Studies on genetic variability and genetic gain in cotton (*Gossypium hirsutum* L.)

M. GNANASEKARAN*, K. THIYAGU AND M. GUNASEKARAN

Tamil Nadu Agricultural University, Tamil Nadu- 641003
Email : gnanasekaran79@gmail.com

Abstract : Research work was carried out at Cotton Research Station, Srivilliputtur, to estimate genetic variability, heritability and genetic advance in upland cotton. The analysis of variance involving a set of thirty two *Gossypium hirsutum* genotypes for sixteen characters *viz.*, days to first flowering,days to 50 per cent flowering, plant height, monopodia sympodia and bolls/plant, boll weight, seed index, lint index, ginning percentage, upper half mean length, bundle strength, fibre fineness, uniformity index, fibre elongation percentage and seed cotton yield (kg/ha) revealed highly significant mean sum of squares for all the characters except sympodia/plant indicating greater diversity among the genotypes. The value of Phenotypic Coefficient of Variation (PCV) is greater than Genotypic Coefficient of Variation (GCV) indicated that the apparent variation is not only due to genotypes but due to influence of environment also. The difference between the estimates of PCV and GCV were low for all the characters except monopodia and sympodia/plant thereby indicating that lesser role played by the environment in the expression of these traits. The characters like days to first flowering, bolls/plant, boll weight, seed index, ginning percentage, upper half mean length, bundle strength, fibre fineness, uniformity index, fibre elongation percentage and seed cotton yield (kg/ha) exhibited high broad sense of heritability and moderate sense of heritability was observed for days to 50 pre cent flowering, plant height, and monopodia/plant. High heritability coupled with high genetic advance as a per cent of mean was recorded for bolls/plant and seed cotton yield indicated the major role of additive gene action in the inheritance of these characters. Hence, these characters may serve as an effective selection parameter during breeding programme in the upland cotton improvement programme.

Keywords : Cotton, heritability, seed cotton yield, variability.

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. India is one of the important cotton growing countries in world and occupies an area of 125.84 lakh hectares, production of 360 lakh bales and productivity of 486 kg/ha (ICAR-AICCIP-Annual Report 2019-20). 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 populations. 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. Germplasm, which is a prerequisite for any breeding programme, serves as a valuable source material as it provides scope for building of genetic variability. Study of variability,

heritability and genetic advance in the germplasm will help to ascertain the real potential value of the genotype. 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. Since several economic characters including yield in cotton are polygenically controlled, it is necessary to partition the observed overall phenotypic variability into heritable (genetic) and non heritable (environment) components with the help of genetic coefficient of variation and heritability. 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. They 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.

MATERIALS AND METHODS

The experiment was conducted in the research field of the Cotton Research Station, Tamil Nadu Agricultural University, Srivilliputtur during the winter 2018. The experimental material comprised of twenty intra *hirsutum* hybrids developed by crossing two female (KC 3 and TSH 330) and ten male parents (RAH 1071, RCH 1217, GISV 310, CPD 1601, Suraj, GJHV 370, SVPR 5, CO 14 and TSH 0499) its parents and checks Mallika non *Bt* and Bunny non *Bt* were raised in a randomized block design with two replications. Two rows of each entry were sown at a spacing of 10 x 30 cm. 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 sixteen characters *viz.*, days to first flowering, days to 50 pre cent flowering, plant height (cm), monopodia sympodia and bolls/plant, boll weight (g), seed index, lint index, ginning percentage, upper half mean length (cm), bundle strength (g/tex), fibrefineness (µ), uniformity index, fibre elongation percentage 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.

STATISTICAL ANALYSIS

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).

RESULTS AND DISCUSSION

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 except sympodia/plant 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 per cent of mean for all the eleven characters are furnished in Table 2. The phenotypic and genotypic variances for days to first flowering were estimated at 4.74 and 3.86 respectively, the phenotypic and genotypic coefficients of variability for days to 50 pre cent flowering were 4.57 and 3.33, respectively. For plant height, phenotypic variance, genotypic variance, phenotypic co efficient of variation and genotypic coefficient of variation were found to be 52.06, 236.31, 7.27 and 5.17, respectively. The mean,

phenotypic variance, genotypic variance, phenotypic coefficient of variation and genotypic coefficient of variation for sympodia/plant were found to be 15.69, 2.33, 0.63, 9.74 and 5.07, respectively. Number of bolls/plant and boll weight recorded a mean value of 22.1and 4.62, respectively. Their phenotypic and genotypic coefficient of variation were also estimated as 14.93, 11.93 (PCV) and 12.10, 10.76 (GCV), respectively. Seed index and lint index recorded a mean value of 10.03 and 5.51, respectively. Their phenotypic and genotypic coefficient of variation were also estimated as 13.02, 10.88 (PCV) and 10.42, 7.81 (GCV), respectively. Ginning percentage had a mean value of 35.54 pre cent while the seed cotton yield was 2035.78 (kg/ha) while their phenotypic and genotypic coefficient of variance were of 5.95, 22.03 (PCV) and 4.81, 20.43 (GCV), respectively. The highest values for phenotypic and genotypic coefficient of variation recorded by quality parameters by fibre fineness and the values were 8.26 and 7.97, respectively. The value of Phenotypic Coefficient of Variation (PCV) is greater than Genotypic Coefficient of Variation (GCV) indicated that the apparent variation is not only due to genotypes but due to influence of environment also. The highest magnitude of both PCV (22.73%) and GCV (20.43%) were observed by seed cotton yield (kg/ha) indicating an inherent but not sufficient variability. However, earlier works by Gnanasekaran *et al.*, 2018, Desmukh *et al.*, 2019, Praveen Sampath Kumar *et al.*, 2019 and Gnanasekaran *et al.*, 2020 reported higher PCV and GCV values for seed cotton yield.The Highest magnitude of both PCV (28.41%) and moderate GCV (19.60%) were observed for monopodia/plant (Eswari *et al.*, (2017) and Gnanasekaran *et al.*, 2020. Bolls/plant, boll weight and seed index 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.

Table 1. Analysis of variance for various yield components and fibre quality traits

Source of Variation	DF	DFF	D (50% F)	PH	NMP	NSyP	NB/P	BW	SI	LI	GP	UHML	BS	FF	UI	FEP	SCY
Replication	1	0.59	0.02	82.32	0.16	0.001	9.15	0.44	3.15	0.11	5.29	0.00	0.01	0.003	0.002	0.002	84780.2
Genotypes	31	9.423*	9.65*	60.19*	0.07*	2.93ns	24.69*	0.51*	3.09*	0.55*	6.83*	4.50*	4.29*	0.20*	0.96*	0.02*	326801.8*
Error	31	2.30	3.07	32.46	0.03	2.47	4.73	0.05	0.47	0.15	1.13	0.04	0.02	0.01	0.01	0.002	42106.3

Table 2. Genetic components of variance for various quantitative traits

Traits	DFF	D (50%F)	PH	NM/P	NSy/P	NB/P	BW	SI	LI	GP	UHML	BS	FF	UI	FEP	SCY
G. Mean	**49.36**	**54.19**	**99.28**	**0.84**	**15.69**	**22.21**	**4.62**	**10.03**	**5.51**	**35.54**	**27.73**	**30.22**	**4.61**	**84.35**	**5.70**	**2035.78**
PV	5.48	6.12	52.06	0.06	2.33	11.00	0.30	1.70	0.36	4.47	2.46	2.73	0.14	0.43	0.01	214052.85
GV	3.62	3.26	26.31	0.03	0.63	7.23	0.25	1.09	0.19	2.93	2.40	2.71	0.13	0.42	0.01	173022.08
PCV	4.74	4.57	7.27	28.41	9.74	14.93	11.93	13.02	10.88	5.95	5.66	5.46	8.26	0.78	2.10	22.73
GCV	3.86	3.33	5.17	19.60	5.07	12.10	10.76	10.42	7.81	4.81	5.59	5.44	7.97	0.77	1.84	20.43
h2 (%)	66.04	53.23	50.54	47.58	27.12	65.69	81.39	64.11	51.55	65.49	97.77	99.24	93.02	98.19	76.43	80.83
GAM	6.45	5.01	7.57	27.85	5.44	20.21	20.00	17.19	11.56	8.02	11.39	11.17	15.83	1.57	3.31	37.84

Days to first flowering (DFF), Days to 50 pre cent flowering (D50%F), Plant height (PH), monopodia/plant (NM/P), sympodia/plant (NSy/P), bolls/plant (NB/P), Boll weight (BW), Seed index (SI), Lint index (LI), Ginning percentage (GP), Upper half mean length (UHML), Bundle strength (BS), Fibre fineness (FF), Uniformity index (UI), Fibre elongation percentage (FEP), Seed cotton yield (kg/ha) (SCY)

These results are in agreement with the earlier findings of Gnanasekaran and Thiyagu (2020) for bolls/plant and seed index; Desmukh *et al.*, 2019 and Praveen Sampath Kumar *et al.*, 2019 reported the same results for boll weight and seed index. The trait lint index recorded for moderate magnitudes of PCV and low GCV (Gnanasekaran and Thiyagu (2020). Low values of phenotypic and genotypic coefficients of variation were observed for days to first flowering, days to 50 pre cent flowering, plant height, sympodia/plant, ginning percentage, upper half mean length, bundle strength, fibre fineness, uniformity index and fibre elongation percentage indicating narrow range of variability for these traits thereby restricting the scope for selection. These results are in agreement with the findings of Gnanasekaran and Thiyagu (2020) for days to first flowering and fibre elongation percentage; Divaya *et al.*, 2014 for days to 50 pre cent flowering and upper half mean length; Gnanasekaran *et al.*, 2020 for plant height, sympodia/plant, upper half mean length and uniformity index; Eswari *et al.*, (2017) for days to 50 pre cent flowering, ginning percentage and uniformity index; Praveen Sampath Kumar *et al.*, 2019 for upper half mean length and bundle strength, Deshmukh *et al.*, 2019 for fibre fineness.In general, the differences between PCV and GCV were less for all the traits except monopodia/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 first flowering, days to 50 pre cent flowering, number of bolls/plant, boll weight, seed index, ginning percentage, upper half mean length, bundle strength, fibre fineness, uniformity index, fibre elongation percentage and seed cotton yield (kg/ha). Similar kind of results was reported by Santosh kumar *et al.*, (2012) for the all traits except uniformity index. Pujer *et al.*, (2014) also reported the same finding except fibre elongation percentage. Easwari *et al.*, 2017, Deshmukh *et al.*, (2019) and Gnanasekaran *et al.*, (2020) have also reported similar results in their studies for traits of bolls/plant, boll weight, ginning percentage, upper half mean length, bundle strength and seed cotton yield. Gnanasekaran and Thiyagu (2020) reported the same kind of results for days to first flowering, number of bolls/plant, ginning percentage, upper half mean length, bundle strength, fibre fineness, uniformity index and seed cotton yield. 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. Days to 50 pre cent flowering, plant height and monopodia/plant showed moderate estimates of heritability. These results are in agreement with the results reported by Eswari *et al.*, (2017) also reported the similar results for days to 50 pre cent flowering and monopodia/plant and Sunayana *et al.*, 2017 for plant height. 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 bolls/plant and seed cotton yield indicating the preponderance of additive gene action in the inheritance of this trait. Praveen Sampath Kumar *et al,*. 2019, Eswari *et al.*, 2017, Gnanasekaran *et al.*, 2020 and Gnanasekaran and Thiyagu (2020) for seed cotton yield and boll number/plant. Pujer *et al.*, 2014, Sunayana *et al.*, 2017 also reported high heritability and high genetic advance for seed cotton yield/plant. 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 monopodia/plant, bolls/plant and boll weight besides seed cotton yield for developing high yielding cotton varieties.

REFERENCES

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? *Internat. J. Pl. Genomi.,* Article ID 670104, 16.

Budak, H., Bolek Y., Dokuyucu T. and Akkaya A. 2004. Potential uses of Molecular Markers in Crop improvement. *KSU J. Sci. Engg.*, **7**: 75 – 76.

Burton, G. W. 1952. Quantitative inheritance in grasses. *Proceeding of sixth International Congress* pp. 277-83.

Deshmukh, M.R., Deosarkar, D.B., Chinchane, V.N. and Deshmukh, S.B. 2019. Studies of genetic parameters for yield, yield contributing and fiber quality characters in *desi* cotton (*Gossypium arboreum* L.) *J. Cotton Res. Dev.* **33** : 44-49.

Dhivya, R., Amalabalu, P., Pushpa, R. and Kavithamani, D. 2014. Variability, heritability and genetic advance in upland cotton (*Gossypium hirsutum* L.). *Afr. J. Plant Sci.* **8**: 1-5.

Eswari, K.B., Sudheer Kumar, S., Gopinath and Rao, M.V.B. 2017. Genetic variability heritability and genetic advance studies in cotton. *Internat. J. Dev. Res.* **07**, Issue, 10902-04.

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.

Gnanasekaran, M. and Thiyagu, K. 2020. Selection Parameters for Improving the Seed Cotton Yield and Fibre Quality Traits in American Cotton (*Gossypium hirsutum* L.). I*nt. J. Curr. Microbiol. App. Sci.* **9**:1333-42.https://doi.org/ 10.20546/ijcmas.2020.910.160.

Gnanasekaran, M., Thiyagu, K. and Gunasekaran, M. 2020. Studies on genetic variability correlation and path analysis in upland cotton. *Elect. J. Pl. Breed.*, **11**:981-86. https://doi.org/ 10.37992/2020.1103.160

Gnanasekaran, M., Thiyagu, K. and Gunasekaran, M. 2018. Genetic variability heritability and genetic advance studies in cotton (*Gossypium hirsutum* l.). *Electronic J. Pl. Breed.*, **9**: 377–82. DOI: 10.5958/0975-928X.2018. 00043.1 ICAR-AICCIP-Annual Report 2019-20 pp: A1

Johnson, H.W., Robinson, H.F. and Comstock, R.E. 1955. Estimates of genetic and environmental variability in soybean. *Agron. J.*, **47**: 314-18

Magadum S., U. Banerjee, R. Ravikesavan, D. Gangapur and N.M. Boopathi. 2012. Variability and Heritability analysis of yield and quality traits in Interspecific Population of Cotton (*Gossypium Spp.*). *Bioinfolet.* **9** : 484 – 85.

Mishra, P.K., Ram, R.B. and Kumar, N. 2015. Genetic Variability, Heritability, and Genetic advance in strawberry (Fragaria × ananassa Duch.). *Turk J Agric.* **39**: 451-58 .

Panse, V.G. 1957. Genetics of quantitative characters in relation to plant breeding. *Indian J. Gene. Pl. Breed.* **17**: 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**: 289–93.

Praveen Sampath Kumar, C., Raju S., Ebenezer Babu Rajan, R., Muraleedharan, Ajish and Suji, Darling B. 2019. Studies on genetic variability, heritability and genetic advance in cotton (*Gossypium hirsutum* L.). *Pl. Arch.*, **19** : 934-37.

Pujer, S., Siwach, S.S., Deshmukh. Jagadeesh, Sangwan, R.S., and Sangwan, O. 2014. Genetic variability, correlation and path analysis in upland cotton (*Gossypium hirsutum* L.). *Electronic J. Pl. Breed.* **5**: 284-89

Ramanjinappa, V., Arunkumar, K.H., Hugar, A.A, and Shashibhaskar, M.S. 2011. Genetic variability in okra (*Abelmoschus esculentus* L. Moench.). *Pl. Arch.* **11**: 435–37.

Santoshkumar M., Banerjee, Urbi, Ravikesavan, R., Doddabhimappa Gangapur and Manikanda Boopathi, N. 2012. Variability and heritability analysis of yield and quality traits ininterspecific population of cotton (*Gossypium* spp.). Bioinfolet. **9** : 484 – 87.

Siva Prasad, U., Chenga Reddy V. and Narisi Reddy, A. 2005. Studies on Genetic Variability in American Cotton (*Gossypium hirsutum* L.). *Karnataka J. Agri. Sci.* **18** :1095-98.

Sunayana., Sangwan R.S. and Nimbal, Somveer 2017. Studies on Association, Path Analysis and Genetic Parameters for Seed Cotton Yield and It's Contributing Characters in *Desi* Cotton (*Gossypium arboreum* L.). I*nt. J. Curr. Microbiol. App. Sci.* **6**:104-111. https://doi.org/ 10.20546/ijcmas.2017.611.013.

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 J. Gen. Pl. Breed.* **22**: 31-36.