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STUDIES ON GENETIC VARIABILITY AND HERITABILITY FOR YIELD, YIELD ATTRIBUTES ALONG WITH FIBER RELATED TRAITS IN UPLAND COTTON (*GOSSYPIMUM HIRSUTUM* L.)

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ABSTRACT

Cotton (*Gossypium* spp.) is world's most important fiber and major cash crop. An experiment was conducted at the Botany Garden, Agriculture College, Dharwad, Karnataka, during 2023-24 *kharif* season to evaluate genetic variability across thirteen traits for 46 genotypes in upland cotton (*Gossypium hirsutum* L.). Thirty hybrids were developed using the mating design Line $\times$ Tester (L $\times$ T) and evaluated for yield, yield-related traits and fiber quality characteristics. The analysis of variance (ANOVA) for the thirteen yield attributes and fiber quality traits revealed highly significant mean sum of squares (MSS) for all the traits studied highlighting considerable genetic variability. The lint index exhibited a high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) indicating substantial variability for the trait lint index. Traits like number of sympodia per plant, number of bolls per plant, number of monopodia per plant, seed index and lint index demonstrated high heritability combined with a high genetic advance (GA) with percentage of means reflecting the predominance of additive gene action, minimal environmental influence and sufficient heritable variation. Consequently, selecting traits such as the number of sympodia per plant, number of bolls per plant, number of monopodia per plant and lint index were likely to be an effective approach in future cotton improvement programs.

Keywords: Cotton, genetic advance, genetic variability, heritability.

Introduction

Cotton (*Gossypium* spp.) is the world's most important fiber crop and a major cash crop. The term "cotton" is derived from Arabic words "Quoton" "Kuton" or "Gytum" referring to a crop that produces spinnable fiber on its seed coat. Cotton, known as the "King of Fiber" crops or "White Gold" is mostly cross-pollinated and belongs to Malvaceae family, *Gossypium* genus. Of the approximately 50 species in this genus, 43 are diploid and 7 are tetraploid and out of these only four species are cultivated.

Cotton has significant genetic variation in yield and quality traits due to its cross-pollinating nature, which also makes hybridization easier and more effective. (Joshi and

Patil, 2018). Genetic variability in the base population is essential for the success of any crop improvement program as a wider range of variability enhances the likelihood of selecting superior genotypes (Mahesh *et al.*, 2020). Heritability consideration is very important in any crop improvement program as it shows how much of a trait's variation is due to genetics and not from environment. Traits with high heritability are easier to pass on to the next generation helping breeders to select better plants for yield, yield attributes and fiber related traits. Understanding the degree of variability along with heritability and genetic advance is essential for successful cotton breeding and the development of superior varieties and hybrids for future sustainability of cotton industries. Genetic variability indicates the feasibility of selection on

Table 1: Experimental materials used in the present study.

S. No.	Parents	Parentage/ Source	Salient Features
Lines			
01	SCS-793	UAS Raichur	Released South zone, irrigated (SCY= 2022 kg/ha, FF= 4.5µg/inch)
02	BGDS-1063	UAS Raichur	Released South zone, central zone, irrigated and rainfed. (SCYP= 2933 kg/ha, FS= 31.1g/tex, FF= 4.4µg/inch, UHML= 30.5mm)
03	RAH-1075	UAS Raichur	Released 2022-23. (SCY= 2665kg/ha, FS= 25-30g/tex, FF= 4.5-4.9µg/inch, UHML= 26.9-29.7mm)
04	RAH 1081	UAS Raichur	Advanced to CVT under irrigated.
05	RAH 1082	UAS Raichur	Advanced to CVT under irrigated.
06	RAH 1083	UAS Raichur	Advanced to CVT under irrigated.
Testers			
01	Sunantha	Surabhi × Rai-4A-3-2	SCY-3675 kg/ha, UHML- 32 mm, tenacity-32.7 g/tex
02	Suraksha	(Surabhi) × (MCU5 × Z2)	SCY-2335-4019 kg/ha, UHML-31.9-32.4, tenacity-33.5-34.3 g/tex
03	Subiksha	(Bunny) × (MCU5 × Z2)	SCY-3325-4201 kg/ha, UHML-32.7, tenacity-33.8 g/tex
04	RAH 19-2	UAS Raichur	SCY-1765 kg/ha, UHML-32.3, tenacity-34.7 g/tex
05	RAH 19-3	UAS Raichur	SCY-2019 kg/ha, UHML-31.9, tenacity-29.6 g/tex
Checks			
01	Nano	CICR regional station Coimbatore	SCY-1815kg/ha, UHML-30.1mm, Teacity-30.2g/tex
02	DHH-11	CPD423 × CPD420	SCY-1825kg/ha
03	DHH-263	CPD-464 × CPD-476	SCY-2500kg/ha, UHML-30mm, Teacity-23g/tex
04	MRC-70717	Private check	SCY-1040kg/ha, UHML-29.7mm
05	Sahana	UAS Dharwad	SCY-1522kg/ha

both phenotypic and genotypic basis.

Cotton breeders continuously worked to utilize cotton germplasm in developing high-yielding varieties with desirable fiber quality. As emphasized Peohlmán and Selper (1995) yield, yield contributing traits and fiber quality traits are heritable, making it possible to enhance both quantitative and qualitative traits through appropriate breeding programs that develop new cross combinations. To achieve this, breeders need a solid understanding of genetic components like genetic variability, coefficient of variation, heritability and genetic advance to design breeding strategies that align with their objectives (Dhamayanathi *et al.*, 2010). Thus, the present study focuses on understanding genetic variability and heritability in upland cotton genotypes for yield and its component traits along with fiber quality traits.

Materials and Methods

The experimental material consists of forty-six genotypes comprising of thirty hybrids developed from six female lines and five male testers through Line × Tester mating design along with five standard checks. The thirty F₁ hybrids along with their parents and five checks were evaluated in Randomized Complete Block Design (RCBD) with three replications during *khari* 2023. Each genotype is planted in 2 rows of 3 m length with a spacing of 90 cm × 60 cm between rows and plants respectively. Observations like plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight, ginning outturn, lint index, seed index and seed cotton yield per plant were taken from five representative plants from each replication. Fibre quality traits such as fibre length, fibre strength, uniformity index and micronaire values were considered for the analysis. Experimental materials used

Table 2: Analysis of variance for various yield and fiber related traits in cotton (*Gossypium hirsutum*L.) genotypes.

	DF	Plant height (cm)	No. of monopodia per plant	No. of sympodia per plant	No. of bolls per plant	Boll weight (g)	Seed cotton yield per plant (g)	Seed index (g)	Lint index (g)	Ginning outturn (%)	Uniformity Half Mean Length (mm)	Uniformity Index (%)	Micronaire Value (µg/inch)	Tenacity (g/tex)
Replication	2	336.78	0.01	2.98	9.36	0.23	73.01	0.01	0.21	14.73	0.09	2.64	0.02	1.56
Treatments	45	588.92*	0.37**	9.58*	48.28**	0.56**	278.64**	3.43**	2.69**	36.63*	6.10**	7.03**	0.28**	3.18*
Error	90	86.34	0.03	0.77	4.44	0.10	23.75	0.28	0.17	4.62	0.14	1.50	0.01	0.33

* Significant at p = 0.05, ** Significant at p = 0.01

Table 3: Genetic parameters of variation for yield and fiber related traits in cotton (*Gossypium hirsutum* L) genotypes.

S. No.	Characters	Mean	Range		Coefficient of Variation		h ² bs (%)	GA	GAM (%)
			MIN	MAX	GCV(%)	PCV(%)			
1	Plant height (cm)	180.78	152.00	203.33	7.16	8.81	65.99	21.66	11.98
2	No. of monopodia per plant	2.32	1.73	3.07	14.40	16.20	79.02	0.61	26.37
3	No. of sympodia per plant	15.62	12.30	20.07	10.97	12.33	79.12	3.14	20.10
4	No. of bolls per plant	21.60	17.33	31.67	17.70	20.21	76.68	6.90	31.92
5	Boll weight (g)	3.90	2.87	4.53	10.07	12.85	61.37	0.63	16.24
6	Ginning outturn (%)	33.51	27.57	42.90	10.75	11.67	69.76	5.62	16.77
7	Seed index (g)	7.33	5.20	9.30	13.96	15.73	78.80	1.87	25.53
8	Lint index (g)	3.81	2.17	6.40	24.03	26.36	83.12	1.72	45.14
9	Seed cotton yield per plant (g)	94.12	76.33	125.67	10.19	11.08	78.16	16.79	17.84
10	Uniformity Half Mean Length (mm)	27.72	24.90	30.40	5.08	5.26	93.25	2.80	10.11
11	Uniformity Index (%)	83.40	80.00	87.00	1.63	2.19	55.05	2.07	2.49
12	Micronaire Value (µg/inch)	3.33	2.80	4.40	8.94	9.48	88.99	0.58	17.38
13	Tenacity (g/tex)	25.54	23.87	28.30	3.82	4.43	74.44	1.73	6.79

for present study are enlisted in Table 1.

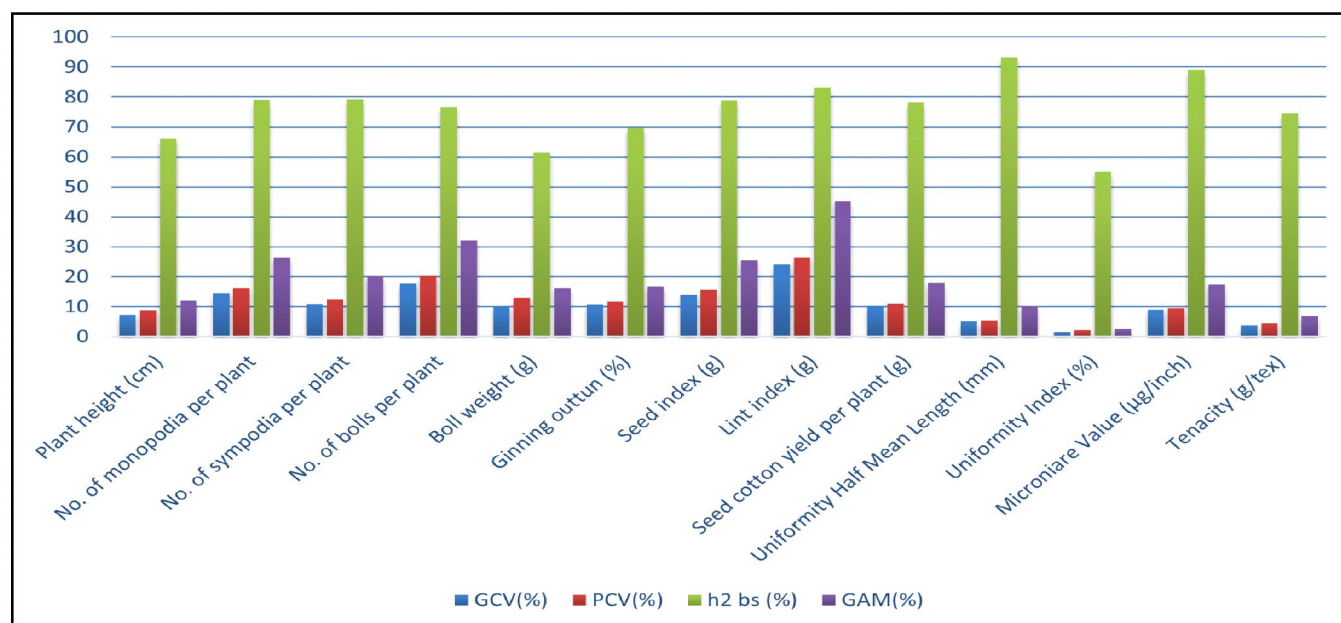
ANOVA was conducted to determine the significant differences among genotypes for the traits under study. The genotypic and phenotypic coefficients of variation (PCV and GCV) were categorized following the classification proposed by Shivasubramanian and Menon (1973), where values of 0-10% indicates low variation, 10-20% represents moderate variation and values greater than 20% reflects high variation. Broad-sense heritability was calculated as the percentage ratio of genotypic variance to phenotypic variance. Based on the classification by Johnson *et al.*, (1955) heritability was grouped into three categories as low (0-30%), moderate (30-60%) and high (>60%). Similarly, genetic advance was classified into three categories referred as low (0-

10%), moderate (10-20%) and high (>20%). The replicated data from the study was analyzed using the software WINDOWSTAT.

Results and Discussion

The analysis of variance for the thirteen yield attributes and fiber quality traits showed that the mean sum of squares for treatments was highly significant for all traits. This indicates the presence of substantial variability in the material studied for these thirteen yields and fiber related traits (Table 2).

The potential for improving economic traits in a crop through selection largely depends on the level of genetic variability present. The genotypic and phenotypic coefficients of variation provide insight into the level of variability within a genetic population, while heritability

**Fig. 1:** Graphical representation of genetic parameters for thirteen characters in cotton (*Gossypium hirsutum* L.).

helps predict the influence of genetic transmission on phenotype expression aiding in the selection of elite genotypes from a segregating population. Heritability combined with genetic advance supports the fixation of genetic factors for a specific trait. The results for the general mean, range, genetic variation parameters, broad-sense heritability (h^2_{bs}) and genetic advance as a percentage of the mean for all the traits studied are presented in Table 3.

High PCV and GCV was observed for lint index (24.03% and 26.36%, respectively) indicating the significant amount of variability for the genotypes studied for this trait. These results align with the findings of Kishore *et al.*, (2011), Dhivya *et al.*, (2014) and Khan *et al.*, (2015). Moderate GCV and PCV were recorded for several traits, including the number of monopodia per plant (14.40% and 16.20%), number of sympodia per plant (10.97% and 12.33%), number of bolls per plant (17.70% and 20.21%), boll weight (10.07% and 12.85%), ginning percentage (9.75% and 11.67%), seed index (13.96% and 15.73%) and seed cotton yield (9.79% and 11.08%). These moderate values suggest the presence of a reasonable level of variability that can be harnessed through selection for effective breeding programs. Similar findings have been reported by Vinodhana *et al.*, (2013), Shruti *et al.*, (2019), Gnanasekaran *et al.*, (2020) and Meena *et al.*, (2022). In contrast, low GCV and PCV were observed for the traits plant height (7.16% and 8.81%), upper half mean length (5.08% and 5.26%), uniformity index (1.63% and 2.19%), micronaire value (8.94% and 9.48%) and tenacity (3.82% and 4.43%) indicating limited variability. These findings are consistent with those of Manonmani *et al.*, (2019), Gnanasekaran *et al.*, (2020), and Meena *et al.*, (2022).

Higher magnitude of heritability was observed for several traits, including plant height (65.99%), number of monopodia per plant (79.02%), number of sympodia per plant (79.12%), number of bolls per plant (76.68%), boll weight (61.37%), ginning outturn (69.76%), seed index (78.80%), lint index (83.12%), seed cotton yield per plant (78.16%), uniformity half mean length (93.25%), micronaire value (88.99%) and tenacity (74.44%). These results indicate a strong genetic influence on these traits and are consistent with the findings of Dhivya *et al.*, (2014), Khan *et al.*, (2015), Manonmani *et al.*, (2019), Shruti *et al.*, (2019) and Meena *et al.*, (2022). Moderate heritability was recorded for the trait uniformity index (55.05%), suggesting a reasonable genetic contribution alongside environmental influence.

High heritability combined with high genetic advance as a percentage of the mean was witnessed for number

of monopodia per plant (26.37%), number of sympodia per plant (20.10%), number of bolls per plant (31.92%), seed index (25.53%), and lint index (45.14%). These results suggest that heritability is predominantly due to additive gene effects, making selection effective for improvement through the utilization of fixable genes. Similar findings have been reported by Dhivya *et al.*, (2014) and Meena *et al.*, (2022). High heritability with moderate genetic advance as a percentage of the mean was recorded for boll weight (16.24%), plant height (11.98%), ginning outturn (16.77%), seed cotton yield per plant (17.84%), uniformity half mean length (10.11%), and micronaire value (17.38%). These results suggest the influence of both additive and non-additive gene actions, indicating that desired outcomes may not be achieved through simple selection alone. Similar results have been noted by Ahsan *et al.*, (2015), Nishanth *et al.*, (2015), Monisha *et al.*, (2018), and Meena *et al.*, (2022). High heritability combined with low genetic advance as a percentage of the mean was noticed for uniformity index (8.45%) and tenacity (5.88%), indicating the predominance of non-additive gene action, which offers limited potential for improvement through selection. High heritability along with low genetic advance as a percentage of the mean was recorded for the trait's uniformity index (8.45%) and tenacity (5.88%). This suggests a predominance of non-additive gene action, limiting the potential for improvement through selection.

The highest values of GCV and PCV were observed for lint index indicating substantial variability among the genotypes. Traits such as the number of monopodia per plant, number of sympodia per plant, number of bolls per plant, seed index and lint index exhibited high heritability coupled with high genetic advance as a percentage of the mean, suggesting the predominance of additive gene action. These traits are ideal for selection in crop improvement programs. Conversely, traits including boll weight, plant height, ginning outturn, seed cotton yield per plant, uniformity half mean length and micronaire value displayed high heritability coupled with moderate genetic advance, indicating the involvement of both additive and non-additive gene effects. Selection for traits with high heritability and genetic advance, such as the number of monopodia, number of sympodia and bolls per plant is likely to be effective for achieving genetic improvement in cotton breeding programs.

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