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## Research Article

### Generation mean analysis study for qualitative and quantitative traits in cotton (*Gossypium hirsutum* L.)

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#### Abstract

Gene effects for six quantitative and two quality traits were estimated from two upland cotton crosses through generation mean analysis from 6 generations ( $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$ , and  $BC_2$ ). Results revealed that the dominant gene action was observed in the majority of the traits. The traits, plant height, number of sympodial branches per plant, number of bolls per plant, seed cotton yield per plant, ginning percentage and micronaire value possessed opposite signs of [h] and [l] indicating the role of duplicate gene action controlling the traits which will pose a hindrance to a plant breeder while attempting selection in long run. Therefore, heterosis breeding would be advantageous and none of the studied traits were found to be controlled by the complementary type of interaction. Epistatic gene interactions also showed a significant role in the inheritance of all characters in one or another cross. Both additive and dominant genetic interactions with inter-allelic interactions should be taken into account for varietal improvement, which is the main breeding objective. Reciprocal recurrent bi-parental mating methods would break the undesirable effects.

**Keywords:** Cotton, gene action, epistasis, fiber quality and generation mean

#### INTRODUCTION

Cotton, also called “White gold”, is one of the most important cash crops. Cotton is a multipurpose crop used for seed cotton, seed oil, lint purpose, seed meal, hull and linters. Cotton belonging to the family of Malvaceae has old and new world cotton species. *Gossypium hirsutum* belonging to the new world tetraploid cotton holds a significant role in the economy of the country. Around 90% of cotton production is derived from this species. The genetic variation present in the population could be identified from the genetic architecture of quantitative traits as suggested by Paramjithsingh *et al.* (2010).

All crop enhancement program relies on the choice of breeding procedures which depends upon the nature and type of gene interaction present in the population as suggested by Naghera *et al.* (2021). According to Giri *et al.* (2020) for polygenic traits like yield and fibre quality, the information on gene interactions should be known for planning breeding activities. Generation mean analysis helps to identify the nature of gene action governing each trait. In this study, six parameter model was utilized for the population involving parents,  $F_1$ ,  $F_2$ ,  $B_1$  and  $B_2$  generations of upland cotton.

## MATERIALS AND METHODS

The experiment was carried out during Summer, 2021 at the Department of Cotton, Tamil Nadu Agricultural University, Coimbatore by using  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $B_1$  and  $B_2$  generations of each of the two upland crosses viz., MCU 5 × KC 3 and CO 14 KC 3. The genotypes were raised in Randomized Block Design with three replications. Observations were recorded on the single plant basis for plant height, number of bolls per plant, number of sympodial branches per plant, seed cotton yield per plant (g), boll weight (g), ginning outturn (g), upper half mean length (mm) and micronaire value ( $\mu$ /inch). Hayman Jinks and Jones (1958) created the notion of generation mean analysis, used to calculate genetic components of variance by including . Parents,  $F_1$ ,  $F_2$ ,  $B_1$  and  $B_2$  The scaling test is used to determine if an additive dominance model is enough or whether there is epistasis. Four alternative measures were developed by Hayman and Mather (1955) for testing the presence and absence of epistasis. Their variances were calculated to test the significance of these four tests. The significance of A, B, C and D was determined by comparing the calculated and table 't' values. The significance of any of the above scales indicates the presence of epistasis or inadequacy of the additive dominance model. The TNAU STAT software was used for this analysis of various gene interactions (m, d, h, i, j and l).

## RESULTS AND DISCUSSION

To understand the gene action for different quantitative and fibre quality traits and to evolve a breeding strategy for the improvement of particular trait, the generation mean analysis was carried out. The generation means analysis which is the first-order biometrical technique was used for partitioning of mean into various genetic components. The result of the joint scaling test, scaling test and gene action for quantitative and qualitative traits are furnished in **Tables 1 and 2**.

Estimation of genetic parameter and *per se* performance of MCU 5 X KC 3: From the estimation of genetic parameter and *per se* performance of MCU 5 X KC 3, the plant height had significance for C and D scales. All types of gene actions were found to be significance for plant height except for (d) and (j). The significant and opposite sign in dominance and dominance × dominance gene had the presence of duplicate gene interaction. Plant height was higher in the female parent MCU 5 (92.20), when compared to the male parent KC 3 (86.60).  $F_1$  generation of the cross recorded highest plant height (93.40) to the parents. The  $B_1$  and  $B_2$  generation of the cross showed mean plant height of 90.98 cm and 93.98 cm respectively. Number of sympodial branches per plant was significant for C and D scales. The mean effects (m), (h), (i), (j) and (l) gene actions showed significance for this trait. The effect (h) and (l) had significant opposite signs indicating the duplicate gene action. Female parent MCU 5 (25.60) had higher number of sympodial branches

per plant than the male parent KC 3 (21.20). The  $F_1$  had a mean value of 29.20 higher than the parents. The generation  $B_1$  (25.91) and  $B_2$  (26.42) had mean values of the number of sympodial branches per plant higher than the parents. The estimate of the scaling test revealed that the scales B, C and D were significant for the trait number of bolls per plant. The (h), (i), (j) and (l) gene interactions exhibited significance for the trait number of bolls per plant. The duplicate gene interaction was expressed because there was a significant and opposite sign recorded in (h) and (l). The trait number of bolls per plant was found to be higher in female (29.60) when compared to male parent KC 3 (22.60). The  $F_1$  had higher mean number of bolls per plant (31.00) than parents. However, the decreased mean effects were observed among  $F_2$  generation (22.35) than parents.  $B_1$  (29.67) and  $B_2$  (30.02) had expressed higher than the male parent KC 3. Epistatic gene interaction was observed in this cross because of the presence of significance in D scale for the trait boll weight. The dominance and additive × additive effects were significant for this trait. The trait boll weight exhibited high mean in male parent KC 3 (4.24 g) and low in female parent MCU 5 (4.16 g). The significance of all the scales expressed the presence of inter-allelic gene action for seed cotton yield per plant. The gene action viz., dominance, additive × additive, additive × dominance and dominance × dominance genetic components showed significance for this trait. Presence of epistatic gene action was confirmed with the significance and opposite sign of (h) and (l). The seed cotton yield per plant has registered the ranged from 97.30 g to 120.71 g. The male parent KC 3 (89.40 g) registered lower seed cotton yield per plant than MCU 5 (101.80). The  $F_1$  generation has recorded lower seed cotton yield per plant (97.30 g) than parents. The generations  $B_1$  (120.46 g) and  $B_2$  (120.71 g) recorded the higher seed cotton yield per plant than other generations. The presence of inter-allelic gene action is due to the significant of scaling test in both B and C for the trait ginning outturn. The additive × dominance gene effect showed significance for this trait. Ginning outturn was higher in the female parent MCU 5 (36.06%), when compare to male parent KC 3 (31.71%). The  $F_1$  generation of the cross has recorded higher ginning outturn (37.03%) than  $F_2$ ,  $B_1$  and  $B_2$ .

The assessment of scaling test indicated the presence of epistatic gene action for the trait upper half mean length. Among the different scales, B alone registered significance. The gene action viz., (h) and (j) expressed significance for this trait. Among the parents and crosses, male showed higher upper half mean length (31.78 mm). The  $F_2$  registered higher upper half mean length (30.33 mm) among the filial generations.  $B_1$  and  $B_2$  had expressed 30.17 mm and 29.44 mm respectively for upper half mean length. The significance of A, B and C scale expressed the presence of epistatic action in this cross for micronaire value. Dominance and dominance × dominance components were significant in this trait.

Table 1. Estimation of *per se* performance, scaling test and gene effects of two crosses for the quantitative traits

GENERATION	Plant height (cm)		Number of sympodial branches per plant (nos.)	
	MCU 5 × KC 3	CO14 × KC 3	MCU 5 × KC 3	CO 14 × KC 3
P <sub>1</sub>	92.20±1.96	96.60±1.33	25.60±1.21	24.40±1.03
P <sub>2</sub>	86.60±1.89	86.60±1.89	21.20±1.39	21.20±1.39
F <sub>1</sub>	93.40±0.88	94.30±2.36	29.20±1.20	28.70±1.03
F <sub>2</sub>	102.25±1.10	96.12±1.13	17.48±0.37	14.88±0.25
B <sub>1</sub>	90.98±2.25	98.53±2.10	25.91±0.53	27.09±0.68
B <sub>2</sub>	93.98±2.17	97.89±2.14	26.42±0.60	26.73±0.71
<b>SCALES</b>				
A	-3.64±4.99	6.17±5.00	-2.98±2.00	1.08±1.99
B	7.96±4.81	14.88**±5.24	2.44±2.20	3.57±2.25
C	43.39**±5.48	12.69±6.94	-35.27**±3.37	-43.46**±2.87
D	19.54**±3.83	-4.18±3.76	-17.37**±1.09	-24.05**±1.10
<b>Genetic effects</b>				
m	102.25**±1.10	96.12**±1.13	17.48**±0.37	14.88**±0.25
d	-3.00±3.13	0.64±3.00	-0.51±0.80	0.36±0.98
h	-35.08**±7.82	11.05*±7.96	40.53**±2.66	54.01**±2.58
i	-39.08**±7.65	8.35±7.51	37.73**±2.19	48.11**±2.20
j	-5.80±3.41	-4.36±3.21	-2.71*±1.22	-1.24±1.31
l	34.77*±13.65	-29.40*±13.86	-34.20**±4.66	-52.75**±4.87
h/d	-2.67	-3.63	-0.61	-1.43
Type of epistasis	Duplicate	-	Duplicate	Duplicate

Table 1. Contd.

GENERATION	Number of bolls per plant (nos.)		Boll weight (g)	
	MCU 5 × KC 3	CO 14 × KC 3	MCU 5 × KC 3	CO 14 × KC 3
P <sub>1</sub>	29.60±1.4	4.16±0.203	4.16±0.203	4.08±0.21
P <sub>2</sub>	22.60±1.36	4.24±0.10	4.24±0.10	4.24±0.10
F <sub>1</sub>	31.00±1.28	4.00±0.18	4.00±0.18	3.80±0.13
F <sub>2</sub>	22.35±0.50	4.26±0.04	4.26±0.04	3.88±0.05
B <sub>1</sub>	29.67±0.52	4.05±0.08	4.05±0.08	3.98±0.08
B <sub>2</sub>	30.02±0.64	4.04±0.08	4.04±0.08	4.07±0.09
<b>SCALES</b>				
A	-1.27±2.66	-0.07±0.33	-0.07±0.33	0.07±0.29
B	6.44**±2.27	-0.17±0.27	-0.17±0.27	0.09±0.24
C	-24.79**±3.79	0.62±0.46	0.62±0.46	-0.41±0.41
D	-14.98**±1.29	0.43**±0.14	0.43**±0.14	-0.28*±0.15
<b>Genetic effects</b>				
m	22.35**±0.50	4.26**±0.04	4.26**±0.04	3.88**±0.05
d	-0.36±0.83	0.01±0.12	0.01±0.12	-0.10±0.12
h	34.87**±3.04	-1.07**±0.35	-1.07**±0.35	0.20±0.35
i	29.97**±2.58	-0.86**±0.28	-0.86**±0.28	0.57*±0.30
j	-3.86**±1.28	0.05±0.14	0.05±0.14	-0.01±0.17
l	-35.14**±5.03	1.11±0.66	1.11±0.66	-0.73±0.62
h/d	-0.92	-1.49	-1.49	4.76
Type of epistasis	Duplicate	-	-	-

Table 1. Contd..

GENERATION	Seed cotton yield per plant (g)		Ginning out turn (%)	
	MCU 5 × KC 3	CO14 × KC 3	MCU 5 × KC 3	CO 14 × KC 3
P <sub>1</sub>	101.80±2.06	116.80±1.93	36.06±0.97	37.58±0.89
P <sub>2</sub>	89.40±2.09	89.40±2.09	31.71±0.74	31.71±0.74
F <sub>1</sub>	97.30±2.48	105.50±2.77	37.03±0.72	36.08±0.67
F <sub>2</sub>	89.49±2.43	68.30±1.45	37.02±0.17	35.84±0.18
B <sub>1</sub>	120.46±3.58	100.64±3.33	36.65±0.30	36.28±0.28
B <sub>2</sub>	120.71±3.21	100.96±3.46	36.39±0.28	36.24±0.30
<b>SCALES</b>				
A	41.82**±7.85	-21.01**±7.47	0.20±1.34	-1.10±1.26
B	54.73**±7.20	7.01±7.73	4.03**±1.78	4.70**±1.16
C	-43.83**±11.30	-44.01**±8.50	6.26**±2.00	1.90±1.93
D	-70.19**±6.84	-65.01**±5.60	1.02±0.53	-0.85±0.54
<b>Genetic effects</b>				
m	85.49**±2.43	68.29**±1.44	37.02**±0.17	35.84**±0.18
d	-0.25±4.81	-0.31±4.80	0.26±0.41	0.03±0.41
h	142.07**±13.98	132.41**±11.64	1.11±1.42	3.13*±1.41
i	140.37**±13.67	130.01**±11.21	-2.04±1.06	1.70±1.10
j	-6.45±5.03	-14.01**±5.00	-1.91*±0.73	-2.89**±0.74
l	-236.92**±22.31	-116.01**±21.01	-2.19±2.59	-5.31**±2.54
h/d	0.52	-1.81	-1.40	-0.99
Type of epistasis	Duplicate	Duplicate	-	Duplicate

Table 2. Estimation of *per se* performance, scaling test and gene effects of two crosses for the qualitative traits

GENERATION	Upper half mean length (mm)		Micronaire value (µg/inch)	
	MCU 5 × KC 3	CO 14 × KC 3	MCU 5 × KC 3	CO 14 × KC 3
P <sub>1</sub>	30.67±0.72	30.27±0.42	3.63±0.26	3.20±0.20
P <sub>2</sub>	31.78±0.54	31.78±0.54	3.40±0.24	3.40±0.24
F <sub>1</sub>	29.78±0.96	29.65±0.83	3.91±0.14	3.93±0.23
F <sub>2</sub>	30.33±0.15	28.31±0.22	4.02±0.04	3.99±0.05
B <sub>1</sub>	30.17±0.33	29.49±0.38	4.15±0.07	4.01±0.08
B <sub>2</sub>	29.44±0.35	29.43±0.36	4.10±0.07	4.09±0.07
<b>SCALES</b>				
A	-0.11±1.37	-0.94±1.20	0.76*±0.33	0.89*±0.34
B	-2.68**±1.31	-2.97*±1.23	0.89**±0.32	0.85*±0.36
C	-0.68±2.20	-8.11**±2.02	1.21*±0.49	1.49*±0.58
D	1.05±0.57	-2.29**±0.69	-0.22±0.14	-0.13±0.14
<b>Genetic effects</b>				
m	30.33**±0.15	28.31**±0.22	4.02**±0.04	3.99**±0.04
d	0.73±0.49	0.36±0.52	0.05±0.11	-0.07±0.11
h	-3.55*±1.56	3.22±1.66	0.83*±0.36	0.90*±0.40
i	-2.11±1.14	4.59**±1.39	0.44±0.27	0.26±0.29
j	1.29±0.66	0.81±0.63	-0.77±0.21	0.02±0.19
l	4.90±2.93	-0.79±2.92	-2.08**±0.65	-2.02**±0.74
h/d	-1.22	1.21	-1.33	-1.89
Type of epistasis	-	-	Duplicate	Duplicate

The female parent MCU 5 (3.63 µg/inch) recorded higher mean value than the male parent KC 3 (3.40 µg/inch). The  $F_1$  recorded higher micronaire value (31.91 µg/inch) than both the parents. The mean value of  $B_1$  and  $B_2$  (4.15 µg/inch, 4.10 µg/inch) were higher than other generations.

Estimation of genetic parameter and *per se* performance of CO 14 X KC 3: In this cross B scale was significant for the trait plant height. Only which indicating dominance x dominance gene action. The mean value of plant height ranged from 94.30 cm ( $F_1$ ) to 96.12 cm ( $F_2$ ). The female parent CO 14 (96.60 cm) recorded high mean value than male parent and  $F_2$ . The scaling test revealed significance of C and D scales for number of sympodial branches per plant. All the types of gene action viz., (m), (h), (i) and (l) expressed as significant except (d) and (j). The dominance and dominance x dominance interaction had opposite sign and significant. This indicates the presence of duplicate gene interaction. The mean value for number of sympodial branches per plant was higher in first filial generation (28.70) than parents and backcrosses. The second filial generation registered less number of sympodial branches per plant (14.88), when compared to parents as well as first filial generation and backcrosses. Inter-allelic gene action expressed because of significance of C and D in scaling test for number of bolls per plant. The dominance and dominance x dominance gene effect recorded significance for this trait. Significant and opposite sign for dominance and dominance x dominance genetic components in the cross indicates the presence of duplicate gene action. The trait, number of bolls per plant exhibited highest mean in  $F_2$  (4.26) then all other generation and parents. Scaling test indicated the presence of epistatic model for the trait, boll weight. Other than (i), both scale and gene action are non-significance. The higher boll weight was showed in male parent KC 3 (4.24 g), when compared to female parent CO 14 (4.08 g).  $F_2$  generation of the cross recorded boll weight (3.88 g). The backcross generations viz.,  $B_1$  and  $B_2$  recorded boll weight of 3.98 g and 4.07 g respectively. The scales A, C and D were significant and indicates the presence of inter-allelic gene action for seed cotton yield per plant. Except (d) all other gene interactions were significant. Significant and opposite sign of (h) and (l) indicated the presence of duplicate gene action. The female parent CO 14 (116.80 g) exhibited higher mean than all other generations. The male parent has recorded low mean value (89.40 g) than female parent.  $F_1$  has registered a higher mean value (105.50) than  $F_2$ ,  $B_1$  and  $B_2$ . B scale alone showed significance depicting the presence of epistatic gene action for ginning out turn. Genetic effects of (m), (h), (j) and (l) showed significance. The significant and opposite signs of (h) and (l) indicated the presence of duplicate gene action. The trait ginning outturn was found to be high in female parent (37.58%) when compared to male parents (31.71%). The range of this trait among all generations was between 31.71% and 37.58%.

The significance of B, C and D scales expressed the presence of epistatic action in this cross for the upper half mean length. Additive, additive x additive and dominance x dominance components were found to be significant for this trait. Among the parents and generations,  $F_2$  showed the lowest upper-half mean length (28.31 mm). The male parent KC 3 registered the highest upper half mean length (31.78 mm) than other populations. For micronaire values A, B and C scales were significant. The components dominance and dominance x dominance gene interaction expressed significant value for this trait and expressed opposite signs indicating duplicate gene action for this trait. The female parent CO 14 (3.20 µg/inch) recorded a lower micronaire value than the male parent KC 3 (3.40 µg/inch). The  $F_1$  (3.93 µg/inch) recorded more micronaire value than both the parents. The mean value of filial generation viz.,  $F_2$  of the crosses registered higher than the parents and lower than  $B_1$  (4.01 µg/inch) and  $B_2$  (4.09 µg/inch) generations.

Out of eight traits studied at least one of the scales (C and D) showed significance except for plant height and ginning out turn in CO 14 x KC 3 and upper half mean length in MCU 5 x KC 3, where the scales were non-significant. However, the significance of any one of the scales indicates the presence of non-allelic gene interaction. Hence simple additive-dominance model was not enough to explain the variation in these traits. Therefore epistatic effects could contribute to the inheritance of these traits. This is by the report suggested by Giri *et al.* (2020).

Both the crosses expressed duplicate gene action for the trait viz., plant height for the cross MCU 5 X KC 3. Similarly, for the cross CO 14 x KC 3 the traits viz., number of sympodial branches per plant for both the cross, number of bolls per plant for both the crosses, seed cotton yield per plant, ginning outturn. However, the trait, micronaire value expressed duplicate gene action for both the crosses both the crosses indicating slowed down progress of selection would be beneficial. Hence heterosis breeding would be advantageous for the improvement of this trait in the respective crosses. This result is by Iqbal *et al.* (2003). Duplicate type of interaction was observed in the majority of the crosses and none of the traits showed the complementary type of interaction as reported by Srinivas *et al.* (2015). Bhatti *et al.* (2006), Refaey and Razeq (2013) and Srinivasan *et al.* (2013) reported duplicate gene interaction for micronaire value.

Dominance gene effect was observed for all traits in the cross MCU 5 x KC 3 except for the trait ginning out turn. Dominance gene effect was observed for all the traits studied in the cross CO 14 x KC 3 except for the trait plant height and boll weight. Recurrent selection and population improvement programs could be followed in the segregating generations when dominance gene effects would have diminished as reported by Kannan *et al.* (2013) and Gawande *et al.* (2016). A

higher magnitude of significant dominance estimate was observed in the majority of the traits, implicating the major role of dominance rather than the additive gene effects in the inheritance of traits. Hence selection of high-yielding genotypes is to be postponed to later generations. These results are in line with the reports by Refaey and Razeq (2013), Komal *et al.* (2014), Naghera *et al.* (2021), Valu *et al.* (2015), Choudhary *et al.* (2017) and AL-Hibbiny *et al.* (2020).

Non-fixable gene effects were observed in both quantitative and qualitative traits taken under study than fixable genes. This result was the result of Thangaraj *et al.* (2020) for fibre quality traits. Dominance effects were found to be greater than additive gene effects and Dominance, additive x dominance and dominance x dominance were significant for seed cotton yield which was similar to the report of Giri *et al.* (2020). Complicated breeding procedures would be required for improving the traits since, (h), (j) and (l) were predominant over (d) and (i). Hence non fixable gene actions were predominant over the fixable genes. This was similar to the finding of Thangaraj *et al.* (2020). However, the presence of non-fixable genetic parameters with the duplicate type of gene action causes delayed improvement in the traits namely, the number of sympodial branches per plant, number of bolls per plant, seed cotton yield per plant and ginning outturn. Hence, selection could be postponed to later generations. These results are in agreement with the conclusions of Kannan *et al.* (2013), Srinivas and Bhadru (2015) and Nand *et al.* (2020).

The results of this study reveal that trait enhancement with high estimates of dominant genes in a particular population affects heterosis breeding. The epistasis types present in a population also affect the breeding techniques. Both additive and dominant genetic interactions with interallelic interactions should be taken into account for varietal improvement, which is the main breeding objective. Reciprocal recurrent selection or bi-parental mating methods would break the undesirable effects.

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