International Journal on Emerging Technologies **16(1): 172-175(2025)**

ISSN No. (Print): 0975-8364
ISSN No. (Online): 2249-3255

Genetic Analysis of Fibre Quality Traits in Interspecific Crosses of Diploid Cotton (*Gossypium herbaceum* L. × *Gossypium arboreum* L.)

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(Received 21 January 2025, Revised 03 March 2025, Accepted 22 March 2025)
(Published by Research Trend, Website: www.researchtrend.net)

ABSTRACT: Using a six-parameter model, generation mean analysis was conducted on two interspecific crosses of diploid cotton, GBhv-302 × PA-812 and GBhv-302 × ARBa-1502. To assess the sufficiency of the additive-dominance model, simple scaling tests and joint scaling tests were performed. In one or more of the characters studied, the magnitude of dominant (h) gene action was larger than estimates of additive (d) gene action. Among epistasis, additive × additive (i) kind of gene action was shown to be significant in cross GBhv-302 × PA-812 for 2.5% span length (mm), fiber strength (g/tex) and fibre length uniformity ratio (%); GBhv-302 × ARBa-1502 for fibre fineness (mv). While, the cross GBhv-302 × PA-812 showed significant contribution of dominance × dominance (l) type of gene action for oil percentage. Duplicate type of gene action was reported for all the traits under all cross, except the cross GBhv-302 × ARBa-1502 for the trait 2.5% span length (mm). None of the traits under study exhibited complementary type of gene interaction.

Keywords: diploid cotton, additive, dominance and epitasis gene interactions.

INTRODUCTION

One of the most significant and major cash crops, cotton is also referred to as "white gold" and has a big impact on global economic and social life. Both the ancient and new worlds have cultivated cotton, which has several uses and meets six essential requirements for people, including seed cotton, lint, oil, seed meal, hull and linters. Cotton fibre are seed hairs from plants in the Malvales order, Malvaceae family, Gossypieae tribe and Gossypium genus. Cotton has four major domesticated species of economic importance: *hirsutum, barbadense, aboreum,* and *herbaceum*. There are now thirty-three species recognized; however, all but four are wild shrubs with no commercial use. Currently more than twenty different wild cotton species have been employed breeding and development programs (Chang *et al.*, 2023). Additionally, there are no or very little costs associated with plant nourishment and plant protection while growing diploid cotton. When considering these traits of diploid cotton, one will be quite interested in its cultivation, provided that it yields as least as much as hybrid tetraploid cotton cultivars and has fibre of comparable quality. Cotton is the natural textile fibre and cellulosic textile fibre in the world and it is used to make clothing, home furnishings and industrial items. Each economically significant species comprises a wide range of variations produced *via* breeding programmes to produce cotton with ever-improving qualities (e.g., quicker maturation, higher yields and enhanced insect and disease resistance) and fibre with greater length strength and uniformity. To understand the potential performance of the cotton, both strength and elongation needs to be characterized (Delhom *et al.*, 2024). The genetic makeup of a variety can have a significant impact on the fibre quality. Producers should consider all fibre quality traits when choosing a variety to assist them decide what is best for their fields. Over the past 50 years, significant progress has been achieved in plant breeding to increase cotton's fibre quality and productivity potential. Quantitative traits' genetic architecture provides insight into the kind and degree of genetic diversity present in the population. The types of gene interaction or effects that are present in the population directly influence the breeding process that should be used in any crop improvement programme. While dominance and epistasis-type gene effects may be used to benefit from hybrid strength, additive gene actions are crucial for the development of pure lines.

MATERIALS AND METHODS

The present study was done at the Main Cotton Research Station, Navsari Agricultural University, Surat, Gujarat during *Kharif*- 2018 with six generations (P_1, P_2, F_1, F_2, B_1 and B_2) of each of the two crosses, GBhv-302 × PA-812 and GBhv-302 × ARBa-1502, in Compact Family Block Design with three replications. The genotype GBhv-302 was used as female parent and from *Gossypium herbaceum* species and the genotypes PA-812 and ARBa-1502 were used as male and from *Gossypium arboreum* species. Per replication, ten random plants were selected from each of the P_1, P_2, F_1, 40 plants from F_2 and 20 plants from each of the B_1 and B_2 generations and observations were made on a single plant basis for 2.5% span length (mm), fibre fineness (mv), fibre strength (g/tex), fibre length uniformity ratio (%) and oil percentage. The scaling tests (A, B, C and D) proposed by Hayman and Mather (1955) were used to assess the adequacy of the additive-dominance model for the several attributes under consideration. The importance of any of the scaling tests revealed the functions of non-allelic gene interactions. Cavalli's joint scaling test was used to verify the adequacy of the additive-dominance model (1952). The various components of gene interactions *viz*., mean (m), additive (d), dominance (h), additive × additive (i), additive × dominance (j) and dominance × dominance (l) were computed using Hayman's six parameter model (1958).

RESULTS AND DISCUSSION

Table 1 shows the analysis of variance over six generations in two cotton crosses for all traits evaluated. The examination of variation across progenies within each cross revealed substantial change between six generation means for all of the traits tested, with the exception of 2.5% span length (mm) in GBhv-302 × ARBa-1502. Further generation mean analysis was not performed for the features that did not show a significant difference between generations in the relevant cross. Considerable variation was reported by Kumar *et al.* (2024) for the traits like fibre length, fibre strength and micronaire value in American cotton.

Many researchers revealed that either additive or non-additive gene actions have a significant impact in the inheritance of fibre quality parameters in cotton. The knowledge of gene action governing numerous qualities in any crop helps in the selection of an appropriate breeding method to improve fibre quality. Generation means analysis, a first order biometrical technique, was used to partition mean into distinct genetic components. Table 2 shows the results of the scaling test, combined scaling test and gene action.

The additive (d) type of gene interaction was shown to be significant and positive in cross GBhv-302 × PA-812 for 2.5% span length (mm), fiber strength (g/tex) and fibre length uniformity ratio (%); and in cross GBhv-302 × ARBa-1502 for fiber strength (g/tex). In the cross GBhv-302 × PA-812, we also discovered significant but negative type additive gene action for fibre fineness (mv) and oil percentage. Furthermore, the additive × additive (i) kind of gene activity was discovered to be substantial and positive in cross GBhv-302 × PA-812 for 2.5% span length (mm), fiber strength (g/tex), and fibre length uniformity ratio (%); and in cross GBhv-302 × ARBa-1502 for fibre fineness (mv). In contrast, for fibre fineness (mv) and oil percentage, a significant and negative additive × additive (i) type of gene effect was seen in cross GBhv-302 × PA-812.

To harness the additive portion of variation, simple pedigree selection can be used. Mass selection can be used in many early generations with the goal of improving the heterozygous population by modifying the frequencies of desirable genes, followed by individual plant selection in the resulting population. However, the presence of non-fixable (h, j, and l) genetic components, as well as a duplicate gene action, may result in delayed improvement in these features through selection in early generations. In such cases, progeny selection might be feasible in later generations. These findings correspond with those of Valu *et al.* (2015); Choudhary *et al.* (2017); Carvalho *et al.* (2019); Nand *et al.* (2020).

Only one cross GBhv-302 × ARBa-1502 showed digenic gene interaction having significant and favorable dominance (h) effect for fibre fineness (mv). The cross GBhv-302 × PA-812 reported a significant and positive estimate of dominance (l) gene action for oil percentage. In cross GBhv-302 × PA-812, 2.5% span length (mm), fiber strength (g/tex) and fibre length uniformity ratio (%) demonstrated substantial and negative dominance gene action. The magnitude of the dominance (h) gene action was higher than that of the additive (d) gene component, indicating that the dominance portion had a greater effect on the expression of the traits under study. To utilize the dominating gene action, traditional breeding processes may be beneficial and the presence of large flower size and an easy hand emasculation process, as well as the availability of a GMS line, heterosis breeding may be used. Siwach *et al.* (2013); Valu *et al.* (2015); Kamaran *et al.* (2018) all cited similar findings (2020).

The opposite sign of dominance (h) and dominance × dominance (l) components revealed the role of duplicate epistasis gene action for all traits across all crosses, except for the trait 2.5% span length in the cross GBhv-302 × ARBa-1502 (mm). Kannan *et al.* (2013); Valu *et al.* (2015); Kamaran *et al.* (2018); Valu *et al.* (2018) all reported duplicate epistasis for different characteristics. Non-additive gene action were reported by Balci *et al.* (2023) in controlling fibre length, fibre strength and fibre fineness in segregating generations.

None of the traits exhibited similar signs of dominance (h) and dominance × dominance (l), implying complimentary epistasis.

Duplicate epistasis is detrimental to quick advancement because it makes it difficult to fix genotypes with enhanced levels of trait exploitation by cancelling the opposing effect of one component by the negative effect of another component.

The negative sign of dominance × dominance (l) effect was exhibited by the trait like 2.5% span length (mm), fiber strength (g/tex) and fibre length uniformity ratio (%) in both the crosses, except for 2.5% span length (mm) observed only in GBhv-302 × PA-812 indicating their reducing effect in the expression of these characters. The sign of dominance × dominance (l) parameter was positive in the remaining character like oil percentage, showing their attractive effect in the expression of that character.

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

Sources of variation	df	Mean Sum of Squares				
		2.5% span length (mm)	Fibre fineness (mv)	Fibre strength (g/tex)	Fibre length uniformity ratio (%)	Oil percentage
GBhv-302 × PA-812						
Replication	2	0.07	0.15	0.10	0.20	0.59**
Generation	5	4.10**	0.34*	3.34**	2.54**	1.09**
Error	10	0.02	0.06	0.28	0.15	0.08
GBhv-302 × ARBa-1502						
Replication	2	0.42	0.33**	0.38	0.11	0.22*
Generation	5	0.03	0.83**	0.66**	1.00**	0.61**
Error	10	0.19	0.03	0.11	0.07	0.03

***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					Gene effects						Type of epistasis
		A	B	C	D	χ^2	m	d	h	i	j	l	
2.5% span length (mm)	GBhv-302 × PA-812	2.99**	-0.24	1.54**	-0.60*	S	26.30**	2.68**	0.22	1.21*	1.61	-3.96**	D
	GBhv-302 × ARBa-1502	-	-	-	-	NS	-	-	-	-	-	-	-
Fibre fineness (mv)	GBhv-302 × PA-812	-0.78**	0.78**	0.77*	0.38*	S	5.34**	-0.40**	-0.33	-0.77*	-0.78	0.77	D
	GBhv-302 × ARBa-1502	1.10**	1.25**	1.26**	-0.54**	S	5.16**	0.00	2.08**	1.09**	-0.07	-3.45**	D
Fiber strength (g/tex)	GBhv-302 × PA-812	4.16*	2.22*	4.04*	-1.17*	S	27.38**	0.90**	0.11	2.34**	0.96	-8.73**	D
	GBhv-302 × ARBa-1502	1.40**	-1.60**	-0.86	-0.33	S	27.14**	1.43**	0.46	0.66	1.50	-0.46	D
Fibre length uniformity ratio (%)	GBhv-302 × PA-812	4.60**	0.60	3.20**	-1.00**	S	79.80**	1.13**	1.20	2.00**	2.00	-7.20**	D
	GBhv-302 × ARBa-1502	1.00*	1.40**	3.20**	0.40	S	80.35**	0.03	0.10	-0.80	-0.20	-1.60	D
Oil percentage	GBhv-302 × PA-812	-2.99**	-0.77**	-2.70**	0.53**	S	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	S	17.32**	-0.06	-0.37	-0.09	-0.73	0.69	D

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

CONCLUSIONS

All of the experiment's findings show that improving such features in a particular population through heterosis breeding depends on greater estimates of dominant genes. In addition, distinct breeding methods are determined by the forms of epistasis. For instance, a duplication kind of epistasis causes genes to mutual cancelation of each other out, preventing heterosis. Since our main breeding goal is varietal development, both dominant as well as additive component with interallelic interactions should be taken into account. This way, bi-parental mating or reciprocal recurrent selection techniques can break undesired effects.

Acknowledgement. The authors are thankful to Department of Genetics and Plant Breeding, N. M. College of Agriculture, Navsari Agricultural University, Navsari and Main Cotton Research Station, Navsari Agricultural University, Surat for providing necessary support and facilities to conduct this experiment successfully.

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How to cite this article: Naghera Y.V., Vavdiya P.A., Mungra K.S. and Prajapati M.R. (2025). Genetic Analysis of Fibre Quality Traits in Interspecific Crosses of Diploid Cotton (*Gossypium herbaceum* L. × *Gossypium arboreum* L.). *International Journal on Emerging Technologies*, *16*(1): 172–175.