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RESEARCH PAPER

Multivariate statistical analysis of genetic parameters of cotton genotypes for yield, yield attributes and fiber quality traits

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Abstract: A successful breeding program fundamentally relies on adequate genetic variability within the base population. To explore this, a comprehensive study was conducted at University of Agricultural Sciences, Dharwad during *kharif* 2023. A field trial was conducted to evaluate yield components and fiber traits in eighteen cotton genotypes, with the experiment arranged in a randomized block design containing two replications. Analysis of variance (ANOVA) demonstrated significant differences ($P < 0.05$, $P < 0.01$) among cotton genotypes across all fourteen measured traits, confirming substantial genetic diversity. The observed phenotypic variation (PCV) was consistently greater than the genetic variation (GCV), demonstrating the strong impact of environmental conditions on how traits were expressed. Of particular interest, seed cotton yield per plant uniquely displayed additive gene action, characterized by high heritability and pronounced genetic advance over mean. This finding suggests its suitability for direct selection protocols, positioning it as crucial parameter for population improvement strategies.

Key words: Cotton, Genotypic coefficient of variation, Phenotypic coefficient of variation

Introduction

Gossypium hirsutum, or upland cotton, white gold, represents approximately 90 per cent of global cotton production. Native to Mexico and Central America, this Malvaceae family member produces white to cream flowers that develop into cotton bolls, yielding fibers crucial for textile manufacturing. Beyond textiles, the crop provides cotton seed oil and animal feed, supporting diverse industrial applications. Modern agriculture has developed numerous cultivars with enhanced pest resistance, yield potential and environmental adaptability. The crop significantly impacts global agricultural economies, particularly in the United States, China, India and Brazil, supporting countless farmers and contributing substantially to international trade.India's textile industry increasingly demands enhanced fiber characteristics, driving the need for improved cotton varieties. Success in plant breeding fundamentally depends on initial genetic variability in base populations and trait stability during selection. Understanding variability among yield-related attributes is essential for implementing effective selection strategies across diverse germplasm.

Trait variability and heritability information guides genetic improvement pathways. Genotypic variability, the heritable component of observable variation, is quantified through heritability—representing the proportion of phenotypic variability attributable to genetic factors. Heritability encompasses both additive and nonadditive effects, offering crucial insights for crop breeding programs. Hanson *et al.* (1956) defined broad-sense heritability as the proportion of genotypic to phenotypic variance, highlighting its importance in understanding trait inheritance. While heritability measures selection potential based on phenotypic expression, Johnson *et al.* (1955) showed that genetic advance provides more precise selection assessment. The coefficient of variation helps to assess genetic variability within populations and facilitates trait comparisons.

The most accurate genetic evaluation occurs when analyzing heritability alongside genetic advance, enabling comprehensive understanding of heritable variation and its breeding implications (Sunilkumar *et al.* 2019). This study aimed to evaluate genetic variability in *G. hirsutum* genotypes for yield and related traits, focusing on identifying and assessing heritable components of phenotypic variability to establish a foundation for targeted selection and genetic enhancement.

Material and methods

The study was conducted during *kharif* 2023 at the University of Agricultural Sciences, Dharwad's botany garden. Eighteen cotton genotypes were evaluated, including three high fiber strength varieties (Sunantha, Suraksha and Subhiksha) from the All India Coordinated Research Project on Cotton in Coimbatore, and fifteen low fiber strength RILs (P1-62, P1-103, P1-82, P1-50, P1-190, P2-17, P2-7, P2-103, P2-3, P2-36, P3-11, P3-59, P3-54, P3-47 and P3-135) from the RHAP series developed at UAS Raichur. The experiment followed a randomized block design with two replications, maintaining standard cultural practices.

The research methodology involved collecting data from five randomly selected plants per replication for each genotype, examining fourteen morphological and fiber-related traits. These included plant architecture parameters (plant height, monopodia and sympodia counts), reproductive traits (boll number and weight), yield components (seed cotton yield, seed index, lint

Table 1. Analysis of variance of cotton genotypes for yield, yield attributes and fiber quality traits

Source	df	NMPP	NSPP	NBPP	BW (gm)	SCYP (gm)	PH (cm)	SI	GOT (%)	LI	FL (mm)	UI	FF (µg/inch)	FS (g/tex)	E (%)
Treatment	17.00	0.34*	6.48**	87.36**	0.30**	301.24**	319.81**	0.96**	10.28**	0.55**	5.09**	4.17**	0.19**	3.71**	0.44**
Replication	1.00	0.44	0.25	1.00	0.02	1.36	0.69	0.05	4.00	0.03	0.18	1.00	0.26	0.87	0.01
Error	17.00	0.20	1.30	3.88	0.02	10.06	28.63	0.11	1.35	0.01	0.01	0.94	0.02	0.11	0.01
Total	35.00														

Note: **Significant at 1% level *Significant at 5% level

NMPP - Number of monopodial branches per plant; NSPP- Number of sympodial branches per plant; NBPP- Number of bolls per plant; BW - Boll weight (g); SCYP - Seed cotton yield per plant (g); PH- Plant height (cm); SI - Seed index; GOT - Ginning outturn (%); LI - Lint index; FL-Fiber length (mm); UI - Uniformity Index (%); FF- Fibre fineness (µg/inch.); FS- Fibre Strength (g/tex.); E - Elongation percentage (%).

index, ginning out-turn percentage) and fiber quality metrics (length, strength, fineness, uniformity ratio and index, elongation percentage).

Analysis of variance (ANOVA) was performed following the protocol outlined by Cochran and Cox (1950), providing insights into the variance components across the studied traits. Genotypic and phenotypic coefficients of variation were calculated using Burton's (1952) recommended formula, enabling quantification of genetic variability. Broad-sense heritability was estimated according to the method proposed by Hanson *et al.* (1956), with results expressed as percentages. Additionally, genetic advance was interpreted and classified based on the criteria established by Robinson *et al.* (1949).

Results and discussion

The analysis of variance revealed significant differences ($P < 0.05$, $P < 0.01$) among cotton genotypes across all 14 measured traits, demonstrating substantial genetic diversity in the studied material (Table 1). This genetic variability suggests promising opportunities for cotton breeding improvement. The mean values for all traits are presented in Figure 1, showing satisfactory yield and fiber quality characteristics. The low coefficient of variation (CV%) observed across all traits confirms the precision and reliability of the experimental results (Table 2).

The analysis included key genetic parameters calculated for all traits under study, as shown in Table 2. These parameters encompassed genotypic and phenotypic coefficients of variation (GCV and PCV), broad-sense heritability (h^2 bs), and genetic advance expressed as a percentage of the mean (GAM). Across all examined characteristics, PCV values were consistently higher than GCV values, suggesting that environmental factors played a significant role in how these traits were expressed. These observations are consistent with research conducted by Monisha *et al.* (2018) and Hussain *et al.* (2010), who documented comparable variation patterns in their studies.

Several traits exhibited low PCV and GCV values, including plant height (6.61 & 7.23), ginning out-turn (6.21 & 7.08), fiber length (5.84 & 5.85), uniformity index (1.53 & 1.93), fiber strength (5.15 & 5.31), fiber fineness (8.49 & 9.42), and elongation (8.25 & 8.53). Number of monopodia per plant showed contrasting coefficients with high PCV (13.47) and moderate GCV (27.11). Two traits displayed moderate PCV with low GCV: number of sympodia per plant (9.42 & 11.56) and boll weight (9.90 & 10.80). Seed cotton yield per plant was unique in showing both high GCV (31.57) and PCV (39.96). These findings partially align with Kumar *et al.* (2021), who also reported high PCV and GCV

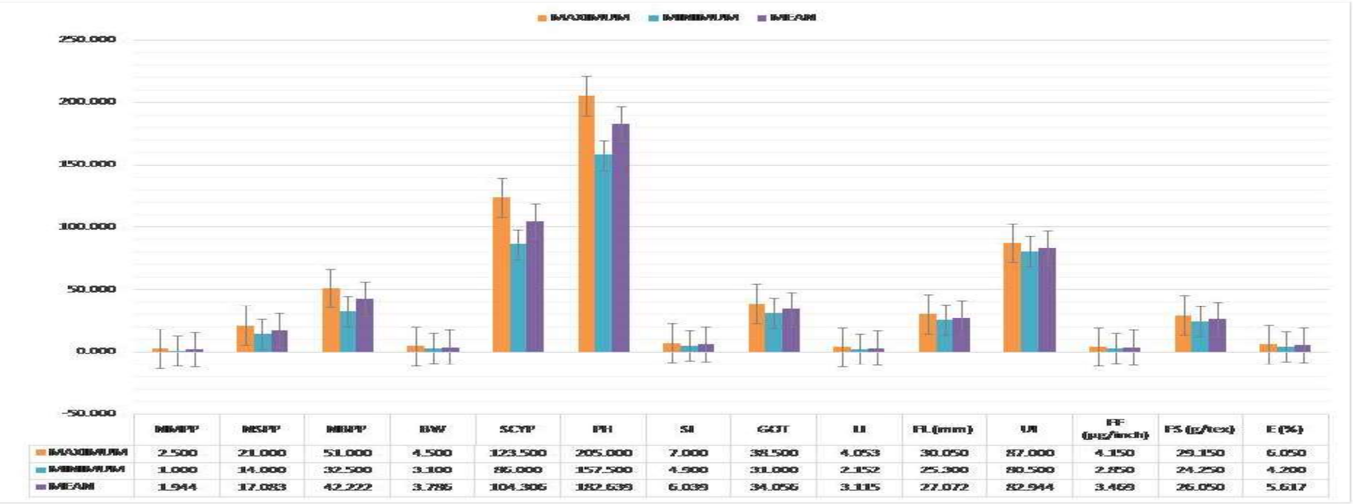

Fig 1. Mean values of cotton genotypes for yield, yield attributes and fiber quality traits

Note: NMPP - Number of monopodial branches per plant; NSPP- Number of sympodial branches per plant; NBPP- Number of bolls per plant; BW - Boll weight (g); SCYP - Seed cotton yield per plant (g); PH- Plant height (cm); SI - Seed index; GOT - Ginning outturn (%); LI - Lint index; FL-Fiber length (mm); UI - Uniformity Index (%); FF- Fibre fineness (µg/inch.); FS- Fibre Strength (g/tex.); E - Elongation percentage (%).

Tale 2. Coefficient of variation for phenotype and genotype followed by heritability and genetic advance as percent of mean for cotton traits

Traits	NMPP	NSPP	NBPP	BW	SCYP	PH	SI	GOT	LI	FL (mm)	UI	FF (µg/inch)	FS (g/tex)	E (%)
GCV	13.473	9.417	15.302	9.899	11.568	6.606	10.821	6.206	16.773	5.838	1.532	8.495	5.149	8.254
PCV	27.105	11.556	15.998	10.796	11.961	7.227	12.152	7.084	17.082	5.854	1.927	9.417	5.309	8.534
h^2(bs)	24.706	66.415	91.491	84.068	93.533	83.564	79.296	76.755	96.408	99.477	63.171	81.371	94.069	93.543
GA	0.268	2.701	12.730	0.708	24.039	22.722	1.199	3.815	1.057	3.247	2.080	0.548	2.680	0.924
GAM	13.795	15.810	30.151	18.697	23.046	12.441	19.851	11.201	33.926	11.996	2.508	15.786	10.288	16.446
S.Em	0.323	0.809	1.393	0.115	2.244	3.784	0.236	0.822	0.071	0.081	0.686	0.100	0.238	0.086
S E.d	0.457	1.144	1.970	0.163	3.173	5.351	0.334	1.163	0.101	0.115	0.970	0.141	0.337	0.122
CV	23.520	6.697	4.667	4.309	3.042	2.930	5.530	3.415	3.238	0.423	1.170	4.065	1.293	2.169
C.D(5%)	0.965	2.414	4.157	0.344	6.694	11.290	0.705	2.454	0.213	0.242	2.047	0.298	0.711	0.257
C.D(1%)	1.325	3.316	5.711	0.473	9.196	15.509	0.968	3.371	0.292	0.332	2.812	0.409	0.976	0.353

Note: NMPP - Number of monopodial branches per plant; NSPP- Number of sympodial branches per plant; NBPP- Number of bolls per plant; BW - Boll weight (g); SCYP - Seed cotton yield per plant (g); PH- Plant height (cm); SI - Seed index; GOT - Ginning outturn (%); LI - Lint index; FL-Fiber length (mm); UI - Uniformity Index (%); FF- Fibre fineness (µg/inch.); FS- Fibre Strength (g/tex.); E - Elongation percentage (%).

values for seed cotton yield, plant height and number of bolls per plant.

Characteristics that show elevated heritability along with substantial genetic advance tend to have improved transmission to offspring generations. Our analysis revealed that seed cotton yield per plant displayed strong broad-sense heritability (H2b) coupled with high genetic advance as percentage of mean (GAM), indicating that additive gene effects were the primary genetic mechanism. These genetic attributes make seed cotton yield per plant an especially useful criterion for selecting promising genotypes during the initial phases of breeding work focused on crop enhancement. Our results align with the work of Nawaz *et al.* (2019), Singh *et al.* (2019), and Bhatti *et al.* (2020), who observed comparable patterns of genetic inheritance in their research.

While genotypic coefficient of variation alone cannot indicate heritable variation, heritability estimates provide insight into the potential effectiveness of selection for genetic improvement based on phenotypic performance.Several traits exhibited high heritability coupled with moderate genetic advance over mean: number of sympodia per plant (66.42 & 15.81), boll weight (84.07 & 18.70), fiber strength (94.07 & 10.29), plant height (83.56 & 12.44), seed index (96.41 & 33.93), fiber length (99.48 & 12.00), fiber fineness (81.37 & 15.79), ginning out-turn (76.75 & 11.20), elongation (93.54 & 16.45), and uniformity index (63.17 & 2.51). These patterns suggest non-additive gene action in trait expression, indicating that simple selection procedures may not be effective for improvement. Instead, these traits may be better enhanced through hybrid breeding approaches.

In contrast, number of bolls per plant (91.49 & 30.15), seed cotton yield per plant (93.53 & 23.05), and lint index (96.41 & 33.93) demonstrated high heritability combined with high genetic advance over mean. This combination indicates additive genetic control, suggesting that rapid improvement could be achieved through simple pureline selection. These findings align with Dhamayanathi *et al.* (2010), who similarly observed high heritability coupled with high genetic advance for seed cotton yield and number of bolls per plant, confirming the potential for trait improvement through selection.

Conclusion

Cotton, the sovereign of fiber crops, commands exceptional economic value across agricultural and industrial domains. The investigation revealed significant genetic diversity among cotton genotypes for quantitative traits, facilitating the identification of superior germplasm. In a comprehensive analysis of phenotypic characteristics, seed cotton yield per plant emerged as uniquely distinguished by its additive gene action, coupled with substantial heritability and remarkable genetic advance as a percentage of mean. This paramount trait presents an optimal target for direct selection in population improvement strategies. Moreover, the synergistic analysis of heritability, genetic advance, and variability illuminates the intergenerational transmission patterns, empowering breeders to devise precisely targeted breeding strategies.

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