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Unravelling genetic variability for yield and fibre quality traits in cotton (*Gossypium hirsutum* L.)

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Abstract

Cotton (*Gossypium hirsutum* L.) is a globally important fibre crop that plays a vital role in the textile industry and agricultural economy. However, its productivity in India remains relatively low due to a narrow genetic base, environmental influences and the complex inheritance of yield and fibre quality traits hence, the present study was conducted to assess genetic variability, heritability and genetic advance among cotton germplasm lines. A total of 207 germplasm lines, along with five checks, were evaluated using an augmented block design. Observations were recorded on 13 yield and fibre quality traits. Statistical analyses were performed to estimate genotypic and phenotypic coefficients of variation (GCV and PCV), broad-sense heritability and genetic advance as percent of mean. Analysis of variance revealed significant differences among germplasm lines for most traits, indicating substantial genetic variability. Higher PCV values compared to GCV for all traits suggested environmental influence on trait expression. High heritability coupled with high genetic advance was observed for lint yield, seed cotton yield, and number of bolls per plant, indicating the predominance of additive gene action and effectiveness of selection. Moderate heritability with moderate genetic advance was recorded for plant height, boll weight and elongation percentage, suggesting partial environmental influence. In contrast, traits such as fibre strength and Micronaire value exhibited low heritability and genetic advance, indicating limited scope for improvement through direct selection. The study highlights the presence of considerable genetic variability among the evaluated germplasm, providing opportunities for selecting superior line. Traits exhibiting high heritability and genetic advance can be effectively utilized in breeding programmes aimed at improving yield and fibre quality in cotton.

Keywords: Phenotypic coefficient of variation, genotypic coefficient of variation, augmented block design, ANOVA and heritability

Introduction

Cotton (*Gossypium* spp.) is one of the most important commercial fibre crops globally, serving as a primary raw material for the textile industry and contributing significantly to the agricultural economy. In addition to fibre, cottonseed provides valuable oil and protein, enhancing its economic importance. Among cultivated species, *Gossypium hirsutum* accounts for the majority of global production due to its wide adaptability and yield potential. Despite its global significance, cotton productivity, particularly in countries like India, remains relatively low compared to the world average. This gap is largely attributed to the narrow genetic base of cultivated varieties, environmental constraints and the complex inheritance of yield and fibre quality traits. Yield in cotton is a polygenic trait influenced by several component characters such as number of bolls, sympodial branches and boll weight, which are often affected by environmental interactions. Therefore, improving yield and fibre quality simultaneously remains a major challenge in cotton breeding programmes. Genetic variability plays a crucial role in crop improvement, as it provides the foundation for selection and hybridisation. The availability of diverse germplasm enables breeders to identify genetically divergent parents, which can be effectively utilised to exploit heterosis and develop superior cultivars. However, continuous selection and domestication have led to a reduction in genetic variability in cultivated cotton, thereby necessitating systematic evaluation of available germplasm to broaden the genetic base. Morphological characterisation based on yield and its component traits remains a

reliable and practical approach for assessing genetic variability under field conditions. Although such traits are influenced by environmental factors, they reflect the actual performance of genotypes and are widely used in breeding programmes. Genetic variability studies have been extensively employed to quantify variance. These methods help in formulating effective hybridisation strategies.

Materials and Methods

The present investigation was conducted during *kharif* 2023 at the College of Agriculture, Bheemarayangudi, Karnataka, India, located in the North-Eastern Dry Zone (Zone II) of Karnataka at an altitude of approximately 412 m above mean sea level. The experimental material comprised a set of 207 cotton (*Gossypium hirsutum* L.) germplasm lines selected based on variation in yield and fibre quality traits. The germplasm lines were obtained from the All India Coordinated Research Project (AICRP) on Cotton, Main Agricultural Research Station (MARS), Raichur. The germplasm lines were evaluated in an augmented block design with appropriate five checks (BGDS-1033, BGDS-1063, SCS-1061, SCS-1062 and SCS-793). Each germplasm lines were sown in rows with recommended spacing and standard agronomic practices were followed to ensure a healthy crop stand throughout the growing season. The randomly selected five plants from each line were used for observing the following parameters: plant height (cm), number of bolls per plant, seed cotton yield per plant (g), seed index (g), boll weight (g), lint index (g), lint yield per plant (g), ginning out turn (%), fibre strength (g/text), UHML (mm), Micronaire value ($\mu\text{g}/\text{inch}$), fibre elongation (%) and fibre uniformity ratio (%). Analysis and estimates of genotypic and phenotypic coefficients of variation, broad sense heritability, genetic advance over mean performed by the R package, Excel (2013) and SPSS (22.0).

Results and Discussion

The means of all observed parameters were calculated and subjected to analysis of variance (ANOVA) following the methods of Johnson *et al.* (1955) [11] and Falconer (1967) [6]. The genotypic and phenotypic coefficients of variation were estimated using the formula proposed by Falconer (1981) [7]. Broad-sense heritability (h^2) was computed according to the procedure outlined by Allard (1960) [2]. Based on the heritability estimates, the expected genetic advance was determined using the formula suggested by Burton (1952) [4].

Analysis of variance for yield and fibre quality parameter

According to Federer's augmented design (1956) [8], The mean values of all quantitative traits under study in the germplasm lines were employed for performing ANOVA. The analysis revealed highly significant mean sum of squares for most traits, indicating substantial variability among the germplasm lines. Detailed results are presented in Table 1. This variability reflects the genetic heterogeneity within the studied germplasm, highlighting promising germplasm for inclusion in breeding programmes aimed at enhancing yield and its component traits. Similar results were demonstrated by choudki *et al.*, 2012 [5], Jarwar *et al.*, 2018 [9]. This collectively suggests that there exists a reasonable amount of variability within the cotton germplasm. Similar results are obtained in our investigation and this presents ample opportunities for plant breeders to select superior and desired germplasms for further genetic enhancement

Genetic variability analysis

The main objective of germplasm conservation is to collect and

preserve the genetic variability of indigenous crop species for use by present and future generations. A higher level of genetic variability in the initial breeding material increases the likelihood of developing improved and desirable crop varieties. The results pertaining to genetic parameters viz., phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability (h^2) and genetic advance as percent of mean for all the 13 characters are furnished in Table 2.

The plant height exhibited the mean (133.49 cm), genotypic coefficient of variation (11.15%), phenotypic coefficient of variation (14.83%), heritability (56.54%) and genetic advance as percent of mean (17.30) respectively. The trait demonstrated the narrow difference between PCV and GCV hence it indicates that there is less influence of environment on trait and heritability and GAM showed a medium range of value for this trait respectively. similar results were reported by Ujjainkar (2024) [20] and Kathiravan *et al.* (2025) [13]. The number of bolls exhibited a mean (16.97), genotypic coefficient of variation (14.62%), phenotypic coefficient of variation (19.11%), heritability (58.49%) and genetic advance as percent of mean (23.06), respectively. The trait showed a moderate difference between PCV and GCV, indicating a moderate influence of environment. Heritability and GAM were in the medium to high range, suggesting good scope for selection. which is in agreement with Meena *et al.* (2024) [16]. Boll weight exhibited a mean (3.91 g), genotypic coefficient of variation (8.88%), phenotypic coefficient of variation (10.76%), heritability (68.13%) and genetic advance as percent of mean (15.12) respectively. The narrow difference between PCV and GCV indicates less environmental influence. High heritability coupled with moderate GAM suggests additive gene action. Singh *et al.* (2018) [19] and lokeshkumar *et al.* (2018) [15]. Seed index exhibited a mean (7.95), genotypic coefficient of variation (12.74%), phenotypic coefficient of variation (18.50%), heritability (47.42%) and genetic advance as percent of mean (18.10), respectively. The moderate difference between PCV and GCV indicates environmental influence. Heritability and GAM were moderate. which is consistent with findings of Adeela *et al.* (2021) [1]. Lint yield exhibited a mean (21.82), genotypic coefficient of variation (20.76%), phenotypic coefficient of variation (25.81%), heritability (64.74%) and genetic advance as percent of mean (34.46), respectively. The moderate difference between PCV and GCV indicates some environmental influence. High heritability along with high GAM suggests strong additive gene effects and good selection potential. Khan *et al.* (2015) [14] and Venkatesan *et al.* (2024) [21]. Lint index exhibited a mean (4.19), genotypic coefficient of variation (10.30%), phenotypic coefficient of variation (17.28%), heritability (35.55%) and genetic advance as percent of mean (12.68), respectively. The wide difference between PCV and GCV indicates higher environmental influence. Heritability and GAM were low to moderate. which aligns with reports of Kathiravan *et al.* (2025) [13]. Ginning outturn exhibited a mean (34.62), genotypic coefficient of variation (6.37%), phenotypic coefficient of variation (7.32%), heritability (75.65%) and genetic advance as percent of mean (11.42), respectively. The narrow difference between PCV and GCV indicates minimal environmental influence. High heritability with moderate GAM suggests selection may be effective as supported by Anitha *et al.* (2016) [3]. Seed cotton yield exhibited a mean (62.90), genotypic coefficient of variation (18.02%), phenotypic coefficient of variation (23.88%), heritability (56.93%) and genetic advance as percent of mean (28.05),

respectively. The moderate difference between PCV and GCV indicates environmental influence. Heritability and GAM were moderate to high, indicating scope for improvement. which is in accordance with Jeyaraj *et al.* (2023) ^[10] and Kathiravan *et al.* (2025) ^[13]. Upper half mean length exhibited a mean (27.03), genotypic coefficient of variation (8.48%), phenotypic coefficient of variation (9.89%), heritability (73.55%) and genetic advance as percent of mean (15.01), respectively. The narrow difference between PCV and GCV indicates less environmental influence. High heritability with moderate GAM suggests effectiveness of selection. which is supported by Adeela *et al.* (2021) ^[1]. Fibre strength exhibited a mean (25.00), genotypic coefficient of variation (6.72%), phenotypic coefficient of variation (11.48%), heritability (34.26%) and genetic advance as percent of mean (8.11), respectively. The wider difference between PCV and GCV indicates greater environmental influence. Heritability and GAM were low. as similarly reported by Lokeshkumar *et al.* (2018) ^[15]. Micronaire exhibited a mean (2.79), genotypic coefficient of variation

(9.65%), phenotypic coefficient of variation (16.25%), heritability (35.22%) and genetic advance as percent of mean (11.81), respectively. The wide difference between PCV and GCV indicates higher environmental influence. Heritability and GAM were low to moderate. as similarly reported by Kadam *et al.* (2025) ^[12]. Uniformity index exhibited a mean (81.26), genotypic coefficient of variation (3.54%), phenotypic coefficient of variation (4.19%), heritability (71.32%) and genetic advance as percent of mean (6.16), respectively. The narrow difference between PCV and GCV indicates minimal environmental influence. High heritability with low GAM suggests limited variability. as also reported by Kumar *et al.* (2014). Elongation percentage exhibited a mean (5.59), genotypic coefficient of variation (13.54%), phenotypic coefficient of variation (18.50%), heritability (53.58%) and genetic advance as percent of mean (20.44), respectively. The moderate difference between PCV and GCV indicates environmental influence. Heritability and GAM were moderate. as also observed by Pradeep *et al.* (2016) ^[18].

Table 1: Analysis of variance for yield, yield component and fibre quality traits in upland cotton (*Gossypium hirsutum* L.)

Source	Df.	Mean Squares												
		PH	NB	BW	SI	LY	LI	GOT	SCY	UHML	STR	MIC	UI	EL
Treatment (ignoring Blocks)	211	388.68**	10.33**	0.18**	2.32**	32.31**	0.52	7.89**	222.69**	7.24**	9.04*	0.21	11.64**	1.10**
Treatment: Check	4	322.17	3.4	0.36**	8.40**	66.91**	0.18	83.52**	107.76	4.64	24.59**	0.1	4.32	0.71
Treatment: Test	206	391.78**	10.52**	0.18**	2.16*	31.70**	0.53	6.42**	225.71**	7.14**	8.24	0.21	11.59**	1.07**
Treatment: Test Vs. Check	1	15.21	0.13	0.16	10.62**	20	1.14	8.03*	60.63	38.54**	112.78**	0.62*	52.50**	7.82**
Block (eliminating Treatments)	8	411.54*	6.75	0.1	1.73	39.52**	0.46	2.47	306.50**	2.94	19.36**	0.1	5.47	0.74
Residuals	32	170.27	4.37	0.06	1.14	11.18	0.34	1.56	97.22	1.89	5.42	0.13	3.32	0.5

^{ns} P > 0.05; * P <= 0.05; ** P <= 0.01

PH- Plant height (cm), NB- Number of bolls per plant, BW-Boll weight (g), SCY- Seed cotton yield per plant (g), LY- Lint yield (g), SI- Seed index (g), GOT- Ginning out turn (%), LI- Lint index, UHML- Upper half mean length, UI- Fibre uniformity index, STR- Fibre strength (g tex⁻¹), EL- Fibre elongation (%) and MIC- Micronaire value

Table 2: Genetic variability parameter for yield and fibre quality traits in cotton (*Gossypium hirsutum* L.)

Trait	Mean	Min	Maxi	GCV	PCV	hBS	GAM
PH	133.49	72.34	185.78	11.15	14.83	56.54	17.3
NB	16.97	11.21	30.88	14.62	19.11	58.49	23.06
BW	3.91	2.77	5.41	8.88	10.76	68.13	15.12
SI	7.95	5.12	13.41	12.74	18.5	47.42	18.1
LY	21.82	9.94	51.14	20.76	25.81	64.74	34.46
LI	4.19	2.47	6.83	10.3	17.28	35.55	12.68
GOT	34.62	26.31	41.32	6.37	7.32	75.65	11.42
SCY	62.9	30.01	142.46	18.02	23.88	56.93	28.05
UHML	27.03	21.09	50.55	8.48	9.89	73.55	15.01
STR	25	17.15	34.15	6.72	11.48	34.26	8.11
MIC	2.79	1.55	4.38	9.65	16.25	35.22	11.81
UI	81.26	48.07	88.59	3.54	4.19	71.32	6.16
EL	5.59	3.28	8.44	13.54	18.5	53.58	20.44

PH- Plant height (cm), NB- Number of bolls per plant, BW-Boll weight (g), SCY- Seed cotton yield per plant (g), LY- Lint yield (g), SI- Seed index (g), GOT- Ginning out turn (%), LI- Lint index, UHML- Upper half mean length, UI- Fibre uniformity index, STR- Fibre strength (g tex⁻¹), EL- Fibre elongation (%) and MIC- Micronaire value

Conclusion

The present study on cotton (*Gossypium hirsutum* L.) germplasm lines revealed significant genetic variability for both yield and fibre quality traits. Traits such as lint yield, seed cotton yield, plant height and number of bolls exhibited moderate to high heritability along with moderate to high genetic advance, indicating strong additive gene action and good potential for selection in breeding programs. Conversely, traits like fibre strength, Micronaire value and lint index showed wider differences between PCV and GCV lower heritability and

limited genetic advance, suggesting greater environmental influence and a comparatively lower scope for direct selection. Overall, the results indicate that selection for yield-related traits is likely to be effective, while improvement of certain quality traits may require careful management of environmental factors. The combination of high heritability and substantial genetic advance for key agronomic traits provides a valuable opportunity for enhancing productivity and quality in cotton breeding programs.

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