

Inheritance studies on yield contribution on yield contributing traits in *desi* cotton (*Gossypium arboreum* L.)

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ABSTRACT : Generation mean analysis was carried out in three crosses of cotton to find out the gene effects for days to first flower, number of bolls/plant, boll weight (g) and seed cotton yield/plant (g). For most of the traits additive dominance model was inadequate except for boll weight. Additive gene effects were more important for number of bolls/plant and seed cotton yield/plant whereas both additive and dominance effect was significant in other two crosses. Among epistatic interactions, additive x additive appeared to be significant for days to first flower and boll weight (g) but additive x dominance and dominance x dominance gene effects were significant for all the traits except boll weight (g). Predominance of complimentary type of gene effects for seed cotton yield/plant (g) was observed in one cross.

Cotton has a unique place in Indian agriculture as well as in commercial sector. Among the four cultivated species, the *Desi* (*Gossypium arboreum* L.) cotton has its own merits because of its desirable attributes like earliness, drought tolerance, hardiness, adaptability to diverse agro climatic regions and resistance to sucking pests. Proper attention for genetic improvement of *Gossypium arboreum* L. might result higher dividend than upland cotton. For its genetic improvement, the knowledge of gene effects is of immense value in deciding the appropriate breeding approach to be followed.

Studies on inheritance of seed cotton yield and its component traits in cotton (*Gossypium arboreum* L.) are limited. In the present study efforts have been made to find out the gene effects for seed cotton yield and its contributing traits in three crosses of *Gossypium arboreum* L..

The present study comprised six generations (P_1 , P_2 , F_1 , F_2 , B_1 and B_2) of three crosses involving six diverse parents, viz., GMS 11 x P502, GMS 1 x ADDH 7 and GMS 21 x GCD 26 of cotton (*Gossypium arboreum* L.). The experiment was conducted at Research Farm of CCS Haryana Agricultural University, Hisar,

in a complete randomized block design with three replications. The plant density was 100 cm between and 30 cm within rows. The plots consisted of one row of parents (P_1 and P_2) and F_1 , six rows of F_2 , three rows of each of the backcrosses (B_1 and B_2) and the length of each row was 4.8 meters. The data were recorded for the days to first flower, number of bolls/plant, boll weight and seed cotton yield/plant (g), on five random plants, each from F_1 's and parents, 10 plants from each backcrosses and 40 plants from F_2 's in each replication. Generation mean analysis was performed according to Mather and Jinks (1971). Cavalli's (1952) joint scaling test was applied to the test of significance of additive and dominant gene effects. Generation means were analysed using the six parameters model of Jinks and Perkins (1969).

The estimates of gene effects were derived from generation means of all the three crosses, viz., GMS 11 x P502, GMS 1 x ADDH 7 and GMS 21 x GCD 26 for days to first flower, number of bolls/plant, boll weight and seed cotton yield/plant (g), by joint scaling test. The significance value of joint scaling test indicated the inadequacy of additive dominance model and hence six parameter

model was applied. The estimates of the gene effects are presented in Table 1.

1) Days to first flower : The joint scaling test indicated the failure of additive dominance model in all the three crosses. Both additive and dominant gene effects was found to be significant in cross, GMS 11 x P 502 and GMS 1 x ADDH 7 whereas only dominant genetic effects was found to be significant in cross GMS 21 x GCD 26. All the three types of gene interaction *i.e.* additive x additive (i) additive x dominance (j) and dominance x dominance type of epistasis were significant in all the three crosses. Opposite signs of dominant and dominance x dominance effects suggested the presence of duplicate type of epistasis in all the three crosses. These results are in agreement with the findings of Bertini *et al.*, (2001) observed more role of dominant gene effects. Contrary finding *i.e.*, more role of additive effects was reported by Muhammad *et al.*, (2003)

2) Number of bolls per plant : The joint scaling test indicated the failure of additive dominance model in all the crosses *viz.*, GMS 11 x P 502, GMS -1 X ADDH 7 and GMS 21 x GCD 26. Additive gene effect was significant in all crosses, whereas dominant gene effect was non significant in all the crosses indicating preponderance of additive gene effect. Additive x dominance (j) type of epistasis was significant in all the crosses. Dominance x dominance (l) type of epistasis was significant in two crosses namely GMS11 x P502 and GMS 1 x ADDH 7. The result suggested the preponderance of dominance x dominance (l) type of epistasis. Similar results were reported different workers. Bertini *et al.*, (2001) observed as dominance; additive with partial dominance by Muhammad *et al.*, (2003); additive and non additive by Basal and Turgut (2005).

3) Boll weight : The joint scaling test indicated the adequacy of additive dominance model in two crosses *viz.*, GMS 11 x P 502 and GMS 1 x ADDH 7. The joint scaling test also suggested the inadequacy of additive-dominance model in the cross, GMS 21 x GCD 26. Additive gene effect was significant in all the three crosses, whereas dominance gene effect was significant only in two crosses *viz.*, GMS 11 x P 502 and GMS 1 x ADDH 7. Additive x additive type of epistasis was significant in one cross, GMS 21 x GCD 26 in which presence of epistasis was indicated by joint scaling test. These results are in agreement with the findings of Basal and Turgut (2005) and Iyanar *et al.*, (2005) where they reported additive gene action, by Bertini *et al.*, (2001) reported dominant gene action and by Esmail (2007) reported both additive and dominance.

4) Seed cotton yield/plant : The joint scaling test indicated the failure of additive dominance model in all the crosses *viz.*, GMS 11 x P 502, GMS 1 x ADDH 7 and GMS 21 x GCD 26 revealed thereby the presence of epistasis. Hence, six parameter model was applied. Additive gene effect was significant in all the three crosses, whereas dominance gene effect was significant only in one cross, GMS 1 x ADDH 7. The magnitude of additive effect was higher than the dominance gene effect indicating the preponderance of additive gene effect. Additive x dominance epistasis was significant in two crosses *viz.*, GMS 11 x P 502 and GMS 21 x GCD 26, whereas dominance x dominance epistasis was significant in cross, GMS 1 x ADDH 7. Complimentary type of epistasis was significant in cross GMS 1 x ADDH 7. These results are in agreement with the findings of Iyanar *et al.*, (2005) where they reported additive x dominance, additive and dominance gene effects for seed cotton yield in *Gossypium hirsutum* cotton.

Table 1. Estimate of gene effects of generation means on three/six parameters model for yield and its component traits in *Gossypium arboreum* L.

CROSS	m	Gene effects						Type of Epistasis	Joint scaling test (c ²)
		(d)	(h)	(i)	(j)	(l)			
		Days to first flower							
GMS 11 X P 502	70.66±0.18	8.28±0.26*	-18.93±0.96*	-24.25±0.90*	9.11±0.63*	34.5±1.42*	D	1158.92*	
GMS-1 X ADDH 7	76.97±0.29	4.37±0.21*	-33.44±1.31*	-33.11±1.25*	-11.59±0.70*	42.40±1.66*	D	978.124*	
GMS 21 X GCD 26	68.18±0.18	-5.04±0.19	8.85±0.93*	1.95±0.83*	-23.8±0.69*	-11.70±1.38*	D	1344.42	
		Number of bolls/Plant							
GMS 11 X P 502	28.28±0.82	-5.2±0.7*	1.15±3.67	-2.73±3.59	-7.06±1.61*	10.33±4.59*	-	31.59*	
GMS-1 X ADDH 7	26.96±1.01	5.26±0.58*	5.74±4.3	-2.53±4.23	3.08±1.46*	15.75±4.92*	-	55.48*	
GMS 21 X GCD 26	32.95±0.99	-6.16±1.46*	7.94±5.0	0.66±4.93	-6.88±3.11*	13.2±7.27	-	43.88*	
		Boll weight							
GMS 11 X P 502	1.63±0.01	-0.15±0.01*	0.23±0.02*	-	-	-	-	7.1	
GMS-1 X ADDH 7	1.82±0.01	0.13±0.01*	0.35±0.03*	-	-	-	-	5.63	
GMS 21 X GCD 26	2.13±0.03	-0.12±0.03*	-0.26±0.15	-0.33±0.15*	0.04±0.07	0.14±0.2	-	15.81*	
		Seed cotton yield/Plant							
GMS 11 X P 502	48.33±1.83	-7.48±1.58*	6.66±8.09	-8.81±8.01	-18.98±3.36*	26.79±9.97	-	57.47*	
GMS-1 X ADDH 7	51.28±2.31	6.4±1.81*	21.53±10.03*	-3.58±9.94	5.5±3.8	29.23±12.07*	C	40.68*	
GMS 21 X GCD 26	65.24±2.12	-15.8±3.18*	8.97±10.77	-7.04±10.62	-14.46±6.62*	28.31±15.71	-	22.23*	

* significant at 5% level

CONCLUSION

Considering overall trend of various kinds of gene effects, the most suitable breeding plan would be one that mops up the additive gene effects and at the same time maintains appropriate homozygosity also for harnessing the interaction effects. In such cases alternative breeding approach like recurrent selection will be most appropriate which give maximum opportunity for rearrangement of genes and to raise genetic ceiling of the concerned population by accumulating concerned population by accumulating favourable additive genes through inter mating the selects. Further the reciprocal recurrent selection seems to be more effective in utilizing both additive and dominance gene effects for faster genetic improvement of *Desi* (*Gossypium arboreum* L.) cotton.

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