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# Genetic analysis of fibre quality traits in interspecific crosses of diploid cotton (*G. herbaceum* × *G. arboreum*)

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**Abstract**
Using a six-parameter model, generation mean analysis was performed 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 tested, estimates of dominant (h) gene action were 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 dominance × dominance (l) type of gene effect contributed significantly in cross GBhv-302 × PA-812 for Oil percentage. Duplicate epistasis gene action 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 showed complementary type of gene interaction.

**Keywords:** Diploid cotton, additive, dominance and epistasis gene actions

## 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 fibres 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 recognised; however, all but four are wild shrubs with no commercial use. 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 fibres with greater length, strength and uniformity. 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 purelines.

## Materials and Methods
During *kharif*-2018, the research experiment was conducted at the Main Cotton Research Station, Navsari Agricultural University, Surat, with six generations (P1, P2, F1, F2, B1 and B2) of each of the two crosses, 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.* Per replication, ten competitive plants were chosen at random 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) [5] 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 numerous gene interactions (m, d, h, i, j and l) were computed using Hayman's six parameter model (1958) [4].

**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 changes 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.

Many researchers have 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 component 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 factors, as well as a duplicate type of action, may result in delayed improvement in these features through selection in early generations. In this case, progeny selection might take place in later generations. These findings correspond with those of Valu *et al*. (2015) [10], Choudhary *et al*. (2017) [3], Carvalho *et al*. (2019) [1] and Nand *et al.* (2020) [8].

Only in the cross GBhv-302 ARBa-1502 did the hybrid displaying digenic gene interaction have significant and favourable dominance (h) effects on fibre fineness (mv). 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 amplitude of the dominance (h) gene component was greater than that of the additive (d) gene component, indicating that the dominance impact had a greater influence on the expression of the traits under study. To utilise 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) [9], Valu *et al*. (2015) [10], Kamaran *et al*. (2018) [6], and Nand *et al*. (2020) [8] all cited similar findings (2020).

The opposing sign of dominance (h) and dominance × dominance (l) components revealed the role of duplicate epistasis gene action for all traits across all crosses, save for the trait 2.5% span length in the cross GBhv-302 ARBa-1502 (mm). Kannan *et al*. (2013) [7], Valu *et al*. (2015) [10], Kamaran *et al*. (2018) [6], and Valu *et al*. (2015) [10] all reported duplicate epistasis for different characteristics. 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 parameter by the negative effect of another parameter.

The negative sign of dominance x dominance (l) effect was observed for 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 traits. The sign of dominance × dominance (l) parameter was positive in the remaining character like Oil percentage, 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, 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.

**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 | $\chi^2$ | 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

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