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## GENETIC VARIABILITY AND ASSOCIATION STUDIES FOR YIELD AND FIBER QUALITY TRAITS IN INTERSPECIFIC HYBRIDS OF CULTIVATED TETRAPLOID COTTON

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### ABSTRACT

The population of interspecific cotton hybrids (*G. hirsutum* × *G. barbadense*) was exploited for genetic variation and trait association. The experiment was laid in randomized complete block design with three replications using forty-five hybrids. Data on fourteen yield and fiber quality related traits were recorded and subjected to statistical analysis. Maximum likelihood test ratio showed significant ( $p < 0.05$ ) genotypic effects for all the traits under study. Evaluated characters were exhibited different levels of variability, heritability and genetic advance among the studied genotypes. Results indicated that, phenotypic coefficient of variation (PCV) was relatively higher than genotypic coefficient of variation (GCV). The highest GCV and PCV values were found particularly for seed cotton yield per plant whereas, monopodia per plant and bolls per plant exhibited moderate GCV and high PCV values indicating high to moderate genetic variability, respectively. Heritability ranges from 19.60% (uniformity index) to 88.20% (seed index). High heritability coupled with high genetic advance expressed as a percent of mean was recorded for monopodia per plant (86.60%, 38.17%), seed cotton yield per plant (71.90%, 36.46%) and bolls per plant (71.10%, 32.97%), respectively suggesting simple selection may be rewarding. Genotypic correlation revealed significant negative association of days to 50% flowering and days to 50% boll bursting with seed cotton yield per plant, while highly significant and positive correlation of seed cotton yield per plant was observed with bolls per plant, boll weight, fiber fineness and uniformity index. Path coefficient analysis revealed highest positive direct effect of bolls per plant (1.09) on seed cotton yield per plant followed by boll weight (0.53). Therefore, the findings of this study suggest existence of ample amount of variability for monopodia per plant, bolls per plant and seed cotton yield per plant with high heritability and high genetic advance. Notably, bolls per plant and boll weight showed true correlation with seed cotton yield per plant as both of these traits exhibited significant positive correlation and highly positive direct effects. Hence, emphasis should be given on these traits, while exercising selection in cotton.

**Key words** : Correlation, Cotton, Genetic variability, Interspecific hybrids, Path analysis.

### Introduction

Cotton (*Gossypium* spp.) is a major global fiber crop, with cultivated tetraploid species – *Gossypium hirsutum* L. (upland cotton) and *Gossypium barbadense* L. (Egyptian or Pima cotton) – accounting for over 95% of the world's cotton production. Upland cotton is predominantly grown due to its high yield potential, while Egyptian cotton is known for its superior fiber quality.

Cotton is the world's most important commercial cash crop and plays a pivotal role in political, economic and social affairs. Cotton constitutes about 85% of raw material of our textile industries and besides this, it also provides raw materials to various agro-based industries like ginning factories and oil mills which provide employment to thousands of peoples. It is one of the major fiber crop of our country hence constitutes a large share

in Indian economy and also the main source of foreign exchange earnings.

India stood on first position for area (12.93 million hectares), while second for production (12.02 million tonnes) after China, whereas, productivity was around 930 kg/ha. In Gujarat, cotton was planted on 2.48 million hectares of land with annual production of 3.14 million tonnes and average productivity is about 1264.7 kg/ha which is higher than the national average (Anonymous, 2023).

The improvement of both yield and fiber quality traits is a critical goal in cotton breeding programs to meet the growing demands of the textile industry. However, these traits are often inversely related and influenced by complex quantitative inheritance patterns, environmental interactions and the narrow genetic base of elite cultivars making it difficult to enhance both attributes simultaneously. Interspecific hybridization, which combines the yield potential of *G. hirsutum* with the fiber quality of *G. barbadense*, offers a promising strategy to overcome these challenges.

Genetic variability is the foundation of any successful plant breeding program. In cotton, maximizing genetic diversity enables breeders to identify and select individuals with enhanced yield and fiber characteristics. Interspecific hybrids between the cultivated tetraploid cotton species have shown significant potential in increasing genetic variability, providing an opportunity to combine high yield and fiber quality traits within a single genotype. However, understanding the extent of this variability is crucial for the efficient selection of genotypes that exhibit desirable combinations of yield and fiber quality traits.

The genetic improvement of yield and fiber quality requires a detailed analysis of the relationships between these traits. Correlation studies provide valuable information on the degree of association between different traits, helping breeders to understand how selection for one trait may affect others. For instance, while yield and fiber quality traits are often negatively correlated, identifying genotypes with a favourable balance of both traits is essential for developing superior cultivars. Understanding these correlations is key to making informed breeding decisions aimed at improving multiple traits simultaneously.

While, correlation analysis offers insights into the associations between traits, it does not reveal the direct and indirect effects of one trait on another. This is where path analysis becomes a powerful tool. Path analysis provides a more detailed understanding of the causal relationships between the traits by partitioning correlation

coefficients into direct and indirect effects. In the context of cotton breeding, path analysis helps breeders to identify traits that have a strong direct influence on yield or fiber quality, as well as traits whose influence is mediated through other factors. By identifying these key traits, breeders can focus on improving those with the most significant impact on overall performance.

The main aim of this study was to investigate the genetic variability, correlation and path analysis of yield and fiber quality traits in interspecific hybrids of cultivated tetraploid cotton. By assessing the extent of genetic variability, this study will provide insights into the potential for improving these traits through selection. Additionally, the correlation analysis will reveal the relationships between yield and fiber quality traits, while the path analysis will help identify the key traits that directly or indirectly influence these important economic characteristics.

## Materials and Methods

### Experimental Details

The experiment was performed at Regional Research Station (RRS), Anand Agricultural University, Anand. Five lines of *hirsutum* and nine testers of *barbadense* were crossed in line  $\times$  tester fashion through hand emasculation and pollination method to generate forty-five interspecific hybrids (Table 1). The generated hybrids were evaluated in Randomized Complete Block Design (RCBD) using three replications during *Kharif* 2021. The experiment was surrounded by guard row to minimize the border effect. Standard package of practices was adopted for raising the good and healthy crop.

### Data collection

Data were collected for fourteen different traits *viz.*, Days to 50% flowering, Days to 50% boll bursting, Plant height (cm), Monopodia per plant, Sympodia per plant, Bolls per plant, Boll weight (g), Ginning Outturn (%), Fiber fineness ( $\mu\text{g}/\text{inch}$ ), Fiber strength (g/tex), Fiber length (mm), Uniformity index (%), Seed index (g) and Seed cotton yield per plant (g). Five competitive plants were selected randomly from all the genotypes in each replication for recording the observations except for days to 50% flowering and days to 50% boll bursting, as they were recorded on plot basis.

### Statistical analysis

For all the genotypes, the replication wise mean values of different characters were subjected to statistical analysis.

### Genetic variability analysis

Analysis of variance technique suggested by Panse

**Table 1 :** Genotypes used in the experiment.

1	BCS-9×ABC-1	16	G.Cot-12×DB-1502	31	Merrell-1-1×GSB-43-1
2	BCS-9×ARBB-27	17	G.Cot-12×RHcb-1014	32	Merrell-1-1×GSB-44
3	BCS-9×GSB-41	18	G.Cot-12×DB-1602	33	Merrell-1-1×GSB-45
4	BCS-9×GSB-43-1	19	G.Cot-20×ABC-1	34	Merrell-1-1×DB-1502
5	BCS-9×GSB-44	20	G.Cot-20×ARBB-27	35	Merrell-1-1×RHcb-1014
6	BCS-9×GSB-45	21	G.Cot-20×GSB-41	36	Merrell-1-1×DB-1602
7	BCS-9×DB-1502	22	G.Cot-20×GSB-43-1	37	AHC-26×ABC-1
8	BCS-9×RHcb-1014	23	G.Cot-20×GSB-44	38	AHC-26×ARBB-27
9	BCS-9×DB-1602	24	G.Cot-20×GSB-45	39	AHC-26×GSB-41
10	G.Cot-12×ABC-1	25	G.Cot-20×DB-1502	40	AHC-26×GSB-43-1
11	G.Cot-12×ARBB-27	26	G.Cot-20×RHcb-1014	41	AHC-26×GSB-44
12	G.Cot-12×GSB-41	27	G.Cot-20×DB-1602	42	AHC-26×GSB-45
13	G.Cot-12×GSB-43-1	28	Merrell-1-1×ABC-1	43	AHC-26×DB-1502
14	G.Cot-12×GSB-44	29	Merrell-1-1×ARBB-27	44	AHC-26×RHcb-1014
15	G.Cot-12×GSB-45	30	Merrell-1-1×GSB-41	45	AHC-26×DB-1602

and Sukhatme (1978) was utilized to test the significance difference among all the genotypes for the studied traits. The mean square due to error and genotypes were used to calculate variance components by manipulation of expected mean squares. Phenotypic, genotypic and environmental variance were calculated as per the formula given by Johnson *et al.* (1955).

#### Genotypic variance ( $\sigma_g^2$ )

$$\sigma_g^2 = \frac{M_g - M_e}{r} \quad (1)$$

Where,

$\sigma_g^2$  = Genotypic variance

$MS_g$  = Mean sum of squares due to genotypes

$MS_e$  = Mean sum of squares due to error

r = Number of replications

#### Phenotypic variance ( $\sigma_p^2$ )

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2 \quad (2)$$

Where,

$\sigma_p^2$  = Phenotypic variance

$\sigma_e^2$  = Error variance

#### Environmental variance ( $\sigma_e^2$ )

$$\sigma_e^2 = M_e \quad (3)$$

Where,

$M_e$  = Error mean sum of square

Phenotypic and genotypic coefficient of variation were analyzed through formula suggested by Burton (1952) and classified into low (0 – 10%), moderate (10 – 20%) and high (20% & above) by classification given by Sivasubramaniam and Menon (1973).

#### Genotypic coefficient of variation (GCV%)

$$GCV\% = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100 \quad (4)$$

Where,

$\bar{X}$  = General mean of trait

#### Phenotypic coefficient of variation (PCV%)

$$PCV\% = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100 \quad (5)$$

#### Broad sense heritability ( $h_b^2$ )

The broad sense heritability was computed for each trait by utilizing the procedure given by Allard (1960) and categorized as low (0 – 30%), moderate (30 – 60%) and high (60% and above) as suggested by Robinson *et al.* (1949).

$$h_b^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100 \quad (6)$$

#### Genetic advance as a per cent of mean

Genetic advance as a per cent of mean was calculated using the below given formula and was classified as low (0 – 10%), moderate (10 – 20%) and

high (20% & above) as per the classification of Johnson *et al.* (1955).

$$GA (\% \text{ of mean}) = \frac{GA}{\bar{X}} \times 100 \quad (7)$$

Where,

GA = Expected genetic advance

### Correlation study

Genotypic correlation coefficient was calculated as per the formula suggested by Hazel (1943).

$$r_{g_i g_j} = \frac{\hat{\sigma}_{g_i g_j}}{\sqrt{\hat{\sigma}_{g_i}^2 \times \hat{\sigma}_{g_j}^2}} \quad (8)$$

Where,

$r_{g_i g_j}$  = Genotypic correlation coefficient between  $i^{\text{th}}$  and  $j^{\text{th}}$  characters

$\hat{\sigma}_{g_i}^2$  = Genotypic variances of  $i^{\text{th}}$  character

$\hat{\sigma}_{g_j}^2$  = Genotypic variances of  $j^{\text{th}}$  character

$\hat{\sigma}_{g_i g_j}$  = Genotypic covariance between  $i^{\text{th}}$  and  $j^{\text{th}}$  characters

### Path coefficient analysis

The path coefficient was analyzed according to the procedure suggested by Wright (1921) and used by Dewey and Lu (1959).

## Results and Discussion

### Analysis of Variance

Analysis of variance showed highly significant difference among the genotypes evaluated for all the quantitative traits except uniformity index indicated the presence of ample amount of genetic variability in the experimental material (Table 2). These results are in accordance with the reports of Meena *et al.* (2024) and Mawblei *et al.* (2022).

### Mean performance

In plant breeding, mean is a simple measure that is used to evaluate phenotypic variability present in the material and forms the foundation for selecting desirable genotype. Mean performance of the genotypes, range and coefficient of variation are presented in Table 3. Days to 50% flowering and boll bursting were varied from 62.67 (Merrell-1-1 × ABC-1) to 80.00 (AHC-26 × GSB-41) and 116.67 (BCS-9 × DB-1502) to 147.67 (AHC-26 × GSB-41), respectively whereas, plant height and

**Table 2 :** Analysis of Variance (ANOVA) showing mean sum of squares for various traits.

Traits	Replication (df = 2)	Genotypes (df = 44)	Error (df = 88)
DFP	0.16	55.44**	2.81
DFBB	27.80	193.68**	16.48
PH	441.11	771.19**	200.03
MPP	0.13	1.98**	0.10
SPP	2.63	11.52**	1.90
BPP	303.39**	384.98**	45.89
BW	0.07	0.48**	0.04
GOT	0.69	8.67**	1.00
FF	0.02	0.28**	0.02
FS	0.64	5.81**	0.68
FL	2.26	6.31**	0.70
UI	1.71	3.25*	1.88
SI	0.12	4.59**	0.20
SCYP	5833.43**	5739.20**	662.36

**Notes:** \*, \*\* Significant at 0.05 & 0.01 levels of probability, respectively. df = Degrees of freedom, DFP = Days to 50% flowering, DFBB = Days to 50% boll bursting, PH = Plant height, MPP = Monopodia per plant, SPP = Sympodia per plant, BPP = Bolls per plant, BW = Boll weight, GOT = Ginning outturn, FF = Fiber fineness, FS = Fiber strength, FL = Fiber length, UI = Uniformity index, SI = Seed index, SCYP = Seed cotton yield per plant.

monopodia per plant showed their range from 219.05 (G.Cot-12 × ABC-1) to 288.66 (BCS-9 × ARBB-27) and 2.53 (G.Cot-12 × GSB-44) to 6.34 (G.Cot-12 × GSB-43-1), respectively. Range for sympodia per plant and bolls per plant was 18.33 (G.Cot-12 × GSB-41) to 27.62 (BCS-9 × GSB-45) and 27.67 (AHC-26 × GSB-41) to 75.80 (BCS-9 × DB-1502), respectively, while for boll weight and ginning outturn range was 2.63 (G.Cot-20 × DB-1602) to 4.57 (AHC-26 × GSB-45) and 25.40 (G.Cot-12 × ARBB-27) to 33.18 (Merrell-1-1 × GSB-43-1), respectively. Fiber fineness and fiber strength showed variable performance from 3.30 (G.Cot-12 × DB-1602) to 4.60 (AHC-26 × ABC-1) and 29.70 (Merrell-1-1 × DB-1502) to 34.60 (G.Cot-20 × GSB-43-1), respectively whereas, fiber length and uniformity index ranged from 29.30 (BCS-9 × GSB-41) to 36.40 (Merrell-1-1 × GSB-43-1) and 83.00 (G.Cot-12 × DB-1602) to 87.00 (G.Cot-12 × GSB-44), respectively. Seed index and seed cotton yield per plant were varied between 10.95 (Merrell-1-1 × DB-1502) & 15.95 (AHC-26 × GSB-45) and 106.27 (AHC-26 × GSB-41) & 290.63 (BCS-9 × DB-1502), respectively.

The general mean for traits DFP, DFBB, PH, MPP, SPP, BPP, BW, GOT, FF, FS, FL, UI, SI and SCYP was

**Table 3 :** Mean performance of the studied genotypes for the various characters.

Genotypes	DF	DFBB	PH	MPP	SPP	BPP	BW
BCS-9×ABC-1	69.67	128.00	254.91	3.33	24.93	51.60	3.73
BCS-9×ARBB-27	69.67	128.67	<b>288.66</b>	3.30	25.41	45.00	3.88
BCS-9×GSB-41	70.67	131.67	265.70	4.87	23.74	49.13	4.29
BCS-9×GSB-43-1	68.67	121.67	252.16	5.47	22.94	75.20	3.68
BCS-9×GSB-44	67.33	120.00	249.76	3.80	23.21	51.33	3.76
BCS-9×GSB-45	68.67	124.00	278.83	4.07	<b>27.62</b>	68.33	4.20
BCS-9×DB-1502	66.00	<b>116.67</b>	249.07	3.33	25.08	<b>75.80</b>	4.19
BCS-9×RHcb-1014	66.00	117.00	249.69	3.62	23.01	68.93	3.93
BCS-9×DB-1602	69.67	131.67	254.92	4.20	26.41	42.67	3.72
GCot-12×ABC-1	70.67	130.00	<b>219.05</b>	3.27	23.01	53.93	3.60
GCot-12×ARBB-27	73.00	134.00	248.60	4.53	22.54	57.93	3.64
GCot-12×GSB-41	79.00	147.33	235.22	4.87	<b>18.33</b>	45.27	3.54
GCot-12×GSB-43-1	68.33	131.00	239.04	<b>6.34</b>	18.74	69.00	3.27
GCot-12×GSB-44	69.33	129.33	245.66	<b>2.53</b>	22.94	52.67	3.35
GCot-12×GSB-45	69.33	129.33	246.48	3.62	21.94	56.20	3.67
GCot-12×DB-1502	67.67	120.00	246.10	3.20	23.27	60.20	3.16
GCot-12×RHcb-1014	68.00	121.33	254.83	4.27	25.54	57.53	3.24
GCot-12×DB-1602	72.00	137.00	232.61	5.94	21.74	43.53	2.93
GCot-20×ABC-1	76.00	141.33	255.45	3.60	24.67	69.20	4.09
GCot-20×ARBB-27	78.67	142.00	286.69	3.87	22.27	62.80	3.53
GCot-20×GSB-41	78.00	140.33	278.05	3.87	21.41	51.00	3.65
GCot-20×GSB-43-1	78.67	134.00	274.81	3.87	19.67	70.53	3.30
GCot-20×GSB-44	70.67	124.33	261.85	3.13	24.08	52.60	3.30
GCot-20×GSB-45	77.67	133.33	249.45	2.87	25.30	50.47	3.62
GCot-20×DB-1502	70.33	122.67	232.43	3.80	23.28	62.20	3.38
GCot-20×RHcb-1014	70.00	121.33	241.01	3.47	21.41	59.20	3.51
GCot-20×DB-1602	79.00	140.00	250.15	4.00	22.81	62.47	<b>2.63</b>
Merrell-1-1×ABC-1	<b>62.67</b>	119.67	234.78	4.13	22.16	74.40	3.14
Merrell-1-1×ARBB-27	69.00	136.00	254.17	3.53	20.54	55.20	3.42
Merrell-1-1×GSB-41	69.33	136.33	255.52	4.13	24.54	49.93	3.58
Merrell-1-1×GSB-43-1	68.67	136.33	257.45	3.60	22.07	44.80	3.44
Merrell-1-1×GSB-44	67.67	126.33	234.28	3.80	21.94	69.67	3.46
Merrell-1-1×GSB-45	67.67	135.00	238.79	3.13	21.28	54.87	3.58
Merrell-1-1×DB-1502	66.33	118.33	236.52	2.67	23.41	58.73	3.54
Merrell-1-1×RHcb-1014	66.00	121.67	249.78	3.80	20.14	67.13	3.69
Merrell-1-1×DB-1602	66.67	131.00	259.57	3.67	23.21	32.33	4.15
AHC-26×ABC-1	68.00	124.67	281.80	4.07	25.14	61.73	3.89

*Table 3 continued...*

Table 3 continued...

AHC-26 × ARBB-27	68.00	130.00	277.18	4.33	23.68	67.33	4.18
AHC-26 × GSB-41	<b>80.00</b>	<b>147.67</b>	280.32	4.86	22.60	<b>27.67</b>	4.04
AHC-26 × GSB-43-1	70.67	137.67	271.18	5.00	22.28	34.73	3.55
AHC-26 × GSB-44	68.00	123.00	252.83	4.40	26.08	56.33	4.27
AHC-26 × GSB-45	64.00	128.67	261.73	4.00	24.60	48.27	<b>4.57</b>
AHC-26 × DB-1502	66.00	119.33	241.56	3.20	24.74	59.87	4.36
AHC-26 × RHcb-1014	69.33	133.33	249.86	4.33	24.82	50.93	4.16
AHC-26 × DB-1602	69.33	124.00	243.30	5.54	22.48	41.40	3.87
<b>General mean</b>	70.22	129.49	253.82	3.98	23.13	56.00	3.68
<b>Range</b>	62.67 – 80.00	116.67 – 147.67	219.05 – 288.66	2.53 – 6.34	18.33 – 27.62	27.67 – 75.80	2.63 – 4.57
<b>CD at 5%</b>	2.72	6.59	22.95	0.51	2.24	10.99	0.31
<b>C.V. (%)</b>	2.39	3.14	5.57	7.84	5.96	12.10	5.19
<b>S. Em. ±</b>	0.97	2.34	8.17	0.18	0.80	3.91	0.11

Table 3 continued...

<b>Genotypes</b>	<b>GOT</b>	<b>FF</b>	<b>FS</b>	<b>FL</b>	<b>U</b>	<b>SI</b>	<b>SCYP</b>
BCS-9 × ABC-1	28.43	4.10	33.60	33.60	<b>87.00</b>	12.71	184.04
BCS-9 × ARBB-27	26.82	4.00	33.50	35.80	<b>87.00</b>	13.08	167.48
BCS-9 × GSB-41	28.29	3.80	32.10	<b>29.30</b>	84.00	13.73	202.48
BCS-9 × GSB-43-1	28.96	3.70	33.90	36.10	<b>87.00</b>	13.31	265.90
BCS-9 × GSB-44	28.84	4.10	33.40	35.00	<b>87.00</b>	13.46	185.34
BCS-9 × GSB-45	28.80	3.90	33.00	34.60	86.00	15.15	278.94
BCS-9 × DB-1502	28.85	3.70	32.20	33.20	85.00	12.87	<b>290.63</b>
BCS-9 × RHcb-1014	29.36	3.90	32.10	34.90	86.00	13.19	262.73
BCS-9 × DB-1602	28.37	3.90	34.40	34.90	<b>87.00</b>	13.14	152.81
G.Cot-12 × ABC-1	27.23	3.70	34.10	33.20	<b>87.00</b>	13.01	188.72
G.Cot-12 × ARBB-27	<b>25.40</b>	3.70	33.70	33.80	<b>87.00</b>	13.89	198.96
G.Cot-12 × GSB-41	29.25	3.50	31.00	35.90	84.00	13.09	156.73
G.Cot-12 × GSB-43-1	27.48	3.50	33.70	34.70	85.00	12.80	219.16
G.Cot-12 × GSB-44	29.84	3.60	33.10	33.80	<b>87.00</b>	13.06	163.44
G.Cot-12 × GSB-45	27.86	3.70	33.20	32.80	<b>87.00</b>	14.19	196.04
G.Cot-12 × DB-1502	30.14	3.70	33.30	32.90	86.00	12.41	183.69
G.Cot-12 × RHcb-1014	28.64	3.40	32.20	32.90	85.00	13.41	176.80
G.Cot-12 × DB-1602	27.25	<b>3.30</b>	33.40	34.00	<b>83.00</b>	13.05	121.15
G.Cot-20 × ABC-1	29.00	4.20	31.50	32.90	85.00	13.56	263.57
G.Cot-20 × ARBB-27	26.88	4.10	34.40	34.40	<b>87.00</b>	13.30	214.80
G.Cot-20 × GSB-41	28.61	3.90	32.80	34.10	84.00	13.31	181.91
G.Cot-20 × GSB-43-1	32.47	3.70	<b>34.60</b>	34.90	86.00	12.90	227.47
G.Cot-20 × GSB-44	30.17	3.90	34.00	34.30	86.00	13.05	166.75

Table 3 continued...

Table 3 continued...

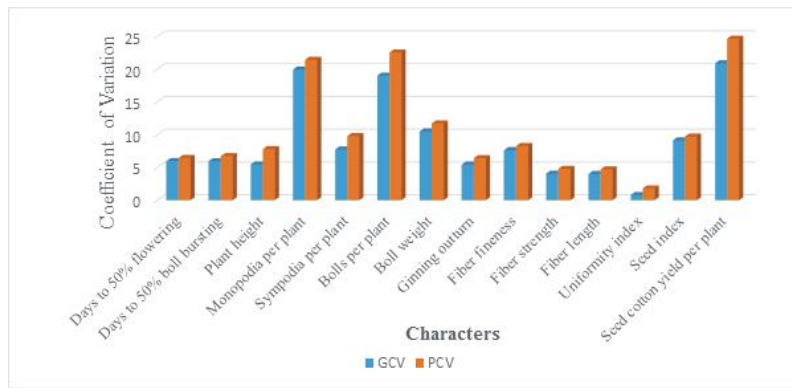
G.Cot-20 × GSB-45	30.27	3.90	32.40	30.00	85.00	12.76	178.36
G.Cot-20 × DB-1502	30.18	3.90	33.30	32.60	86.00	12.33	202.10
G.Cot-20 × RHcb-1014	29.82	3.90	32.70	33.60	86.00	12.89	199.90
G.Cot-20 × DB-1602	31.35	4.00	31.90	34.20	85.00	12.71	160.37
Merrell-1-1 × ABC-1	31.39	4.40	32.70	33.10	86.00	11.40	222.20
Merrell-1-1 × ARBB-27	29.06	4.30	32.60	35.90	86.00	11.37	182.39
Merrell-1-1 × GSB-41	32.70	3.60	32.00	34.00	85.00	11.87	174.85
Merrell-1-1 × GSB-43-1	<b>33.18</b>	3.90	31.20	<b>36.40</b>	86.00	11.97	147.08
Merrell-1-1 × GSB-44	31.61	4.10	30.80	33.60	86.00	11.70	236.63
Merrell-1-1 × GSB-45	30.42	4.00	31.40	34.30	85.00	13.37	192.07
Merrell-1-1 × DB-1502	31.73	4.20	<b>29.70</b>	33.50	86.00	<b>10.95</b>	199.55
Merrell-1-1 × RHcb-1014	32.02	4.00	30.60	34.30	<b>87.00</b>	11.54	222.46
Merrell-1-1 × DB-1602	31.87	3.70	29.80	34.00	85.00	11.27	123.55
AHC-26 × ABC-1	28.33	<b>4.60</b>	32.80	35.40	85.00	15.40	236.47
AHC-26 × ARBB-27	28.45	4.20	31.30	36.20	85.00	15.33	269.04
AHC-26 × GSB-41	27.57	3.50	30.00	35.90	84.00	14.90	<b>106.27</b>
AHC-26 × GSB-43-1	29.75	3.90	34.50	35.50	86.00	15.02	117.75
AHC-26 × GSB-44	28.55	4.50	30.80	33.70	86.00	15.81	232.24
AHC-26 × GSB-45	29.59	4.40	31.00	35.50	86.00	<b>15.95</b>	213.42
AHC-26 × DB-1502	29.99	4.50	29.80	34.30	86.00	14.41	244.24
AHC-26 × RHcb-1014	28.64	4.30	31.10	36.10	85.00	14.66	204.03
AHC-26 × DB-1602	29.42	4.20	30.70	35.20	84.00	14.65	155.20
<b>General mean</b>	29.40	3.93	32.36	34.21	85.69	13.29	197.10
<b>Range</b>	25.40 – 33.18	3.30 – 4.60	29.70 – 34.60	29.30 – 36.40	83.00 – 87.00	10.95 – 15.95	106.27 – 290.63
<b>CD at 5%</b>	1.62	0.20	1.34	1.36	2.22	0.72	41.76
<b>C.V. (%)</b>	3.40	3.16	2.55	2.45	1.60	3.34	13.06
<b>S. Em. ±</b>	0.58	0.07	0.48	0.48	0.79	0.26	14.86

70.22, 129.49, 253.82, 3.98, 23.13, 56.00, 3.68, 29.40, 3.93, 32.36, 34.21, 85.69, 13.29 and 197.10, respectively. The number of genotypes showing superior performance in desired direction as compared to general mean for traits DFF, DFBB, PH, MPP, SPP, BPP, BW, GOT, FF, FS, FL, UI, SI and SCYP were 30, 23, 20, 25, 22, 23, 20, 20, 26, 24, 23, 27, 20 and 22, respectively.

The genotypes Merrell-1-1 × ABC-1 (62.00 days), AHC-26 × GSB-45 (64.00 days) and BCS-9 × DB-1502, BCS-9 × RHcb-1014, Merrell-1-1 × RHcb-1014, AHC-26 × DB-1502 (66.00 days) were early maturing in nature. BCS-9 × DB-1502 (75.80), BCS-9 × GSB-43-1 (75.20) and Merrell-1-1 × ABC-1 (74.40) were identified as a

best genotypes for bolls per plant. The genotypes AHC-26 × GSB-45 (4.57 g), AHC-26 × DB-1502 (4.36 g) and BCS-9 × GSB-41 (4.29 g) showed superior performance for boll weight. For fiber fineness, the genotypes G.Cot-12 × DB-1602 (3.30 ñg/inch), G.Cot-12 × RHcb-1014 (3.40 ñg/inch) and G.Cot-12 × GSB-41, G.Cot-12 × GSB-43-1, AHC-26 × GSB-41 (3.50 ñg/inch) were adjudged as a best performing genotypes. The superior genotypes for fiber length were Merrell-1-1 × GSB-43-1 (36.40 mm), AHC-26 × ARBB-27 (36.20 mm) and BCS-9 × GSB-43-1, AHC-26 × RHcb-1014 (36.10 mm). Genotypes BCS-9 × DB-1502 (290.63 g), BCS-9 × GSB-45 (278.94 g) and AHC-26 × ARBB-27 (269.04 g) were found excellent for seed cotton yield per plant.





**Fig. 1 :** Genotypic and Phenotypic coefficient of variation for different characters.

population.

The Genotypic Coefficient of Variation (GCV%) and Phenotypic Coefficient of Variation (PCV%) analyzed for 14 seed cotton yield and its component traits in 45 cotton genotypes are presented in Table 4. The results depicted that the difference between GCV% and PCV% was low for all the studied traits, suggesting traits have low environmental influence (Table 4 and Fig. 1). High GCV and PCV was observed for seed cotton yield per plant (20.87, 24.62) showing the plenty amount of variation among the genotypes for this trait.

**Table 4 :** Estimation of genetic variability parameters for the various traits in cotton.

Characters	$\sigma_g^2$	$\sigma_p^2$	$\sigma_e^2$	GCV (%)	PCV (%)	$h_b^2$ (%)	GAM
Days to 50% flowering	17.54	20.36	2.81	5.96	6.43	86.17	11.41
Days to 50% boll bursting	59.06	75.55	16.48	5.94	6.71	78.18	10.81
Plant height	190.39	390.42	200.03	5.44	7.78	48.77	7.82
Monopodia per plant	0.63	0.73	0.10	19.92	21.40	86.57	38.17
Sympodia per plant	3.21	5.11	1.90	7.74	9.77	62.81	12.64
Bolls per plant	113.03	158.92	45.89	18.98	22.51	71.12	32.98
Boll weight	0.15	0.19	0.04	10.48	11.69	80.32	19.35
Ginning outturn	2.56	3.56	1.00	5.44	6.41	71.87	9.50
Fiber fineness	0.09	0.11	0.02	7.62	8.25	85.33	14.51
Fiber strength	1.71	2.39	0.68	4.04	4.78	71.51	7.04
Fiber length	1.87	2.57	0.70	4.00	4.69	72.66	7.02
Uniformity index	0.46	2.33	1.88	0.79	1.78	19.58	0.72
Seed index	1.47	1.66	0.20	9.11	9.70	88.15	17.62
Seed cotton yield per plant	1692.28	2354.64	662.36	20.87	24.62	71.87	36.45

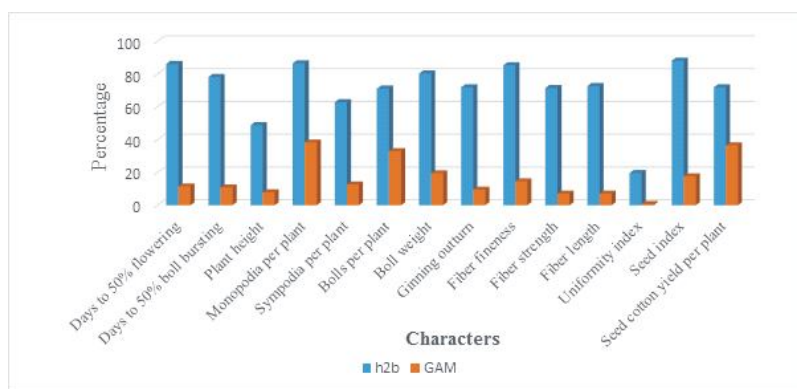
Notes:  $\sigma_g^2$  = Genotypic variance,  $\sigma_p^2$  = Phenotypic variance,  $\sigma_e^2$  = Environmental variance, GCV= Genotypic Coefficient of Variation, PCV = Phenotypic Coefficient of Variation,  $h_b^2$  = Heritability in broad sense, GAM= Genetic Advance as per cent of Mean.

### Estimation of Variability parameters

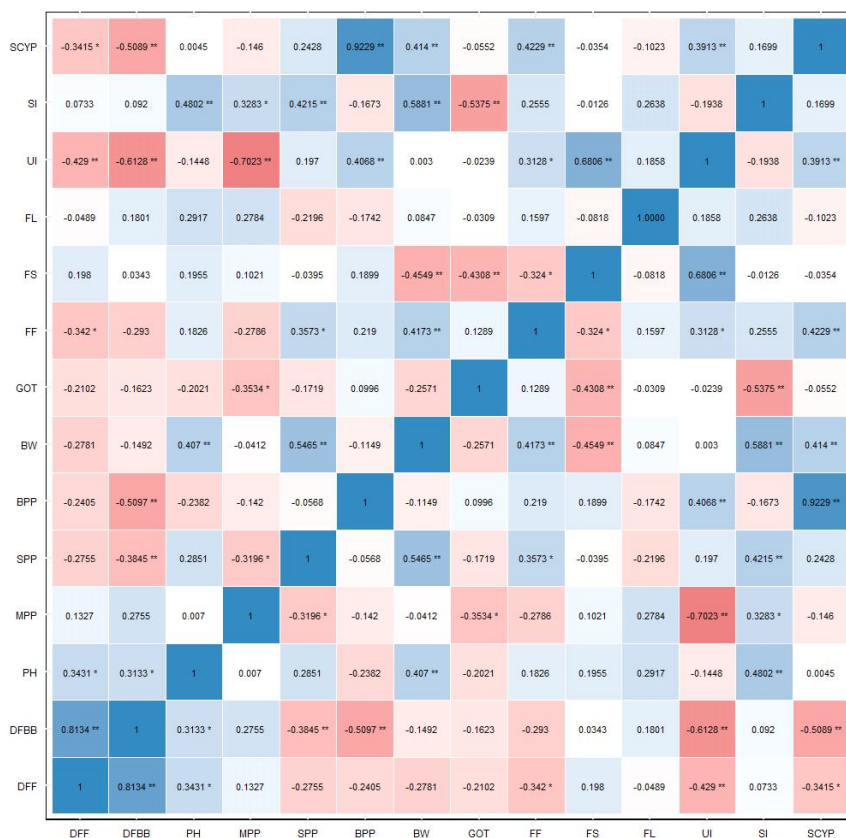
Those traits having high genotypic and total phenotypic variability is strongly influenced by genetic factors but environmental factors also play a significant role. Besides this, high genetic variability suggests excellent potential for improvement through selection. In contrast, the traits with low genotypic and total phenotypic variability suggests that, the trait is relatively stable and have minimal influence of both genetic and environmental factors. The lack of variability might indicate that the trait is either highly conserved or reached a selection plateau thus offering very little scope for further improvement through simple selection. Moderate to low variability indicates the need for improvement of base

Therefore, simple selection would be rewarding for further improvement of seed cotton yield per plant. This was in conformity with the findings of Manonmani *et al.* (2019), Chaudhari *et al.* (2017) and Rathinavel *et al.* (2017). Moderate GCV and high PCV values were observed for monopodia per plant (19.91, 21.40) and bolls per plant (18.98, 22.51). Boll weight (10.48, 11.69) showed moderate estimates of GCV and PCV hence suggesting the moderate variability present in the materials for boll weight. These results are in accordance with the reports of Meena *et al.* (2024), Manonmani *et al.* (2019) and Chaudhari *et al.* (2017). Low estimates of GCV and PCV were found for days to 50% flowering (5.96, 6.43), days to 50% boll bursting (5.94, 6.71), plant height (5.44,





**Fig. 2 :** Heritability and genetic advance as a % of mean of various characters.



**Fig. 3 :** Correlogram showing correlation between seed cotton yield and its attributing traits. **Notes:** \*, \*\* Significant at 0.05 & 0.01 levels of probability, respectively. DFF = Days to 50% flowering, DFBB = Days to 50% boll bursting, PH = Plant height, MPP = Monopodia per plant, SPP = Sympodia per plant, BPP = Bolls per plant, BW = Boll weight, GOT = Ginning outturn, FF = Fiber fineness, FS = Fiber strength, FL = Fiber length, UI = Uniformity index, SI = Seed index, SCYP = Seed cotton yield per plant.

7.78), sympodia per plant (7.74, 9.77), ginning outturn (5.44, 6.41), fiber fineness (7.62, 8.25), fiber strength (4.04, 4.78), fiber length (4.00, 4.69), uniformity index (0.79, 1.78) and seed index (9.11, 9.70) indicating low range of variation in the genotypes for these traits, thus providing little scope for further improvement of these traits through simple selection. Similar results were reported earlier by

Meena *et al.* (2024), Mawblei *et al.* (2022) and Manonmani *et al.* (2019).

Heritability and genetic advance as a percent of mean for all the traits are presented in (Table 4 and Fig. 2). High heritability helps breeders to select superior genotypes based on phenotypic expression of quantitative traits (Johnson *et al.*, 1955). The result showed that, the heritability varies from 19.58% (uniformity index) to 88.15% (seed index). High heritability values were obtained for days to 50% flowering (86.17%), days to 50% boll bursting (78.18%), monopodia per plant (86.57%), sympodia per plant (62.81%), bolls per plant (71.12%), boll weight (80.32%), ginning outturn (71.87%), fiber fineness (85.33%), fiber strength (71.51%), fiber length (72.66%), seed index (88.15%) and seed cotton yield per plant (71.87%). Moderate heritability estimate was obtained for plant height (48.77%) indicating that selection based on phenotypic performance would be rewarding on partitioning of environmental variances. Low heritability was recorded for uniformity index (19.58%). This is an indicative of the fact that character is rather more influenced by environment and may not respond much to selection.

The results of genetic advance as a percent of mean indicated that the characters *viz.*, monopodia per plant (38.17), bolls per plant (32.98) and seed cotton yield per plant (36.45) exhibited high genetic advance as per cent of mean. Moderate genetic advance as per cent of mean was depicted by days to 50% flowering (11.41), days to 50% boll bursting (10.81), sympodia per plant (12.64), boll weight (19.35), fiber fineness (14.51) and seed index (17.62). The traits *viz.*, plant height (7.82), ginning outturn (9.50), fiber strength (7.04), fiber length (7.02) and uniformity index (0.72) exhibited low genetic advance as a per cent of mean.

Knowledge of heritability coupled with genetic advance is most useful than heritability alone in predicting the scope for genetic improvement of the character through selection. In the current investigation, high heritability ( $h^2_p$ ) accompanied with high genetic advance

as a per cent of mean (GAM) was observed for monopodia per plant, bolls per plant and seed cotton yield per plant. Hence phenotypic selection would be more effective for improvement of these traits. These results corroborates the findings of Mawblei *et al.* (2022), Manonmani *et al.* (2019) and Chaudhari *et al.* (2017). High heritability associated with moderate genetic advance as a per cent of mean was observed for days to 50% flowering, days to 50% boll bursting, sympodia per plant, boll weight, fiber fineness and seed index. High heritability with low genetic advance as a per cent of mean was found for ginning outturn, fiber strength and fiber length. Moderate heritability in association with low genetic advance as a percent of mean was present in plant height. Low heritability coupled with low genetic advance as a per cent of mean was observed in uniformity index indicates high influence of environment and consequently its selection may not be effective, thus limited scope for improvement of this trait by selection. The obtained results were in line with Mawblei *et al.* (2022) for boll weight; Manonmani *et al.* (2019) for ginning outturn and fiber length; Chaudhari *et al.* (2017) for days to 50% flowering and fiber fineness; Rathinavel *et al.* (2017) for seed index.

### Correlation study

Genotypic correlations for all trait combinations are presented in Fig. 3. Genetic correlations may be due to pleiotropy, tight linkage, linkage disequilibrium or relationship with other unrecorded traits. Linkage can be broken through recombination but in case of pleiotropy induced correlation, genetic improvement in one trait is not possible without a change in other associated traits, as it can't be manipulated through recombination. When two characters are highly correlated, selecting one will automatically results in the selection of another one.

### Correlation between yield and other component traits

The genotypic correlation coefficient estimates varied from -0.70 (MPP *vs.* UI) to 0.92 (BPP *vs.* SCYP). The seed cotton yield per plant exhibited significantly positive genotypic correlation with bolls per plant, boll weight, fiber fineness and uniformity index. The outcome suggests that, seed cotton yield can be improved in these genotypes by using above traits as selection criteria in advanced generations. Positive association of seed cotton yield per plant with bolls per plant, boll weight and fiber fineness was also reported by Kadam *et al.* (2024). Mawblei *et al.* (2022) reported positive association of bolls per plant and boll weight; Jyoti *et al.* (2021), Bhatti *et al.* (2020) and Chapepa *et al.* (2020) reported positive correlation

of bolls per plant with seed cotton yield per plant. Days to 50% flowering and days to 50% boll bursting were significantly and negatively associated with seed cotton yield per plant. It was in confirmation with Kadam *et al.* (2024).

### Path Coefficient analysis

The character association as determined by simple correlation may not provide an exact relationship between yield and its attributes. In contrast, path analysis divides the correlation coefficients into direct as well as indirect effects, elucidating the causal relationships among traits that cannot be explained by correlation studies.

In present investigation, seed cotton yield per plant was considered as the dependent variable and remaining thirteen yield contributing traits were taken as independent variables. The findings of genotypic path co-efficient analysis showing direct (diagonal values) and indirect effects of different attributing traits on seed cotton yield per plant was given in Table 5. According to the results, bolls per plant had highest direct effect on seed cotton yield per plant (1.0911) followed by boll weight (0.5348), days to 50% boll bursting (0.2452), sympodia per plant (0.1131), fiber length (0.0487), fiber strength (0.0454), ginning outturn (0.0250) and seed index (0.0113). These traits can be considered as a primary selection criterion in breeding programs for improvement of seed cotton yield. Remaining traits *viz.*, uniformity index (-0.0190), monopodia per plant (-0.0223), fiber fineness (-0.0329), plant height (-0.0478) and days to 50% flowering (-0.1009) exerted negative direct effect on seed cotton yield per plant. The correlation of bolls per plant and boll weight with seed cotton yield was significantly positive with their high positive direct effects. This results indicates that seed cotton yield was in true correlation with bolls per plant and boll weight. Uniformity index and fiber fineness showed significant positive correlation with seed cotton yield per plant, but they have negative direct effect on seed cotton yield. Thus its positive correlation with seed cotton yield per plant was mainly due to its indirect effect *via* bolls per plant.

Jyoti *et al.* (2021) also reported positive direct effect of boll weight, ginning outturn, sympodia per plant and seed index on seed cotton yield per plant. Positive and direct effects of bolls per plant on seed cotton yield per plant was reported earlier by Mawblei *et al.* (2022) and Pujer *et al.* (2014). The residual effect of -0.1412 suggested that, the characters included in the study were sufficient to explain variability present in the material.

In cotton, a greater number of bolls per plant and higher boll weight are desirable for high seed cotton yield;

**Table 5 :** Genotypic path coefficient analysis showing direct as well as indirect effects of different traits on seed cotton yield in cotton.

Traits	DFB	DFBB	PH	MPP	SPP	BPP	BW	GOT	FF	FS	FL	U	SI	SCYP
DFB	<b>-0.1009</b>	0.1994	-0.0164	-0.0030	-0.0312	-0.2624	-0.1487	-0.0053	0.0113	0.0090	-0.0024	0.0081	0.0008	-0.342*
DFBB	-0.0821	<b>0.2452</b>	-0.0150	-0.0061	-0.0435	-0.5562	-0.0798	-0.0041	0.0097	0.0016	0.0088	0.0116	0.0010	-0.509**
PH	-0.0346	0.0768	<b>-0.0478</b>	-0.0002	0.0322	-0.2599	0.2177	-0.0051	-0.0060	0.0089	0.0142	0.0027	0.0054	0.005
MPP	-0.0134	0.0676	-0.0003	<b>-0.0223</b>	-0.0361	-0.1549	-0.0220	-0.0088	0.0092	0.0046	0.0136	0.0133	0.0037	-0.146
SPP	0.0278	-0.0943	-0.0136	0.0071	<b>0.1131</b>	-0.0620	0.2923	-0.0043	-0.0118	-0.0018	-0.0107	-0.0037	0.0048	0.243
BPP	0.0243	-0.1250	0.0114	0.0032	-0.0064	<b>1.0911</b>	-0.0615	0.0025	-0.0072	0.0086	-0.0085	-0.0077	-0.0019	0.923**
BW	0.0281	-0.0366	-0.0194	0.0009	0.0618	-0.1254	<b>0.5348</b>	-0.0064	-0.0137	-0.0207	0.0041	-0.0001	0.0066	0.414**
GOT	0.0212	-0.0398	0.0097	0.0079	-0.0194	0.1087	-0.1375	<b>0.0250</b>	-0.0042	-0.0196	-0.0015	0.0005	-0.0061	-0.055
FF	0.0345	-0.0718	-0.0087	0.0062	0.0404	0.2389	0.2232	0.0032	<b>-0.0329</b>	-0.0147	0.0078	-0.0059	0.0029	0.423**
FS	-0.0200	0.0084	-0.0093	-0.0023	-0.0045	0.2072	-0.2433	-0.0108	0.0107	<b>0.0454</b>	-0.0040	-0.0129	-0.0001	-0.035
FL	0.0049	0.0441	-0.0139	-0.0062	-0.0248	-0.1901	0.0453	-0.0008	-0.0053	-0.0037	<b>0.0487</b>	-0.0035	0.0030	-0.102
UI	0.0433	-0.1503	0.0069	0.0157	0.0223	0.4439	0.0016	-0.0006	-0.0103	0.0309	0.0090	<b>-0.0190</b>	-0.0022	0.391**
SI	-0.0074	0.0226	-0.0229	-0.0073	0.0477	-0.1826	0.3145	-0.0134	-0.0084	-0.0006	0.0128	0.0037	<b>0.0113</b>	0.170

**Notes:** \*, \*\* Significant at 0.05 & 0.01 levels of probability, respectively. DFB = Days to 50% flowering, DFBB = Days to 50% boll bursting, PH = Plant height, MPP = Monopodia per plant, SPP = Symopodia per plant, BPP = Bolls per plant, BW = Boll weight, GOT = Ginning outturn, FF = Fiber fineness, FS = Fiber strength, FL = Fiber length, UI = Uniformity index, SI = Seed index, SCYP = Seed cotton yield per plant.

fiber fineness and uniformity index are important fiber quality traits. The path coefficient analysis revealed that bolls per plant and boll weight could be considered as major yield contributing traits and should be given due weightage while exercising selection for improvement in seed cotton yield as they exhibited high positive direct effect as well as positive correlation with seed cotton yield and positive indirect effect of fiber fineness and uniformity index *via* bolls per plant.

## Conclusion

The genetic improvement of yield and fiber quality in cotton is a complex but crucial task for enhancing the productivity and competitiveness of the cotton industry. Interspecific hybridization between *G. hirsutum* and *G. barbadense* is attempted in cotton to combine desirable traits from both the species. In this study, we observed large spectrum of variation for all the studied traits among developed interspecific hybrids thus, there is a scope for further improvement in advanced segregating generations. Many hybrids were also recorded superior performance for various traits than their parents which showed improvement in genotype after hybridization. All the component traits are differently correlated with seed cotton yield. Among all, Bolls per plant and boll weight showed true correlation with seed cotton yield per plant hence, these traits should be considered as important selection criteria for future cotton breeding programme. Through the combined use of genetic variability assessment, correlation studies and path analysis, this study provide a comprehensive understanding of the genetic architecture governing important traits, ultimately contributing to more efficient and targeted breeding strategies for producing high-yielding cotton cultivars with superior fiber quality.

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