Study of Gene Effects for Seed Cotton Yield and Its Attributing Traits in Upland Cotton (*Gossypium hirsutum* **L.**)

Sonika[*] and R. S. Sangwan

Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar-125004, India
*Corresponding Author E-mail: sonikabhankhar@gmail.com

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 the seed cotton yield and its attributing traits 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 boll weight, seed index and seed cotton yield indicated the presence of non-allelic interactions. Dominance component was significant for the characters such as seed index and seed cotton yield. 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.

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

INTRODUCTION

Cotton is a major fibre crop of global importance and has high commercial value. The word 'cotton' refers to four species in the genus *Gossypium* (*Malvaceae*), namely G. *hirsutum* L., G. *barbadense* L., G. *arboreum* L., and G. *herbaceum* L., that were domesticated independently as sources of textile fiber. Globally, the *Gossypium* genus comprises about 50 species[9]. 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[20]. Cotton is harvested as 'seed cotton' which is then 'ginned' to separate the seed and lint. The long 'lint' fibers are further processed by spinning to produce yarn which is knitted or woven into fabrics. Cotton as a crop as well as commodity plays an important role in the agrarian and industrial activity of the nation and has a unique place in the economy of our country. It is contributing about 65% of the raw material for the textile industry.

Our 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. The knowledge of genetic architecture of the varieties and nature of gene action governing seed cotton yield and its related attributes besides the quality traits is a pre–requisite for deciding the breeding strategy to be followed for desired improvement of any crop. 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[22,5,1]. Every plant breeding program aims at efficient utilization of genetic variation present in the populations. 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 past many scientists conducted studies to identify the inheritance pattern of quantitative /metric traits and revealed additive type of gene action such as the investigations carried out by Khan *et al.*[16], Ahmad *et al.*[4], Nadeem and Azhar[22], Basal and Turgut[8], Ali and Khan[5], and Ali and Awan[6], revealed additive type of gene action with partial dominance in most of the traits under study. Some other scientists studied and revealed the presence of genes showing over-dominance for seed cotton yield[12].

The present study was also conducted to reveal the information about gene effects for seed cotton yield and its attributing traits in upland cotton.

MATERIAL 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.* GCH 3, H 1353, RST 9 and HS 6 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 and 50 plants from F_2 generations and 10 plants from each of backcrosses were taken at random for recording observations on the following economic characters:

1. Boll weight (g): The seed cotton of five well opened bolls taken from a plant was weighed in grams and averaged.

2. Seed index (g): Weight of 100 seeds of each plant was recorded in grams.

3. Lint index (g): The weight of lint produced by 100 seeds in grams was calculated by using the formula given below:

$$Lint\ index = \frac{Seed\ index\ x\ Ginning\ Out\ Turn}{100 - Ginning\ Out\ Turn}$$

4. Seed cotton yield / plant (g): The seed cotton of all the well-opened bolls of a plant were weighed 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[18,13,15].

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 has been presented in Table 1 and described character wise.

Boll weight (g)

Significant variation was observed for this trait among parents (Table 1) in all the crosses except cross I. Boll weight was observed to be maximum in H 1353 (3.10) and minimum for RST 9 (2.59). The mean values of F_1 in all crosses except in cross II (2.20), were mid parent

value. The F_2 mean values were lower than those of F_1s in cross GCH 3 x HS 6 (2.78), GCH 3 x RST 9 (2.10), H 1353 x HS 6 (2.50) and H 1353 x RST 9 (2.61). The backcross generations (BC_1 and BC_2) tended to be equivalent to that of respective recurrent parent of its backcross (Table 1).

Seed index (g)

The significant magnitude of variation for this trait among parents (Table 1) involved in all

the four crosses was relatively high. The parent GCH 3 in cross GCH 3 x HS 6 recorded maximum seed index (6.46) and the parent RST 9 in cross GCH 3 x RST 9 registered minimum seed index value (4.85). The F_1 hybrids were found to be intermediate in almost all of the cases. F_2 means were almost similar to F_1s. The backcross generations BC_1 and BC_2) tended to be towards the parents used as recurrent one (Table 1).

Table 1: **Mean performance for seed cotton yield and its attributing characters in different generations in four crosses of upland cotton**

Character	Cross	P_1	P_2	F_1	F_2	BC_1	BC_2
Boll weight (g)	**GCH 3 x HS 6**	3.06±0.06	2.63± 0.11	2.80 ±0.34	2.78±0.48	3.02 ±0.78	2.96 ±0.88
	GCH 3 x RST 9	2.77±0.21	2.59 ±0.06	2.20± 0.33	2.10 ±0.53	2.71±0.69	2.67 ±0.76
	H 1353 x HS 6	3.10±0.81	2.70 ±0.42	2.90±0.22	2.50 ±0.47	2.81±0.89	2.73±0.95
	H 1353 x RST 9	2.80±0.97	2.62 ±0.12	2.68 ±0.56	2.61 ±0.53	2.62 ±0.60	2.43 ±0.77
Seed index (g)	**GCH 3 x HS 6**	6.46±0.41	4.97±0.11	5.51±0.26	5.10 ±0.06	5.75 ±0.12	5.40 ±0.13
	GCH 3 x RST 9	6.15±0.36	4.85 ±0.23	5.25 ±0.25	5.14 ±0.12	5.43 ±0.15	5.32±0.16
	H 1353 x HS 6	5.93±0.34	5.31 ±0.20	5.59 ±0.28	5.17 ±0.09	5.52 ±0.17	5.18 ±0.13
	H 1353 x RST 9	6.35±0.40	5.27 ±0.22	5.54 ±0.23	5.50 ±0.13	5.69± 0.14	5.31 ±0.13
Lint index (g)	**GCH 3 x HS 6**	3.76±0.50	2.36±0.23	3.04 ±0.47	2.76 ±0.12	3.18 ±0.23	2.91±0.29
	GCH 3 x RST 9	3.48±0.48	2.11 ±0.25	2.84±0.30	2.72 ±0.14	2.75 ±0.24	2.48±0.27
	H 1353 x HS 6	3.35±0.51	2.34 ±0.24	2.95±0.34	2.56±0.16	3.15± 0.29	2.79±0.33
	H 1353 x RST 9	3.65±0.39	2.39 ±0.25	2.98 ±0.45	2.97 ±0.16	3.06 ±0.27	2.45±0.26
Seed cotton yield / plant (g)	**GCH 3 x HS 6**	59.02 ± 9.53	48.17 ±3.53	61.32 ±10.11	59.26±4.92	61.60 ±5.80	41.19 ± 5.26
	GCH 3x RST 9	57.92± 7.17	50.58 ±3.52	60.66 ± 9.67	45.63±5.03	60.32 ±9.40	52.62 ± 6.22
	H 1353 x HS 6	60.57 ± 9.16	57.87±6.26	61.07± 9.45	55.07 ±6.26	58.43 ±7.61	57.95 ± 9.43
	H 1353 x RST 9	60.10 ± 6.21	57.12± 3.51	63.78 ±9.91	53.81±7.02	59.73 ±9.07	53.04 ±6.20

*Heterosis was over mid-parent in all the characters

Lint index (g)

The parents involved in all the crosses depicted significant magnitude of variation for this trait (Table 1). The GCH 3 in cross GCH 3 x HS 6 had maximum lint index (3.76) whereas RST 9 in cross GCH 3 x RST 9 had minimum lint index (2.11). F_1 hybrid showed the lint index towards the intermediate value for the parents involved. The mean value of F_2 generation was lower in all crosses. The average lint index in the backcross generations (BC_1 and BC_2) tended towards their respective recurrent parents (Table 1).

Seed cotton yield / plant (g)

The parents possessed significant amount of variability for seed cotton yield (Table 1).

Highest mean value for seed cotton yield was recorded in H 1353 for the cross H 1353 x HS 6 (60.57) and lowest mean value was recorded in HS 6 (48.17). The mean value of F_1 in all the four crosses was higher than parental values showing heterotic effect. The mean values of F_2 generation were lower in all the four crosses. The backcross generations (BC_1 and BC_2) means, tended towards the recurrent parent of the crosses (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.

Boll weight (g)

The individual scaling test indicated the presence of epistasis in cross III (Table 2). The joint scaling test also confirmed the inadequacy of three parameter model as χ^2 values were significant in cross III whereas the individual scaling test showed the adequacy of additive dominance model in cross I, II and IV. It was also substantiated by non-significant χ^2 value of joint scaling test which suggested that three parameter model was sufficient for cross I, II and IV while in cross III three parameter models was not sufficient.

Seed index (g)

The individual scaling test indicated the presence of epistasis in all the crosses except cross IV (Table 2) where the additive-dominance model was not adequate. The joint scaling test showed the inadequacy of additive-dominance model for crosses I, II and

III while in cross IV joint scaling test showed the adequacy of three parameter model which was also indicated by non-significant χ^2 values.

Lint index (g)

The individual scaling test indicated that additive-dominance model was adequate for all four crosses.

Seed cotton yield (g)

The scaling test indicated the failure of additive-dominance model in cross II but in other crosses the additive-dominance model was adequate, which was further confirmed by joint scaling test (Table 2).

Six parameter model

It was evident that the additive-dominance model was inadequate in some cases. Therefore, digenic epistatic model as described[15], 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.

Table 2: Estimates of different scaling tests and genetic effects for boll weight, seed index and seed cotton yield in four upland cotton crosses

Boll weight	Cross Parameter	Cross I (GCH 3 x HS 6) Estimates± SE	Cross II (GCH 3 x RST 9) Estimates± SE	Cross III (H 1353 x HS 6) Estimates± SE	Cross IV (H 1353 x RST 9) Estimates± SE
		Scaling test			
	A	-0.060 ±0.286	0.471±0.266	-0.532±0.327	0.053±0.329
	B	- 0.300±0.258	0.325±0.272	-0.308±0.303	-0.654*±0.292
	C	-0.790±0.397	0.393±0.437	0.243±0.447	-0.145±0.509
	D	0.215±0.157	0.202±0.175	-0.542**±0.185	-0.228±0.173
		Joint scaling test (three parameter model)			
	m	3.137**±0.327	3.234**±0.362	1.837**±0.392	2.013**±0.371
	d	0.73±0.89	0.236*±0.093	-0.001±0.133	-0.069±0.131
	h	-0.326±0.913	-1.456±0.950	2.304±1.078	1.726±0.984
	χ^2 (df=3)	**5.14**	**3.80**	**9.07****	**6.40**
		Six parameter model			
	m	2.991**±0.043	2.806**±0.062	2.508**±0.055	2.612**±0.061
	d	-0.47**±0.131	0.163±0.125	0.111±0.148	-0.423**±0.123
	h	-0.256±0.362	-0.257±0.394	0.379±0.417	0.669±0.412

i	-0.430±0.314	-0.403±0.350	1.084**±0.369	0.456±0.347
j	-0.240±0.317	-0.146±0.311	0.224± 0.398	-0.708±0.359
l	0.070±0.658	1.200*±0.663	-1.925*±0.742	-1.057±0.707
Type of epistasis	-	-	-	-

Mather and Jinks

E	0.019	0.020	0.030	0.034
D	-0.031	-0.023	-0.038	-0.023
H	-0.006	-0.016	-0.034	-0.075
Heritability	1.741	1.170	0.919	0.355
Inbreeding depression	-0.110	0.171	-0.292	0.070

Seed index	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

Scaling test

A	0.47±0.31	0.52±0.31	0.06±0.32	0.52±0.31
B	-0.32±0.22	-0.53*±0.27	0.11±0.25	0.19±0.24
C	-0.37±0.42	-1.06*±0.48	-0.80*±0.45	0.40±0.49
D	0.26*±0.12	0.53**±0.19	0.49**±0.16	0.15±0.19

Joint scaling test (three parameter model)

m	5.58**±0.08	5.50**±0.09	5.68**±0.09	5.67**±0.09
d	-0.54**±0.07	-0.41**±0.08	-0.36**±0.08	-0.42**±0.08
h	0.12±0.16	-0.07±0.18	-0.41*±0.18	-0.24±0.18
χ^2 (df=3)	**13.35****	**19.35****	**9.51****	**3.01**

Six parameter model

m	5.70**±0.03	5.64**±0.07	5.59**±0.05	5.58**±0.08
d	0.34**±0.10	0.11±0.13	0.33**±0.12	0.37**±0.11
h	-0.72*±0.32	-1.31**±0.43	-1.43**±0.39	-0.57±0.43
i	-0.52*±0.25	-1.06**±0.38	-0.98**±0.33	-0.30±0.39
j	-0.80**±0.32	-1.05**±0.36	0.04±0.34	-0.32±0.34
l	0.67±0.59	1.05±0.71	1.16 ±0.68	1.01±0.67
Type of epistasis	-	-	-	-

Mather and Jinks

E	0.02	0.02	0.02	0.03
D	-0.01	-0.02	-0.02	-0.01
H	-0.07	-0.04	-0.03	-0.06
Heritability	0.30	0.59	0.68	0.25
Inbreeding depression	-0.19	-0.39	-0.42	-0.03

Seed cotton yield	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

Scaling test

A	9.60±8.20	-16.53±9.61	8.26±9.68	-8.20±8.09

B	-5.06±9.21	-6.20±11.46	2.40±10.00	-16.00±9.24
C	-13.86±11.92	-71.60**±15.70	-4.37±13.90	-27.00*±13.42
D	9.20±5.37	24.43**±7.03	7.52±6.30	1.40±6.64
Joint scaling test (three parameter model)				
m	56.32**±2.30	43.00**±3.36	54.84**±3.07	50.38**±2.43
d	-2.86±2.57	-4.93±4.88	2.96±3.76	-7.63**±2.97
h	-37.73±31.01	-86.66±39.05	-71.85±35.73	11.96±35.20
χ^2 (df=3)	**6.17**	**26.54****	**1.65**	**4.99**
Six parameter model				
m	59.26**±4.92	45.63**±5.03	55.07**±6.26	53.81**±7.02
d	-10.20**±1.41	0.23±5.03	0.03±4.97	-11.53*±4.68
h	-14.80±11.96	-60.53**±15.33	-46.14**±13.86	-9.43±14.12
i	-18.40±10.75	-48.86**±14.06	-15.04± 12.60	-2.80±13.29
j	-14.66±10.49	10.33±14.01	-5.86±12.47	-7.80±11.09
l	22.93±21.84	26.13±25.52	25.71±24.27	-21.40±23.04
Type of epistasis	-	-	-	-
Mather and Jinks				
E	15.81	36.31	25.26	16.45
D	-37.88	-38.58	-41.99	-32.75
H	20.49	-43.95	-2.10	21.93
Heritability	0.73	-16.60	-28.13	-14.26
Inbreeding depression	24.04	0.83	2.23	0.21

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

DISCUSSION

In the present investigation analysis of variance revealed that mean squares due to generations were significant for boll weight, lint index, seed index and seed cotton yield in all of the four crosses. Traits like boll weight directly contributed toward economic yield of seed cotton[2], and Abdullah *et al.*[3], also reported that the analysis of variance showed that significant differences existed among the genotypes studied. Similarly, Baloch *et al.*[7], studied analysis of variances which revealed that significant differences (P ≤ 0.05) existed among the varieties for all the studied traits such as boll weight (g), seed cotton yield / plant (g) and seed index (g) and depicted the availability of substantial genetic variability among the genotypes.

In the present investigation additive x additive gene action was found significant for boll weight which indicated that boll weight character was under the control of additive gene action. These results are in conformity with the results of Girase *et al.*[10], Gittie *et al.*[11] and Rao *et al*[23].

In the present investigation additive and dominance gene effects were found for the seed cotton yield where digenic epistatic model was found as significant and dominance effects were involved in the inheritance of boll weight and 100-seed weight/ seed index. Similarly, Mert *et al.*[19], revealed that additive, dominance and epistatic gene effects were found responsible for the inheritance of seed cotton yield whereas, only dominance effects were involved in the inheritance of boll weight

and 100-seed weight. Additive effects for seed cotton yield and its attributing characters were also reported[17,14]. Seed cotton yield / plant was significantly and positively correlated with boll weight (r = 0.68**), seed index (r = 0.91**) and lint percentage (r = 0.70**)[21].

Ali *et al.*[6], found additive component fit for seed cotton yield and in our study dominance component was found fit for seed cotton yield. More role of additive genetic effects for these parameters also reported by Khan *et al.*[16], Ahmed *et al.*[4]; Haq and Azhar[12], Nadeem and Azhar[22], Basal and Turgut[8], Ali and Khan[5], and additive genetic effects for seed cotton yield and some other characters was 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; boll weight, seed index, lint index and seed cotton yield. The traits with inadequate additive-dominance model were subjected further to six-parameter model. The magnitude was more for dominance component than additive component. All the three types (i, j and 1) 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 boll weight.

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