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

R.K. Giri\(^1\), S.K. Verma\(^2\), Jaya Parkash Yadav\(^1\)

**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, 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 from six generations *viz.*, \(P_1\), \(P_2\), \(F_1\), \(F_2\), BC, 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 \(\times\) additive \([l]\), additive \(\times\) dominance \([j]\) and dominance \(\times\) dominance \([l]\) 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...
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 with 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 and 8 parental combinations 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 generations 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) 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 |
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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 F2 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 | P1 | P2 | F1 | F2 | BC1 | BC2 |
|--------|------------|----|----|----|----|-----|-----|
| 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 Sympos | Means | 11.32 | 10.93 | 11.58 | 14.03 | 14.1 | 14.75 |
|         | Variance | 9.24 | 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 | ±6.718 | ±8.049 | ±3.183 | ±1.471 | ±3.043 | ±2.579 |
|         | Seed Cotton Yield | Means | 0.049 | 0.043 | 0.127 | 0.048 | 0.047 | 0.049 |
|         | 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 | 3.41 | 1.91** | -0.6 | -0.79 | 1.05** | 2.895** |
|         | Stand. Error | ±0.541 | ±0.438 | ±0.688 | ±0.377 | ±0.125 | ±0.282 |

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 Sympos | 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** | 0.199** | 0.108** | -0.109** | -0.134** |
|         | Stand. Error | ±0.006 | ±0.01 | ±0.012 | ±0.002 | ±0.004 | ±0.012 | ±0.012 | ±0.001 | ±0.002 | ±0.002 |
| 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, l = (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 F1 | Potence Ration (h2) in F2 | 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 Symmonds      | 0.26*     | -2.45                 | -21.157               | 2.333                     | 29.795                    | -16.943                |
| 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 ** gives the significance at 0.01 percent level.

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 trend with those reported by Abd El-Haleem et al. (2010) and Karademir and Gencer (2010).

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

The dominance [h] were similar to the [i] type of epistasis, for boll size, number of monopods, 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 Ziema (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-Rafaey 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 monopodidia 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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