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## Research Article

### Genetic analysis for seed cotton yield and its contributing traits in interspecific crosses of diploid cotton (*G. herbaceum* × *G. arboreum*)

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#### Abstract

Generation mean study was carried out in two interspecific crosses of diploid cotton *i.e.*, GBhv-302 × PA-812 and GBhv-302 × ARBa-1502 using six parameter model. Simple scaling tests along with joint scaling test were carried out to check the sufficiency of additive-dominance model. The estimates of dominant (h) gene action were higher than the additive (d) gene action in one or more characters studied. Among epistasis, additive × additive (i) type of gene action was found to be significant in cross GBhv-302 × PA-812 for sympodia per plant and ginning outturn and in cross GBhv-302 × ARBa-1502 for sympodia per plant, bolls per plant and seed cotton yield per plant. While dominance × dominance (l) type of gene effect contributed significantly in cross GBhv-302 × PA-812 for sympodia per plant and in cross GBhv-302 × ARBa-1502 for sympodia per plant, average boll weight, bolls per plant, average boll weight and seed cotton yield per plant. Duplicate type of epistasis was observed for sympodia per plant in both the crosses, for bolls per plant and seed cotton yield per plant in cross GBhv-302 × ARBa-1502 and for ginning outturn in cross GBhv-302 × PA-812. While complementary type of gene interaction was detected for bolls per plant and seed cotton yield per plant in cross GBhv-302 × PA-812 and for average boll weight and ginning outturn in cross GBhv-302 × ARBa-1502.

#### Key words

Diploid cotton, additive, dominance and epistasis gene actions

## INTRODUCTION

Cotton, known as the white gold, is one of the significant and an important cash crop having tremendous influence on economic and social associations of the world. Cotton is domesticated in both the old and new world having multipurpose utility that provides six basic needs of the humankind *viz.*, seed cotton, lint, oil, seed meal, hull and linters. Moreover, the cultivation of diploid cotton involves low seed cost with low or no cost for plant protection and crop nutrition. Looking to these characteristics of diploid cotton, one will really be interested for cultivation of diploid cotton provided that it yield at least at par with hybrid varieties of tetraploid cotton and having equivalent fibre quality. Though, the inherited potential of diploid

cotton still remains underutilized suggesting use of strong and appropriate breeding procedures for its genetic augmentation to avoid genetic erosion of these species possessing tolerance to both biotic and abiotic stresses. In prevailing situation, diploid cotton can obtain higher prices, so diploid cotton breeding has its own importance. Genetic architecture of quantitative traits helps to make clear the nature and magnitude of genetic variation present in the population. In any crop improvement program, the choice of breeding procedures to be followed directly rely upon the type of gene interaction or effects which are present in the population. To develop pureline, additive gene actions are of prime importance, whereas

dominance and epistasis type of gene effects could be utilize to take advantage of hybrid vigor.

### MATERIALS AND METHODS

The research experiment was conducted during *kharif*, 2018 at Main Cotton Research Station, Navsari Agricultural University, Surat by using six generations ( $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$ ) of each of the two crosses viz., GBhv-302 × PA-812 and GBhv-302 × ARBa-1502 in Compact Family Block Design with three replications. Female parent GBhv-302 was from *G. herbaceum* and male parents PA-812 and ARBa-1502 were from *G. arboretum*. Randomly selected ten competitive plants from each of the  $P_1$ ,  $P_2$ ,  $F_1$ , 40 plants of  $F_2$  and 20 plants of each of the  $BC_1$  and  $BC_2$  generations were utilized per replication and observations were recorded on the single plant basis for monopodia per plant, sympodia per plant, bolls per plant, average boll weight, seed cotton yield per plant and ginning outturn. The scaling tests (A, B, C and D) as given by Hayman and Mather (1955) were utilized to check the adequacy of additive-dominance model for various traits under study. The roles of non-allelic gene interactions were indicated by the significance of any of the scaling tests. The sufficiency of an additive-dominance model was also checked by joint scaling test illustrated by Cavalli (1952). The various gene interactions (m, d, h, i, j and l) were calculated by using six parameter model given by Hayman (1958).

### RESULTS AND DISCUSSION

The analysis of variance for six generations in two crosses of cotton for all characters studied is presented in **Table 1**. The analysis of variance among progenies within each cross showed significant differences among six generation means for all the characters studied except monopodia per plant in GBhv-302 × ARBa-1502. Further generation mean analysis was not carried out for the traits which failed to record significant differences among the

generations in respective cross.

Many workers have reported prime role of either additive or non-additive gene actions in the inheritance of seed cotton yield and its attributing traits in cotton. The information related to gene action controlling various traits in any crops that helps in the selection of appropriate breeding procedure. First order biometrical technique i.e. the generation means analysis was adapted to partition mean into various genetic components. The result of scaling test, joint scaling test and gene action are furnished in **Table 2**.

The additive (d) type of gene interaction was found significant and negative only in cross GBhv-302 × PA-812 for bolls per plant and seed cotton yield per plant. Moreover, additive × additive (i) type of gene action was found significant and positive in cross GBhv-302 × PA-812 for sympodia per plant and ginning outturn. In contrast, significant and negative additive × additive (i) type of gene effect was recorded in cross GBhv-302 × ARBa-1502 for sympodia per plant, bolls per plant and seed cotton yield per plant.

Simple pedigree selection can be adopted to exploit the additive component of variation. Mass selection can be utilized in several early generation with an aim to improve the heterozygous population by changing the frequencies of desirable genes followed by individual plant selection in resulting population might be the cheapest and quickest procedure. But, the presence of non-fixable (h, j and l) genetic parameters along with duplicate type of action may result in delayed improvement in these characters using selection in early generations. In this condition, progeny selection could be done at later generations. These results are in agreement with the conclusion of Kannan *et al.* (2013), Srinivas and Bhadru (2015), Yehia and El-Hashash (2019) and Nand *et al.* (2020).

**Table 1. Analysis of variance for six generations in two crosses of cotton**

Sources of variation	df	Mean Sum of Squares					
		Monopodia per plant	Sympodia per plant	Bolls per plant	Average boll weight	Seed cotton yield per plant	Ginning outturn
<b>GBhv-302 × PA-812</b>							
Replication	2	0.10	4.95	10.37	0.01	16.17	0.42
Generation	5	0.99*	20.67*	53.04**	0.14*	320.63**	3.75**
Error	10	0.30	3.81	8.57	0.03	53.92	0.50
<b>GBhv-302 × ARBa-1502</b>							
Replication	2	1.49	7.19	11.81	0.00	113.37*	0.39
Generation	5	1.18	9.57*	55.33**	0.24**	676.24**	2.86*
Error	10	0.43	2.33	3.88	0.02	23.48	0.67

\*Significant at 5% level, \*\*Significant at 1% level

**Table 2. Estimation of scaling test, joint scaling test and genetic parameters for different characters of two crosses in cotton**

Characters	Crosses	Scaling tests				$\chi^2$	Gene effects						Type of epistasis
		A	B	C	D		m	d	h	i	j	l	
Monopodia per plant	GBhv-302 × PA-812	1.13	1.13	2.46	0.10	NS	-	-	-	-	-	-	-
	GBhv-302 × ARBa-1502	-	-	-	-	-	-	-	-	-	-	-	-
Sympodia per plant	GBhv-302 × PA-812	6.53**	1.86	-5.53	-6.96**	**	21.30**	-0.03	18.03**	13.93**	2.33	-22.33**	D
	GBhv-302 × ARBa-1502	-3.26	-4.20*	2.93	5.20**	**	23.23**	-1.46	-8.60**	-10.4**	0.46	17.86**	D
Bolls per plant	GBhv-302 × PA-812	-6.86*	-3.46	-19.07**	-4.36	**	28.51**	-5.93**	14.70**	8.73	-1.70	1.60	C
	GBhv-302 × ARBa-1502	-5.73	-7.06	9.20	11.00**	**	36.48**	-3.50	-15.16*	-22.00**	0.66	34.80**	D
Average boll weight	GBhv-302 × PA-812	-0.03	0.13	0.14	0.02	NS	-	-	-	-	-	-	-
	GBhv-302 × ARBa-1502	-0.95**	-0.50**	-1.08**	0.18	**	2.38**	0.02	0.13	-0.37	-0.22	1.82**	C
Seed cotton yield/plant	GBhv-302 × PA-812	-19.85	-11.49	-43.11	-5.88	**	67.28**	-8.23*	37.17**	11.76	-4.18	19.58	C
	GBhv-302 × ARBa-1502	-38.71**	-36.65**	33.95*	54.66**	**	89.39**	-6.76	-81.92**		-1.03	184.68**	D
Ginning outturn	GBhv-302 × PA-812	-3.64**	0.26	-8.91**	-2.76*	**	34.91**	-1.27	7.10**	5.53*	-1.95	-2.15	D
	GBhv-302 × ARBa-1502	-3.32*	-0.08	-5.93**	-1.26	**	35.19**	-0.72	4.10*	2.52	-1.62	0.89	C

\*Significant at 5% level, \*\*Significant at 1% level

The hybrid exhibiting digenic gene interaction had a significant and positive dominance (h) effects for sympodia per plant, bolls per plant and seed cotton yield per plant in cross GBhv-302 × PA-812; and ginning outturn in both the crosses. While cross GBhv-302 × ARBa-1502 showed a significant and negative dominance (h) gene effects for sympodia per plant, bolls per plant and seed cotton yield per plant.

A significant and positive estimate of dominance × dominance (l) gene effect was reported by cross GBhv-302 × ARBa-1502 for all traits studied except monopodia per plant and ginning outturn. While only sympodia per plant showed a significant and negative dominance × dominance gene action in cross GBhv-302 × PA-812. The magnitude of dominance (h) gene component was higher than that of additive (d) gene component, signifying higher influence of dominance effect in the expression of the traits under study. To exploit dominance gene effect conventional breeding procedures might be rewarding, and presence of large flower size and easy hand emasculatation process as well as availability of GMS line, heterosis breeding might be adopted. Similar results were

also quoted by Kannan *et al.* (2013) Srinivas and Bhadru (2015), Valu *et al.* (2015), Choudhary *et al.* (2017), AL-Hibbiny *et al.* (2020) and Nand *et al.* (2020).

The opposite sign of dominance (h) and dominance × dominance (l) components indicated the role of duplicate epistasis for sympodia per plant in both the crosses; bolls per plant and seed cotton yield per plant in cross GBhv-302 × ARBa-1502; and ginning outturn in cross GBhv-302 × PA-812. While bolls per plant and seed cotton yield per plant in cross GBhv-302 × PA-812; and average boll weight and ginning outturn in cross GBhv-302 × ARBa-1502 showed a similar sign of dominance (h) and dominance × dominance (l) presuming complementary type of epistasis. Complementary type of epistasis was also reported by Patel *et al.* (2014) for sympodia per plant, bolls per plant, average boll weight and seed cotton yield per plant. While duplicate type of epistasis was reported by Patel *et al.* (2014), Srinivas and Bhadru (2015), Valu *et al.* (2015) for various characters.

The existence of duplicate epistasis would be harmful for rapid progress because it creates difficulties in fixing

the genotypes with amplified level of trait exploitation by cancelling the opposite effect of one parameter by the negative effect of another parameter.

The negative sign of dominance x dominance (I) effect was recorded for sympodia per plant and ginning outturn in cross GBhv-302 × PA-812 indicating their reducing effect in the expression of these characters. The sign of dominance x dominance (I) parameter was positive in the remaining characters stating their attractive effect in the expression of that character.

All the results of this experiment depict that improvement of such traits in a certain population through heterosis breeding is affected by higher estimates of dominant genes. Besides that types of epistasis also decide different breeding techniques. As for example duplicate type of epistasis resulting mutual cancellation of genes resulting in no heterosis. Since, the varietal improvement is our primary breeding objective, both additive and dominant components with interallelic interactions should be taken into consideration, so that undesirable effects could be broken by bi-parental mating or reciprocal recurrent selection methods.

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