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Genetic diversity and association studies in cotton

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ABSTRACT

One ninety-six (including four checks) of upland cotton genotypes (*Gossypium hirsutum* L.) were evaluated for genetic variability and divergence for seed cotton yield and it's attributing traits at Regional Agricultural Research Station, ANGRAU, Lam, Guntur during *kharif,* 2024. The analysis of variance indicated significant genetic variability among the germplasm lines. Genetic parameters such as genotypic and phenotypic coefficients of variation (GCV and PCV), heritability and genetic advance were calculated to understand the nature of trait inheritance and potential for improvement. Traits such as number of bolls per plant, number of sympodia, lint yield, and seed cotton yield showed high heritability coupled with high genetic advance, indicating predominant additive gene action. This implies that these traits can be effectively improved through simple selection. In contrast, traits like boll weight and uniformity ratio had lower GCV, PCV, and genetic advance, indicating a greater environmental influence or non-additive genetic control.

Keywords: *Cotton, Genetic advance, Heritability and Variability*

Cotton is a major fibre crop of global importance and addressed as the King of fibre crops (Komala *et al*., 2018). It belongs to the genus *Gossypium* family Malvaceae, which has extensively phenotypic diversity among the approximately 50 species representing in this genus. Currently, *Gossypium* includes 50 species, among these 44 are diploids, two are wild tetraploid and only four are cultivated species: *Gossypium herbaceum*, *Gossypium arboreum* (Asian diploid species; $2n = 2x = 26$), *Gossypium hirsutum* and *Gossypium barbadense* (American tetraploid species; $2n = 4x = 52$). Among the four cultivated species, upland cotton (*Gossypium hirsutum* L.) is mostly under cultivation because it is highly adaptable to various environments and higher yields.

The heritability estimated in the broad sense and expected genetic advance estimates reflects the preponderance of additive genetic effects controlling various attributes (Reddy and Reddy, 2016) and enable breeders in the execution of early generation phenotypic selection procedure for yield attributes which could result in better response to selection (Vineela *et al*., 2013). Hence, the information regarding genetic variability, heritability and genetic advance existing in the material under study is significantly essential for any crop improvement program (Reddy and Reddy, 2016).

Seed cotton yield and fibre quality in cotton depends on sympodia and monopodia/plant, No. of bolls/plant, seed index, boll weight, lint index and ginning out-turn and their association with yield is of utmost importance (Latif *et al*., 2015). Keeping in view the significance of genetic diversity, the present research was conducted to explore the genetic divergence and relationship among cotton germplasm for yield, yield-related traits, and fibre quality attributes.

MATERIAL AND METHODS

The experiment was laid out at Regional Agricultural Research Station, Lam, Guntur, Andhra Pradesh (situated at 28.290 E longitude, 16.100N latitude, and 31.5m altitude) during *Kharif,* 2024. The experimental material comprised of 196 (including Checks) germplasm accessions, which were planted in an augmented block design (Federer, 1956). Each genotype was sown in two rows with a row length of six m each with a spacing of 105 x 60 cm. Recommended package of practices were followed for better crop growth during the crop period. Data was collected in five randomly selected plants on various seed cotton yield contributing traits like plant height (cm), number of monopodia/plant, number of sympodia, number of bolls/plant, boll weight (g), lint index (g), seed index (g), ginning out turn (%) and fibre quality parameters like Fibre length (cm), uniformity Ratio, micronaire (µg/inch), fibre strength (g/ tex) and The analysis of variance was performed as per Johnson *et al*. (1955) and Falconer (1967).

Five plants at random in each replication were chosen and labelled for recording observations. The mean of five plants was used for statistical analyses. The data on the following yield and yield components and quality parameters were recorded. The characters *viz.,* days to 50% flowering, plant height at maturity, number of sympodial branches per plant, number of bolls per plant, single boll weight, seed index, ginning out turn, lint index, biological yield per plant, 2.5 per cent span length, micronaire, bundle strength and seed cotton yield. Genotypic co-efficient of variation (GCV) and phenotypic (PCV) co-efficient of variation were calculated based on the formula advocated by Burton (1952). Heritability in broad sense was calculated according to Hanson *et al.* (1956) and expressed in percentage. The GA as per cent of mean was classified according to Robinson *et al*. (1949)

RESULTS AND DISCUSSION

The analysis of variance (ANOVA) revealed highly significant differences among the treatments for most of the characters studied, indicating substantial genetic variability present among the genotypes evaluated. Out of 16 traits, all showed significant treatment effects except boll weight, which was non-significant, suggesting limited variation for this trait. Traits such as plant height, days to 50 % flowering, number of sympodia per plant, number of bolls per plant, ginning outturn, seed index, lint index, yield per plant, lint yield per plant, fibre length, micronaire, fibre strength, uniformity ratio, and day of emergence exhibited significant mean square values, reflecting adequate scope for genetic improvement. (Table 1 and 2)

Correlation analysis revealed that seed cotton yield per plant was significantly and positively correlated with lint yield, number of bolls, boll weight,

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

Mean sum of Square

Source	Df	PH	DFF	NMP	NSP	NBP	BW	GOT	SI
Treatment (ignoring Blocks)	5	195	386.15**	21.06**	0.24**	10.15**	113.59**	0.21*	12.18**
Treatment: Check	195	3	800.82**	52.00**	1.14**	7.26**	420.78**	0.01ns	8.82**
Treatment: Test	3	191	351.68**	9.44**	0.23**	9.23**	109.11**	0.20ns	10.88**
Test vs. Check	192	1	5724.48**	2146.69**	0.05**	193.90**	47.34**	2.76**	270.09**
Residuals	15	15	106.78	3.20	0.09	2.70	13.82	0.02	3.80

Mean Sum of Square

Source	Df	LI	SCYP	LYPP	FL	MIC	FS	UR	DE
Block (ignoring Treatments)	5	0.77**	681.11**	95.73**	3.09**	0.22**	3.97**	2.97**	0.46**
Treatment (eliminating Blocks)	195	3.78**	1537.50**	396.00**	1.73**	0.02*	3.56**	2.00**	1.50**
Treatment: Check	3	0.45**	506.04**	65.39**	2.78**	0.20**	3.46**	2.39**	0.45**
Treatment: Test and Test vs. Check	192	51.94**	31550.11**	4989.06**	67.41**	3.93**	100.78**	116.67**	0.04**
Residuals	15	0.13	128.77	14.3	0.26	0.02	0.31	0.21	0.09

*Indicates 5 % level of significance, ** indicates 1 % level of significance

LI: Lint index, LYPP: Lint yield per plant, FL: Fibre length, MIC: Micronaire value, FS: Fibre Strength, UR: Uniformity Ratio, DE: Days of emergence, SCYP: Yield yield per plant, MSS- Mean Sum of Square

Table 2. Variability parameters for yield, yield attributing and fibre quality traits of 196 (including four checks) Cotton (*Gossypium hirsutum* L.)

Trait	Mean	Mean	Std. Deviation	Min	Max	GCV (%)	PCV (%)	h^2 (%)	GA	GAM (%)
PH	120.11	120.11	19.1	82.04	213.54	13.03	15.61	69.64	26.9	22.4
DTFF	61.17	61.17	3.38	52	75	4.08	5.02	66.1	4.18	6.84
NMP	0.3	0.3	0.47	0	1.67	124.72	159.86	60.87	0.6	200.45
NSP	11.26	11.26	2.94	3.96	21.21	22.69	26.98	70.75	4.43	39.32
NB	31.47	31.47	10.97	17	73	31.02	33.19	87.33	18.79	59.72
BW	4.17	4.17	0.45	2.7	5.66	10.17	10.72	90	0.83	19.88
GOT	31.27	31.27	3.32	22.05	37.55	8.51	10.55	65.07	4.42	14.14
SI	7.21	7.21	1.42	3.52	10.24	15.57	19.81	61.76	1.82	25.21
LI	3.18	3.18	0.71	1.63	5.8	17.79	21.09	71.11	0.98	30.9
YPP	113.58	113.58	23.01	62	175	17.1	19.81	74.55	34.55	30.42
LYPP	35.02	35.02	8.35	15	62	20.41	23.09	78.13	13.02	37.16
FL	27.43	27.43	1.67	24.3	31.5	5.79	6.08	90.65	3.11	11.35
MIC	4.1	4.1	0.45	2.97	4.95	10.35	10.91	90	0.83	20.22
FS	27.57	27.57	1.87	24.1	31.7	6.44	6.75	91.04	3.49	12.65
UR	82.21	82.21	1.57	80	85	1.8	1.88	91.21	2.9	3.53
DE	4.21	4.21	0.67	3	5	14.25	15.93	80	1.11	26.26

and lint index. These traits could be considered as important indirect selection criteria for yield improvement. Negative correlations were observed between seed index and lint yield, as well as between plant height and some fibre traits, suggested the need for careful trait balancing in breeding programs.

Path coefficient analysis provided further insight by breaking down the correlations into direct and indirect effects. The highest positive direct effect on yield was observed for lint yield, followed by number of bolls per plant and boll weight. This reinforces the findings of the correlation study and highlights the importance of these traits in selection strategies. Traits like ginning outturn and seed index had negative direct effects, even when their correlation with yield was weakly positive, suggesting that their positive influence was indirectly via other traits.

Genetic parameters such as genotypic and phenotypic coefficients of variation (GCV and PCV), heritability, and genetic advance were calculated to understand the nature of trait inheritance and potential for improvement. Traits such as number of bolls per plant, number of sympodia, lint yield, and seed cotton yield showed high heritability coupled with high genetic advance, indicating predominant additive gene action. This implies that these traits can be effectively improved through simple selection. In contrast, traits like boll weight and uniformity ratio had lower GCV, PCV, and genetic advance, indicating a greater environmental influence or non-additive genetic control.

Very highest heritability estimates were observed for uniformity ratio followed by fibre strength, fibre length, micronaire, boll weight, number of bolls, days of emergence, lint yield per plant, lint index, number of sympodia, plant height, days to 50% flowering, ginning outturn, seed index and number of monopodia.

The clustering pattern and trait means suggested that Cluster V genotypes were most promising for yield improvement, while Clusters I and IV offered balanced traits for adaptability and fibre quality. Crosses between genetically distant clusters-particularly Cluster V with Clusters II or IV hold the potential to generate high heterosis and transgressive segregants. Such combinations are likely to enrich the genetic base of future breeding populations and might in the development of superior cotton varieties.

Ginning outturn trait heritability was 65.07%, with GAM of 14.14%, suggesting some potential for selection gain. GOT, being a key determinant of fibre yield, can benefit from selection if high-value genotypes such as L 1612 are utilized. For lint yield per plant heritability was high (78.13%), and the GAM was 37.16%, reflecting a strong potential for improving this trait through selection. Genotypes like LHDP cotton 1, which showed the highest lint yield per plant, could serve as donors for lint productivity improvement.

A comparative analysis of inter-cluster distances revealed that the maximum genetic divergence occurred between Clusters II and V

Table 4.3 Correlation among yield, yield attributing and fibre quality traits in Cotton genotypes

	PH	DTFF	NMP	NSP	NB	BW	GOT	SI	LI	LYPP	FL	MIC	FS	UR	DE	SCYP
PH	1	-0.165*	0.079	-0.033	0.159*	0.056	-0.102	-0.08	-0.227**	-0.11	-0.046	-0.2**	-0.161*	-0.149*	0.024	-0.019
DTFF	-0.165*	1	-0.048	0.242***	-0.011	0.305***	0.2**	0.026	0.433***	0.413***	0.188**	0.188**	0.203**	0.29***	-0.07	0.424***
NMP	0.079	-0.048	1	0.029	0.003	0.034	-0.089	0.014	-0.045	-0.107	0.06	0.043	0.139*	-0.024	0.027	-0.079
NSP	-0.033	0.242***	0.029	1	0.083	0.206**	-0.055	0.04	0.266***	0.157*	0.145*	-0.055	0.09	-0.019	0.165*	0.279***
NB	0.159*	-0.011	0.003	0.083	1	0.472***	-0.06	-0.117	-0.075	0.486***	0.043	-0.024	-0.007	-0.13	0.122	0.637***
BW†	0.056	0.305***	0.034	0.206**	0.472***	1	0.023	-0.19**	0.067	0.568***	0.162*	0.143*	0.156*	-0.033	0.102	0.676***
GOT	-0.102	0.2**	-0.089	-0.055	-0.06	0.023	1	-0.107	0.145*	0.454***	-0.012	0.12	0.234***	0.095	-0.039	0.117
SI	-0.08	0.026	0.014	0.04	-0.117	-0.19**	-0.107	1	0.656***	-0.19**	-0.083	-0.041	-0.114	0.031	-0.02	-0.169*
LI	-0.227**	0.433***	-0.045	0.266***	-0.075	0.067	0.145*	0.656***	1	0.205**	0.171*	0.119	0.103	0.304***	0.019	0.222**
LYPP	-0.11	0.413***	-0.107	0.157*	0.486***	0.568***	0.454***	-0.19**	0.205**	1	0.178**	0.222**	0.314***	0.13	0.043	0.853***
FL	-0.046	0.188**	0.06	0.145*	0.043	0.162*	-0.012	-0.083	0.171*	0.178**	1	0.091	0.111	0.197**	-0.05	0.211**
MIC	-0.2**	0.188**	0.043	-0.055	-0.024	0.143*	0.12	-0.041	0.119	0.222**	0.091	1	0.095	0.141*	0.082	0.168*
FS	-0.161*	0.203**	0.139*	0.09	-0.007	0.156*	0.234***	-0.114	0.103	0.314***	0.111	0.095	1	0.09	-0.023	0.24***
UR	-0.149*	0.29***	-0.024	-0.019	-0.13	-0.033	0.095	0.031	0.304***	0.13	0.197**	0.141*	0.09	1	-0.098	0.146*
DE	0.024	-0.07	0.027	0.165*	0.122	0.102	-0.039	-0.02	0.019	0.043	-0.05	0.082	-0.023	-0.098	1	0.053
SCYP	-0.019	0.424***	-0.079	0.279***	0.637***	0.676***	0.117	-0.169*	0.222**	0.853***	0.211**	0.168*	0.24***	0.146*	0.053	1

PH: Plant height, DFF: Days of 50 % flowering, NMP: Number of Monopodia, NSP: Number of Sympodia, BW: Boll Weight, GOT: Ginning Outturn, SI: Seed index, LI: Lint index, LYPP: Lint yield per plant, FL: Fibre length, MIC: Micronaire value, FS: Fibre Strength, UR: Uniformity Ratio, DE: Days of emergence, SCYP: Seed Cotton Yield per Plant.

Table 4.4 Path analysis for yield, yield attributing and fibre quality traits in cotton genotypes

	PH	**DTFF**	**NMP**	**NSP**	**NB**	**BW**	**GOT**	**SI**	**LI**	**LYPP**	**FL**	**MIC**	**FS**	**UR**	**DE**	**SCYP**
PH	0.031	0.002	-0.001	0.006	0.061	0.018	0.006	0.006	-0.006	0.025	-0.001	-0.001	0	-0.002	-0.001	**0.031**
DTFF	0.001	0.054	0.001	0.011	0.01	0.015	0.002	-0.001	0.005	0.102	0	0	0	0.002	0.005	**0.054**
NMP	0.001	-0.002	-0.016	-0.001	-0.023	0.003	0.023	0	-0.002	-0.071	-0.001	0	0.001	-0.001	-0.001	**-0.016**
NSP	0.002	0.006	0	0.104	0.044	0.019	0.034	0	0.008	0.044	-0.001	-0.001	0	-0.008	-0.008	**0.104**
NB	0.006	0.002	0.001	0.014	0.332	0.061	0.006	0.011	-0.005	0.391	-0.001	0	0	-0.005	-0.005	**0.332**
BW	0.005	0.007	0	0.016	0.172	0.119	-0.012	0.009	0	0.336	-0.002	0.001	0.001	-0.006	-0.007	**0.119**
GOT	-0.001	0	0.002	-0.015	-0.008	0.006	-0.232	0.008	-0.003	0.227	0.002	0	0.001	-0.002	0.001	**-0.232**
SI	-0.003	0.001	0	0.001	-0.058	-0.018	0.03	-0.061	0.044	-0.113	0.001	0	-0.001	0.002	0.001	**-0.061**
LI	-0.004	0.004	0.001	0.015	-0.029	0.001	0.013	-0.048	0.056	-0.026	-0.001	0	-0.001	0.007	-0.002	**0.056**
LYPP	0.001	0.009	0.002	0.008	0.222	0.068	-0.09	0.012	-0.003	0.585	0	0.001	0.001	-0.005	-0.002	**0.585**
FL	0.001	0	-0.001	0.008	0.027	0.011	0.025	0.005	0.002	0.016	-0.018	0	0	0.004	0.003	**-0.018**
MIC	-0.005	0	-0.001	-0.015	-0.008	0.013	-0.012	0.003	-0.001	0.064	0	0.009	0	0.001	-0.004	**0.009**
FS	-0.002	-0.001	-0.003	0	0.012	0.013	-0.031	0.007	-0.005	0.1	0	0	0.007	-0.003	0.001	**0.007**
UR	-0.001	0.002	0	-0.016	-0.035	-0.015	0.007	-0.003	0.008	-0.056	-0.001	0	0	0.051	0.006	**0.051**
DE	0.001	-0.006	0	0.019	0.038	0.019	0.006	0.001	0.003	0.029	0.001	0.001	0	-0.007	-0.044	**-0.044**

PH: Plant height, DFF: Days of 50 % flowering, NMP: Number of Monopodia, NSP: Number of Sympodia, BW: Boll Weight, GOT: Ginning Outturn, SI: Seed index, LI: Lint index, LYPP: Lint yield per plant, FL: Fibre length, MIC: Micronaire value, FS: Fibre Strength, UR: Uniformity Ratio, DE: Days of emergence, SCYP: Seed cotton Yield per Plant.

(7.49), followed by Clusters IV and V (6.98), and Clusters III and V (6.51). This clearly suggests that genotypes in Cluster V are the most genetically distinct from the rest. The minimum inter-cluster distance was recorded between Clusters III and IV (5.25), indicating a close relationship and lesser divergence among their genotypes. These findings suggest that crossing genotypes from highly divergent clusters such as Cluster II × V or Cluster IV × V could yield promising segregants with superior recombinants in the progeny, due to the likely presence of complementary alleles.

CONCLUSION

Genotypes L 1659 and LHDP cotton 5 which appeared in distinct and diverse clusters in genetic divergence analysis and showed high performance for multiple traits, could serve as promising parents for hybridization to generate high heterotic combinations.

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