



Generation Mean Analysis for Yield and Its Component Traits in a Diallel Population of Cotton (*Gossypium hirsutum* L.)

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ABSTRACT

Background: The nature and magnitude of gene action decides the choice of breeding procedure for achieving desired genetic improvement in any crop. It is particularly important to have an idea of gene interactions for getting genetic advance for polygenic traits such as yield and fiber traits in cotton.

Method: The current study was undertaken to investigate the gene action controlling yield and components traits in eight *Gossypium hirsutum* varieties by using means of the six generations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) of 8 x 8 diallel crossing program. The mean of the crosses for the traits in each generation were used for generation mean analysis.

Conclusion: Results revealed that the estimated mean effects (m) were highly significant for all traits, indicating quantitative inheritance of these traits. Out of the seven traits under study five traits showed significance for at least one scaling test. Additive and dominant gene effects were significant for seed cotton yield and number of monopods with larger magnitude of dominance effects than additive ones. Dominance, additive x dominance and dominance x dominance were significant for boll weight, number of monopods, seed cotton yield and seed index. Narrow-sense heritability and genetic advance were found low for most of the traits.

Key words: Generation mean analysis, *Gossypium hirsutum*, Seed cotton yield, Upland cotton.

INTRODUCTION

Cotton (*Gossypium hirsutum* L.) is one of the most important fiber crop all over the world. Cotton is cultivated in tropical and sub-tropical regions of about 80 countries. Despite the introductions of artificial fiber, cotton continues to enjoy its status as most widely used textile fiber in the world due to its natural qualities such as softness, durability and versatility. *G. hirsutum* covers more than 90% of Indian cotton acreage (Verma *et al.*, 2020). 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 across the world have played significant role in improving fiber quality characters which are quantitatively inherited. The details about the nature and magnitude of gene action of 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 yield and its contributory 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). The magnitude of additive as well as nonadditive gene effects for cotton traits have been 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 and Mather (1955) proposed a model partitioning the estimation of additive, dominance and epistasis effects

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from six generations *viz.*, P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 of a cross. Hayman (1958) described the procedure for partitioning of generation mean into 6 parameters *viz.*, mean (m), additive [d], dominance [h], additive x additive [ij], additive x dominance [ji] and dominance x dominance [II] gene effects. 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.

If dominance variance especially over-dominant is predominant, then the hybrid program for commercial purpose may be the appropriate choice. Therefore, the estimation of gene action and the inheritance of the traits especially seed yield is an interesting procedure for the breeders in order to formulate the most efficient breeding method to bring about the maximum improvement of the attribute in question. Both additive and non-additive genetic

effects control seed cotton yield (Kalsy and Garg, (1988); Deshpande and Baig, (2003).

The information of gene action is critical for any breeding program to achieve desirable results. Keeping that in mind the present study was undertaken to understand the gene effects for seed cotton yield and its contributory traits in upland cotton (*G. hirsutum* L.).

MATERIALS AND METHODS

The parental material multiplication and crossing program for this research work was undertaken at ICAR-CICR Regional Research Station, Sirsa. The experimental material was comprised of eight *G. hirsutum* lines viz., RS-2013, RST-9, RS-810, F-1378, F-2164, F-2228, LH-2076 and LH-2108. The details of parental lines, their origin and characteristics are provided in Table 1. These eight parents were crossed in diallel manner with reciprocals to produce 56 F₁ hybrids at ICAR-CICR Regional Research Station, Sirsa during kharif-2015. During Kharif 2016 season, these 56 F₁'s were selfed and backcrossed with their respective parents to obtain the F₂ and backcross (BC₁ and BC₂) generations respectively. Selfed seed was also obtained for all the parents. Thus, six basic generations viz., P₁, P₂, F₁, F₂, BC₁ and BC₂ were developed for all the 56 crosses. In kharif 2017, evaluation of P₁, P₂, F₁, F₂, BC₁ and BC₂ generations was undertaken in Randomized Block Design with 2 replications at three different locations to understand the genetic nature of seed cotton yield and its contributing traits through generation mean analysis. The aggregate numbers of plants studied in different generation were 120 in F₂ generation and 30 plants each in P₁, P₂, F₁, BC₁ and BC₂ generation for all the traits under study. Parental testing (P₁ and P₂) was undertaken with 67.5 x 60 cm² spacing whereas the F₁, F₂, BC₁ and BC₂ populations were tested in 105 x 60 cm² row to row and plant to plant spacings. The recommended package of practices was followed to raise a good crop.

The analysis of generation mean analysis was done by using OP STAT software developed by CCSHAU, Hisar. The mean of across location data from the multilocation trials was used to calculate the scaling test by Hayman and Mather (1955). The significance of scaling tests (A, B, C and D) determines the presence or absence of non-allelic interactions. 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. After confirmation of the presence of epistasis, joint scaling test of six parameter model was applied to estimate the significance of m, [d], [h], [i], [j] and [l]. For the estimation of the gene effects six parameter model developed by Hayman, 1958 was used to get the estimates of (mean (m), additive gene effects (d), dominance gene effects (h) and 3 types of non-allelic gene interactions viz., additive x additive (i), additive x dominance (j) and dominance x dominance (l). The standard error and 't' values for these parameters were calculated in similar manner as done in scaling tests. The data was subjected to analysis of variance (ANOVA) using OPSTAT computer software for all the traits to test the null hypothesis. Simple additive-dominance model approach (Hayman, 1954, 1958) modified by Mather and Jinks (1982) was followed for genetic analysis and for estimation of the components of genetic variation.

RESULTS AND DISCUSSION

The data presented in Table 2 revealed the mean performance of the six generations and variance of mean advanced from the diallel crosses of cotton for the traits in view. The trait data used to calculate the scaling test by Hayman and Mather (1955) and six parameters of generation mean analysis were calculated using Hayman (1958) approach. Out of seven traits under study six traits showed significance for at least one of the scales except for boll weight, where scales were not significant. For Ginning Out-turn (GOT) only scale B was found significant whereas for seed cotton yield and plant height all the four scales were found significant. However, the significance of any one of the scales reveals the presence of non-allelic interactions. Values for scaling tests and gene action are provided in Table 3.

For the traits where scales are significant, simple additive/dominance model was not enough to explain most the genetic variation for the expression of these traits. This shows that epistatic effects contributed to the inheritance of these traits which might suggest that, the inheritance of these

Table 1: Parental lines, their origin and Characteristics.

Line Code	Origin	Characteristics
RS 2013	Sri Ganganagar, Rajasthan	Average yielder, open plant type with average fiber
RST 9	Sri Ganganagar, Rajasthan	Average yielder, spreading type plant, high GOT, poor fiber
RS 810	Sri Ganganagar, Rajasthan	Poor yielder, Short and Erect Plant type, below average fiber
F 1378	Faridkot, Punjab	Good yield potential, Erect Plant Type, Good fiber
F 2164	Faridkot, Punjab	High yields, Tall plant type and good fiber
F 2228	Faridkot, Punjab	Good yields, open and tall plant type with superior fiber
LH 2076	Ludhiana, Punjab	Poor yielder, open plant type and superior fiber
LH 2108	Ludhiana, Punjab	Good yielder, high GOT, medium tall with average fiber

traits is complex and polygenic (Warnock *et al.*, 1998). On the other side, the insignificance of all scales for the excepted trait mentioned indicates that a simple additive-dominance model was adequate for estimating the genetic components of variance of these traits. This indicates that, selection could be practiced effectively in F_2 generation for improving these traits. However, for boll size- scales are non-significant, but

the dominance (h) component of gene action came out as highly significant, suggesting the importance of hybrid breeding for exploitation genetic advance. For monopods- Scale A and D are significant suggesting the presence of additive x dominance and dominance x dominance epistatic effect. For number of sympods- A, B and C scales were significant showing the presence of additive x dominance

Table 2: Performance of six generations with respect to mean and variance for yield and related traits.

Traits	Statistics	P ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂
Boll Size	Means	2.41	2	2.54	2.255	2.4	2.37
	Variance	0.032	0.069	0.038	0.098	0.033	0.027
	Stand. Error	±0.08	±0.117	±0.087	±0.07	±0.082	±0.073
No. of Monopodia	Means	3.59	2.44	2.38	2.895	2.03	2.71
	Variance	0.841	0.22	0.297	0.622	0.447	0.35
	Stand. Error	±0.41	±0.21	±0.244	±0.176	±0.299	±0.265
No. of Sympods	Means	11.32	10.93	11.58	14.03	14.1	14.75
	Variance	0.924	1.753	2.486	3.331	1.122	1.214
	Stand. Error	±0.43	±0.592	±0.705	±0.408	±0.474	±0.493
Plant Height	Means	88.69	100.34	116.24	135.935	129.76	131.29
	Variance	225.652	323.907	50.663	43.251	46.307	33.245
	Stand. Error	±6.718	±8.049	±3.183	±1.471	±3.043	±2.579
Seed Cotton Yield	Means	0.049	0.043	0.127	0.066	0.067	0.119
	Variance	0.002	0.003	0.012	0.016	0.004	0.008
	Stand. Error	±0.004	±0.008	±0.005	±0.003	±0.003	±0.005
Seed Index	Means	8.03	6.62	7.22	7.195	7.95	7.56
	Variance	0.118	0.142	0.642	0.387	0.634	0.438
	Stand. Error	±0.154	±0.168	±0.358	±0.139	±0.356	±0.296
Ginning Out-turn	Means	30.23	29.42	33.38	31.383	32.03	29.66
	Variance	1.856	1.428	7.031	3.335	6.727	6.087
	Stand. Error	±0.609	±0.534	±1.186	±0.408	±1.16	±1.103

Table 3: Estimate of scaling test and type of gene action for the seven traits under discussion.

Traits	Statistic	A	B	C	D	M	D	H	i	j	l
Boll Size	Estimate	0.15	-0.2	0.47	-0.26	2.255**	0.03	0.855**	0.52*	-0.35	-0.57
	Stand. Error	±0.143	±0.146	±0.254	±0.126	±0.049	±0.078	±0.264	±0.251	±0.185	±0.401
No. of Monopods	Estimate	1.91**	-0.6	-0.79	1.05**	2.895**	-0.68*	-2.735**	-2.1**	-2.51**	3.41*
	Stand. Error	±0.541	±0.438	±0.688	±0.377	±0.125	±0.282	±0.79	±0.753	±0.652	±1.322
No. of Sympods	Estimate	-5.3**	-6.99**	-10.71**	-0.79	14.03**	-0.65	2.035	1.58	-1.69	-13.87**
	Stand. Error	±0.889	±0.954	±1.611	±0.753	±0.289	±0.483	±1.607	±1.506	±1.096	±2.516
Plant Height	Estimate	-54.59**	-46**	-122.23**	10.82**	135.93**	-1.53	0.085	-21.64**	8.59	-78.95**
	Stand. Error	±6.794	±7.124	±9.619	±3.504	±1.04	±2.821	±8.242	±7.009	±9.315	±14.826
Seed Cotton Yield	Estimate	0.042**	-0.068**	0.082**	-0.054**	0.066**	-0.051**	0.189**	0.108**	-0.109**	-0.134**
	Stand. Error	±0.006	±0.01	±0.012	±0.006	±0.002	±0.004	±0.012	±0.012	±0.011	±0.021
Seed Index	Estimate	-0.65	-1.28*	0.31	-1.12**	7.195**	0.39	2.135*	2.24**	-0.63	-4.17**
	Stand. Error	±0.574	±0.504	±0.661	±0.382	±0.098	±0.327	±0.809	±0.764	±0.674	±1.467
Ginning Out-turn	Estimate	-0.45	3.48*	0.88	1.075	31.383**	2.37*	1.405	-2.15	3.93	5.18
	Stand. Error	±1.892	±1.811	±2.115	±1.271	±0.289	±1.132	±2.692	±2.542	±2.335	±4.998

Note: */** gives the significance at 0.05 and 0.01 percent level.

Abbreviations-

A, B, C and D stands for scaling test- A, B, C and D

m = (mean); d = (additive effect); h = (dominance effect);

i, j, k = (additive x additive), (additive x dominance) and (dominance x dominance) epistatic effects.

Table 4: Heterosis, Inbreeding depression and Potence Ratio for studied traits.

Traits	Heterosis	Inbreeding Depression	Inbreeding Effect (%)	Potence Ration (h1) in F ₁	Potence Ration (h2) in F ₂	No. of Effective genes
Boll Size	0.13	0.285	11.22	1.634	0.488	0.376
No. of Monopodia	-0.06	-0.515	-21.639	-1.104	-0.417	2.962
No. of Sympods	0.26*	-2.45	-21.157	2.333	29.795	0.024
Plant Height	15.9**	-19.695	-16.943	-3.73	-14.221	-39.859
Seed Cotton Yield	0.078**	0.061	48.013	24.606	12.227	27.808
Seed Index	0.6	0.025	0.346	-0.149	-0.369	-3.23
Ginning Out-turn	3.15	1.997	5.984	8.778	7.691	-0.532

Note: */** gives the significance at 0.05 and 0.01 percent level.

type of interaction. Plant height- all the four Scales were significant at 0.01% level of significance which suggests the presence of high epistatic effect. Seed cotton yield also showed the significance for all the Scales with all the epistatic interaction also showing significance showing the complexity of the inheritance of the trait. Seed Index- scales B and D are significant whereas for Ginning out-turn scale B was found significant. The estimated mean effect (m) was found to be highly significant for all studied traits in all crosses, indicated that these traits were quantitatively inherited. From the obtained results (Table 3), it could be detected that, additive [d] gene effect was significant for ginning out turn and dominant [h] gene effects were highly significant for boll size, number of monopods, seed cotton yield and seed index, indicating that both additive and dominant inheritance are present for these traits, which suggests that 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 Esmail (2007), El Refaey and Razek (2013) and Srinivasan *et al.* (2013). It could be observed that dominance effects are several times larger than additive one and this might indicate that dominance gene effects play the major role in controlling the genetic variation of most studied traits. These results are in the same trend with those reported by Abd El-Haleem *et al.* (2010) and Karademir and Gencer (2010).

For the number of monopods and ginning out-turn the additive effects are larger than non-additive ones, it is suggested that selection in early segregating generations would be effective for these traits. Similar conclusions were drawn by Srinivasan *et al.* (2013). The non-additive portion are larger in magnitude than additive ones for most of the traits under study which indicated that the improvement of the characters need intensive selection through later generation. These conclusions are in the same line with those found by Dhillon and Singh (1980), Lin and Zhao (1988), Mert *et al.* (2003), Murtaza (2005) and Srinivas and Bhadru (2015).

Apart from the magnitude of dominance effect [h] its sign also plays important role. Positive sign of [h] suggests its enhancing effects on the performance of traits. The negative values observed either for main effects; [d] and [h] or the non-allelic interactions; [i], [j] and [l], these might

indicate that, the alleles responsible for less values traits were over dominant over the alleles controlling high value. However, it could be detected that the effects of additive and dominant genes were in the opposite direction, where its signs were not similar. This was true for number of sympods, plant height and seed cotton yield whereas for all other traits as boll size, number of monopods, seed index and ginning out-turn, the effect of additive and dominant were in the same direction.

For all the studied traits, it could be observed that the signs of dominance [h] and dominance x dominance [l] gene effects were opposite, except for only one trait ginning out-turn suggesting the presence of duplicate type of non-allelic interaction in these traits.

The signs of dominance [h] were similar to the [i] type of epistasis, for boll size, number of monopodia, number of sympods, seed cotton yield and seed index. This show the chances of the presence of complementary type of gene interaction in these crosses whereas the sign of [h] and [i] were not similar for plant height and ginning out-turn suggesting that no complementary type of interaction was present in the genetic control of these two traits.

The dominance [h], additive x dominance [j] and dominance x dominance [l] which referred as non-additive genetic variance were significant for number of monopodia per plant and seed cotton yield. This would indicate that, these traits were greatly affected by dominance as main effect and their non-allelic interactions as epistatic effects. These results are in good agreement with those reported by Bhardwaj and Kapoor (1998), Esmail *et al.* (1999), El-Disouqi and Ziena (2001), Abdul-Hafeez *et al.* (2007) and Abd El-Haleem *et al.* (2010). However, when epistatic effects were significant for a trait, the possibility of obtaining desirable segregates through inter-mating in early segregations by breaking undesirable linkage could be desirable or it is suggested to adopt recurrent selection for handling the above crosses for rapid improvement. Abo El-Zahab and Amein (2000), Dong *et al.* (2006), Hendawy *et al.* (2009) and EL-Refaeey and El-Razek (2013) have previously given the same conclusion for such crosses.

Heterosis over mid-parent, inbreeding depression, potence ratio (F₁ and F₂) and number of effective genes for all the traits under study are presented in Table 4. Significant

heterotic effects relative to mid-parent was detected in number for sympods, Plant height and seed cotton yield whereas heterotic effects were non-significant for boll size, number of monopods, seed index and ginning out-turn. However, if we look at the potence ratio values, they indicate over-dominant effects for most of the traits under study except for seed index which was a case of partial dominance.

Potence ratio values for F_2 generation reflected the similar trend as in heterosis where overdominance was observed for number of sympods, plant height, seed cotton yield and ginning out-turn and partial dominance effects were found for boll size, number of monopodia and seed index. The low values of inbreeding depressions indicate the less reduction in the performance (mean) of F_2 generation due to the direct effect of homozygosity; this low reduction might be attributed to the low sensitivity of the present materials to the inbreeding processes. If we compare the inbreeding values for our traits in discussion boll weight, seed cotton yield, seed index and ginning out turn are showing some inbreeding depression apart from these all other traits show low inbreeding depression. Abdalla (2007) and EL-Refaey and El-Razek (2013) reported that cotton has a relatively low inbreeding depression.

CONCLUSION

From this investigation it could be concluded that (1) dominance gene effects play the major role in controlling the genetic variance of yield and most of its components. This suggests the selection of high yielding genotypes need to be postponed till later generations in order to diminish the dominance effect (2) heterosis over mid parent were significant for major traits under study i.e. number of sympods, plant height and seed cotton yield. This indicated the importance of F_1 hybrids to exploit the genetic gain in commercial crop. (3) The inbreeding depression values indicated the low reduction in mean for F_2 generation. Low inbreeding depression provides freedom to breeders to develop highly pure lines by going for prolonged selfings cycles. (4) Opposite sign of additive and dominance variance components indicates low narrow sense heritability and genetic advance for the traits under study. From the present study, it could be concluded that dominance and epistatic gene effects played major role in controlling the genetic variance in most of the studied traits.

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