

## Research Note

# Genetic variability studies in germplasm of upland cotton (*Gossypium hirsutum* L.)

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### Abstract

Three hundred and ninety nine germplasm lines of upland cotton (*Gossypium hirsutum* L.) were evaluated for fifteen traits to assess the *per se* performance, magnitude of genetic variability, heritability and genetic advance as percent of mean. *Per se* performance study revealed the top entries for yield, early maturing, high boll weight, high boll number and fibre quality characters among the 399 entries used for the study. The estimates of PCV were higher than the GCV for all the characters under studied, this shows the influence of environmental factors on the characters. Highest estimates of PCV and GCV were observed for number of monopodia and seed cotton yield. While lowest estimates of PCV and GCV were observed for days to 50% flowering, seed index, bundle strength, uniformity and elongation percent. The four characters *viz.*, number of sympodia, boll weight, lint index and micronaire value showed the moderate estimates of PCV and GCV. High heritability coupled with high genetic advance as percent of mean was observed for number of monopodia, number of sympodia, boll weight, lint index, micronaire value and seed cotton yield and these characters were controlled by additive gene effects, hence selection of genotypes based on these characters would be effective in the improvement of yield.

### Keywords

*Gossypium hirsutum* L., *Per se* performance, genetic variability, heritability and genetic advance.

Cotton is the King of the fibre crops commonly known as the “White gold”. It is the main economic and industrial crop of our country serving prime raw material for textile mills. The genus *Gossypium* belongs to the family Malvaceae and there are about 50 different species of cotton among which four species are cultivated having spinnable lint and the remaining 46 species are in wild form. Among four cultivated species *Gossypium hirsutum* L. is cultivated more than 90% of the area throughout the world. It is having wide range of yield components and fibre quality traits.

In *Gossypium hirsutum* L. cotton there are many varieties and hybrids are under cultivation which gives profitable yield but they are highly uniform with narrow genetic background. Germplasm is the only source to broaden the genetic base of the cotton species. So study of germplasm having high genetic variability and desirable genes will guide us to design breeding strategies for increasing the genetic base. Understanding the extent of variability and magnitude of heritability and genetic advance as percent mean is important for the formulation of successful breeding program. The genetic improvement in cotton crop is depends on the existence of initial genetic variability among the population. The initial variability and the

degree of heritability amongst yield and yield attributing traits are prime important for developing superior genotypes in cotton.

The present study was carried out at the Department of Cotton, TNAU, Coimbatore. A total of 399germplasm of upland cotton were sown on Augmented Block Design along with nine checks during the *Kharif* season. The observations were recorded on three selected plants from each entry for 15 characters *viz.*, Days to 50% flowering, Plant height, Number of monopodia, Number of sympodia, Number of bolls, Boll weight, Seed cotton yield per plant, Ginning outturn, Seed index, Lint index, 2.5% span length, Micronaire value, Bundle strength, Uniformity ratio, Elongation percentage. The variability parameters were calculated according to the formula of Burton (1952) and heritability in broad sense was estimated as per suggestion of Lush (1949). The expected genetic advance was calculated according to method suggested by Johnson *et al.* (1955).

The study of *per se* performance of 399germplasm of upland cotton revealed the top entries with better performance in yield and quality. The entries like SS 264-N (178.47), RU 4\4 (176.67), IGM 28-1

(176.67), KC 2 (165), D 20 (156) were found to be better yielding (g). The entries *viz.*, 134-CO-3M (48), CT 13-14-15 (51) and Delta Pine 16 (51) were observed to be early maturing (days) among the 400 entries. Highest boll weights (g) were observed for TCH 1811 (6.9), RS 253 (6.4), EWLS-403-2 (6.37), TCH 1806 (6.3) and RS 252 (6.28). The entries having more number of bolls per plant were IGM 28-1 (56.6), D 16 (48.67), Okra Leaf (42.33), IARI 16-18-13 (41.33), BP-6871 (41). The germplasm entries *viz.*, Delta Pine 16 (42.35%), Buri 147 (40.91%), PRS 2 (40.37%), 5\44 (40%), AC 114 (40%) recorded top position for ginning outturn (%). The high fibre strength (g/tex) entries were K 51 (28), Cerro (P) (27.3), SH 469(1-1) (27.2), 418\49-45F×LSS 1\63 (26.8) and CC 29-2-3-20 (26.5). The lines with higher 2.5% span length (mm) include BW-12-5-1 (36.4), C 34 (36), GISV 01/876 (35.9), CAT 728-1 (35.6) and BP-52 NC-62 (35.5). The entries such as IC 1903 SF (7.3), EC 2 (6.94), B-61-1862 (6.65), SRT 1 (6.62) and CPD 431 (6.6) were having highest micronaire value ( $\mu\text{g}/\text{in}$ ) which can be suggested for surgical cotton. The above mentioned entries can be used in the breeding program for the improvement of its respective characters mentioned.

A wide range of data was observed for all the characters under study. The average values in respect of 15 characters were used for the analysis (Table 1). The analysis of variance revealed significant differences among the genotypes for 14 characters except number of bolls per plant (Table 2.) thereby indicating the presence of significant genetic variability among the experimental material. Phenotypic coefficient of variation was greater than the genotypic coefficient of variation for all the characters studied and this proves that environment plays a significant role in the expression of these traits. The PCV, GCV, heritability and genetic advance as percent mean for the different characters are shown in the Table 3.

Highest estimates of PCV and GCV were recorded for the characters, number of monopodia and seed cotton yield. These results are in accordance with by Neelam and Potdukhe (2002), Altaher and Singh (2003), Kaushik *et al.* (2003) and Vijayalaxmi (2007). For the characters *viz.*, number of sympodia, boll weight, lint index and micronaire value, moderate PCV and GCV was observed. Moderate PCV and low GCV were observed for plant height and 2.5 % span length which is in accordance with Sakthi *et al.* (2007), and Dhivya *et al.* (2014). Characters like days to 50 % flowering, seed index, ginning out-turn bundle strength, uniformity ratio and elongation

percent had shown low PCV and GCV. Similar results were recorded by Dinakaran *et al.* (2012), Usharani *et al.* (2014) and Reddy *et al.* (2015).

Study of heritability and genetic advance as percent mean helps in selecting a character for breeding program. In the present study high heritability coupled with high genetic advance as percentage of mean was observed for number of monopodia, number of sympodia, boll weight, lint index, micronaire value and seed cotton yield. This indicated the less influence of environment on the expression of these traits and presence of additive gene action in the inheritance of these traits and it is amenable for simple selection. These results fall in line with the results of Vijayalaxmi (2007), Padmavathi (2008), Dinakaran *et al.* (2012), Vinodhana *et al.* (2013) and Reddy *et al.* (2015).

The characters like plant height, ginning out-turn, 2.5 % span length, bundle strength, uniformity ratio and micronaire value had shown high heritability with moderate genetic advance as percentage of mean. So the possibility for improving these characters through mass selection, progeny selection or any modified selection procedure aiming to exploit the additive gene effects. Preetha and Raveendran (2007) and Dhivya *et al.* (2014) also observed the similar results. The character seed index showed low heritability coupled with low genetic advance and the similar findings were reported by Vinodhana *et al.* (2013). The trait days to 50% flowering showed high heritability combined with low genetic advance. High heritability is being exhibited due to favorable influence of environment rather than genotype and selection for such traits may not be rewarding.

## References

- Altaher, A., & Singh, R. 2003. Genetic diversity studies in upland cotton (*Gossypium hirsutum* L.). *Journal of the Indian Society for Cotton Improvement*, **28**(3): 158-163.
- Burton, G. W. 1952. Quantitative inheritance in grasses. Proceedings of the 6<sup>th</sup> International Grassland Congress Research p. 277-283.
- Dhivya, R., Amalabalu, P., Pushpa, R., & Kavithamani, D. 2014. Variability, heritability and genetic advance in upland cotton (*Gossypium hirsutum* L.). *African Journal of Plant Science*, **8**(1): 1-5.
- Dinakaran, E., Thirumeni, S., & Paramasivam, K. 2012. Yield and fibre quality components analysis in upland cotton (*Gossypium hirsutum* L.) under



- salinity. *Annals of Biological Research*, **3**(8): 3910-3915.
- Johnson, H. W., Robinson, H., & Comstock, R. 1955. Estimates of Genetic and Environmental Variability in Soybeans . *Agronomy Journal*, **47**(7):314-318.
- Kaushik, S., Kapoor, C., & Koli, N. 2003. Association and path analysis in American cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*, **17**(1): 24-26.
- Lush, J. L. 1949. Heritability of quantitative characters in farm animals. *Hereditas*, **35**(S1): 356-375.
- Neelam, G., & Potdukhe, N. 2002. Studies on variability and correlations in upland cotton for yield and its components. *Journal of the indian society for cotton improvement*, **27**(3): 148-152.
- Padmavathi, A. 2008. Characterization of cotton germplasm (*Gossypium hirsutum* L.).M.Sc. (Ag) thesis Acharya N.G. Ranga Agricultural University, Rajendranagar, Hyderabad.
- Preetha, S., & Raveendran, T. 2007. Genetic variability and association analysis in three different morphological groups of cotton (*Gossypium hirsutum* L.). *Asian Journal of Plant Sciences*, **6**(1): 122-128.
- Reddy, K. B., Reddy, V. C., Ahmed, M. L., Naidu, T., & Srinivasarao, V. 2015. Correlation and path coefficient analysis in upland cotton (*Gossypium hirsutum* L.).*International Journal of Pure & Applied Bioscience*, **3**(3): 70-80.
- Sakthi, A., Kumar, M., & Ravikesavan, R. 2007. Variability and association analysis using morphological and quality traits in cotton (*Gossypium hirsutum*). *Journal of Cotton Research and Development*, **21**(2): 148-152.
- Usharani, K., Vindhivarman, P., & Amalabalu, P. 2014. Combining ability analysis in intraspecific F1 diallel cross of upland cotton (*Gossypium hirsutum* L.). *Electronic Journal of Plant Breeding*, **5**(3): 467-474.
- Vijayalaxmi, G. 2007. *Genetic divergence in cotton (Gossypium hirsutum L.)*. Acharya N.G. Ranga Agricultural University, Rajendranagar, Hyderabad.
- Vinodhana, K., *et al.* 2013. "Genetic studies of variability, correlation and path coefficient analysis in cotton genotypes." *International Journal of Pure & Applied Bioscience* **1**(5): 6-10.



**Table 1. Mean and range of performance for different characters among the accessions of *G. hirsutum***

<b>Characters</b>	<b>Mean</b>	<b>Maximum value</b>	<b>Minimum value</b>
<b>Days to 50% flowering</b>	56.16	66.00	48.00
<b>Plant height (cm)</b>	119.90	168.33	83.67
<b>Number of monopodia</b>	1.43	3.67	0.00
<b>Number of sympodia</b>	19.19	32.30	13.13
<b>Number of bolls</b>	25.35	56.67	10.00
<b>Boll weight (g)</b>	4.78	6.93	2.77
<b>Lint index</b>	5.01	6.96	2
<b>Seed index</b>	9.93	11.40	7.00
<b>Ginning outturn (%)</b>	33.39	42.35	22.22
<b>2.5% span length (mm)</b>	29.05	36.40	16.40
<b>Uniformity ratio (%)</b>	47.37	56.10	38.90
<b>Bundle strength (g/tex)</b>	21.34	28.00	17.00
<b>Elongation percent</b>	5.78	6.80	3.90
<b>Micronaire value (<math>\mu\text{g}/\text{inch}</math>)</b>	4.90	7.33	3.27
<b>Seed cotton yield (g)</b>	73.78	178.47	2.33



**Table 2. ANOVA table for quantitative traits**

Characters	Mean sum of squares				
	Treatment	Checks	Test entry	Check vs test	Error
Days to 50 % flowering	9.73**	32.23	9.30**	0.17	3.03
Plant height(cm)	223.74**	1005.71	203.63*	1975.25	103.54
Number of monopodia	0.62*	0.74	0.62*	1.48	0.38
Number of sympodia	6.54**	15.52	6.30**	27.95	1.69
Number of Bolls	34.74	40.35	34.3	165.75	36.13
Boll weight (g)	0.47**	1.43	0.45**	0.89	0.07
Seed index	0.81*	2.62	0.68*	35.1	0.64
Lint index	0.677**	0.4	0.60**	32.25	0.05
Ginning outturn (%)	9.30**	10.99	9.15**	58.26	1.77
2.5% Span length (mm)	8.45*	37.7426	7.8524*	14.33	6.45
Bundle strength (g/tex)	3.94**	6.2	3.87**	14.53	0.96
Uniformity ratio (%)	12.46**	31.77	12.0976**	4.08	1.22
Elongation percent (g)	0.030**	0.02	0.03**	0.06	0.004
Micronaire value ( $\mu\text{g}/\text{inch}$ )	0.42**	1.5	0.40**	0.5031	0.03
Seed cotton yield (g)	1026.77**	457.36	1033.24**	3198.24	330.68

\*- Significant at 5 % level

\*\* - Significant at 1 % level



**Table 3. Variability, heritability and genetic advance as percent mean**

<b>Characters</b>	<b>PCV</b>	<b>GCV</b>	<b>Heritability</b>	<b>GA</b>	<b>GAM</b>
<b>Days to 50% flowering</b>	5.55	4.34	61.11	3.92	6.99
<b>Plant height (cm)</b>	12.20	8.81	52.19	15.73	13.12
<b>Number of monopodia</b>	55.14	36.81	44.57	0.73	50.62
<b>Number of sympodia</b>	13.23	11.40	74.20	3.88	20.22
<b>Boll weight (g)</b>	14.55	13.54	86.60	1.24	25.95
<b>Seed index</b>	8.99	4.12	20.99	0.39	3.89
<b>Lint index</b>	16.11	15.5	92.54	1.56	30.72
<b>Ginning outturn (%)</b>	9.11	8.19	80.97	5.09	15.19
<b>2.5% Span length (mm)</b>	10.05	7.18	51.48	3.08	10.61
<b>Bundle strength (g/tex)</b>	9.47	8.46	79.71	3.32	15.56
<b>Uniformity ratio (%)</b>	7.48	7.10	90.08	6.56	13.89
<b>Elongation percent</b>	3.06	2.57	70.06	0.26	4.42
<b>Micronaire value (<math>\mu\text{g}/\text{inch}</math>)</b>	13.40	12.78	91.00	1.23	25.12
<b>Seed cotton yield (g)</b>	43.43	35.14	65.45	43.20	58.56

PCV- Phenotypic coefficient of variance  
GA –Genetic advance

GCV- Genotypic coefficient of variance  
GAM- Genetic advance as percent mean