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Estimating Genetic Variability for Yield, Yield Contributing and Fibre Quality Traits in Upland Cotton (*Gossypium hirsutum* L.)

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ABSTRACT

The study was conducted during the *kharif* season (July-October, 2022) at Cotton Research Station in Nanded to explore the genetic variability in upland cotton (*Gossypium hirsutum* L.) using 46 elite genotypes and four reference checks, which had been planted in a Randomized Block Design. The study assessed 13 key traits encompassing morphology, fibre quality, and yield. Understanding the association between yield components and fibre characteristics required data on the diversity and scope of variation, genetic progress, and heritability. Notably, traits such as seed cotton yield plant^{-1}, number of bolls plant^{-1}, number of sympodia plant^{-1}, plant height and boll weight exhibited substantial genotypic and phenotypic variation. Phenotypic variances surpassed genotypic variances across nearly all traits, indicating that the observed variation arose from both genotypes and environmental influences. This suggested that these traits had a strong additive genetic component, making them suitable for efficient improvement through selection. Notably, SCS 793, ARBH 83, SCS 1061, and NDLH 2061-1 emerged as superior genotypes for seed cotton yield per plant, while ARBC 1352, GBHV 180, BWR-152-1, G.Cot 22, CNH 1122 and PH 1060 outperformed the control varieties in terms of fibre quality traits. The study's findings highlighted that the number of bolls plant^{-1}, plant height, boll weight, number of sympodia plant^{-1}, ginning percentage, lint index, and fibre fineness were the most critical traits for the effective selection of superior American cotton genotypes.

KEYWORDS: Upland cotton, genetic variability, genetic advance, phenotypic variance

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1. INTRODUCTION

Cotton has been mentioned in ancient Indian Vedas, where the Vedic people had knowledge about weaving methods. Cotton (*Gossypium hirsutum* L.) serves primarily for fibre and oil production, playing a pivotal role in the country's economic landscape (Satish, 2021). Cotton is a major crop, with 64% of its fiber used in apparel, 28% in household furnishings, and 8% in industrial applications (Venkatesan et al., 2024). It's the leading non-food crop, supporting the $3 trillion global fashion industry and contributing $1.3 trillion to global garment exports in 2019 (Tridge, 2019). Cotton is grown in tropical and subtropical regions, with India, China, the U.S., and Brazil accounting for 75% of production. In India, cotton is grown in three main zones: Northern (Punjab, Haryana, Rajasthan), Central (Gujarat, Maharashtra, Madhya Pradesh), and Southern (Andhra Pradesh, Tamil Nadu, Karnataka). India is the top producer of cottonseed, with 126.14 lakh hectares cultivated and a productivity of 439 kg ha^{-1}. In 2022-23, India produced 337 lakh bales. Maharashtra leads in area, Gujarat in yield, and Tamil Nadu in total production. The Gossypium genus encompasses 50 species, consisting of 45 diploids (2n=2x=26) and 5 tetraploids (2n=4x=52), spread across different regions worldwide (Ahsan et al., 2015). India holds a unique distinction as the sole country cultivating all four commercially viable Gossypium species: *Gossypium arboreum* and *G. herbaceum* (Asiatic cotton), *G. barbadense* (Egyptian cotton), and *G. hirsutum* (American upland cotton), in addition to hybrid cotton (Deshmukh and Reddy, 2023). *Gossypium hirsutum*, also referred to as upland cotton or Mexican cotton, stands as the most extensively planted cotton species globally. Within *Gossypium hirsutum*, various varieties or crossbred cultivars exhibit diverse fibre lengths and resilience to different growing conditions (Gibely et al., 2015). Longer-length varieties are called "long-staple upland," while shorter-length varieties are referred to as "short-staple upland." *G. hirsutum* L. (American cotton) and *G. barbadense* L. (Egyptian cotton) are known for their superior fibre quality (Eldessouky et al., 2021). In India, *Gossypium hirsutum* accounts for 99.9% of the hybrid cotton, and all existing Bt cotton hybrids belong to either *G. hirsutum* or are inter-specific hybrids involving *G. barbadense* (Kumar et al., 2019). Genetic improvement in fibre quality is one of the main challenges for cotton breeders. In response to the requirements of the contemporary textile industry, genetic enhancements have been implemented in cotton to improve fibre quality and yield traits across various populations and systems of cotton production (Mawblei et al., 2022). Therefore, simultaneously improving fibre quality and increasing yield potential in diverse areas and planting systems pose a significant challenge in cotton production. Fiber quality traits typically encompass characteristics such as fibre length, uniformity, strength, elongation, and micronaire value (Gnanasekaran et al., 2020). Among these, fibre strength and length are deemed the most crucial properties that significantly influence yarn quality. The uniformity ratio, which determines fibre uniformity, is calculated as the ratio between 50% span length and 2.5% span length. Micronaire serves as a gauge of the air permeability of compressed cotton fibres, commonly utilized as an indicator of both fibre fineness and maturity (Sarwar et al., 2021). Genetic diversity is an essential tool in plant breeding for producing cultivars with desired characteristics (Miranda et al., 2020). Studying the relationship between yield components and fibre characters requires information about the nature and extent of variation, genetic advances, and heritability (Iqbal and Farooq, 2023). The current research endeavours to explore the genetic variability concerning yield, yield-contributing factors, and the quality of fibre traits in cotton. The present research aimed to study genetic variability for yield, yield contributing, and fibre quality traits in cotton.

2. MATERIALS AND METHODS

The present study comprised of forty-six diverse genotypes along with four standard checks of cotton (*Gossypium hirsutum* L.) that had been obtained from different sources. The experiment was conducted at Cotton Research Station, Nanded during *kharif* (July-October, 2022). These elite genotypes of *G. hirsutum* were sown in a plot using Randomized Block Design with two replications and involving two rows per genotype per plot of size 1.2×4.5 m^2. Spacing was maintained at approximately 60 cm between row-row and 30 cm between each plant. Four standard checks such as PH 348, NH 545, NH 615 and Suraj were obtained from CRS, Nanded and CICR, Nagpur respectively.

Recommended cultivation practices and plant protection measures had been adopted as per recommendations and efforts were made to keep experimental plot free from weeds and pest. Five plants at random in each plot and replication were chosen and utilized for recording observations for thirteen characteristics such as days to 50% flowering, plant height (cm), number of sympodia plant^{-1}, number of bolls plant^{-1}, boll weight (g), seed index (g), lint index, ginning percentage (%) on plot basis in each replication. The fibre quality traits viz., upper half mean length (mm), fibre strength (g tex^{-1}), fibre fineness (μg inch^{-1}) and uniformity ratio (%) were assessed using the high-volume instrument (HVI) in the well-equipped laboratory of CICR, Nagpur. Mean values for all the traits per replication were subjected to statistical analysis. Analysis of variance was conducted to determine the significance of disparities among genotypes for each trait. The mean and variance of each character were calculated by standard statistical procedure suggested by Panse and Sukhatme (1961). The genotypic and phenotypic coefficient of variation (GCV and PCV) were computed following Burton's method (1952). Broad sense heritability (h^2) was determined based on Allard's method (1960) and categorized as low (<30%), moderate (30–60%), and high (>60%) as outlined by Johnson et al. (1955). Pairwise analysis of covariance involved examining two characters simultaneously. Genotypic and phenotypic covariances were calculated using the formulas described by Singh and Chaudhary (1977).

3. RESULTS AND DISCUSSION

The analysis of variance for thirteen traits was displayed in Table 1 indicating significant differences among the treatments for all the studied traits. The mean performance of the forty-six genotypes and four checks was evaluated for thirteen diverse traits contributing to yield and fibre quality as shown in Table 2. The mean for days to 50% flowering ranged from 63.50 to 70 days wherein ARBC 64 and CNH 2050 were identified as early flowering genotypes while RHC-HD 1312 was identified as a late flowering genotype. Plant height exhibited a wide range, varying from 46.90 to 118.10 cm, with the highest plant height observed in CNH 1122 and KH 113 while ARBC 1352 was found as a dwarf genotype. Strains such as ARBC 64, ARBC 757, CCH 1110, H 1236, and CNH 1122 recorded higher number of sympodia compared to control varieties.

The number of bolls plant^{-1} exhibited a wide variation, ranging from 9 to 26.20, with NDLH 1061-1 recording the most bolls per plant. The mean value for the seed index was 8.71 g, with BS 2 recording the highest seed index and lint index values. Seed cotton yield per plant displayed a wide range with an average of 35.02 g and SCS 793 recorded the highest seed cotton yield per plant (53.80 g). The genotype NH 545 recorded the highest boll weight. Ginning percent exhibited significant variation with a mean of 35.77, and ADB 102 exhibited the highest ginning percent (39.40%). Most genotypes displayed similar values for the uniformity ratio (78–82%). BWR-152-1, PAIG 363, JLA-804 and NDLA-3089 recorded higher fibre strength values. DSC 1351, ARBC 1352, TCH 5811 and ARBC 757 exhibited good micronaire values.

Table 1: Analysis of Variance (ANOVA) for thirteen characters in cotton

Sl. No.	Source of variation	D.F.	Mean sum of squares					
			Days to 50% flowering	Plant height (cm)	No. of sympodia plant^{-1}	No. of bolls plant^{-1}	Seed cotton yield plant^{-1} (g)	Seed index (g)
			1	2	3	4	5	6
1.	Replication	1	1.44	1.081	0.462	0.270	3.132	0.36
2.	Treatments	49	5.607**	460.635**	5.173**	25.607**	98.749**	1.353**
3.	Error	50	0.480	13.555	0.228	0.666	14.385	0.465

Table 1: Continue...

Sl. No.	Source of variation	D.F.	Mean sum of squares						
			Lint index (g)	Ginning outturn (%)	Boll weight (g)	Upper half Mean Length (mm)	Uniformity ratio (%)	Fiber strength (g/tex)	Fiber fineness (µg/inch)
			7	8	9	10	11	12	13
1.	Replication		0.0237	0.921	0.174	0.0227	0.5155	0.0005	0.0054
2.	Treatments		0.361**	6.726**	0.793**	4.307**	4.747**	5.755**	0.503**
3.	Error		0.026	0.471	0.081	0.431	0.2896	0.371	0.019

*,** = Significant at (*p*=0.05) and (*p*=0.01) level of significance respectively

A considerable range of variability was noted across the majority of traits related to yield contribution. Similar results were reported by Vinodhana et al. (2013), Dhivya et al. (2014), Reddy et al. (2014), Dahiphale et al. (2015), Latif et al. (2015), Hussain et al. (2020) where they found the major amount of variability among the morphological traits they have studied. GCV values ranged from 1.17 to 21.64 and PCV values ranged from 2.20 to 22.21. In Table 3, it was evident that the phenotypic variance exceeded the genotypic variance across nearly all the characters. This indicated that the observed variation was not solely attributed to genotypes but was also influenced by environmental factors. Reddy et al. (2014), Farooq et al. (2014), Santoshkumar et al. (2014), Aarthi et al. (2018), Gnanasekaran et al. (2018), Bhatti et al.

Table 2: Mean performance of thirteen characters in fifty genotypes of cotton

Sl. No.	Genotype	DF	PH	NSP	NBP	SCYP	SI	LI	GO	BW	UHML	UR	FS	FF
1.	SCS 793	64.50	98.70	10.30	22.60	53.80	9.75	3.67	37.85	3.30	25.10	79.00	26.30	5.50
2.	SCS 1061	65.00	90.50	9.70	14.40	45.80	9.25	3.37	39.25	3.32	27.50	80.00	27.30	4.70
3.	DSC 55	68.50	95.10	8.50	13.20	33.70	8.00	3.00	36.60	3.06	25.50	81.00	23.30	5.20
4.	DSC 1351	66.50	87.30	7.50	10.60	24.30	9.25	3.19	33.40	3.15	26.90	79.00	24.90	3.60
5.	BS 41	66.50	85.50	11.10	18.10	40.50	9.75	3.75	34.25	2.66	26.60	80.00	27.10	4.50
6.	BS 2	64.50	73.70	11.10	18.30	30.90	10.75	4.54	35.40	2.48	24.50	80.00	23.90	4.80
7.	CCH 2629	66.00	69.00	7.50	11.60	29.15	8.75	3.23	38.80	3.36	24.80	81.00	25.80	4.70
8.	CCH 1110	69.00	69.40	11.90	17.50	26.70	7.25	3.73	34.50	2.56	23.60	80.00	25.50	4.60
9.	ARBC 757	66.00	70.10	11.50	15.50	26.90	10.50	3.41	39.30	2.44	26.60	80.00	26.20	4.20
10.	ARBC 64	63.50	65.30	13.10	22.80	28.20	7.50	3.03	32.00	2.44	23.90	80.00	22.20	4.70
11.	ARBC 1352	68.50	46.90	5.50	9.00	17.50	8.50	3.73	33.85	2.20	28.90	81.00	27.30	3.70
12.	TCH 5811	67.00	69.80	10.80	19.90	30.40	8.00	3.86	35.35	2.50	26.20	82.00	25.40	4.10
13.	TSH 0430	66.50	69.70	10.50	14.50	30.70	8.75	3.82	35.65	3.02	24.40	82.00	23.70	4.80
14.	RAH 101	66.50	64.40	8.90	12.80	35.10	9.25	3.66	35.40	1.64	24.60	78.00	24.90	4,50
15.	RAH 1271	64.50	95.60	10.30	21.50	37.10	7.25	3.27	33.90	3.13	25.60	79.00	25.60	4.60
16.	AKH 2013-2	66.00	93.20	10.20	16.20	36.00	8.00	2.76	32.10	3.56	27.60	79.00	25.40	5.30
17.	AKH 2016-1	68.50	69.80	9.00	12.30	32.90	9.75	3.73	35.25	3.18	27.40	81.00	27.70	4.30
18.	ADB 102	66.50	92.20	10.70	17.30	38.20	8.25	2.97	39.40	2.59	25.00	80.00	24.90	4.90
19.	KH 113	65.00	106.10	7.30	10.90	33.30	8.50	3.65	35.45	3.94	25.00	80.00	23.60	4.70
20.	IH 71	64.50	83.60	10.60	20.90	30.00	8.25	3.45	34.70	3.62	26.70	80.00	23.60	5.00
21.	IH 11	68.00	87.00	8.70	13.90	32.50	9.25	4.14	35.90	3.38	24.60	82.00	23.30	4.80
22.	H 1236	66.50	92.60	11.40	17.30	26.10	9.25	3.94	36.25	2.80	25.10	79.00	23.70	4.80
23.	NDLH 1943	65.50	92.50	9.10	15.90	30.00	8.25	3.17	35.35	3.90	26.00	79.00	22.80	4.90
24.	ARBH 83	64.50	94.00	8.50	16.30	48.70	9.25	3.50	35.70	3.85	25.70	81.00	23.10	4.40
25.	ARBH 813	66.50	91.90	7.30	18.90	28.45	8.25	3.58	36.00	4.16	25.90	80.00	26.20	4.70
26.	GBHV 180	66.00	71.30	11.40	17.20	36.45	8.00	3.99	36.90	3.48	28.70	79.00	23.90	5.10
27.	GBHV 170	63.50	85.20	8.90	13.10	36.50	9.25	3.87	38.50	3.75	22.70	79.00	22.10	5.90
28.	GBHV 198	66.50	65.80	7.10	11.80	35.00	8.25	3.07	37.10	3.57	24.70	79.00	23.20	5.10
29.	CNH 1122	68.50	108.00	11.30	19.10	36.00	8.25	3.94	36.55	3.65	24.90	79.00	25.30	5.80
30.	CNH 1137	65.50	96.30	6.20	10.30	32.30	9.25	4.14	39.25	3.80	25.50	80.00	25.40	4.60
31.	CNH 2050	63.50	59.70	8.30	16.70	35.90	8.25	3.94	35.20	3.70	24.00	81.00	22.90	4.90
32.	CNH 15	67.50	93.20	8.20	16.00	35.40	8.25	3.27	35.90	4.04	24.20	79.00	25.60	4.30
33.	G.Cot 18	64.00	77.40	8.80	15.50	35.40	10.50	4.24	38.10	4.19	27.50	80.00	27.30	4.40
34.	G.Cot 22	64.00	80.70	8.30	15.10	31.80	9.75	3.26	34.55	4.24	23.10	80.00	22.50	6.10
35.	BWR-152-1	64.00	88.40	8.30	17.30	32.90	9.50	2.91	34.30	4.30	28.40	81.00	27.80	5.00
36.	RB 611	67.00	93.20	7.60	14.10	42.30	7.75	2.77	34.10	2.74	25.80	80.00	25.60	5.10
37.	RB 616	67.00	80.60	8.80	16.50	43.30	8.25	3.17	34.25	3.72	25.90	80.00	25.40	4.90
38.	NH 688	64.50	80.10	9.30	18.30	39.30	8.75	3.80	35.70	2.45	23.90	80.00	23.50	4.90
39.	NH 662	67.00	96.10	7.10	12.80	36.90	8.00	3.93	35.55	2.94	23.70	81.00	23.20	5.40

Table 2: Continue...

Sl. No.	Genotype	DF	PH	NSP	NBP	SCYP	SI	LI	GO	BW	UHML	UR	FS	FF
40.	PH 1060	68.00	87.20	8.60	17.00	32.40	7.75	3.17	34.65	3.44	23.90	82.00	22.40	5.20
41.	PH 1070	67.00	102.20	9.20	19.60	44.30	8.75	3.99	33.35	3.72	25.20	82.00	25.40	5.20
42.	RHC-HD 1405	67.00	61.00	7.10	12.50	28.90	8.25	3.87	33.85	2.64	24.80	78.00	25.90	4.30
43.	RHC-HD-1312	70.00	103.70	8.50	18.80	24.90	9.75	4.29	37.60	3.30	26.00	79.00	26.40	5.20
44.	L 1536	67.00	68.20	8.00	14.10	33.70	8.75	3.78	36.75	3.70	22.50	79.00	21.90	5.50
45.	NDLH 2061-1	67.00	93.90	8.30	26.20	46.10	8.25	3.81	36.35	3.32	24.40	81.00	24.10	5.10
46.	NDLH 2071-1	69.00	98.10	8.40	14.80	33.30	9.00	3.23	34.75	3.54	25.80	80.00	25.00	4.90
Checks														
47.	PH 348	64.00	103.20	8.80	18.50	40.20	8.25	2.90	33.55	4.06	25.70	80.00	23.70	5.30
48.	NH 545	64.00	118.10	10.50	20.50	39.60	9.25	3.87	38.25	4.35	25.30	80.00	26.00	5.30
49.	NH 615	65.00	92.00	9.40	17.20	42.05	8.25	3.41	36.55	3.88	27.20	82.00	28.30	4.20
50.	Suraj	68.00	112.50	11.00	20.60	49.30	7.75	3.81	35.60	4.05	25.70	79.00	27.40	4.60
	Mean	66.18	85.40	9.16	16.31	35.02	8.71	3.57	35.77	3.33	25.46	80.06	24.87	4.84
	SEm±	0.48	2.60	0.33	0.57	2.68	0.48	0.11	0.48	0.20	0.48	1.41	0.43	0.09
	CD (p=0.05)	1.39	7.39	0.96	1.63	7.61	1.36	0.32	1.38	0.57	1.38	-	1.22	0.28
	CV (%)	3.04	8.31	7.21	8.00	10.82	7.82	4.51	1.91	8.55	2.7	2.50	2.45	2.90

DF: Days to 50% flowering; PH: Plant height (cm); NSP: No. of sympodia plant^{-1}; NBP: No. of bolls plant^{-1}; SCYP: Seed cotton yield plant^{-1} (g); SI: Seed index (g); LI: Lint index (g); GO: Ginning outturn (%); BW: Boll weight (g); UHML: Upper half mean length (mm); UR: Uniformity ratio (%); FS: Fiber strength(g/tex); FF: Fiber fineness (μg inch^{-1})

Table 3: Estimates of variability parameters for thirteen characters in cotton

Characters	Range	Genotypic variance (2 g)	Phenotypic variance (2 p)	GCV (%)	PCV (%)	Heritability (BS) (%)	Genetic advance	Genetic advance as % of mean
Days to 50% flowering	63.50-70.00	2.56	3.04	2.41	2.63	84.23	3.03	4.57
Plant height (cm)	46.9-118.10	223.53	237.09	17.5	18.03	94.28	29.91	35.01
No. of sympodia plant^{-1}	5.5-13.10	2.47	2.70	17.15	17.92	91.53	3.09	33.80
No. of bolls plant^{-1}	9-26.2	12.47	13.13	21.64	22.21	94.93	7.08	43.44
Seed cotton yield plant^{-1} (g)	17.50-53.80	42.18	56.56	18.54	21.47	74.57	11.55	32.98
Seed index (g)	7.25-10.75	0.44	0.90	7.65	10.94	48.87	0.96	11.02
Lint index (g)	2.76-4.54	0.16	0.19	11.45	12.31	86.55	0.78	21.96
Ginning outturn (%)	32-39.4	3.12	3.59	4.94	5.30	86.90	3.39	9.49
Boll weight (g)	1.64-4.35	0.35	0.43	17.87	19.82	81.37	1.11	33.22
Upper half mean length (mm)	22.5-28.9	1.91	2.39	5.43	6.07	80.20	2.55	10.03
Uniformity ratio (%)	78.00-82.00	-0.89	3.12	1.17	2.20	28.47	1.04	1.29
Fiber strength (g tex^{-1})	21.90-28.30	2.69	3.06	6.59	7.03	87.86	3.17	12.73
Fiber Fineness (μg inch^{-1})	3.60-6.10	0.24	0.26	10.15	10.55	92.43	0.97	20.10

GCV: Genotypic coefficient of variation; BS: Broad sense; PCV: Phenotypic coefficient of variation

(2020) and Sahar et al. (2021) were observed the variation among genotypes affected by the environmental factors also.

Days to 50% flowering showed high heritability (84.23%) with a low expected genetic advance (4.57%) which was indicative of non-additive gene action. Plant height exhibited higher heritability (94.28%) with a substantial expected genetic advance (35.02%), indicating additive gene action and suggesting that selection might have been effective for that trait. These findings aligned with the results reported by Adsare and Salve (2017). PCV and GCV values were approximately equal in number of bolls per plant. High heritability estimates coupled with moderate genetic advance were observed for lint index, seed index, fibre strength and micronaire value. Similar results were reported by Elango et al. (2012) for micronaire value and by Dahiphale and Deshmukh (2018) for seed index.

Seed cotton yield plant^{-1} displayed a higher estimate of heritability with a high expected genetic advance. These results conformed to the findings of Erande et al. (2014), Baloch et al. (2015), Naik et al. (2016), Bhatti et al. (2020) and Sahar et al. (2021). The lowest genotypic and phenotypic coefficients of variation were observed for uniformity ratio, fibre strength, and ginning percent. Similar results were found by Vinodhana et al. (2013) and Patil et al. (2014). In the current study, traits such as plant height, number of sympodia plant^{-1}, number of bolls plant^{-1}, lint index, boll weight and seed cotton yield plant^{-1} exhibited both high heritability and a significant expected genetic advance. Among the genotypes studied, SCS 793, ARBH 83, SCS 1061 and NDLH 2061-1 showed superiority for seed cotton yield per plant. The genotypes ARBC 1352, GBHV 180, BWR-152-1, G.Cot 22, CNH 1122 and PH 1060 showed superiority for fibre quality traits over the checks. This suggested that these traits had a strong additive genetic component, making them suitable for efficient improvement through selection. It was advisable to prioritize these traits and assign them due importance in breeding programs.

4. CONCLUSION

SCS 793, ARBH 83, SCS 1061, and NDLH 2061-1 were identified as superior genotypes for seed cotton yield per plant, while ARBC 1352, GBHV 180, BWR-152-1, G.Cot 22, CNH 1122, and PH 1060 excelled in terms of fibre quality traits. Several traits, including the number of bolls per plant, plant height, boll weight, number of sympodia per plant, ginning percentage, lint index, and fibre fineness, were found to be most effective for the selection of superior genotypes of American cotton.

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