 420 X LK 861	1.70±0.14	1.33±0.05	1.63±0.08	0.97±0.00	1.70±0.05	1.93±0.02
	CPD420 X 4084	1.07±0.07	2.27±0.10	1.00±0.00	1.20±0.02	1.90±0.03	1.30±0.05
	NA 1325 X LK 861	1.50±0.14	1.53±0.11	1.97±0.16	1.13±0.02	1.13±0.02	1.07±0.02
	NA 1325 X 4084	1.67±0.13	1.87±0.09	2.20±0.04	1.33±0.03	2.03±0.08	1.43±0.06
No. Of sympodia per plant	CPD 420 X LK 861	16.00±0.02	15.67±0.13	14.67±0.13	16.67±0.12	17.33±0.09	17.67±0.09
	CPD420 X 4084	17.67±0.25	16.33±0.27	17.67±0.13	16.33±0.06	15.67±0.09	17.33±0.09
	NA 1325 X LK 861	15.87±0.09	17.07±0.07	16.47±0.10	14.00±0.11	14.67±0.18	13.33±0.23
	NA 1325 X 4084	16.33±0.13	16.23±0.26	14.67±0.33	17.33±0.16	17.67±0.23	16.33±0.09
No. Of bolls per plant	CPD 420 X LK 861	27.87±0.78	32.67±0.55	29.67±0.33	32.00±0.21	38.67±0.49	44.67±0.53
	CPD420 X 4084	31.33±0.55	31.43±0.48	34.33±0.25	31.33±0.34	34.33±0.38	37.67±0.18
	NA 1325 X LK 861	29.20±0.53	32.00±0.46	29.20±0.96	30.00±0.21	32.67±0.23	34.67±1.27
	NA 1325 X 4084	36.00±1.00	31.13±0.70	24.33±0.45	25.33±0.22	40.67±0.78	35.67±0.76
Boll weight (g)	CPD 420 X LK 861	5.69±0.05	5.05±0.02	5.25±0.03	5.06±0.01	5.58±0.03	6.07±0.02
	CPD420 X 4084	5.34±0.13	4.57±0.13	4.55±0.22	4.87±0.02	6.46±0.12	4.84±0.04
	NA 1325 X LK 861	4.21±0.09	4.65±0.07	5.08±0.16	5.04±0.07	4.44±0.03	6.07±0.08
	NA 1325 X 4084	4.31±0.05	3.66±0.08	4.38±0.07	4.83±0.04	4.06±0.06	5.46±0.12
No. Of seeds per boll	CPD 420 X LK 861	35.61±0.39	29.50±0.12	31.64±0.26	28.20±0.16	29.30±0.25	35.00±1.24
	CPD420 X 4084	32.08±0.70	31.67±0.88	30.43±0.27	30.02±0.16	35.89±0.58	31.13±0.16
	NA 1325 X LK 861	23.10±1.13	28.53±0.98	31.63±0.78	26.89±0.20	28.87±0.62	33.70±0.33
	NA 1325 X 4084	26.43±0.08	28.20±1.29	27.57±0.45	31.25±0.24	28.78±0.25	26.40±0.48
Seed cotton yield per plant (g)	CPD 420 X LK 861	169.07±1.27	150.68±3.39	160.49±1.27	175.12±0.90	235.37±2.61	280.77±3.92
	CPD420 X 4084	135.63±1.85	155.63±2.28	149.15±3.87	167.22±0.87	207.49±2.68	172.96±1.50
	NA 1325 X LK 861	153.05±2.62	173.20±4.05	146.23±2.70	150.58±1.62	130.68±1.48	185.35±1.99
	NA 1325 X 4084	148.74±1.11	142.29±1.61	130.41±1.77	123.68±2.03	146.32±2.58	205.93±3.70

Table 3: Estimates of scaling tests for seed cotton yield and its components in four cotton crosses

Trait	Cross	A	B	C	D
Days to 50% flowering	CPD 420 X LK 861	-13.34**±0.5	-17.77**±0.35	-5.17**±1.09	7.97**±7.97
	CPD420 X 4084	4.98**±0.8	2.66**±0.5	7.75**±0.86	1.27±0.52
	NA 1325 X LK 861	-13.27**±0.35	29.80**±0.41	-1.61±0.62	-13.30**±0.33
	NA 1325 X 4084	-4.18**±0.4	-10.15**±0.66	-11.39**±0.62	2.04*±0.33
No. of monopodia per plant	CPD 420 X LK 861	0.37±0.18	11.20**±0.09	-10.50**±0.21	-33.82**±0.05
	CPD420 X 4084	20.42**±0.09	-4.85**±0.14	-3.57**±0.15	-11.84**±0.07
	NA 1325 X LK 861	-5.62**±0.21	-6.99**±0.2	-6.55**±0.37	1.26±0.05
	NA 1325 X 4084	0.94±0.21	-7.56**±0.16	-12.78**±0.2	-6.98**±0.12
No. of sympodia per plant	CPD 420 X LK 861	16.35**±0.24	20.02**±0.25	9.81**±0.57	-6.06**±0.27
	CPD420 X 4084	-12.06**±0.33	1.94±0.34	-7.87**±0.51	-1.91±0.17
	NA 1325 X LK 861	-7.99**±0.38	-14.34**±0.48	-20.39**±0.48	-
	NA 1325 X 4084	7.41**±0.58	3.85**±0.46	7.62**±0.98	1.63±0.41
No. of Bolls per plant	CPD 420 X LK 861	15.35**±1.29	21.71**±1.24	5.65**±1.44	-23.08**±0.84
	CPD420 X 4084	3.08**±0.97	14.80**±0.65	-3.74**±1.63	-11.64**±0.8
	NA 1325 X LK 861	5.83**±1.19	2.95**±2.76	0.18±2.21	-5.39**±1.36
	NA 1325 X 4084	11.03**±1.91	9.12**±1.74	-8.22**±1.76	-21.82**±1.18
Boll weigt (g)	CPD 420 X LK 861	2.78**±0.08	31.56**±0.06	-12.49**±0.08	-38.23**±0.04
	CPD420 X 4084	8.91**±0.34	2.14±0.26	1.00±0.47	-12.26**±0.13
	NA 1325 X LK 861	-2.06*±0.2	9.99**±0.24	2.58**±0.44	-2.75**±0.16
	NA 1325 X 4084	-4.03**±0.14	11.04**±0.26	11.84**±0.22	0.91±0.15
No. of seeds per boll	CPD 420 X LK 861	-12.57**±0.69	3.55**±2.49	-16.86**±0.93	-6.06**±1.31
	CPD420 X 4084	6.66**±1.4	0.17±0.97	-3.24**±1.4	-10.25**±0.68
	NA 1325 X LK 861	1.63±1.85	5.10**±1.42	-3.19**±2.31	-10.87**±0.81
	NA 1325 X 4084	5.20**±0.68	-1.78±1.66	8.32**±1.83	10.23**±0.72
Seed cotton yield per plant (g)	CPD 420 X LK 861	25.58**±5.52	28.98**±8.64	10.49**±5.7	-32.91**±5.04
	CPD420 X 4084	18.98**±6.86	7.61**±5.41	8.83**±8.98	-13.05**±3.53
	NA 1325 X LK 861	-7.92**±4.79	8.16**±6.28	-1.69±9.7	-3.65**±4.07
	NA 1325 X 4084	2.43**±5.56	17.89**±7.78	-6.29**±9.07	-17.28**±6.07

*Significant at 5% level, **Significant at 1% level

Table 4: Estimates of components of generation mean analysis for yield and its components for various traits in four cotton crosses.

Character	Cross	m	d	h	i	j	l	χ2
Days to 50% flowering	CPD 420 X LK 861	64.46** ± 0.97	0.48** ± 0.08	-21.04** ± 2.23	-7.29** ± 0.97	-	20.25** ± 1.43	0.45NS
	CPD420 X 4084	59.11** ± 0.21	-2.64** ± 0.18	-	-	3.21** ± 0.76	-6.13** ± 0.35	1.66NS
	NA 1325 X LK 861	51.07** ± 0.66	-	21.80** ± 1.66	8.67** ± 0.65	-14.00** ± 0.43	-14.53** ± 1.04	113.42**
	NA 1325 X 4084	62.17** ± 0.18	-0.50** ± 0.18	-11.32** ± 0.62	-	4.29** ± 0.66	7.15** ± 0.61	3.41NS
No. of monopodia per plant	CPD 420 X LK 861	-2.20** ± 0.11	-	8.83** ± 0.34	3.40** ± 0.10	-0.47** ± 0.10	-5.00** ± 0.27	15.21**
	CPD420 X 4084	1.60** ± 0.07	-0.60** ± 0.06	-	1.67** ± 0.06	2.31** ± 0.19	-2.81** ± 0.10	0.09NS
	NA 1325 X LK 861	-	-	-	-	-	-	-
	NA 1325 X 4084	1.08** ± 0.07	-	3.11** ± 0.10	1.75** ± 0.07	1.45** ± 0.25	-0.91** ± 0.13	2.35NS
No. of sympodia per plant	CPD 420 X LK 861	12.51** ± 0.56	-	14.56** ± 1.26	3.33** ± 0.55	-0.67** ± 0.25	-12.30** ± 0.76	3.8*
	CPD420 X 4084	15.85** ± 0.09	0.67** ±0.18	-	1.03** ± 0.20	-4.68** ± 0.44	1.80** ±0.19	1.60NS
	NA 1325 X LK 861	16.47** ± 0.06	-0.60** ± 0.06	-9.87** ± 0.40	-	3.87** ± 0.58	9.87** ± 0.41	0.08NS
	NA 1325 X 4084	17.65** ± 0.83	-	-	-	2.67** ± 0.50	-4.70** ± 1.38	0.84NS
No. of Bolls per plant	CPD 420 X LK 861	-8.32** ± 1.74	-3.49** ± 0.40	123.29** ± 4.88	38.22**± 1.67	-	-85.31**± 3.23	17.34**
	CPD420 X 4084	12.72** ± 1.64	-	52.83** ± 3.88	18.67**± 1.60	-6.67** ± 0.84	-31.22** ± 2.34	0.02NS
	NA 1325 X LK 861	-	-	-	-	-	-	-
	NA 1325 X 4084	-17.48** ± 2.43	3.05** ± 0.53	129.44** ± 7.02	51.26**± 2.35	-	-87.63** ± 4.69	4.22**
Boll weigt (g)	CPD 420 X LK 861	2.03** 0.08	-	8.90** ± 0.24	3.08** ± 0.08	-0.98** ± 0.08	-5.52** ± 0.17	177.27**
	CPD420 X 4084	1.84** ± 0.27	-	9.41** ± 0.82	3.12** ± 0.24	3.24** ± 0.24	-6.70** ± 0.68	18.65**
	NA 1325 X LK 861	4.43** ± 0.06	-0.22** ± 0.06	2.38** ± 0.28	-	-2.63** ± 0.20	-1.74** ± 0.37	7.58**
	NA 1325 X 4084	3.99** ± 0.04	0.33** ± 0.04	2.92** ± 0.20	-	-3.59** ± 0.25	-2.52** ± 0.21	0.83NS
No. of seeds per boll	CPD 420 X LK 861	24.80** ± 0.41	3.10** ± 0.20	6.92** ± 0.61	7.81** ± 0.46	-10.47** ± 1.20	-	9.71**
	CPD420 X 4084	-	-	-	-	-	-	-
	NA 1325 X LK 861	6.97** ± 1.68	-3.84** ± 0.51	54.99** ± 4.76	18.69**± 1.53	-	-30.33** ± 3.42	4.24**
	NA 1325 X 4084	-	-	-	-	-	-	-
Seed cotton yield per plant (g)	CPD 420 X LK 861	-165.0** ± 10.15	-	1035.00**± 29.41	331.83**±10.08	-90.80** ± 9.42	-709.5**±19.50	25.88**
	CPD420 X 4084	51.53** ± 7.20	-	365.14** ± 20.52	92.03** ± 7.05	69.05** ± 6.14	-267.51**±5.20	46.42**
	NA 1325 X LK 861	155.20** ± 2.00	-10.97** ± 2.9	-	10.10** ± 3.36	-84.81** ± 6.71	-8.06** ± 4.11	6.99**
	NA 1325 X 4084	-63.11** ± 12.18	-	553.64** ± 31.74	209.78**± 2.14	19.23 ** ± 9.02	-360.1**±20.19	10.90**

*Significant at 5% level, **Significant at 1% level