The Pharma Innovation Journal 2021; 10(9): 487-490

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2021; 10(9): 487-490

www.thepharmajournal.com
Received: 28-07-2021
Accepted: 30-08-2021

V Thirumala Rao
Regional Agricultural Research Station, Professor, Jayashankar Telangana State Agricultural University, Rajendranagar, Hyderabad, Telangana, India

A Sudarshanam
Regional Agricultural Research Station, Professor, Jayashankar Telangana State Agricultural University, Rajendranagar, Hyderabad, Telangana, India

B Ramprasad
Regional Agricultural Research Station, Professor, Jayashankar Telangana State Agricultural University, Rajendranagar, Hyderabad, Telangana, India

D Aswini
Regional Agricultural Research Station, Professor, Jayashankar Telangana State Agricultural University, Rajendranagar, Hyderabad, Telangana, India

Corresponding Author:
V Thirumala Rao
Regional Agricultural Research Station, Professor, Jayashankar Telangana State Agricultural University, Rajendranagar, Hyderabad, Telangana, India

Genetic variability and association studies in upland cotton (*Gossipium hirsutum* L.)

V Thirumala Rao, A Sudarshanam, B Ramprasad and D Aswini

Abstract
The research was carried out for genetic variability, heritability and genetic advance of eighteen germplasm lines. Analysis of variance revealed significant difference among genotypes for all the eleven characters studied. The magnitude of PCV and GCV was moderate to high for seed cotton yield, number of sympodia per plant and boll weight. High heritability was recorded for tenacity, upper half mean length, seed cotton yield, boll weight, micronaire, palnt height and number of sympodia per plant. High heritability combined with high genetic advance was recorded for seed cotton yield, Plant height, boll weight, micronaire and number of sympodia per plant indicating that these characters are controlled by additive gene effect and phenotypic selection of these characters would be effective for further breeding purpose. Seed cotton yield has positive correlations boll weight, number of bolls per plant, number of sympodia per plant and palnt height along with quality parameters Uniformity index, upper half mean length, tenacity and these are major characters to be given selection pressure for improving yield.

Keywords: genetic variability, heritability, correlation and cotton

Introduction
Cotton (*Gossypium hirsutum* L.) is a king of fibre crops and plays a vital role as a cash crop in economy of many countries *viz*., USA, China, India, Pakistan, Uzbekistan, Australia and Africa. The demand of cotton is increasing at a rapid pace, more than the world's population growth rate, so we have to increase the yield per unit area. In India, cotton is cultivated in 129.57 lakh ha producing 371 lakh bales (170 kgs) with a productivity of 487 kg/ha whereas, in Telangana state, cotton is cultivated in 23.73 lakh ha producing 60 lakh bales (170 kgs) and 430 kg/ha as productivity (AICCIP Annual Report 2020-21). In India productivity is very low compared to all other cotton growing countries. Therefore it is essential to develop new high yielding cultivars with good fibre quality parameters.

Genetic variability is essential for plant breeders to exercise selection and the phenotypic and genotypic coefficients of variation were estimated using genotypic and phenotypic variances respectively. The coefficient of variation gives only the extent of existing variability for various traits, but that does not give any information about the heritable portion of it. Therefore, the heritability accompanied with estimates of genetic advance and genetic advance over mean were also estimated. Heritability itself provides no indication about the genetic progress that would result from selection. However, at a fixed selection pressure, the amount of advance varies with magnitude of heritability. Further, the efficiency of selection in any breeding programme mainly depends upon the knowledge of association of the characters. Phenotypic correlation indicated the extent of the relation between two characters while genotypic correlation provides an estimate of inherent association between the genes controlling them. Hence the present study was planned to assess the genetic variability and correlation for various yield and yield contributing characters in a set of genotypes. Such information may be fruitful in formulating efficient selection programme for synthesis and development of new cotton genotypes with improved yield and its contributing traits.

Materials and Methods
The experiment was conducted at Professor Jayashankar Telangana State Agricultural University, Regional Agricultural Research Station, Warangal during *Kharif*, 2019-20. The mean maximum and minimum temperature prevailed during the cropping period was 30.4 ˚C & 20.1 ˚C respectively and an average rainfall of 1265 mm which was received in 57 rainy days. The experimental site is located at Longitude 79° 22¹ E and Latitude 18° 03¹ N). In the present study eighteen genotypes were sown in randomized complete block design (RBD) with

two replications at each genotype was raised in 4.5m length with spacing of 120 X 45 cm in two rows. Recommended agronomic practices were followed to raise a good crop. Observations were recorded on plant height (cm), number of monopodia per plant, number of sympodia per plant, number of bolls per planr, boll weight (g), Upper half mean length(mm), Uniformity index, micronaire (ug/inch), Tenacity (g/tex), Elongation ratio(%), Seed cotton yield(Kg/plot). Observations on fibre quality traits in each replication were recorded by High Volume Instrument (HVI) in ICC mode. Good crop was raised by using recommended agronomic practices and need based plant protection measures.

Statistical analysis: Data were subjected to analysis of variance using INDOSTAT statistical software. The means for all the observed parameters were worked out and were further subjected to Analysis of variance (ANOVA) according to Johnson *et al.* (1955) [9]. The genotypic and phenotypic coefficients of variation were calculated according to the formula given by Falconer (1981) [6]. Heritability (h^2) in the broad sense was calculated according to the formula given by Allard (1960) [2]. Genetic advance was estimated by the following formula given by Burton (1953) [4] from the heritability. Correlation coefficients at phenotypic and genotypic level were calculated as per procedure given by Al-Jibouri *et al.* (1958) [1].

Results and Discussion

The analysis of variance revealed significant differences among the genotypes for all the traits studied. The general mean, range and genetic variability of different parameters presented in Table 1, revealed that sufficient variability was present in the genotypes for all the characters. High variability in the breeding material ensures better chances of producing required forms of a crop plant. This variability can be utilized effectively to develop high yielding cultivars through hybridization followed by selection. 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 over mean for all the characters are furnished in Table 1. Moderate estimate of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was observed for seed cotton yield (18.56% and 15.97%), number of sympodia per plant (13.00% and 10.07%) and boll weight (12.20% and 10.41%). High phenotypic coefficient of variation and moderate genotypic coefficient of variation was observed for the number of monopodia per plant (43.54%, 19.88%) whereas the moderate estimates of phenotypic coefficient of variation and low estimates of genotypic coefficient of variation were recorded for traits like number of bolls per plant (13.33% and 9.23%) and miconaire (11.98% and 9.75%). Plant height (7.98% and 6.39%), Upper half mean length (7.60%,6.93%), Tenacity (6.71%,6.57%), Elongation ratio(6.79%, 4.91%,) and Uniformity index (4.76% and 0.83%) exhibited low PCV and GCV which indicated that the characters were highly influenced by the environmental factors. The phenotypic coefficient of variation which measures the total variation was found to be greater than the genotypic coefficient of variation for all the characters indicated some degree of environmental influence on the traits. Selection for improvement of such traits may sometimes be misleading due to environmental influence. These findings were also supported by Kulkarni *et al.*, 2011 [11], Pujer *et al.*, 2014 [13], Sunayana *et al.*, 2017 [18] and Gnanasekaran *et al.*, 2020.

High heritability value was observed for characters like tenacity (95.8%), upper half mean length (83.2%), seed cotton Yield (74%), boll weight (72.9%) Micronaire (66.2) palnt height (64.1%) and number of sympodia per plant(60.0%). This finding was agreed with earlier finding of Pujer *et al.*, 2014 [13]. Eswari *et al.*, 2017 [5] and Gnanasekaran *et al.*, 2018 [7, 8] have also reported similar results for the number of bolls per plant, 2.5% span length, bundle strength and seed cotton yield per plant. Sunayana *et al.*, 2017 [18] have reported the same results for the number of bolls per plant (79.39%), seed index (64.20%), lint index (77.27%), ginning percentage (81.10%), and seed cotton yield per plant (88.67%). This suggested the greater effectiveness of selection and improvement to be expected for these characters in future breeding programmes as the genetic variance is mostly due to the additive gene action. Number of bolls per plant (48.0%), elongation ratio (52.2%) showed moderate estimates of heritability and Uniformity index (22.4%), number of monopodia per plant (20.%) showed low estimates of heritability. Heritability estimates along with genetic advance would be more useful in predicting yield under phenotypic selection than heritability estimates alone as suggested by Johnson *et al.* (1955) [9]. If heritability is mainly due to non-additive gene effect, the expected genetic advance would be low, and if there is additive gene effect, a high genetic advance may be expected (Panse, 1957) [12]. In the present investigation high heritability coupled with high genetic advance as percentage of mean was observed for seed cotton yield(36.29), boll weight(23.48), micronaire(20.94) and number of sympodia per plant(20.6) indicating the preponderance of additive gene action in the inheritance of these traits. Pujer *et al.* (2014) [13], Eswari *et al.* (2017) [5] and Sunayana *et al.* (2017) [18] reported high heritability and high genetic advance as percentage of mean for the number of bolls per plant, seed cotton yield per plant revealed the influence of additive gene action for these traits. Hence the improvement of these traits can be made through direct phenotypic selection.

The traits such as Tenacity (95.8 and 16.98%) and upper half mean length (83.2 and 16.7%), Plant height (64.1 and 13.50%) in which high heritability accompanied by medium genetic advance was recorded indicates the effect of non-additive gene action and hence heterosis breeding may be rewarding for these traits. Siva Prasad *et al.* (2005) [16] for ginning percentage and Pujer *et al.* (2014) [13] for uniformity ratio reported the similar results.

Seed cotton yield is a complex character governed by several contributing traits. Hence, it is important to understand the association of different characters with seed yield for enhancing the usefulness of selection criterion to be followed while developing varieties. In the present investigation the genotypic and phenotypic correlations are on par with each other suggesting the less influence of environment (Table 2). Seed cotton yield was significant positive correlation with Boll weight, Upper half mean length, Uniformity index and Tenacity. Hence, the selection for these traits will help in selecting genotypes with higher seed cotton yield per plant. The close association between yield and yield attributing traits can be exploited in the selection programme which might be helpful in evolving high yielding genotypes. Such positive association of seed cotton yield per plant with these traits was also observed by Pujer *et al.* (2014) [13], Asha *et al.* (2015) [3], and Sunayana *et al.* (2017) [18].

The traits like number of bolls per plant, Plant height, number of sympodia per plant and Micronaire exhibited non-significant positive association with seed cotton yield. Similar results were reported by Srinivas *et al.* (2015) [17] for ginning percentage and bundle strength; Sunayana *et al.* (2017) [18] for lint index; Rao and Gopinath (2013) [14] for 2.5% span length (mm), bundle strength (g/tex), fibre fineness (µg/inch) and uniformity ratio (%). Number monopodia per plant exhibited non-significant negative association with seed cotton yield.

The inter correlation between the quantitative yield contributing traits *viz*., Plant height has significant negative association with number of monopodia per plant, non-significant negative association with number of sympodia per plant and number of bolls per plant, significant positive association with upper half mean length, uniformity index, Micronaire and non-significant positive association with boll weight, Elongation ratio, Tenacity. Number of monopodia per plant has significant negative association with number of bolls per plant, Micronaire, number of sympodia per plant, significant positive association with boll weight, uniformity index, upper half mean length, Tenacity and non-significant positive association with Elongation ratio. Number of sympodia per plant has significant positive association with Number of bolls per plant, non-significant positive association with Micronaire, Elongation ratio and non-significant negative association with uniformity index, upper half mean length, boll weight, Tenacity. Number of bolls per plant has significant positive association with Elongation ratio, non-significant positive association with Micronaire, Tenacity, significant negative association with uniformity index and non-significant negative association with upper half mean length, boll weight. Boll weight has significant positive association uniformity index, upper half mean length, Tenacity, Elongation ratio, non-significant negative association with Micronaire. Upper half mean length has significant positive association with uniformity index, Tenacity and non-significant positive association with Elongation ratio, Micronaire. Uniformity index has significant positive association with Tenacity and non-significant positive association with Elongation ratio, Micronaire. Micronaire has significant positive association with Elongation ratio and non-significant positive association with Tenacity. Tenacity has significant positive association with Elongation ratio. These findings are in accordance with the results of Sakthi *et al.* (2007) [15], Kalpande *et al.* (2008) [10], Rao and Gopinath (2013) [14]. Gnanasekaran *et al*., (2020) [7, 8]. Hence, the selection based on plant height, the number of monopodia, the number of sympodia, the number of bolls per plant, boll weight along with quality traits will bring about breakthrough in cotton yields.

In the present investigation high heritability was recorded for tenacity, upper half mean length, seed cotton Yield, boll weight, Micronaire, palnt height and number of sympodia per plant. High heritability combined with high genetic advance was recorded for seed cotton yield per plant, Plant height, boll weight and micronaire indicating that these characters are controlled by additive gene effect and phenotypic selection of these characters would be effective for further breeding purpose. Present study revealed that boll weight, number of bolls per plant, number of sympodia per plant and palnt height along with quality parameters Uniformity index, upper half mean length Tenacity were positively associated with seed cotton yield. Selection pressure on these traits is the key to obtain higher seed cotton yield.

Table 1: Estimates of variability, heritability and genetic advance in Cotton

Character	Mean	Range	GCV (%)	PCV (%)	Heritability in Broadsence (H^2)	Genetic advance	GA as percent of mean
Plant Height	143.50	120-158	6.39	7.98	64.1	19.383	13.508
No of monopodia per plant	1.22	0.5-1.9	19.88	43.54	20.9	0.294	23.974
No of sympodia per plant	21.90	16.7-25.3	10.07	13.00	60.0	4.513	20.607
Number of bolls per plant	43.83	34.5-55.3	9.23	13.33	48.0	7.407	16.890
Boll weight	4.83	3.7-5.5	10.41	12.20	72.9	1.135	23.483
Upper Half mean length(UHML)	28.01	24.2-30.3	6.93	7.60	83.2	4.680	16.707
Uniformity Index(UI)	82.36	80-84	0.83	1.76	22.4	0.859	1.043
Micronaire	4.46	3.3-5.3	9.75	11.98	66.2	0.934	20.947
Tenacity	28.16	24.4-30.9	6.57	6.71	95.8	4.782	16.983
Elongation	6.43	5.75 -6.90	4.91	6.79	52.2	0.603	9.366
Seed cotton yield(kg/pl)	3.37	1.78-4.09	15.97	18.56	74.0	1.222	36.294

Table 2: Genotypic correlation coefficients between different traits in Cotton

Character	PH	NMP	NSP	NB	BW	UHML	UI	M	T	E	Seed cotton Yield/ Plant
Plant Height (PH)	1.0000	-0.7702*	-0.3711	-0.1470	0.3819	0.5317*	0.6749*	0.4754*	0.2379	0.2646	0.3584
No of monopodia per plant (NMP)		1.0000	-0.5278*	-1.1689*	1.0005*	0.6247*	0.9398**	-1.0473**	0.4475*	0.3588	-0.2304
No of sympodia per plant(NSP)			1.0000	1.0106*	-0.2870	-0.3385	-0.4292	0.2470	-0.0278	0.0487	0.3145
Number of bolls per plant(NB)				1.0000	-0.1720	-0.3526	-0.4670*	0.2927	0.2125	0.5292*	0.4229
Boll weight(BW)					1.0000	0.7275*	1.0965**	-0.2498	0.6457*	0.6276*	0.4573*
Upper Half mean length(UHML)						1.0000	1.5356**	0.0362	0.7105*	0.2378	0.6340*
Uniformity Index(UI)							1.0000	0.1537	1.1657**	0.2669	1.0373**
Micronaire(M)								1.0000	0.1537	0.5524*	0.0956
Tenacity(T)									1.0000	0.8707**	0.6742*
Elongation										1.0000	0.6462*

*, ** Significant at P=0.05 and P = 0.01 level respectively

References

1. Al-Jibouri HA, Miller PA and Robinson HF. Genotypic and environmental variances and covariances in upland cotton crosses of inter-specific origin. Agron. J 1958;50:633-637.
2. Allard RW. Principles of Plant Breeding. Publishers by John Wiley and Sons Inc. New York, USA 1960; 485.
3. Asha R, Ahamed ML, Babu, DR, Kumar PA. Character association and path coefficient analysis for yield and component traits in upland cotton. J Cotton Res. Dev. 2015;29:31-35.
4. Burton GW, De Vane EW. Estimating heritability in tall fescue (*Feetuca circuhinoceae*) from replicated clonal material. Agron. J 1953;45:478-481. [Cross Ref]
5. Eswari KB, Sudheer Kumar S, Gopinath and Rao MVB. Genetic variability heritability and genetic advance studies in cotton. International Journal of Development Research 2017;07:10902-10904.
6. Falconer DS. Introduction to quantitative genetics. Second Edition. Longman, New York 1981.
7. Gnanasekaran M, Thiyagu K, Gunasekaran M. Genetic variability heritability and genetic advance studies in cotton (*Gossypium hirsutum* L.) Electronic J Pl. Breeding 2018.;9:377-382.
8. Gnanasekaran M, Thiyagu K, Gunasekaran M. Studies on Genetic variability correlation and path analysis in upland cotton (*Gossypium hirsutum* L.) Electronic J Pl. Breeding 2018;11(3):981-986.
9. Johnson HW, Robinson H, Comstock RE. Estimates of genetic and environmental variability in soybean. Agron. J 1955;47:314-318.
10. Kalpande HV, Bhale SD, Kale UV, Deshmukh JD, Gite VK, Kakde SS. Genetic variability and correlation studies in F3 generation of cotton (*Gossypium hirsutum* L.) Intl. J plant Sci 2008;3:94-97.
11. Kulkarni AA, Nand HC, Patil SG. Studies on genetic divergence in upland cotton (*Gossypium hirsutum* L.). J cotton Res. Dev 2011;25:9-13.
12. Panse VG. Genetics of quantitative characters in relation to plant breeding. Indian Journal of Genetics and Plant Breeding 1957;17(3):318-328.
13. Pujer SK, Siwach SS, Sangwan RS, Sangwan O, Deshmukh J. Correlation and path coefficient analysis for yield and fibre quality traits in upland cotton (*Gossypium hirsutum* L.). J. Cotton Res. and Dev 2014;28:214-216.
14. Rao PJM, Gopinat, M. Association analysis of Yield and Fibre quality Characters in upland cotton (*Gossypium hirsutum* L.) Australian Journal of Basic and Applied Sciences 2013;7:787-790.
15. Sakthi AR, Kumar M, Ravikesavan R. Variability and association analysis using morphological and quality traits in cotton (*Gossypium hirsutum* L.). J Cotton Res. Dev 2007;21:148.
16. Siva Prasad U, Chenga Reddy V, Narisi Reddy A. Studies on genetic variability in American cotton (*Gossypium hirsutum* L.). Karnataka Journal of Agricultural Sciences 2005;18:1095-1098.
17. Sriniva B, Bhadru D, Brahmeswara Rao, MV. Correlation and path coefficient analysis for seed cotton yield and its components in American cotton (*Gossypium hirsutum* L.). Agric. Sci. Digest 2015;35:13-18.
18. Sunayana R, Sangwan, S, Somveer Nimbal. Studies on Association, Path Analysis and Genetic Parameters for Seed Cotton Yield and Its Contributing Characters in Desi Cotton (*Gossypium arboreum* L.). Int. J Curr. Microbiol. App. Sci 2017;6:104-111.