



Evaluation of genetic variability parameters for yield, yield attributes and fibre quality traits in the F₂ population of *Gossypium hirsutum* L.

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ARTICLE INFO	ABSTRACT
Received : 26 December 2022	<p>The F₂ populations of the crossings CO 14 × NDLH 1938 and CO17 × NDLH 1755 were used to investigate variability and heritability studies in order to better understand the gene action involved in each characteristic studied. Morphological data viz., days to first flowering, plant height (cm), number of sympodials, number of bolls per plant, boll weight (g), ginning outturn (%), upper half mean length (mm), elongation percentage (%) and micronaire value (µg/inch) were all recorded in each plant of both the populations. Studies of heritability and genetic advance as a percent of mean help us determine if a gene is additive or epistatic in nature, and so undergo appropriate breeding programmes for population enhancement. The value of PCV (Phenotypic Coefficient of variation) was always greater than GCV (Genotypic coefficient of variation) indicating the environment also plays a major role in contributing to the variations. The seed cotton yield per plant alone was shown to exhibit additive gene action with high heritability and strong genetic advance as percent of mean, suggesting that it might be used in direct selection since it is the most important attribute for population development.</p>
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Introduction

Cotton is a valuable fibre crop with a high commercial and export value, accounting for 70% of fibre use in the textile industry. It is known as the "King of Fibre Crops" and contributes significantly to the Indian economy (Boopathi *et al.*, 2011). In India's textile sector, cotton is the most common fibre. The area, production and productivity of cotton in India are, 123.50 lakh hectares, 340.62 lakh bales (1 bale = 170 kg of lint) and 469 kg per hectare respectively. India occupies the largest area under cotton cultivation of about 37% compared to world level (32.29 million hectares) between 12 million hectares and 13.5 million hectares. The cotton exports from India

have increased from 47.04 lakh bales to 77.59 lakh bales during the year 2020-21 compared to previous crop year. (Committee on Cotton Production and Consumption (COCPC) in its meeting held on 22.03.2022). The genetic variability among parents is crucial for the generation of high heterotic hybrids with high yield potential. Cotton selection improvement will thus be heavily reliant on the finding and production of genetic variation. Superior genotypes produced by recombination of superior alleles at distinct loci are then carefully chosen at various breeding stages. Selection is frequently made exclusively on the basis of phenotypic expression, which might be deceiving

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due to environmental factors (Budak *et al.*, 2004). As a result, data on genotypic, phenotypic, and environmental heterogeneity is critical for efficient selection. Their coefficient of variation is used to quantify them. The genotypic coefficient of variation, on the other hand, does not provide a precise estimate of the total heritable variation. According to Magadum *et al.* (2012) heritability may be used to determine the proportional amount of heritable variation. Heritability will have to be calculated to account for the fraction of phenotypic diversity that may be attributed to genetic variance. This is crucial because it lays the groundwork for effective choosing genotypes Kale *et al.* (2007) and Eswari *et al.* (2017). Magadum *et al.* (2012) also said that the genetic variability of a character as well as its heritability, will suggest the ability and amount of phenotypic improvement. The breeding value may not be predictable based just on its heritability (Mishra *et al.*, 2015). As a result, combining genetic advance over means with prediction of the ensuing effect of selection is more effective and dependable (Patil *et al.*, 1996). When there is a lot of genetic variety, knowing about heritability and genetic progress can assist the breeder rapidly reach the goal by exercising selection on the desired features. As a result, in order to increase a desired attribute in any crop, complete knowledge of variability, heritability, and genetic advance is required (Burton, 1952; Swarup and Chaugle, 1962). Given the relevance of these factors, research was done to determine the genotypes' true potential usefulness.

Material and Methods

The experiment was conducted in the research field of the Department of Cotton at the Tamil Nadu Agricultural University, Coimbatore, in the summer of 2022. The experiment employed two F₂ populations of *G. hirsutum* segregants (CO 14 × NDLH 1938 and CO17 × NDLH 1755). The two F₂ populations were grown using a Randomized Block Design with two replications. For each population, twenty rows of 90 cm × 45 cm spacing were sown. The plant population was maintained upto 200 plants in each F₂ cross. Standard field care practices, as well as basic agronomic approaches including irrigation, fertilizer maintenance, weed control and pest management, were followed.

Morphological data viz., days to first flowering, plant height (cm), number of symposia's, number of bolls per plant, boll weight (g), ginning outturn (%), upper half mean length (mm), elongation percentage (%) and micronaire value (µg/inch) were all recorded in each entry. Using the High Volume Instrument 900 classic, the resulting lint was examined for fibre quality characteristics. The variances were calculated using Singh and Choudhary's (1977) technique, and the genetic components of variation were assessed using the same formula.

Phenotypic variance

The phenotypic variance was calculated using individual observations made for each characteristic on the F₂ population.

$$\text{Phenotypic variance } (\sigma^2p) = \text{Var } F_2$$

Where,

Var F₂ = variance of F₂ population

Environmental variance

The environmental variation was estimated using the average variance of the parents.

$$\text{Environmental variance } (\sigma^2e) = \frac{(\sigma^2p_1) + (\sigma^2p_2)}{2}$$

Where,

σ^2p_1 = Variance of parent P1

σ^2p_2 = Variance of parent P2

Genotypic variance

$$\text{Genotypic variance } (\sigma^2g) = \sigma^2p - \sigma^2e$$

Where,

σ^2p = Phenotypic variance

σ^2e = Environmental variance

Genetic advance (GA):

According to Johnson *et al.* (1955) genetic advance was divided into three categories: low, moderate and high.

$$GA = h^2K \sigma p$$

Where,

H² = Heritability in broad sense

K = Selection intensity which is equal to 2.06 at 5 per cent intensity of selection

σp = Phenotypic standard deviation.

Genetic advance as per cent of mean (GAM)

$$\text{GAM} = \frac{\text{GA}}{\text{X}} \times 100$$

Where,

GA = Genetic advance

X = General mean of the character

Coefficient of Variability (CV)

The approach proposed by Burton and Devane (1953) was used to calculate genotypic and phenotypic coefficients of variation. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were characterized as low (less than 10%), moderate (10–20%), and high (more than 20%) by Sivasubramanian and Menon (1973).

$$\text{GCV (\%)} = \sqrt{V_g / \text{mean}} \times 100$$

$$\text{PCV (\%)} = \sqrt{V_p / \text{mean}} \times 100$$

Heritability (h^2) (Broad Sense):

Robinson *et al.* (1949) defined heritability percentages as low (0–30 percent), moderate (30–60 percent), and high (> 60 percent).

$$\text{Heritability } (h^2) = V_g / V_p \times 100$$

Results and Discussion

The mean of F_2 populations of two crosses were given in table 1 for eleven biometrical traits taken under study. The results of the phenotypic, genotypic variances along with their coefficient of variation, heritability and genetic advance as percent of mean were given in the table 2, for the crosses CO 14 × NDLH 1938 and CO 17 × NDLH 1755. Both the crosses had low PCV (7.62%, 7.14%), low GCV (6.19%, 6.31%), high heritability (65.98%, 78.21%) and low GAM (8.85%, 9.82%) for the trait days to first flowering. The trait plant height exhibited moderate PCV (13.17%, 10.67%), high heritability (79.40%, 77.75%) and low GAM (18.41%, 14.60%) for both the crosses. Lokesh kumar *et al.* (2018) also found a high heritability for the trait plant height. The cross CO 14 × NDLH 1938 was observed to have moderate GCV (11.74%) and the cross CO 17 × NDLH 1755 was observed to have low GCV (9.41%) for plant height. The trait number of sympodia's exhibited

low PCV (16.19%), low GCV (11.76%), low heritability (52.81%) and low GAM (15.05%) in the cross CO 14 × NDLH 1938. High PCV (23.58%), moderate GCV (19.61%), high heritability (69.14%) and high GAM (28.69%) were noted in the cross CO 17 × NDLH 1755 for the trait number of sympodial branches. Similar results of high PCV, high GAM for the trait number of sympodial branches per plant was reported by Nandhini *et al.* (2018). Similar results of high GAM and high heritability for the same trait was reported by Gitte *et al.* (2007). Same trait with high GAM was reported by Lokeshkumar *et al.* (2018). Number of bolls per plant had moderate GCV (12.60%, 17.05%) and high heritability (67.52%, 66.70%) for both the crosses CO 14 × NDLH 1938 and CO 17 × NDLH 1755. The former cross had low PCV (15.34%), low GAM (18.23%) while the latter had high PCV (20.87%) and high GAM (24.50%) for the trait number of bolls per plant. Same trait with high GAM was reported by Lokesh kumar *et al.* (2018).

Table 1: The mean of F_2 populations of two crosses for eleven biometrical traits.

Traits	Crosses	Mean (m)
Days to first flowering	CO 14 × NDLH 1938	54.32
	CO 17 × NDLH 1755	56.35
Plant Height (cm)	CO 14 × NDLH 1938	101.69
	CO 17 × NDLH 1755	106.52
Number of sympodial branches	CO 14 × NDLH 1938	27.70
	CO 17 × NDLH 1755	19.91
Number of bolls per plant	CO 14 × NDLH 1938	32.69
	CO 17 × NDLH 1755	23.37
Boll Weight (g)	CO 14 × NDLH 1938	4.01
	CO 17 × NDLH 1755	4.03
Lint index (g)	CO 14 × NDLH 1938	6.26
	CO 17 × NDLH 1755	5.67
Ginning outturn (%)	CO 14 × NDLH 1938	37.61
	CO 17 × NDLH 1755	36.75
Seed cotton yield per plant (G)	CO 14 × NDLH 1938	130.84
	CO 17 × NDLH 1755	94.35
Upper Half Mean Length (mm)	CO 14 × NDLH 1938	27.01
	CO 17 × NDLH 1755	26.92
Elongation percent (%)	CO 14 × NDLH 1938	5.34
	CO 17 × NDLH 1755	5.49
Micronaire Value (µg/inch)	CO 14 × NDLH 1938	3.73
	CO 17 × NDLH 1755	4.03

Both the crosses had moderate PCV (12.09%, 13.43%), low GCV (6.96%, 3.95%) and low GAM (7.04%, 2.05%) for the boll weight character. The cross CO 14 × NDLH 1938 (33.10%) had moderate heritability while the cross CO 17 × NDLH 1755 (8.66%) had low heritability for the trait boll

Table 2: Variances and coefficient of variation for phenotype and genotype followed by heritability and genetic advance as percent of mean

Traits	Crosses	Variance		PCV	GCV	h^2 (bs)	GAM
		σ_p^2	σ_g^2				
Days to first flowering	CO 14 × NDLH 1938	17.12	11.30	7.62	6.19	65.98	8.85
	CO 17 × NDLH 1755	16.17	12.65	7.14	6.31	78.21	9.82
Plant height (cm)	CO 14 × NDLH 1938	179.35	142.41	13.17	11.74	79.40	18.41
	CO 17 × NDLH 1755	129.10	100.38	10.67	9.41	77.75	14.60
Number of sympodial branches	CO 14 × NDLH 1938	20.11	10.62	16.19	11.76	52.81	15.05
	CO 17 × NDLH 1755	22.04	15.24	23.58	19.61	69.14	28.69
Number of bolls per plant	CO 14 × NDLH 1938	25.14	16.98	15.34	12.60	67.52	18.23
	CO 17 × NDLH 1755	23.78	15.86	20.87	17.05	66.70	24.50
Boll weight (g)	CO 14 × NDLH 1938	0.23	0.08	12.09	6.96	33.10	7.04
	CO 17 × NDLH 1755	0.29	0.03	13.43	3.95	8.66	2.05
Lint index (g)	CO 14 × NDLH 1938	0.83	0.28	14.56	8.46	33.74	8.65
	CO 17 × NDLH 1755	0.39	0.16	10.97	6.99	40.59	7.84
Ginning outturn (%)	CO 14 × NDLH 1938	4.42	0.89	5.59	2.50	20.02	1.97
	CO 17 × NDLH 1755	5.18	2.03	6.20	3.87	39.07	4.26
Seed cotton yield per plant (g)	CO 14 × NDLH 1938	616.25	592.55	18.97	18.60	96.15	32.11
	CO 17 × NDLH 1755	588.62	568.45	25.71	25.27	96.57	43.71
Upper half mean length (mm)	CO 14 × NDLH 1938	6.18	2.42	9.21	5.76	39.18	6.35
	CO 17 × NDLH 1755	3.74	1.70	7.19	4.84	45.38	5.74
Elongation percent (%)	CO 14 × NDLH 1938	0.02	0.01	2.68	1.38	26.68	1.26
	CO 17 × NDLH 1755	0.06	0.02	4.34	2.83	42.61	3.26
Micronaire value (µg/inch)	CO 14 × NDLH 1938	0.27	0.06	13.88	6.39	21.18	5.18
	CO 17 × NDLH 1755	0.31	0.16	13.76	10.04	53.24	12.90

weight. Similar result of moderate heritability for the trait boll weight was reported by Nandhini *et al.* (2018). Both the crosses had moderate PCV (14.56%, 10.97%), low GCV (8.46%, 6.99%), low GAM (8.65%, 7.84%) and moderate heritability (8.65%, 7.84%) for the lint index trait. The cross CO 14 × NDLH 1938 had moderate PCV (18.97%), moderate GCV (18.60%) and the cross CO 17 × NDLH 1755 had high PCV (25.71%), high GCV (25.27%) for the trait seed cotton yield per plant. Both the crosses had high heritability (96.15%, 96.57%) and high GAM (32.11%, 43.71%) for the same trait. Similar results of high GCV, high PCV and high heritability for the trait seed cotton yield per plant was reported by Lokeshkumar *et al.* (2018), Jarwar *et al.* (2018) and Hampannavar *et al.* (2020). Both the crosses had low PCV (5.59%, 6.20%), low GCV (2.50%, 3.87%) and low GAM (1.97%, 4.26%) for the ginning outturn trait. The cross CO 14 × NDLH 1938 had low heritability (20.02%) and the cross CO 17 × NDLH 1755 showed moderate heritability (39.07%) for the ginning outturn character. Similar results of low GAM for the same trait was reported by Gitte *et al.* (2007). Both the crosses had low PCV (9.21%, 7.19%), low GCV (5.76%, 4.84%),

moderate heritability (39.18%, 45.38%) and low GAM (6.35%, 5.74%) for the qualitative trait upper half mean length. The crosses CO 14 × NDLH 1938 and CO 17 × NDLH 1755 recorded low PCV (2.68%, 4.34%), low GCV (1.38%, 2.83%) and low GAM (1.26%, 3.26%) for elongation percent. Low heritability (26.68%) and high heritability (42.61%) was observed for the trait elongation percent for the crosses CO 14 × NDLH 1938 and CO 17 × NDLH 1755 respectively. Similar results of low GCV, low PCV and high heritability for the qualitative traits namely, upper half mean length and elongation percent were reported by Lokeshkumar *et al.* (2018). Similar results for the same trait with low GCV and low PCV were reported by Srinivas *et al.* (2014), Kumar *et al.* (2017). Both the crosses had moderate PCV (13.88%, 13.76%) for the trait micronaire value. The same trait had low values for GCV (6.39%), low heritability (21.18%) and low GAM (5.18%) for the cross CO 14 × NDLH 1938 and the cross CO 17 × NDLH 1755 reported moderate GCV (10.04%), moderate heritability (53.24%) and moderate GAM (12.90%) for the same trait. Regardless of the fact that the magnitude of the phenotypic coefficient of variation was greater than that of the genotypic coefficient of

variation in the current study, the PCV and GCV values for all of the traits tested showed a narrow variance as reported by Gitte *et al.* (2007). Certain findings suggested that the environment had less impact on the expression of these traits but then that further breeding may be used to improve them as suggested by Johnson *et al.* (1955). Important selection characteristics include heritability and genetic advance. Heritability estimates combined with genetic advance are usually more useful than heritability estimates alone in estimating the gain under selection as reported by Lokesh Kumar *et al.* (2018). Among all the traits studied, seed cotton yield per plant is determined to have additive gene action, high heritability, and high genetic advance as a percent of mean in both the crosses. Hence, this trait may be chosen as the key attribute for population development. Other traits included non-additive or epistatic gene action, with either high heritability with medium or low genetic advance as a percent of mean, which Pujer *et al.* (2014)

proposed could be improved by heterosis breeding programmes.

Conclusion

For majority of the characteristics, PCV and GCV had a high level of agreement, indicating that the observed variance might be mostly genetic. Among all the characters taken under study, the seed cotton yield per plant alone was found to have additive gene action with high heritability and high genetic advance as percent of mean, hence could be involved in direct selection as it is the major trait for improvement of the population of that trait. Other traits had non-additive or epistatic gene action with either high heritability with medium or low genetic advance as percent of mean which could be improved through heterosis breeding programmes.

Conflict of interest

The authors declare that they have no conflict of interest.

References

- Boopathi, N. M., Thiyagu, K., Urbi, B., Santhoshkumar, M., Gopikrishnan, A., Aravind, S. & 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*, 4 (8), 56-67.
- Budak, H., Bolek, Y., Dokuyucu, T., & Akkaya, A. (2004). Potential uses of molecular markers in crop improvement. *KSU Journal of science and Engineering*, 7(1), 75-79.
- Burton, G. W. (1952). Qualitative inheritance in grasses. Vol. 1. In *Proceedings of the 6th International Grassland Congress, Pennsylvania State College* 3 (9), 17-23.
- Burton, G. W., & Devane, D. E. (1953). *Estimating heritability in tall fescue (Festuca arundinacea)* from replicated clonal material. *Agronomy journal*, 45(10), 478-481.
- 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*. 07: 10902-10904.
- Gitte, V. K., Misal, M. B., Kalpande, H. V., & Deshmukh, J. D. (2007). Genetic variability studies in F₂ populations of upland cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*, 21(1), 27-28.
- Hampannavar, M. R., Patil, B. R., Katageri, I. S., Kumar, B. A., & Janagoudar, B. S. (2020). Genetic variability and correlation analysis for agronomic and fibre quality traits in intra-specific cotton (*G. hirsutum* × *G. hirsutum*) recombinant inbred lines (RILs). *International Journal Current Microbiological Applied Sciences*, 9(1), 493-503.
- Jarwar, A. H., Wang, X., Wang, L., Ma, Q., & Fan, S. (2018). Genetic advancement, variability and heritability in upland cotton (*Gossypium hirsutum* L.). *Journal of Environmental and Agricultural Sciences*, 6, 24-31.
- Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans 1. *Agronomy journal*, 47(7), 314-318.
- Kale, U. V., Kalpande, H. V., Gunjkar, A. S., & Gite, V. K. (2006). Variability, heritability and genetic advance studies in cotton. *Journal-Maharashtra Agricultural Universities*, 31(3), 389.
- Kumar, N. M., & Katageri, I. S. (2017). Genetic variability and heritability study in F₂ population of *Gossypium barbadense* L. cotton for yield and its components. *International Journal of Current Microbiological Applied Sci*, 6(6), 975-983.
- Lokeshkumar, B. M., & Patil, B. R. (2018). Estimation of genetic variability parameters in F₂ population of *Gossypium hirsutum* L. for yield, yield attributes and fiber quality traits. *Electronic Journal of Plant Breeding*, 4(3), 756-763.

- Magadum, S., Banerjee, U., Ravikesavan, R., Gangapur, D., & 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.). *Turkish Journal of Agriculture and Forestry*, 39(3), 451-458.
- Nandhini, K., Balu, P. A., & Isong, A. (2018). Genetic analysis and inheritance studies in F₂ population of upland cotton (*G. hirsutum* L.). *International Journal of Pure and Applied Biosciences*, 6(2), 1499-1505.
- Patil, Y.B., Madalageri B.B, Biradar, B.D, and Hoshmani, R.M. (1996). Variability studies in okra (*Abelmoschus esculentus* L. Moench.). *Karnataka Journal of Agricultural Sciences*. 9: 289–293.
- Pujer, S., Siwach, S. S., Deshmukh, J., Sangwan, R. S., & Sangwan, O. (2014). Genetic variability, correlation and path analysis in upland cotton (*Gossypium hirsutum* L.). *Electronic Journal of Plant Breeding*, 5(2), 284-289.
- Robinson, H. F., Comstock, R. E., & Harvey, P. H. (1949). Estimates of heritability and the degree of dominance in corn. 41, 353-359.
- Singh, R. K., & Chaudhary, B. D. (1977). Biometrical methods in quantitative genetic analysis. *Biometrical methods in quantitative genetic analysis*. Kalyani Publishers, New Delhi, 57-58.
- Sivasubramanian, S., & Menon, M. (1973). Heterosis and inbreeding depression in rice. *Madras Agricultural Journal*, 60(7), 1139-1140.
- Srinivas, B., Bhadr, D., Rao, M. V., & Gopinath, M. (2014). Genetic studies in yield and fibre quality traits in American cotton (*Gossypium hirsutum* L.). *Agricultural Science Digest-A Research Journal*, 34(4), 285-288.
- Swarup, V., & Chaugle, 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(1), 31-36.

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