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Generation mean analysis of interspecific diploid cotton crosses

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Abstract
The magnitude of various gene actions governing various traits in interspecific diploid cotton crosses were traced out by using the generation mean analysis. Six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) each of the two crosses *viz*, GBhv-302 × PA-812 and GBhv-302 × ARBa-1502 were utilized. The significance of one or more simple scaling test as well as χ^2 values of joint scaling test indicated presence of non-allelic gene interactions for most of the traits. The magnitude of additive type of gene actions were found to be lower that dominance gene interactions in most of the characters. The values of dominance gene actions were higher for days to first flower, seed index and lint yield per plant. Epistasis component of gene actions like additive × additive (I) and dominance × dominance (l) were found to be involved in inheritance of days to first flower, plant height, leaf area, seed index, lint yield per plant and oil percentage. Duplicate type of epistasis was observed for all traits in one or both crosses, while complementary epistasis was present for plant height in cross GBhv-302 × ARBa-1502 and for lint yield per plant in cross GBhv-302 × PA-812.

Keywords: Generation mean analysis, diploid cotton, gene action, epistasis

Introduction

Cotton, known as "King of fiber" is one of the significant fiber crop which is having profound effect on socio-economic status of the world. Lint is the main product for which cotton is cultivated, besides it also provides oil, hull and seed meal. In addition, cottonseed oil is also consumed by human. It is having 18 to 26 percent oil. Low seed cost along with low or no cost for plant protection attracted farmers to cultivate diploid cotton as it gives at par yield to that of hybrids of tetraploid cotton with somewhat comparable fiber quality. The inherent potential of diploid cotton remains untapped, which suggested use of proper breeding techniques for its genetic enhancement to prevent genetic loss of these species. Diploid cottons are also having tolerance to biotic and abiotic stresses. Further, genetic analysis of various traits gives clear cut idea about the nature and magnitude of genetic variation present in particular population. In any crop improvement strategy, the use of breeding technique to be utilized is directly depends on the type of gene effects present in the population. Additive type of gene actions are of prime importance to develop pure line, where dominance and epistasis type of gene interactions can be exploited to take benefits of hybrid vigor.

Materials and Methods

The research was carried out at Main Cotton Research Station, Navsari Agricultural University, Surat during *Kharif*-2018. 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 were analyzed in Compact Family Block Design with three replications. Selected female parent was from *G. herbaceous* and male parents were of *G. arboretum* species. Ten competitive plants each of the P_1, P_2 and F_1, 40 plants of F_2 and 20 plants of each of the BC_1 and BC_2 generations were used for recording of observations per replication. Observations were recorded on individual plant basis for days to first flower, plant height (cm), leaf area (cm^2), seed index (g), lint yield per plant (g) and oil percentage. The simple scaling tests (A, B, C and D) as illustrated by Hayman and Mather (1955) [6] were used to ensure the adequacy of additive-dominance model for different characters studied. The significance of any of the scaling tests suggested presence of non-allelic gene effects for the inheritance of traits. The adequacy of additive-dominance model was also tested by Cavalli (1952) [2] joint scaling test. Six parameter model suggested by Hayman (1958) [5] was used for calculation of various gene interactions (m, d, h, i, j, l).

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Result and discussion

The mean values of all six generations *viz.*, P_1, P_2, F_1, F_2, BC_1 and BC_2 for all characters studied was subjected to analysis of variance for both the crosses (Table- 1). The analysis of variance indicated significant differences among all six generation means for all the traits under study in both the crosses except leaf area in GBhv-302 × ARBa-1502. Additional generation mean analysis was not carried out for

this trait which failed to account significant difference among the generations in particular cross. Further, mean values of all generations of both crosses were used to estimate various scaling tests and gene interaction using six parameter model (Table - 2). Significance of any simple scaling tests as well as joint scaling test indicated inadequacy of additive-dominance model and presence of non-allelic gene interactions.

Table 1: Analysis of variance for six generations in interspecific crosses of diploid cotton

Sources of variation	DF	Mean Sum of Squares					
		Days to first flower	Plant height (cm)	Leaf area (cm^2)	Seed index (g)	Lint yield per plant (g)	Oil percentage
GBhv-302 × PA-812							
Replication	2	5.20	94.01	3.52	0.06	2.19	0.59**
Generation	5	281.37**	318.37*	17.17**	0.71**	58.41**	1.09**
Error	10	4.30	94.86	2.73	0.04	6.95	0.08
GBhv-302 × ARBa-1502							
Replication	2	2.26	10.38	4.43	0.03	13.11	0.22*
Generation	5	105.99**	425.60*	7.34	2.06**	96.80**	0.61**
Error	10	6.51	117.70	3.70	0.08	3.79	0.03

*Significant at 5% level
**Significant at 1% level

Table 2: Estimates of scaling tests, joint scaling test, gene effects and epistasis in interspecific crosses of diploid cotton

Characters	Crosses	Scaling tests					Gene effects (Hayman, 1958)						Type of epistasis
		A	B	C	D	χ^2	M	D	H	I	J	L	
Days to first flower	GBhv-302 × PA-812	-4.80*	-13.00**	17.86**	17.83**	**	99.33**	15.83**	-31.00	-35.67**	4.10	53.46**	D
	GBhv-302 × ARBa-1502	-7.77**	1.53	10.53*	8.36**	**	96.98**	4.20**	-17.03**	-16.73**	-4.63	22.93**	D
Plant height (cm)	GBhv-302 × PA-812	-31.00**	-41.40**	-32.00	20.20	**	143.68**	-3.16	-31.23	-40.40	5.20	112.80**	D
	GBhv-302 × ARBa-1502	-14.26	-41.73**	-77.33**	-10.66	**	134.58**	0.96	31.10	21.33	13.73	34.66	C
Leaf area (cm^2)	GBhv-302 × PA-812	-4.72	-11.03**	2.32	9.04**	**	31.15**	2.91*	-15.44**	-18.00**	3.15	33.84**	D
	GBhv-302 × ARBa-1502	-	-	-	-	-	-	-	-	-	-	-	-
Seed index (g)	GBhv-302 × PA-812	-1.13**	-0.97*	-0.44	0.83*	**	7.83**	-0.53*	-0.88	-1.66*	-0.08	3.77**	D
	GBhv-302 × ARBa-1502	-0.55	-0.63	-3.55**	-1.18**	**	7.47**	-0.53*	4.24**	2.36**	0.04	-1.18	D
Lint yield per plant (g)	GBhv-302 × PA-812	-9.94**	-4.36*	-21.97**	-3.83	**	23.59**	-3.81*	18.38**	7.66	-2.78	6.63	C
	GBhv-302 × ARBa-1502	-16.50**	-13.82**	6.46	18.40**	**	31.38**	-2.78	-25.40**	-36.80**	-1.34	67.13**	D
Oil percentage	GBhv-302 × PA-812	-2.99**	-0.77**	-2.70**	0.53**	**	17.36**	-0.60**	-0.49	-1.06**	-1.11	4.83**	D
	GBhv-302 × ARBa-1502	-1.03**	0.43	-0.50	0.04	**	17.32**	-0.06	-0.37	-0.09	-0.73	0.69	D

*Significant at 5% level
**Significant at 1% level

Days to first flower

GBhv-302 × PA-812: All simple scaling tests as well as joint scaling test were significant implies presence of non-allelic gene interactions. The result obtained from six parameter model indicated highly significant estimates of mean (m) which shows significant difference among the generations. The other parameters like additive (d), additive × additive (i) and dominance × dominance (l) gene interactions were also found highly significant. Looking to the sings of (h) and (l),

duplicate type of epistasis was responsible for inheritance of this trait.

GBhv-302 × ARBa-1502: Simple scaling tests A, C and D along with χ^2 test of joint scaling test were highly significant indicated role of non-allelic gene action. Estimation of genetic parameters by six parameter model revealed that all the parameters were highly significant except additive × dominance (j) gene interaction. Opposite signs of dominance (h) and dominance × dominance (l) showed role of duplicate

type of epistasis for the trait under study. Similar results were obtained by Haleem *et al*. (2010), Srinivas and Bhadru (2015) and Choudhary *et al*. (2017) [4, 12, 3].

Plant height (cm)

GBhv-302 × PA-812: Scaling tests A and B along with joint scaling test was highly significant suggested presence of non-allelic gene interactions. According to six parameter model, only dominance × dominance (l) gene effect was significant. Duplicate type of epistasis was observed for controlling this character.

GBhv-302 × ARBa-1502: Inadequacy of additive-dominance model was supported by highly significant values of scaling test B and C along χ^2 value of joint scaling test. None of the genetic parameters were significant except mean (m). Further, similar signs of dominance (h) and dominance × dominance (l) depicted presence of complementary type of epistasis. These findings are in accordance with Choudhary *et al*. (2017) and Nand *et al*. (2020) [3, 9].

Leaf area (cm^2)

GBhv-302 × PA-812

Out of four scales, only scaling tests B and D were found significant and χ^2 value of joint scaling test was also found significant. As per six parameter model, all genetic parameters were significant except additive × dominance (j) gene interaction. Duplicate type of epistasis was observed for inheritance of this trait. The similar result was reported by Hussain *et al*. (2008) [7].

Seed index (g)

GBhv-302 × PA-812: The presence of non-allelic gene interactions were confirmed by significance of all scaling tests except scale C as well as significance of χ^2 value of joint scaling test. The result of six parameter model showed significance of mean (m), additive (d), additive × additive (i) and dominance × dominance (l) type of gene effects. The opposite signs of dominance (h) and dominance × dominance (l) revealed presence of duplicate type of epistasis.

GBhv-302 × ARBa-1502: For this trait, scaling tests C and D were highly significant indicated existence of epistasis. As far as the gene effects are concerned, additive (d), dominance (h) and additive × additive (i) were found highly significant. This character was governed by duplicate type of epistasis as confirmed by opposite signs of dominance (h) and dominance × dominance (l) gene interactions. These results are similar with the findings of Sarwar *et al*. (2011), Kannan *et al*. (2013), Siwach *et al*. (2013) and Yehia and Hashash (2019) [10, 8, 11, 14].

Lint yield per plant (g)

GBhv-302 × PA-812: All scaling tests except scale D and χ^2 value of joint scaling test were highly significant depicted the inadequacy of additive-dominance model and existence of non-allelic interactions for this trait. As per Hayman six parameter model additive (d) and dominance (h) gene effects were significant. Complementary type of epistasis was found to be responsible for controlling this trait due to similar signs of dominance (h) and dominance × dominance (l) genetic components.

GBhv-302 × ARBa-1502: The presence of non-allelic gene interaction was supported by significance of scaling tests A, B

and D as well as joint scaling test. Other genetic parameters like dominance (h), additive × additive (i) and dominance × dominance (l) gene components were found to be highly significant in six parameter model. This trait was found to be governed by duplicate type of epistasis. These results are in agreement with the conclusion of Choudhary *et al*. (2017), Yehia and Hashash (2019) and AL-Hibbiny *et al*. (2020) [3, 14, 1].

Oil percentage

GBhv-302 × PA-812: All simple scaling tests as well as χ^2 value of joint scaling test were highly significant depicted role of non-allelic gene interactions for the inheritance of this particular trait. In context to Hayman six parameter model, mean (m) value was found highly significant, which shows presence of variability and differences among the generations. According to six parameter model additive (d), additive × additive (i) and dominance × dominance (l) gene effects were found to be highly significant. This trait was governed by duplicate type of epistasis as suggested by opposite signs of dominance (h) and dominance × dominance (l) gene effects.

GBhv-302 × ARBa-1502: Out of four simple scaling tests, only scale A was found significant and result of joint scaling test showed significance of χ^2 value. As per six parameter model none of the genetic parameters were found significant. Moreover, opposite signs of dominance (h) and dominance × dominance (l) represent the duplicate type of epistasis controlling this trait. Similar results were also quoted by Valu *et al*. (2018) [13].

Conclusion

For lint yield per plant, most of the scaling tests were significant indicated the existence of considerable amount of epistasis and inadequacy of additive- dominance model and role of non-allelic gene interactions. For most of the characters, both additive and non-additive gene interactions were found to be significant. In present investigation, non-allelic gene interactions along with the additive and dominant gene actions were found to played significant role in inheritance of various traits under study particularly in cotton. When both additive and non-additive gene effects are involved in inheritance of the traits, it is suggested to use parental mating followed by population improvement method of breeding including conventional methods of selection of desirable recombinant. Their inter-mating can be done to develop elite homozygous recombinants with desirable quality and high yielding ability. Duplicate type of epistasis was observed for most of the traits, which makes it difficult to fix genotypes because effect of one parameter would be nullified by negative effect of another parameter. In such situation, selection in later generations would be rewarding.

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