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Genetic variability analysis for seed cotton yield, its component and fibre quality traits in upland cotton (*Gossypium hirsutum* L.)

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Abstract : The present investigation was undertaken to evaluate genetic variability for seed cotton yield and fibre quality traits in fifty diverse genotypes of upland cotton (*Gossypium hirsutum* L.). The experiment was laid out in randomized block design (RBD) with three replications at the Farm Research Area, Cotton Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar during *kharif*, 2020-2021. The analysis of variance revealed significant differences among genotypes for all the traits. High phenotypic coefficients of variance (PCV) and Genotypic coefficients of variance(GCV) were recorded for the characters *viz.*, monopods /plant (28.45 and 27.15 %), bolls /plant (22.99 and 21.73 %) and seed cotton yield /plant (25.27 and 23.24 %). Moderate values of PCV and GCV were recorded for boll weight (12.06 and 10.17 %) and Low estimates of PCV and GCV were recorded for days to first flower (3.62 and 3.19 %), days to 50 pre cent flowering (1.79 and 1.37 %), seeds /boll (9.04 and 8.97%) and ginning outturn (6.52 and 5.35 %). High heritability coupled with high genetic advance as per cent mean was observed in case of seed cotton yield /plant (84.56 %, 44.02 %), bolls/ plant (89.30 %, 42.29 %) and monopods /plant (91.03 %, 53.35 %). This clearly indicated the existence of additive genetic control in the expression of these traits. All the fibre quality traits *i. e.* fibre length, fibre strength, fineness and uniformity index showed low estimates of GCV and PCV. High heritability and low genetic advance as percent of mean was detected in case of fibre length (90.31%, 8.40%), fibre strength (98.98%, 8.35%) and fibre uniformity (67.97%, 1.49%).

Key words: Genetic advance, GCV, genetic variability, heritability, PCV, seed cotton yield

Cotton is one of the most important and extensively grown cash crops in the world. It is also known as “King of Fibre” or “White Gold” which plays a dominant role in the industrial and agricultural economy of the country (Ranganatha *et al.*, 2013). Cotton provides employment and sustenance to a population of nearly 60 million people, who are involved directly or indirectly in cotton production, processing, textiles and related activities. Although many other natural and synthetic fibers have been available but advantages related to the cost of production and many unique features offered by cotton lint, and the growing world population will ensure a continued increase in the demand for seed cotton (Rajan *et al.*, 2014). It belongs to genus *Gossypium* which consists of 50 species of which 43 are diploid (2n=2x=26) and seven are allotetraploid (2n=4x=52). Mainly cultivated species of diploid cotton are G. *arboreum* and G. *herbaceum* and cultivated allotetraploid species are G. *barbadense* and G. *hirsutum* (Karena *et al.*, 2021). The *Gossypium hirsutum* also known as upland cotton/American cotton/Mexican cotton has long staple cotton, it’s occupied nearly 95 per cent of the global cotton area because of its wider adaptability and high lint yield. India has the distinction of having the largest area under cotton cultivation which is about 37 pre cent of the world area under cotton cultivation and the largest producer of cotton in the world accounting for about 22 per cent of the world cotton production. The yield/kg/ac which is presently 469 kg/ha (Anonymous, 2022).

Major goal of the cotton improvement programme through breeding is enhancing seed cotton yield. Because seed cotton yield itself being a complex trait, polygenic in inheritance, more prone to environmental fluctuations than other characters and depend up on the various component traits, selection based only on yield may not be effective. The scientists therefore has developed ways of selecting for high seed cotton yield indirectly through yield associated and highly heritable traits after eliminating environmental components of variation.

Now the cotton breeders facing the challenge for continuously development of new hybrids/varieties with superior performance for seed cotton yield and fiber quality traits over the existing hybrids/varieties to meet the demands of cotton grower and cotton industries. But development of such improved cultivars largely depends upon magnitude and nature of genetic variation present in breeding population. Besides genetic variability, knowledge on heritability and genetic advance measures the relative degree to which a character is transmitted to progeny, there by helps the breeder to employ a suitable breeding strategy to achieve the objective quickly (Chaudhari, *et al.*, 2017). Genetic advance as percent of mean together with heritability estimates gives a relatively better picture of the amount of advance to be expected through selection (Johnson *et al.*, 1955a). A relative comparison of heritability values and expected genetic advance expressed as the percent of means gives an idea about the nature of gene action governing a particular character. Therefore, for successful improvement of any crop, it is necessary to have a thorough knowledge on the variability (Shruti *et al.*, 2019). Considering the above point of view, this present study was carried out with an objective to assess the genetic variability for seed cotton yield, its component and fibre quality traits in fifty diverse genotypes of upland cotton.

The present investigation has been carried out at the farm research area of cotton section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar during *kharif*, 2020. The study was planned with fifty diverse genotypes of upland cotton and experiment was laid out in a randomized block design (RBD) with three replications, row length 6 m, row to row distance 67.5 cm and plant to plant distance was 30 cm. The observations were recorded on five randomly selected plants from each line in each replication for 14 characters viz., days to first flower, days to 50 per cent flowering, plant height, monopods/plant, bolls/plant, seeds/boll, boll weight, seed cotton yield/plant, ginning outturn, seed index, fibre Length, fibre strength, fibre fineness and uniformity index. Fibre quality parameters were analyzed in Central Institute for Research on Cotton Technology (CIRCOT), Regional Research Station, Sirsa through High Volume Instrument. Data on each observation were recorded and subjected to the analysis. The analysis of variance for a randomized block design was carried out as per the method suggested by R.A. Fisher (1925). Genotypic and phenotypic coefficients of variation were estimated based on the estimates of genotypic and phenotypic variances. Phenotypic and genotypic coefficient of variance (PCV and GCV) and heritability was calculated by using the method of Burton and De Vane (1953). Genetic advance as percent of mean were calculated by using method suggested by Johnson *et al.*, (1955a).

The analysis of variance showed that the mean sum of squares due to genotypes were highly significant for all the characters studied (Table1). This indicated that the fifty genotypes differed genetically among themselves for most of the characters. Similar observations were also made by Kumar, *et al.*, (2019) and Reddy *et al.*, (2019).

Genetic variability in terms of genotypic and phenotypic coefficients of variation, heritability and genetic advance as per cent of mean was assessed among all the genotypes for the purpose of comparison across different characters. The phenotypic coefficient of variance was slightly higher than the genotypic coefficient of variance, small difference between them indicates that, most of the variability observed was due to the predominance of genotype but environmental had also a little influence on the expression of a character. The PCV, GCV, heritability and genetic advance as percent mean for the different characters are shown in the (Table 2). High estimates of PCV and GCV were recorded for the characters *viz.*, monopods/plant (28.45 and 27.15 %), bolls/ plant (22.99 and 21.73 %) and seed cotton yield/plant (25.27 and 23.24 %) which indicated that these traits contributed markedly to the total variability and there is greater scope for improvement for these traits either by direct selection or by involving chosen parents in hybridization. The results were in also confirmation with those reported by Khokher *et al.*, (2017); Chaudhari *et al.*, (2017); Adsare and Salve (2017). Moderate values of PCV and GCV were recorded for boll weight (12.06 and 10.17 %) and seed index (11.08 and 10.36 %) indicating that these are amenable for improvement and selection for these traits will be ineffective. Moderate GCV and PCV for boll weight were also reported by Dinakaran *et al.*, (2012); Adsare and Salve (2017). Low values of PCV and GCV were recorded for days to first flower (3.62 and 3.19 %), days to 50 per cent flowering (1.79 and 1.37 %), seeds per boll (9.04 and 8.97%) and ginning out turn (6.52 and 5.35%), indicating the impediment in improvement these traits through selection. Erande *et al.*, (2014) and Anjani, *et al.*, (2020) also found low values of GCV and PCV for days to 50 per cent flowering. Similar finding were obtained by Reddy *et al.*, (2015) and Anjani, *et al.*, (2020) in case of ginning outturn. Similarly, for seeds/boll low level of GCV and PCV were reported by Kulkarni *et al.*, (2011). Monisha (2018) and Manonmani *et al.*, (2019) reported low GCV and PCV for days to first flowering. Low PCV and GCV were observed for the fibre quality parameters *viz*; ibre length (4.51 and 4.29 %), fibre fineness (6.77 and 6.37 %), fibre strength (4.09 and 4.07%) and fibre uniformity (1.06 and 0.88 %). Low GCV and PCV values for fibre quality traits combined with small difference between them indicate lesser extent of environmental influence for the development of fibre quality traits. Similar findings were reported by Shao *et al.*, (2016); Chaudhari *et al.*, (2017); and Shruti *et al.*,(2019).

The degree to which a character is transmitted on from parent to offspring is referred to as heritability. Heritability in the wide definition includes both additive and non-additive gene effects (Hanson *et al.*, 1956), but heritability in the narrow sense only includes those attributable to additive components (Lush, 1949). High heritability values indicate that the character under study is less influenced by the environment in their expression, and that such characters could be improved using simple selection methods. Furthermore, knowing about genetic variation, heritability, and genetic advance as a percentage of mean can help predict the genetic gain that could be achieved in future generations if selection is used to improve the characteristic under study. The nature of gene action influencing a given character can be determined by comparing heritability values and predicted genetic advance expressed as a percentage of means.

High heritability coupled with high genetic advance as per cent mean was observed in case of seed cotton yield/plant (84.56 %, 44.02 %), bolls/plant (89.30 %, 42.29 %) and monopods/plant (91.03 %, 53.35 %). This clearly indicated the existence of additive genetic control in the expression of these traits and quick improvement could well be expected for these characters by following simple selection. Similar findings were observed by Dahiphale *et al.*,

Table 1. Analysis of variance of various morphological characters and fibre quality traits

Source of	D.F	PH cm	DFF	FPF	NMP	NBP	BW (g)	SCYP (g)
variation Replication	2	239.76	0.83	23.33	0.121	19.127	0.193	30.77
Treatment	49	485.17**	9.246*	6.0**	2.158**	308.774**	0.308**	3,567.39**
Error	98	112.93	0.813	1.15	0.069	11.86	0.037	204.642
Source of variation	D.F	SI (g)	NSB	GOT (%)	UHML (mm)	UI (%)	BS (g/tex)	FF (µg/inch)
Replication	2	0.029	0.021	1.005	0.028	0.694	0.057	0.016
Treatment	49	1.305**	19.3*	12.5**	3.749**	1.674**	3.911**	0.24**
Error	98	0.06	0.1	1.744	0.147	0.225	0.014	0.01

PH- plant height, DFF- days to first flower, FPF- fifty percent flowering, NMP- number of monopods, NBP- number of bolls, BW- boll weight, SCYP- seed cotton yield per plant, SI- seed index, NSB- number of seeds per boll, GOT- ginning out turn, FL- fibre length, UI- uniformity index, FS- fibre strength, FF- fibre fineness

Table 2: Genetic components of variance for fibre quality traits, seed cotton yield and its component traits

Characters	Genetic components of variance				
	PCV (%)	GCV (%)	h2bs(%)	GA(%)	GAM (%)
Plant height(cm)	10.09	7.30	52.38	16.61	10.89
Days to first flower	3.62	3.19	77.56	3.04	5.78
Days to 50 per cent flowering	1.79	1.37	58.44	2.00	2.15
Monopods/plant	28.45	27.15	91.03	1.64	53.35
Bolls/plant	22.99	21.73	89.30	19.37	42.29
Boll weight (g)	12.06	10.17	71.09	0.52	17.67
Seeds/boll	9.04	8.97	98.44	5.18	18.33
Seed index (g)	11.08	10.36	87.35	1.24	19.94
Ginning outturn (%)	6.52	5.35	67.28	3.20	9.04
Seed cotton yield/plant (g)	25.27	23.24	84.56	63.42	44.02
Fibre length (UHML) (mm)	4.51	4.29	90.31	2.15	8.40
Fibre Uniformity (%)	1.06	0.88	67.97	1.18	1.49
Fibre fineness (Micronaire value)	6.77	6.37	88.55	0.54	12.35
Fibre strength (g/tex)	4.09	4.07	98.98	2.34	8.35

(2015), Kumar *et al.*, (2019), Shruti *et al.*, (2019) and Gnanasekaran (2020). High heritability and moderate genetic advance as per cent mean was observed in case of boll weight (71.09 %, 17.67%), seeds/boll (98.44%, 18.33%) and seed index (87.35%, 19.94%) indicating that both additive and non additive type of gene action and environment effect is more compared to genetic effect, hence selection could be ineffective for improvement of these traits. Similar findings were reported by Sambamurthy (1999) and Rasheed *et al.*,(2009). High heritability coupled with low genetic advance was recorded for days to first flower (77.56 %, 5.78%) and ginning outturn (67.28%, 9.04%). This clearly indicated the characters are mainly under the control of non-additive types of genes. Moderate heritability coupled with low to moderate genetic advance was recorded for plant height (52.38%, 10.89%) and days to 50 per cent flowering (58.44%, 2.15%) indicating that these traits are under the control of non- additive type of gene. These results were in confirmation with the findings of Kulkarni *et al.*, (2011) and Dhivya *et al.*, (2014).

For the fibre quality traits high heritability and low genetic advance as percent of mean was detected in case of fibre length (90.31%, 8.40%), fibre strength (98.98%, 8.35%) and fibre uniformity (67.97%, 1.49%) whereas, high heritability with moderate genetic advance as per cent of mean was reported in case of fibre fineness (88.55%, 12.35%). The results indicating that the fibre quality traits are mainly under the control of non-additive types of genes action. Hence, simple selection could not be effective for improvement in these traits. Similar findings were reported by Lacape *et al.*, (2005) and Nawaz *et al.*, (2019). Kumar *et al.*, (2019) studied genetic diversity for fibre quality traits in 30 genotypes of cotton and observed high heritability coupled with low genetic advance in case of fibre length and bundle strength. Shruti *et al.*, (2019) observed high heritability and moderate genetic advance for fibre length and fibre strength. Similar findings were reported by Sahar *et al.*, (2021) for upper half of mean length.

CONCLUSION

According to the findings of the variability, heritability and correlations coefficients it had been concluded that monopods/plant, bolls/ plant and boll weight are the most essential component characters for improving seed cotton yield. Hence, selection for these traits would be quite effective in improving the seed cotton yield in upland cotton.

REFERENCES

Adsare, A. D. and Salve, A. N. 2017. Study on genetic variability for the quantitative traits in some genotypes of upland cotton (*Gossypium hirsutum* L.). *Biosci.* Discov., **8**: 365-68.
Agricul. J. **86:** 39-42.

Anjani, A., Padma, V., Ramana, J. V. and Satish, Y. 2020. Evaluation of genetic parameters of agro- morpho-quality traits in American cotton (*Gossypium hirsutum* L.). *Elect. J. Pl. Bree.*, **11**: 279-82.

Anonymous. 2022. (https://cotcorp.org.in/national-cotton.aspx)

Burton, G. W. and DeVane, E. W. 1953. Estimating heritability in tall fescue (Feetucacircuhinoceae) from replicated clonal material. *Agronomy Journal*, **45**: 478-81.

Chaudhari, M. N., Faldu, G. O. and Ramani, H. R. 2017. Genetic variability, correlation and pathcoefficient analysis in cotton (*Gossypium hirsutum* L.). *Adv. Biores.*, **8**: 226-33.

Dahiphale, K. D., Deshmukh, J. D., Jadhav, A. B. and Bagade, A. B. 2015. Genetic variability, correlation and path coefficient analysis for yield and its attributing traits in cotton (*Gossypium hirsutum* L.). *Internat. J. Trop. Agri.*, **33**:15-22.

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

Dinakaran, E., Thirumeni, S. and Paramasivam, K. 2012. Yield and fibre quality components analysis in upland cotton (*Gossypium hirsutum* L.) under salinity. *Ann. Bio. Res.*, **3**: 3910- 15.
Elect. J. Pl. Bree., **9**: 1053-59.

Erande, C. S., Kalpande, H. V., Deosarkar, D. B., Chavan, S. K., Patil, V. S., Deshmukh, J. D., Chinchane, V. N., Kumar, A., Utpal, D. and Puttawar, M. R. 2014. Genetic variability, correlation and path analysis among different traits in desi cotton (*Gossypium arboretum* L.). *African J. Agri. Res.* **9**: 2278-86.

Fisher, R.A. 1925. *Statistical methods* for *research workers*. Oliver and Boyd, Edinburg.

Gnanasekaran, M., Thiyagu, K. and Gunasekaran, M. 2020. Studies on genetic variability, correlation and path analysis in upland cotton. *Electronic J. Pl. Bree*d. **11**: 981-86.

Hanson, C. H., Robinson, H. F. and Comstock, R. E. 1956. Biometrical studies of yield and segregating populations of Korean lespedza. *Agronomy. Journal.* **47**: 313-18.

Johanson, H. W., Robinson, H. and Comstock, R. E. 1955a. Estimates of genetic and environmental variability in soybean. *Agronomy Journal*, **47**: 314 – 18.

Karena, R.G., Sapovadiya, M.H., Mehta, D.R. (2021). Characterization of American Cotton (*Gossypium hirsutum* L.) genotypes based on morphological characters. *J. Pharma. Phytochem.* **10**: 135-45.

Khokhar, E. S., Shakeel, A., Maqbool, M. A., Anwar, M. W., Tanveer, Z. and Irfan, M. F. 2017. Genetic study of cotton (*Gossypium hirsutum* L.) genotypes for different agronomic, yield and quality traits. *Pak. J. Agri. Res.* **30**: 363-72.

Kulkarni, A. A., Nanda, H. C. and Patil, S. G. 2011. Studies on genetic divergence in upland cotton (*Gossypium hirsutum* L.). *J. Cotton Res. Dev.* **25**: 9-13.

Kumar, C.P.S., Raju, S., Rajan, R.E.B., Muraleedharan, A. and Suji, D. B. 2019. Studies on genetic variability, heritability and genetic advance in cotton (*Gossypium hirsutum* L.). *Plant Archives.* **19**: 618-20.

Lacape, J. M., Nguyen, T. B., Courtois, B., Belot, J. L., Giband, M., Gourlot, J. P. and Hau, B. 2005. QTL analysis of cotton fiber quality using multiple *Gossypium hirsutum* × *Gossypium barbadense* backcross generations. *Crop Sci.* **45**: 123-40.

Lush, J. L. 1949. Heritability of seed cotton yield and important yield components characters in farm animals. *Hereditas.*, **35**: 356 –75.

Manonmani, K., Mahalingam, L., Malarvizhi, D., Sritharan, N. and Premalatha, N. 2019. Genetic variability, correlation and path analysis for seed cotton yield improvement in upland cotton (*Gossypium hirsutum* L.). *J Pharma. Phytochemi*, **8**: 1358-61.

Nawaz, B., Sattar, S. and Malik, T. A. 2019. Genetic analysis of yield components and fiber quality parameters in upland cotton. *Internati. Multi discipl. Res. J.* **9:** 13-19.

Ranganatha, H. M., Patil, S. S., Manjula, S. M. and Arvindkumar, B. N. 2013. Genetic variability studies in segregating generation of upland cotton (*G. hirsutum* L.). *Mole. pl. breed.*, **4**: 84-88.

Ranjan, R.U.M.E.S.H., Sangwan, R.S., Siwach, S.S., Sangwan, O. and Sah, M.K. 2014. Studies of genetic parameters for seed cotton yield and its contributing characters in *Gossypium arboreum* L. *J. Cotton Res. Dev.* **28**: 227-29.

Rasheed, A., Malik, W., Khan, A. A., Murtaza, N., Qayyum, A. and Noor, E. 2009. Genetic evaluation of fiber yield and yield components in fifteen cotton (*Gossypium hirsutum* L.) genotypes. *International J. Agri. Bio.* **11**: 581-85.

Reddy, B., Nimbal, S., Sangwan, R. S. Kumar, P., S. and Jangid, K. 2019. Genetic parameters, correlation and path analysis of agro-morphological traits in elite genotypes of upland cotton (*Gossypium hirsutum* L.). *Internat. J. Chem. Stud.*,**7:** 1885-89.

Reddy, K. B., Reddy, V. C., Ahmed, M. L., Naidu, T. and Srinivasarao, V. 2015. Correlation and path coefficient analysis in upland cotton (*Gossypium hirsutum* L.). *Internat. J. Pure Appl. Biosci.*, **3**: 70- 80.

Sambamurthy, J.S.V. 1999. Character association and component analysis in upland cotton. Madras Shao, D., Wang, T., Zhang, H., Zhu, J. and Tang, F. 2016. Variation, heritability and association of yield, fiber and morphological traits in a near long staple upland cotton population. *Pak. J. Bot.* **48**: 1945-49.

Shruti, H., Sowmya, C. H., Nidagundi, J. M., Lokesha, R., Arunkumar, B. and Murthy, M. S. 2019. Genetic variability studies for yield, yield attributing and fibre quality traits in cotton (*Gossypium hirsutum* L.). *Internat. J. Curr. Micro. Appl. Sci.* **8**: 2677-87.

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