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Research Note

Genetic variability heritability and genetic advance studies in cotton (*Gossypium hirsutum* l.)

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Abstract

The present experiment was carried out at research farm of Cotton Research Station, Srivilliputtur, to determine genetic variability, heritability and genetic advance estimates in upland cotton. The analysis of variance involving a set of fourty two improved *hirsutum* genotypes received from various research institutes under AICRP on Cotton for eleven characters *viz.,* Days to 50 % flowering, Plant height, Number of monopodia per plant, Number of sympodia per plant, Number of bolls per plant, Boll weight**,** Ginning percentage, Upper Half Mean Length, Bundle strength, Micronaire value, and Seed cotton yield (kg/ha) revealed highly significant mean sum of squares for all the characters indicating greater diversity among the genotypes. The value of Phenotypic Coefficient of Variation (PCV) is greater than Genotypic Coefficient of Variation (GCV); it means that the apparent variation is not only due to genotypes but also due to influence of environment. The difference between the estimates of PCV and GCV were low for all the characters except number of monopodia per plant, number of sympodia per plant and number of bolls per plant thereby indicating that lesser role played by the environment in the expression of these characters. The traits like Days to 50% flowering, Plant height, Boll weight, Seed cotton yield (kg/ha), Upper half mean length, Micronaire value and Bundle strength exhibited high broad sense of heritability and moderate sense of heritability was observed for Number of monopodia per plant, Number of sympodia per plant, Number of bolls per plant and Ginning percentage. High heritability coupled with high genetic advance as a percent of mean was recorded for boll weight, seed cotton yield and micronaire value indicated the major role of additive gene action in the inheritance of these characters. Thus, these characters may serve as an effective selection parameter during breeding programme in the upland cotton.

Key Words
Variability, Heritability, Seed Cotton Yield, Gossypium hirsutum.

Cotton (*Gossypium species*), is the world's most utilized natural textile fibre and global textile industry depends largely on natural fibre. Majority of plant trichomes are multicellular, but *Gossypium spp*. produce unicellular seed trichomes known as fibre, making cotton the leading cash crop with significant economic and social impact on Indian economy (Boopathi *et al.,* 2011). Cotton provides numerous useful products and supports millions of jobs as it moves from field to fabric. It is also one of the most important cash crops of India, which accounts for 60% of total foreign exchange earnings through export of lint and value added cotton products. India is one of the important cotton growing countries in world and occupies an area of 105 lakh hectares, production of 351 lakh bales and productivity of 568kg per hectare (AICCIP Annual Report 2016-17). Improving cotton fibre quality and lint yield remains challenging for cotton breeders. The success of any breeding programme depends on the spectrum of genetic variability present in the population. The major target of cotton breeding in the world has been to improve fibre yield and quality. Remarkable advances in cotton yield and quality improvement has been recorded in both conventional and molecular approaches in the last few decades. Yield potential is reportedly plateaued due to complex and antagonistic genetic relationship amongst the cultivated species. For instance, continuous incorporation of genes and selection from the same breeding stock of cultivated species has resulted in narrow genetic base for most of the elite types which is a major bottleneck for cotton breeding, cultivation and production. Selection changes the genetic structure of population due to preservation of superior alleles and discarding the undesirable alleles (Budak *et al*., 2004). Cotton improvement by selection therefore will largely depend on discovery and creation of genetic variability. Superior genotypes resulting from the recombination of superior alleles at different loci are then precisely selected at different breeding stage. Often the selection is based solely on phenotypic expression which is often misleading because of the influence of environment. Therefore, data information on genotypic, phenotypic and environmental variability is of great importance in making effective selection. They are measured by their coefficient of variation. However, genotypic coefficient of variation does not give an exact idea on the total heritable variation. According to Magadum *et al*., (2012), the relative amount of heritable variation could be assessed by heritability. To account for the proportion of phenotypic variance attributable to genetic variance, heritability will have to be estimated. This is vital as it also provides the basis for effective selection. Magadum *et al.*, (2012) also pointed out that genetic variability along with heritability of a character will indicate the possibility and extent to which improvement is feasible through selection on phenotypic basis. Heritability value alone may not provide clear predictability of the breeding value (Mishra *et al.*, 2015). Hence, combination with genetic advance over means is more effective and reliable in predicting the resultant effect of selection (Ramanjinappa *et al*., 2011, Patil *et al.*, 1996). In the presence of high amount of genetic variability, knowledge on heritability and genetic advance helps the breeder to exercise selection on the desired characters to achieve the objective quickly. Therefore, for improvement of target trait in any crop, it is necessary to have full information on the variability, heritability and genetic advance (Burton, 1952 and Swarup and Chaugle, 1962). Keeping in view the importance of these aspects a study was conducted to ascertain the real potential value of the genotypes.

The experiment was conducted in the research field of the Cotton Research Station, Tamil Nadu Agricultural University, Srivilliputtur during the winter 2016. The mean maximum and minimum temperature of this region is 37.2 ^{0}C to 25.5 ^{0}C and an annual rainfall is 818.8 mm by northeast and southwest monsoons contributing to 59.9% and 18.4% respectively and during summer it received 21.6% of rainfall to the total rainfall. The experimental site is located at 9” 5’N latitude, 77” 6’E longitudes and an altitude of 137.92m above mean sea level. The crop has grown in sandy clay loam soil texture with pH of 8.2.

The experimental material comprised of fourty two improved *G.hirsutum* cultures received from various research institutes under AICRP on Cotton. The fourty two cotton cultures were raised in a Randomized Block Design with three replications. Two rows per each entry were sown at a spacing of 90cm x 45cm. Standard procedure for field maintenance was adhered to; basic agronomic practices like irrigation, fertilizer application, weeds and pest control were practiced. Data were recorded from five selected plants in each entry for twelve characters *viz.*, Days to 50 % flowering, Plant height, Number of monopodia per plant, Number of sympodia per plant, Number of bolls per plant, Boll weight**,** Ginning percentage, Upper Half Mean Length, Bundle strength, Micronaire value and Seed cotton yield (kg/ha). Seed cotton was pooled from the sampled plants, ginned and the lint obtained was evaluated for fibre quality characters estimation using High Volume Instrument 900 classic.

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) and Falconer (1967). The genotypic and phenotypic coefficients of variation were calculated according to the formula given by Falconer (1981). Heritability (h^2) in the broad sense was calculated according to the formula given by Allard (1960). From the heritability estimates the genetic advance was estimated by the following formula given by Burton (1952).

Greater variability in the initial breeding material ensures better chances of producing desired forms of a crop plant. Thus, the primary objective of germplasm conservation is to collect and preserve the genetic variability in indigenous collection of crop species to make it available to present and future generations. The analysis of variance (Table. 1) revealed significant differences among the genotypes for all the characters studied indicating that the data generated from the above diverse material will yield reliable information. 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 as percent of mean for all the eleven characters are furnished in Table 2. Days to 50% flowering ranges from 45.7 to 53.3 days with a mean of 49.14 days. The phenotypic and genotypic variances for this character were estimated at 5.47 and 4.23 respectively, the phenotypic and genotypic coefficients of variability for days to 50% flowering were also found to be 4.76 and 4.18 respectively. Plant height recorded a mean value of 87.03 cm and it ranges between 72.3 cm and 111.7 cm. The phenotypic variance, genotypic variance, phenotypic coefficient of variation and genotypic coefficient of variation were found to be 82.05, 50.46, 10.40 and 8.16 respectively. The mean, range, phenotypic variance, genotypic variance, phenotypic coefficient of variation and genotypic coefficient of variation for number of sympodia per plant were found to be 14.7, 12.8-17.1, 1.66, 0.62, 8.79 and 5.40 respectively. Number of bolls per plant and boll weight recorded a mean value of 27.45 and 3.39 respectively. Their phenotypic and genotypic coefficient of variation were also estimated as 13.46, 12.95 (PCV) and 8.81, 11.24 (GCV) respectively. Ginning percentage had a mean value of 35.09 % while the seed cotton yield was 1377.65 (kg/ha). Seed cotton yield also recorded a phenotypic and genotypic coefficient of variance of 32.55 and 30.50 respectively. The highest values for phenotypic and genotypic coefficient of variation recorded by quality parameters were 17.25 and 14.66 respectively only by micronaire value. The low PCV and GCV result by quality parameters (Upper Half Mean Length and bundle strength) has also been reported by Preetha and Raveendran (2007). Environmental influence was found to be effective in all the characters since, PCV values were found to be higher than GCV in all characters. This result is in agreement with the findings of Sakthi *et al*. (2007) and Tomar *et al*., (1992). The Highest magnitude of both PCV (59.66%) and GCV (39.57%) were observed for number of monopodia per plant followed by Seed cotton yield (kg/ha) (32.55%, 30.50%) indicating an inherent but not sufficient variability. However, earlier work by Ganesan and Raveendran (2007) showed a higher PCV and GCV values for seed cotton yield and Siva Prasad *et. al.*, (2005) for number of monopodia per plant. Boll weight, micronaire value showed moderate estimates of phenotypic and genotypic coefficients of variation indicating diversity among the material studied depicting the possibility of improvement in the yield by further selection in segregating generations. These results are in agreement with the findings of Ahuja and Tuteja (2000), Rao and Reddy (2001). Siva Prasad *et. al.*, (2005) also reported the same results for boll weight and Eswari *et al.*, (2017) for micronaire value. The trait plant height and number of bolls per plant recorded for moderate magnitudes of PCV and low GCV. Low values of genotypic and phenotypic coefficients of variation were observed for days to 50% flowering, number of sympodia per plant, ginning percentage, upper half mean length and bundle strength indicating narrow range of variability for these traits thereby restricting the scope for selection. These results are in agreement with the findings of Rao and Reddy (2001), Girase and Mehetre (2002) and Siva Prasad *et. al.*, (2005). In general, the differences between PCV and GCV were less for all the traits except number of monopodia per plant indicating that these traits were not much influenced by the environment, thus suggesting ample scope for improvement through selection (Siva Prasad *et. al.*, 2005)

Heritability estimate was high for days to 50 % flowering, plant height, boll weight**,** upper half mean length, bundle strength, micronaire value and seed cotton yield. This finding was agreed with earlier finding of Pujer *et. al.*, (2014). Ahuja and Tuteja (2000), Girase and Mehetre (2002) and Siva Prasad *et. al.,* (2005) have also reported similar results in their studies for seed cotton yield. Eswari *et al.*, (2017) have also reported similar results for days to 50 % flowering, boll weight**,** upper half mean length, bundle strength and seed cotton yield. Rokadia and Vaid (2003) reported the similar results for pant height. 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 monopodia per plant, number of sympodia per plant, number of bolls per plant and ginning percentage, showed moderate estimates of heritability. These results are in agreement with the results reported by Ahuja and Tuteja (2000), Rao and Reddy (2001), Girase and Mehetre (2002) and Siva Prasad *et. al.*, (2005). Eswari *et al.*, (2017) also reported the similar results for number of monopodia per plant, number of sympodia per plant. High heritability indicates the amenability of the traits in selection process. Johnson *et al*., (1955) and Swarup and Chaugale (1962) indicated that a high value of heritability is not always an indication of high genetic gain. 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). In the present investigation high heritability coupled with high genetic advance was observed for boll weight, seed cotton yield and micronaire value indicating the preponderance of additive gene action in the inheritance of this trait. Ahuja and Tuteja (2000), Girase and Mehetre (2002), Kumari and Chamundeshwari (2005), Kale *et. al.*, (2006) and Preetha and Raveendran (2007) reported high heritability and high genetic advance for seed cotton yield per plant and Narisireddy and Ratnakumari (2004) for boll weight. Similar report was observed by Siva Prasad *et al.*, (2005) for seed cotton yield and Pujer *et al.*, (2014) and Eswari *et al.*, (2017) for seed cotton yield and boll weight. Hence pedigree method of breeding would be rewarding one to improve the traits under investigation. From the present study, taking into consideration the amount of variability, heritability and genetic advance as per cent of mean, it may be concluded that selection would be effective in cotton for number of monopodia per plant, number of bolls per plant and boll weight besides seed cotton yield for developing high yielding cotton varieties.

References

Ahuja, S.L. and Tuteja, O.P. (2000). Variability and association analysis for chemical components imparting resistance to *Gossypium hirsutum* cotton. *Journal of Cotton Research and Development*, **14**(1): 19-22. AICCIP Annual Report. 2016-17. pp: A1-A5

Allard, R. W. (1960). Principles of Plant Breeding. Publishers by John Wiley and Sons *Inc. New York,* USA: pp. 485.

Boopathi N. M., Thiyagu K., Urbi B., Santhoshkumar M., Gopikrishnan A., Aravind S., Swapnashri G., and Ravikesavan R. (2011). Marker-Assisted Breeding as Next-Generation Strategy for Genetic Improvement of Productivity and Quality: Can It Be Realized in Cotton? *International Journal of Plant Genomics*, Article ID 670104, 16

Budak, H., Bolek Y., Dokuyucu T. and Akkaya A. (2004). Potential uses of Molecular Markers in Crop improvement. *KSU Journal of science and Engineering*, **(7**) 1, pp. 75 – 76

Burton, G. W. (1952). Quantitative inheritance in grasses. *Proceeding of sixth International Congress* pp.277-283.

Eswari, K.B., Sudheer Kumar, S., Gopinath and Rao, M.V.B. (2017). Genetic variability heritability and genetic advance studies in cotton. *International Journal of Development Research:* Vol. 07, Issue, 01, pp.10902-10904.

Falconer D. S. (1967). The inheritance of liability to diseases with variable age of onset, with particular reference to diabetes mellitus. *Ann. Hum. Genet*. **31**:1-20.

Falconer, D. S. (1981). Introduction to quantitative genetics. *Oliver and Boyd, London*, pp.340.

Ganesan K.N. and Raveendranm, T.S., (2007). Enhancing the breeding value of genotype through genetic selection in cotton (*Gossypium hirsutum* L.) *Bull. Inst. Trop. Agr., Kyushu Univ.*, **30**:1-10.

Girase, V.S. and Mehetre, S.S. (2002). Variability, heritability and genetic advance studies in cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*, **16**(1): 81-82.

Johnson H.W., Robinson H.F. and Comstock R.E. (1955). Estimates of genetic and environmental variability in soybean. *Agron. J.*, **47**: 314-318

Kale, U. V., Kalpande, H. V., Gunjkar, A. S. and Gite, V. K. (2006). Variability, heritability and genetic advance studies in cotton. *Journal of Maharashtra Agricultural Universities* **31**(3): 389-390.

Kumari, S. R. and Chamundeshwari, N. (2005). Studies on genetic variability, heritability and genetic advance in cotton (*Gossypium hirsutum* L.). *Research on Crops* **6**(1): 98-99.

Magadum S., Banerjee U., Ravikesavan R., Gangapur D. and Boopathi N. M. (2012). Variability and Heritability analysis of yield and quality traits in Interspecific Population of Cotton (*Gossypium Spp*.). *Bioinfolet **9** (4A):* 484 – 485

Mishra P. K., Ram R. B., Kumar N. (2015). Genetic Variability, Heritability, and Genetic advance in strawberry (Fragaria × ananassa Duch.). *Turk J Agric.* **39**: 451-458

Narisireddy, A, and Ratnakumari, S. (2004). Genetic components of variation of physiological attributes for drought screening of genotypes in American cotton (*Gossypium hirsutum* L.). *Annals of Agricultural Research* **25**(3): 412-414.

Panse, V.G. (1957). Genetics of quantitative characters in relation to plant breeding. *Indian Journal of Genetics and Plant Breeding*, **17(3)**: 318-328.

Patil, Y.B., Madalageri B.B, Biradar, B.D, and Hoshmani, R.M. (1996). Variability studies in okra (*Abelmoschus esculentus* L. Moench.). *Karnataka J. Agr. Sci*. **9**: 289–293

Preetha, S. and Raveendran, T. S. (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.

Pujer, S., Siwach, S.S., Jagadeesh Deshmukh., Sangwan, R.S. and Sangwan, O. (2014). Genetic variability, correlation and path analysis in upland cotton (*Gossypium hirsutum* L.). *Electronic Journal of Plant Breeding*, *5(2):* 284-289

Ramanjinappa, V., Arunkumar, K.H., Hugar, A., and Shashibhaskar, M.S. (2011). Genetic variability in okra (*Abelmoschus esculentus* L. Moench.). *Plant Archives*. **11**: 435–437.

Rao, G. N. and Reddy, M. S. S. (2001). Studies on heritability and variability for yield and its components in *hirsutum* cottons. *Journal of Cotton Research and Development* **15**(1): 84-86.

Rokadia, P and Vaid, B. (2003). Variability Parameters in American Cotton *(Gossypium hirsutum* L.). *Annals of Arid Zone **42**(1):* 105-106.

Sakthi A. R., Kumar M. and Ravikesavan R. (2007). Variability and association analysis Using morphological and quality traits in cotton (*Gossypium hirsutum*). *J. Cotton Res. Dev.**21**(2)*:148.

Siva Prasad, U., Chenga Reddy.,V and Narisi Reddy, A. (2005). Studies on Genetic Variability in American Cotton (*Gossypium hirsutum* L.). *Karnataka Journal of Agricultural Sciences:* **18** (4):1095-1098

Swarup, V. and Chaugale, B. S. (1962). Studies on genetic variability in sorghum. Phenotypic variation and heritable component in some quantitative characters contributing towards yield. *Indian Journal of Genetics and Plant Breeding* **22**: 31-36.

Tomar, S.K., Singh, S.P. and Tomar, S.R.S. (1992). Correlation and path coefficient analysis for yield components in desi cotton (*Gossypium arboretum* L.). *Crop Res.*, **5**: 274.

Table 1. Analysis of variance for different traits in cotton

Source of variation	Degrees of freedom	DFF	PH	NOM	NOS	NOB	BW	GP	SCY	UHMC	MIC	BS
Replication	2	3.17	86.54	0.34	0.17	1.79	0.05	2.19	23827	9.53	3.17	53.74
Treatment	41	13.94*	182.98*	0.66*	2.92*	25.35*	0.49*	10.79*	554291*	11.25*	0.97*	9.81*
Error	82	1.24	31.58	0.19	1.04	7.81	0.05	2.12	24512	0.09	0.11	0.07

*Significant at P=0.05 level

Table 2. Estimates of mean, range, variability, heritability and genetic advance in cotton

Traits	Mean ± SE	Range	PV	GV	PCV	GCV	h^2	GA	GAM
Days to 50% Flowering	49.14±0.64	45.7-53.3	5.47	4.23	4.76	4.18	77.34	3.72	7.58
Plant Height (cm)	87.03±3.24	72.3-111.7	82.05	50.46	10.40	8.16	61.50	11.47	13.18
Number of Monopodia per plant	0.99± 0.26	0.3-1.8	0.35	0.15	59.66	39.57	43.99	0.53	54.07
Number of Sympodia per plant	14.66±0.59	12.8-17.1	1.66	0.62	8.79	5.40	37.74	1.00	6.84
Number of Bolls per plant	27.45±1.61	21.9-32.7	13.65	5.84	13.46	8.81	42.83	3.26	11.87
Boll Weight (g)	3.39±0.13	2.5-4.1	0.19	0.14	12.95	11.24	75.45	0.68	20.13
Ginning Percentage	35.09± 0.84	31.5-41.0	5.01	2.89	6.38	4.84	57.62	2.65	7.57
Seed Cotton Yield (kg/ha)	1377.65±90.31	756.0-2613.3	201105.68	176592.97	32.55	30.50	87.81	811.20	58.88
Upper Half Mean Length (cm)	28.15± 0.18	24.7-32.3	3.81	3.72	6.93	6.85	97.56	3.92	13.94
Micronaire Value (µ)	3.64± 0.19	3.0-5.7	0.39	0.28	17.25	14.66	72.21	0.93	25.66
Bundle Strength (g/tex)	29.95± 0.15	27.0-33.0	3.31	3.24	6.08	6.01	97.84	3.67	12.26

SE=Standard Error; **PV**=Phenotypic Variation; **GV**=Genotypic Variation; **PCV**=Phenotypic Co-efficient of Variation; **GCV**=Genotypic Co-efficient of Variation; **h^2**=Heritability (Broad sense); **GA**=Genetic Advance; **GAM**=Genetic Advance as % of Mean.