

## Research Article

# Study of Gene Effects for Some Quantitative Traits in Upland Cotton (*Gossypium hirsutum* L.)

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**Abstract**

The present investigation comprising of six generations ( $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$ ) of four crosses *viz.* GCH 3 x HS 6, GCH 3 x RST 9, H 1353 x HS 6 and H 1353 x RST 9 was conducted to estimate the gene effects for some quantitative or metric traits in upland cotton during *kharif* 2013-2016. The experimental material was grown in a randomized block design with three replications during *kharif*, 2015 in Cotton Research Area of CCS Haryana Agricultural University, Hisar. The “t” statistical test was applied to test the differences between parental genotypes for the characters studied before considering the biometrical analysis. The gene effects were estimated by employing generation mean analysis which revealed significant differences for all the characters in all the four crosses. Traits namely days to flowering, plant height and number of bolls / plant indicated the presence of non-allelic interactions. Dominance component was significant for the characters; days to flowering and plant height.

Either all or any of the three types of epistatic interactions (i, j and l) were significant for the cases where simple additive-dominance model was found inadequate. Duplicate type of interaction was apparent for days to flower (cross IV) and plant height (cross I, II and IV).

**Keywords:** Additive, Dominance, Epistasis, Gene effects, Generation mean analysis.

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**Introduction**

Cotton is a major fibre crop of global importance and has high commercial value. It is grown commercially in the temperate and tropical regions of more than 70 countries. These include periods of hot and dry weather and adequate moisture obtained through irrigation. The leading cotton producing countries are China, USA, India and Pakistan where climatic conditions suit the natural growth requirements of cotton [1]. Indian economy is consistently influenced by cotton through its production, processing and by generating direct and indirect employment to more than eight million people. There has also been a manifold improvement in production, productivity and quality with no virtual increase in area.

As this crop is highly important for the economy of our country, efforts have been placed and should continue in future on various aspects of cotton production to increase the production and productivity of cotton. The choice of suitable breeding procedure depends upon the nature and magnitude of gene action involved in the inheritance of various characters of economic importance in the crop or we can say that the estimates of gene effects in a crop improvement program have a direct bearing upon the choice of selection procedure to improve a quantitative character. Hence, it is obvious that the efficiency of selection for the improvement of quantitative traits depends on the nature and magnitude of gene effects involved in the inheritance of a specific character. In order to breed high yielding varieties of cotton, the information on genetic effects/ gene action of different quantitative traits may help cotton breeders for improving genetic architecture of cotton plant in particular direction for maintaining and improving the proper level of crop production and productivity [2] and [3].

The use of already existing genetic variability in the breeding material as well as, the creation of new variability along with understanding of its genetic mode is of crucial importance for a plant breeder to run an efficient breeding program. In recent past many scientists conducted studies to identify the inheritance pattern (genetics) and association of some agronomic, morphological, quantitative /metric traits in upland cotton [4], [5], [6]. The present study was also conducted to reveal the information about gene effects for some of the morphological/ quantitative traits in upland cotton.

**Materials and Methods**

The present investigation was conducted in Cotton Research Area, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar from *kharif* 2013 to 2016. Experimental material consists of four parents *i.e.*

GCH3, H1353, RST9 and HS6 differing for different characteristics. These four parents were used to develop four crosses, GCH 3 x HS 6, GCH 3 x RST 9, H 1353 x HS 6 and H 1353 x RST 9. These crosses were designated as cross I, cross II, cross III and cross IV, respectively.

During *Kharif*, 2013, the parents were identified and  $F_1$  crosses were made. The  $F_1$  and parents were raised in next season. Each  $F_1$  was selfed to obtain  $F_2$  generation and simultaneously backcrossed to both of its parents to produce backcross generations  $BC_1$  (backcross to parent 1) and  $BC_2$  (backcross to parent 2). Fresh crosses were also made to obtain the  $F_1$  seed and all the parents were selfed to get their seeds for the next year and finally experimental material comprised of six generations *i.e.*  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$ .

The experimental material comprised of six generations *i.e.* parents ( $P_1$  and  $P_2$ ),  $F_1$ ,  $F_2$  and back crosses ( $BC_1$  and  $BC_2$ ) of four crosses was grown in a randomized block design with three replications during *kharif*, 2015 in Cotton Research Area of CCS Haryana Agricultural University, Hisar. There were two rows of non segregating generations ( $P_1$ ,  $P_2$  and  $F_1$ ), 10 rows of  $F_2$ , and 4 rows of each back cross 1 and back cross 2 generations. The length of each row was 6 m with a spacing 67.5 cm x 30 cm. Normal cultural practices were followed during crop season. Observations were taken during *kharif* 2015-16.

### ***Observations on Economic Traits***

Five competitive plants from each row of non-segregating generations, fifty plants from  $F_2$  generations and ten plants from each of backcrosses were taken at random for recording observations on the following economic characters:

- **Days to Flower:** It was measured by the number of days counted from the date of sowing to the emergence of the first flower on particular plant in each replication and then averaged.
- **Plant Height (cm):** The observation was taken at the time of maturity of crop. The measurement was taken from the cotyledonary node to the apex of main stem.
- **Number of Bolls / Plant:** The total number of effective bolls picked from a plant were counted and recorded.
- **Ginning Out turn (%):** It is the proportion of lint to seed cotton expressed in percentage. It was estimated by taking 100 g of seed cotton from each plant. The lint weight was calculated on electronic balance in grams.

### ***Biometrical Analysis for Estimation of Gene Effects***

The “t” statistical test was applied to test the differences between parental genotypes for the characters studied before considering the biometrical analysis. The gene effects were estimated by employing generation mean analysis [7], [8], [9].

### ***Genetic Analysis of Means Based on Six Generations***

The following assumptions were made for estimating the parameters of gene effects from the generation mean analysis *viz.*

- Parents are homozygous
- Diploid inheritance
- Absence of linkage
- Absence of lethal genes
- Absence of multiple alleles
- Absence of maternal effects
- Equal viability of all genotypes
- Absence of genotype x environment interaction

The plant material used in the present investigation included the parents which were inbred varieties, continuously selfed for many generations, and thus fulfill these assumptions to a greater extent. The assumption of diploid segregation, homozygous parents, absence of multiple alleles and constant viability of all the genotypes could be clearly fulfilled as the parental material constituted highly homozygous selected genotypes.

The significance of gene effects was tested by t-test. It comprised of estimating the parameters  $m$ ,  $d$  and  $h$ , using weighted least square method followed by a comparison of observed means with expected means. A weighted least square analysis was performed on the model using parameter ‘ $m$ ’ only. Further model of increasing complexity were fitted, where chi-square value was significant. The best-fitted model was chosen as the one, which had significant

estimates of all parameter along with non-significant chi-square. This can be affected by Chi-square test with the degree of freedom equal to the number of generations minus number of parameters estimated.

## Results

### Generation Mean Analysis

The mean performance of six generations of all the four crosses viz. GCH 3 x HS 6, GCH 3 x RST 9, H 1353 x HS 6 and H 1353 x RST 9 for different characters are presented in **Table 1** and described character wise.

**Table 1** Mean performance for some quantitative or yield attributing characters in different generations in four crosses of upland cotton

Character	Cross	P <sub>1</sub>	P <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>	BC <sub>1</sub>	BC <sub>2</sub>
Days to flower	GCH 3 x HS 6	54.33± 1.17	58.60 ± 1.22	57.40 ±0.80	57.26±0.59	55.80±0.82	57.60±1.28
	GCH 3 x RST 9	58.53± 1.61	56.13± 7.09	60.20± 2.11	58.68±0.72	57.46± 1.20	56.80±3.35
	H 1353 x HS 6	55.93 ±1.45	57.13±1.15	56.40±1.56	56.75±0.59	56.43±0.90	57.66 ±1.10
	H 1353 x RST 9	56.93±2.33	54.60±1.13	57.60±1.63	57.22 ±0.68	55.50 ±0.74	54.33±0.80
Plant height (cm)	GCH 3 x HS 6	120.66±8.01	118.00 ±7.21	120.66 ±6.20	117.02±2.62	116.16 ±7.17	114.00 ±4.77
	GCH 3 x RST 9	131.00 ±6.71	128.00 ±10.44	134.66±11.19	120.61 ±4.25	128.33 ±5.74	122.16 ±4.28
	H 1353 x HS 6	143.33±9.84	131.00 ±8.50	145.33± 11.46	143.50 ±3.14	145.00± 5.38	135.16±6.89
	H 1353 x RST 9	143.33±9.77	118.66 ±8.51	135.33±8.21	132.44 ±2.80	135.00±5.93	120.00 ±9.55
No. of bolls/plant	GCH 3 x HS 6	21.86± 3.56	18.53 ±2.40	23.33±3.40	21.95±12.76	20.40±1.91	19.13 ±6.11
	GCH 3 x RST 9	18.93±3.17	19.53±3.09	30.33 ±6.94	21.73 ±1.09	22.26 ±4.67	15.43 ±3.21
	H 1353 x HS 6	23.33±2.95	22.26 ±2.72	23.13 ±3.70	22.03 ±4.11	22.93±2.87	21.23 ±2.91
	H 1353 x RST 9	22.26± 5.54	23.80 ±3.57	23.86 ±5.10	20.62±4.43	22.80 ±3.08	21.83 ±3.44
Ginning out turn (%)	GCH 3 x HS 6	36.18 ±1.97	31.91±2.17	32.42 ±2.77	31.15±0.87	35.25±1.67	32.26 ±2.03
	GCH 3 x RST 9	35.45±3.26	29.95±2.31	34.79±2.44	32.02 ±1.08	33.06 ±1.79	31.01 ±2.25
	H 1353 x HS 6	34.99 ±2.73	30.39 ±1.91	32.70 ±2.65	31.93 ±1.19	33.69 ±3.39	30.52±4.18
	H 1353 x RST 9	36.56±2.11	30.92 ±2.32	34.04 ± 3.03	33.78 ±1.22	34.36 ±2.19	30.81 ±1.95

\*Heterosis was over mid-parent in all the characters

### Days to Flower

There was non-significant variation for this trait among the parents of all the four crosses. The mean values of F<sub>1</sub> in the crosses I and III (57.40 and 56.40) were near mid parent value and higher than parent value in crosses II and IV (60.20 and 57.60) showing heterotic effect. F<sub>2</sub> means were lower than that of F<sub>1</sub> in cross II (GCH 3 x RST 9) (58.68) while in other crosses means were almost same as that of F<sub>1</sub>. The backcross generations (BC<sub>1</sub> and BC<sub>2</sub>) tended to be equivalent to that of respective recurrent parents of its backcross as presented in Table 1.

### Plant Height (cm)

Significant variation existed among parents in all the four crosses where the maximum plant height was recorded in H 1353 (143.33) and minimum plant height was recorded in HS 6 (118.00), F<sub>1</sub> of cross II and III (134.66 and 145.33) showed heterotic effect and same as parental value in cross I (120.66). The mean values of F<sub>2</sub> generation was lower than that of F<sub>1</sub> in all crosses. The average plant height in the backcross generations (BC<sub>1</sub> and BC<sub>2</sub>) tended towards their respective recurrent parents as shown in the Table 1.

### Number of Bolls / Plant

Boll number / plant is the most important trait in cotton for seed cotton yield. The parents involved in all the four crosses exhibited significant variation for this trait. The parent H 1353 (CR III) recorded maximum number of bolls (23.33) and HS 6 (CR I) contained minimum number of bolls (18.53). The F<sub>1</sub> hybrid exhibited heterotic effect in all crosses. The F<sub>2</sub> mean values were found lower than those of F<sub>1</sub> in all four crosses and the backcross generations (BC<sub>1</sub> and BC<sub>2</sub>) tended to be towards their recurrent parents as presented in the Table 1.

### Ginning Out turn (%)

The significant magnitude of variation for this character was present in parents as depicted in the Table 1. The ginning out turn was maximum in H 1353 in cross H 1353 x RST 9 (36.56) and was minimum in RST 9 in cross GCH 3 x

RST 9 (29.95). The F<sub>1</sub> hybrids were found to be intermediate in all four crosses. The F<sub>2</sub> generation had lower mean values than the F<sub>1</sub> in all four crosses. The backcross generations (BC<sub>1</sub> and BC<sub>2</sub>) tended to be towards their recurrent parents for the performance in respect of this trait as indicated in Table 1.

### Three Parameter Model

Both individual (A, B, C, and D) and joint scaling tests were used in all the crosses to determine whether at all the additive-dominance model was adequate for different traits. Further the three parameters m, (d) and (h) were estimated through joint scaling test wherever the additive-dominance model was satisfactory under three parameters.

### Days to Flowering

The individual scaling test showed the significance of additive-dominance model in cross I, II and III whereas, the cross IV indicated the failure of additive-dominance model as presented in **Table 2**. It was also substantiated by non-significant  $\chi^2$  value of joint scaling which suggested that three parameter model was sufficient for cross I, II and III while in cross IV three parameter models was not sufficient.

**Table 2** Estimates of different scaling tests and genetic effects for days to flowering, plant height and boll no./plant in four upland cotton crosses

Days to flowering	Cross	Cross I	Cross II	Cross III	Cross IV
		(GCH 3 x HS 6)	(GCH 3 x RST 9)	(H 1353 x HS 6)	(H 1353 x RST 9)
	Parameter	Estimates $\pm$ SE	Estimates $\pm$ SE	Estimates $\pm$ SE	Estimates $\pm$ SE
<b>Scaling test</b>					
	A	0.13 $\pm$ 1.25	3.80* $\pm$ 2.07	-0.53 $\pm$ 1.62	5.86** $\pm$ 1.85
	B	0.80 $\pm$ 1.70	2.73 $\pm$ 5.77	-1.80 $\pm$ 1.70	1.40 $\pm$ 1.47
	C	-1.33 $\pm$ 1.92	0.31 $\pm$ 5.14	-1.15 $\pm$ 2.51	-2.15 $\pm$ 2.87
	D	1.13 $\pm$ 1.11	3.11 $\pm$ 2.22	-0.58 $\pm$ 1.07	4.71** $\pm$ 1.00
<b>Joint scaling test ( three parameter model)</b>					
	m	56.54** $\pm$ 0.40	57.76** $\pm$ 1.07	56.66** $\pm$ 0.47	54.63** $\pm$ 0.55
	d	2.11** $\pm$ 0.42	-0.09 $\pm$ 1.07	0.73 $\pm$ 0.44	0.32 $\pm$ 0.46
	h	0.92 $\pm$ 0.67	1.41 $\pm$ 1.86	0.22 $\pm$ 0.94	2.42* $\pm$ 1.09
	$\chi^2$ (df = 3)	1.11	4.60	1.12	28.44**
<b>Six parameter model</b>					
	m	57.26** $\pm$ 0.34	58.68** $\pm$ 0.42	56.75** $\pm$ 0.34	57.22** $\pm$ 0.39
	d	-1.80* $\pm$ 0.88	0.66 $\pm$ 2.06	-1.23 $\pm$ 0.82	-1.06 $\pm$ 0.63
	h	-1.33 $\pm$ 2.33	-3.35 $\pm$ 5.07	1.04 $\pm$ 2.39	-7.58** $\pm$ 2.34
	i	-2.26 $\pm$ 2.23	-6.22 $\pm$ 4.45	1.17 $\pm$ 2.15	-9.42** $\pm$ 2.01
	j	0.66 $\pm$ 2.01	-1.06 $\pm$ 5.88	-1.26 $\pm$ 1.97	-4.46* $\pm$ 1.95
	l	3.20 $\pm$ 4.01	12.75 $\pm$ 9.71	-3.51 $\pm$ 4.15	16.68** $\pm$ 3.82
	Type of epistasis	-	-	-	Duplicate
<b>Mather and Jinks</b>					
	E	0.39	6.38	0.65	1.04
	D	-1.31	-8.14	-1.13	-0.48
	H	-1.52	-8.55	0.11	-2.58
	Heritability	-2.18	0.79	3.10	0.24
	Inbreeding depression	0.13	1.51	-0.35	0.37
Plant height(cm)	Cross	Cross I	Cross II	Cross III	Cross IV
		(GCH 3 x HS 6)	(GCH 3 x RST 9)	(H 1353 x HS 6)	(H 1353 x RST 9)
	Parameter	Estimates $\pm$ SE	Estimates $\pm$ SE	Estimates $\pm$ SE	Estimates $\pm$ SE
<b>Scaling test</b>					
	A	9.00 $\pm$ 10.14	29.00** $\pm$ 10.04	-34.33** $\pm$ 10.71	28.66** $\pm$ 10.06
	B	-29.33** $\pm$ 7.78	-1.66 $\pm$ 10.13	-27.00* $\pm$ 11.54	-6.00 $\pm$ 12.97
	C	11.89 $\pm$ 11.25	5.88 $\pm$ 17.75	-75.00** $\pm$ 16.86	-37.11** $\pm$ 13.71
	D	-16.11** $\pm$ 5.82	10.72 $\pm$ 6.42	6.83 $\pm$ 6.22	29.88** $\pm$ 7.25

<b>Joint scaling test ( three parameter model)</b>					
m	118.93**±2.54	130.04**±3.08	144.75**±3.31	133.54**±3.08	
d	5.89*±2.59	3.96±2.63	-8.20*±2.98	-5.06±3.14	
h	2.21±4.70	-22.12**±6.34	-9.29±6.67	7.58±5.90	
$\chi^2$ (df=3)	25.38**	11.19**	19.96**	35.71**	
<b>Six parameter model</b>					
m	117.02**±1.51	120.61**±2.45	143.50**±1.81	142.44**±1.62	
d	-17.83**±4.97	-13.83**±4.13	9.83*±5.04	-5.00±6.49	
h	33.56**±12.57	-36.27**±14.82	-38.50**±14.58	-55.44**±15.71	
i	32.22**±11.64	-21.44±12.84	-13.66±12.43	-59.77**±14.51	
j	-38.33**±11.74	-30.66**±10.95	7.33±12.58	-34.66*±14.98	
l	-52.56*±22.87	48.77*±24.27	-47.66 ±26.30	82.44**±29.36	
Type of epistasis	Duplicate	Duplicate	-	Duplicate	
<b>Mather and Jinks</b>					
E	17.18	31.06	33.39	26.15	
D	-44.97	-22.18	-44.37	-78.99	
H	30.35	-55.76	-31.61	63.87	
Heritability	-17.49	0.47	1.04	-7.15	
Inbreeding depression	0.00	-5.94	-31.16	-7.11	
Boll no. / plant	Cross	Cross I (GCH 3 x HS 6)	Cross II (GCH 3 x RST 9)	Cross III (H 1353 x HS 6)	Cross IV (H 1353 x RST 9)
	Parameter	Estimates ± SE	Estimates ± SE	Estimates ± SE	Estimates ± SE
<b>Scaling test</b>					
A	4.40 ± 3.60	4.73±6.96	6.60±4.30	-2.26±5.62	
B	-20.40** ± 7.46	-1.00±5.74	2.93±4.28	-4.80±5.36	
C	-36.74±29.84	12.20±8.78	-88.26±101.98	-110.28±102.85	
D	10.37± 15.19	-4.23±3.51	48.90±50.99	51.61±51.37	
<b>Joint scaling test( three parameter model)</b>					
m	19.66**±1.09	18.75**±1.22	22.22**±1.09	23.53**±1.66	
d	-0.28±1.07	0.90± 1.18	-0.13±1.04	0.95±1.52	
h	-0.38±2.24	7.07**±2.60	-0.94±2.24	-0.78±3.27	
$\chi^2$ (df=3)	11.80**	4.51	3.28	1.89	
<b>Six parameter model</b>					
m	28.953**±7.36	21.73**±0.63	45.03±25.46	49.62±25.65	
d	-10.73**±3.70	-3.16±3.27	-1.30±2.36	-2.03±2.67	
h	-21.61± 61	19.56**±8.18	- 97.46±102.01	-105.18±102.81	
i	-20.74±30.39	8.46±7.02	-97.80±101.98	-103.22±102.75	
j	-24.80**±7.80	-5.73±7.03	-3.66±5.26	-2.53±6.56	
l	4.74±33.31	-4.73±15.77	107.33±102.42	96.15±103.40	
Type of epistasis	-	-	-	-	
<b>Mather and Jinks</b>					
E	3.34	7.54	3.32	7.73	
D	81.20	-20.62	1.286	1.30	
H	41.43	12.70	9.07	-2.41	
Heritability	0.64	54.01	0.99	0.99	
Inbreeding depression	-9.62	8.60	-21.90	-28.55	
df = degrees of freedom, calculated as the number of generations minus the number of estimated genetic parameters (*,**) indicates that the value was significant by the t-test at the 5% and 1% probability level respectively					

### ***Plant Height (cm)***

The significant values of scale A, B, C, D in all most all the four crosses presented in the Table 2 indicated that the non-allelic interactions were present and additive-dominance model was not fit for this trait. It was also substantiated by significant  $\chi^2$  value which suggested that three parameter model was not sufficient. The additive-dominance effects were found significant in joint scaling test for this trait.

### ***Number of Bolls / Plant***

The individual scaling test showed the adequacy of additive-dominance model in all the crosses except in cross I, presented in the Table 2 and hence indicated presence of epistasis for this trait. The joint scaling test showed the inadequacy of three parameter model which was also indicated by significant  $\chi^2$  values in cross I for this trait whereas the individual scaling test showed the adequacy of additive-dominance model in cross II, III and IV. It was also substantiated by non-significant  $\chi^2$  value of joint scaling which suggested that three parameter model was sufficient for cross II, III and IV while in cross I three parameter models was not sufficient.

### ***Ginning Out turn (%)***

The individual scaling test showed the fitness of additive-dominance model in all the four crosses for ginning out turn. It was also substantiated by non-significant  $\chi^2$  value which suggested that three parameter model was sufficient for all the four crosses.

### ***Six Parameter Model***

It was evident that the additive-dominance model was inadequate in some cases. Therefore, digenic epistatic model as described by Jinks and Jones, 1958 [9] was applied to all the cases where the additive-dominance model was inadequate to estimate epistatic effects *i.e.* additive x additive (i), additive x dominance (j) and dominance x dominance (l) effects. These estimates along with their standard errors in the four crosses are presented in Table 2.

## **Discussion**

In the present investigation analysis of variance revealed that mean squares due to generations were significant for plant height, number of bolls / plant and ginning out turn in all of the four crosses. Traits like days to flower and number of bolls / plant also directly contributed toward economic yield of seed cotton [10] and Abdullah *et al.* (2016) [11] also reported that the analysis of variance showed that significant differences existed among the genotypes studied. Similarly, Baloch *et al.* (2016) [12] studied analysis of variances which revealed that significant differences ( $P \leq 0.05$ ) existed among the varieties for all the studied traits such as plant height (cm), bolls / plant, ginning out turn (GOT %) and seed index (g) and depicted the availability of substantial genetic variability among the genotypes.

In the present investigation additive gene effect was found significant for number of bolls per plant. The estimation of gene effects revealed the presence of significant additive gene effect for boll number per plant [13]. Genetic analysis in an inter varietal cross (H 777 x Tamcot SP 37H) of upland cotton disclosed that all the three digenic interactions were significant for boll number [14] and in our study 'j' type of interaction was found as significant for no. of bolls /plant.

Similarly, Mert *et al.* (2003) [15] revealed that additive, dominance and epistatic gene effects were found responsible for the inheritance of boll number per plant and ginning out turn. Ali *et al.* (2009) [16] found additive component fit for number of bolls, ginning out turn and plant height and in our study dominance component was found fit for plant height and additive component for number of bolls/plant. More role of additive genetic effects for these parameters also reported by Khan *et al.* (2003) [17]; Iqbal *et al.* (2003) [18]; Haq and Azhar (2004) [19]; Ali and Khan (2007) [2] and additive (d), additive x additive (i) genetic effects for days to flower, plant height and no. of bolls/ plant were also found in our study.

## **Conclusion**

Analysis of variance revealed that mean squares due to generations were significant for all of the characters in all crosses. Scaling tests revealed that additive-dominance model was fit for the characters, namely; days to flower, boll number and ginning out turn, The traits with inadequate additive-dominance model were subjected further to six-

parameter model. The magnitude was more for dominance component than additive component in days to flower. All the three types (i, j and l) or either of epistatic effects of them were significant for most of the cases wherein dominance x dominance (l) type of interaction was reported for days to flower and plant height. Duplicate type of interaction was apparent for days to flower and plant height. Genotype H 1353 was found as most promising for having maximum plant height (cm), maximum no. of bolls/plant (gm) and ginning out turn (%).

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