



Genetic Variability and Heritability Study in Double Cross F2Linesof Cotton (*G. hirsutum* L.)

A. K. Meena ^{a++*}, S. S. Patil ^{b#} and L. K. Verma ^{a†}

^a University of Agriculture Sciences, Dharwad, India.

^b GPB, SKNAU, Jobner, Jaipur, India.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/JABB/2024/v27i5812

Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://www.sdiarticle5.com/review-history/114581>

Original Research Article

Received: 05/02/2024

Accepted: 09/04/2024

Published: 18/04/2024

ABSTRACT

An effective breeding programme requires precise information regarding the degree of link between different genotypes. The difference in gene frequencies between populations is represented by genetic variability. Genetic diversity was thought to be a key factor in achieving heterotic responses in F1 and a wide range of variability in segregating generations. As a result, any breeding effort must have information on the estimates of variability in yield and its heritable components in the material with which the breeder is working. As a result, using genetic parameters like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2), and genetic advance as a percent of mean (GAM). It becomes important to divide total variability into heritable and non-heritable components. Attempts were made to take use of the heterogeneity seen in segregating cotton generations through the current study. In Kharif 2016, at Botany Garden UAS, Dharwad, 80 Double Cross F2lines from staygreen (SG) and high relative growth rate (high RGR)

⁺⁺ Ph. D. Scholar and Assistant Professor;

[#] Professor (Retirement.) and Emeritus Scientist;

[†] Ph. D. Scholar;

*Corresponding author: E-mail: akmeena.pbg@sknau.ac.in;

heterotic groups of cotton were assessed in a Randomized Block Design with two replications. With the exception of inter-boll distance, which helps in the selection and identification of beneficial transgressive segregants, RBD analysis lines in the DCF₂ generation revealed substantial variations for every character.

Keywords: DCF₂ generation; GCV; GAM; genetic variability; heritability; PCV.

1. INTRODUCTION

Cotton can be grown in a wide variety of climates as it is being grown by about 77 countries across the globe which makes it an international crop. India occupies a unique place in the global cotton field because of several unique features, such as the largest cotton growing area, cultivation of all four cultivated species, a large area under tetraploid cotton, possibly the only country to grow hybrid cotton involving different species of cotton, the native home of old world cultivated cotton, and a wide range of agro-climatic conditions under which cotton is grown. The quality of cotton farmed in India is extremely diverse, ranging from 5s to 120s counts.

In the World, cotton occupies an area of 323.61 lakh hectares and production of 242.59 million bales of 170 kg with average productivity of 749 kg lint/ha Anon., [1] of cotton lint. In India cotton occupies an area of 130.49 lakh hectares and recorded production of 337.23 lakh bales of 170 kg of cotton lint with the productivity of 439 kg lint/ha. India is the world leading cotton growers and second largest cotton producer after China [1]. India is still recognized as a native to old world cultivated cotton and it is endowed with a wide diversity in agro-climatic condition in which cotton is grown.

One of the primary goals of plant breeders is to create new variability when existing natural variability is depleted or constrained. Better reshuffling of genes can be achieved by hybridization, which is a major source to create variability. Understanding the extent and magnitude of genotypic and phenotypic diversity in any crop species is critical to the development of improved cultivars. Hutchinson [2] has addressed "the need of estimating genotypic and phenotypic variability while designing efficient breeding strategies in cotton. He discovered that genetic variation has a direct impact on the probability of cotton breeding programme advancements. Information on heritability and genetic advance, in addition to genetic variability, evaluate the relative degree to which a trait is transferred to its offspring, assisting the breeder

in selecting a suitable breeding approach to meet the objectives".

In the present study 80 Double Cross F₂ lines from stay green (SG) and high relative growth rate (high RGR) groups were evaluated to estimate the genetic parameters like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h²) and genetic advance as percent of mean (GAM).

2. MATERIALS AND METHODS

The present study on measurement of variability consists of 80 Double Cross F₂ which consists of 40 DCF₂ lines from stay green (SG) group and 40 DCF₂ lines from relative growth rate (high RGR) group with commercial check. During Kharif 2016, selected lines were tested in a Randomized Block Design with two replications at Botany Garden UAS, Dharwad. "The data was analysed and observations for quantitative traits such as seed cotton yield (SCY), lint yield (LY), number of bolls per plant (NBP), boll weight (BW), plant height (PH), number of monopodia per plant (NMP), number of sympodia per plant (NSP), inter boll distance (IBD), ginning outturn (GOT), seed index (SI), lint index (LI) were recorded" [3].

The analysis of variance was carried out according to Panse and Sukhatme [4] recommendations. Burton and Devane [5] formula was used to determine genotypic and phenotypic coefficients of variation, while Johnson et al. [6], formula's was used to calculate heritability and GAM. According to Robinson et al. [7] GCV, PCV, and heritability were divided into three categories: low, moderate, and high.

3. RESULTS AND DISCUSSION

Analysis of variance DCF₂ segregating generation for eleven characters was presented in Table 1. In RBD analysis lines in DCF₂ generation showed significant differences for all the characters except for inter boll distance. In the present study mean, GCV, PCV, heritability

and GAM of DCF₂ lines were measured and significant variability was recorded for most of the traits.

In the present investigation, estimates of genetic factors revealed that the phenotypic coefficient of variability was larger than the genotypic coefficient of variability for all of the traits tested, indicating that they all interacted with the environments to a certain degree. In the present study, eleven different characters were considered to evaluate genetic variability and results were discussed for each character separately in the following heads.

3.1 Seed Cotton Yield (kg ha^{-1})

This trait ranged from 660 kg ha^{-1} (RGR-15) to 1935 kg ha^{-1} (SG-31) among DCF₂ lines, with an overall mean of 1174 kg ha^{-1} . "The Lines of DCF₂ generation was estimated moderate GCV (17.05) coupled with high PCV (24.30) and moderate heritability (41.14) coupled with high GAM (24.64)" [3].

The GCV and PCV ranges in the DCF₂ lines were high, showing that this trait provides more variability and that there is scope for improvement by direct selection for this characteristic. Vinodhana et al. [8], Ahsan et al. [9], Gnanasekaran et al. [10], Kumar et al. [11] also reported the same result for this trait.

"Seed cotton yield was estimated to have a moderate heritability. GAM, when coupled with heritability, provides a more accurate view of the amount of progress that may be expected by selection" [6]. As a result, the genotypes in the present investigation have a good chance to improve seed cotton yield through selection. Rao and Gopinath [12], Vinodhana et al. [13], Dhivya et al. [14], Pujer et al. (2014), and Khokher et al. [15] were also reported moderate heritability and GAM.

3.2 Lint Yield (kg ha^{-1})

This trait ranged from 218 kg ha^{-1} (RGR-15) to 674 kg ha^{-1} (SG-31) among DCF₂ lines, with an overall mean of 405 kg ha^{-1} . The lines in DCF₂ generation estimated low GCV (13.91) coupled with high PCV (24.35) and moderate heritability (49.60) coupled with moderate GAM (16.37) were also recorded. These findings were in accordance of Ahuja and Tuteja [16], Rao and Reddy [17], Vinodhana et al. [8],

Eswari et al. [18] and Gnanasekaran et al. (2018).

3.3 Number of Bolls Per Plant

This trait ranged from 14.38 (SG-13) to 30.25 (SG-18) among DCF₂ lines, with an overall mean of 20.81. The PCV (19.60) was moderate and the estimated GCV (9.98) was low. There was a low heritability (25.93) and a moderate GAM (10.47). Similar findings were also reported by Ahuja and Tuteja (2000), Rao and Reddy [17], Vinodhana et al. [8], Eswari et al. [18] and Gnanasekaran et al. [10].

3.4 Boll Weight (g)

The variation for this trait among the lines in DCF₂ generation was from 3.05 (RGR-31) to 6.08 (RGR-3) with an overall mean of 3.96 g. The moderate GCV (10.36) and moderate PCV (16.09) were estimated for this trait. Moderate heritability (41.50) coupled with moderate GAM (13.75) were recorded.

The boll weight expressed moderate genotypic and phenotypic coefficients of variation for DCF₂ generation. This was in agreement with the findings of Pujer et al. (2014), Preetha and Raveendran [19], Vinodhana, et al. [8], Eswari et al. [18] and Kumar et al. [11]. The same heritability and GAM response were reported by Vinodhana et al. [8].

3.5 Plant Height (cm)

The variation for this trait among the lines in DCF₂ generation was from 108.40 (SG-2 and SG- 21) to 195.50 cm (RGR-1) with an overall mean of 139.70 cm. DCF₂ lines were registered with low GCV (7.60), moderate PCV (12.21), moderate heritability (38.75) coupled with low GAM (9.47).

This trait had low GCV and PCV values, and the little difference between them indicated that the majority of the variability was attributable to genotype dominance in the ultimate expression of its phenotype. Vinodhana et al. [8], Pujer et al. (2014), Ahsan et al. [9], Dahiphaleet al. [20], and Shruti et al. [21] all provided similar reports. In DCF₂ generation, moderate heritability was seen along with moderate GAM, while Gnanasekaran et al. [10] were also reported similar results for plant height.

Table 1. ANOVA of DF₂ lines for different quantitative characters

Source variation	of df	SCY (kg ha⁻¹)	LY (kg ha⁻¹)	NBP	BW (g)	PH (cm)	NMP	NSP	IBD (cm)	GOT (%)	SI (g)	LI (g)
Replication	1	6320.25	274.46	35.96	6.69**	3498.57**	0.27	0.04	4.36	0.00	1.27	0.65
Treatments	80	121373.23**	12914.41**	20.94**	0.57**	403.46**	0.17**	7.60**	1.51	22.86**	0.96**	1.19**
Error	80	41297.74	6558.94	12.31	0.24	178.09	0.09	3.86	2.48	11.99	0.39	0.46

Table 2. Mean value, GCV, PCV, Heritability and genetic advance for eleven different quantitative characters of DCF₂ lines

DCF₂	SCY (kg ha⁻¹)	LY (kg ha⁻¹)	NBP	BW (g)	PH (cm)	NMP	NSP	IBD (cm)	GOT (%)	SI (g)	LI (g)
Mean	1174	405.32	20.81	3.96	139.70	1.66	11.67	9.13	34.79	8.39	4.52
GCV	17.05	13.91	9.98	10.36	7.60	12.18	11.72	7.63	6.70	6.34	13.32
PCV	24.30	24.35	19.60	16.09	12.21	21.93	20.52	15.50	12.00	9.81	20.10
<i>h²</i> (Broad Sense)	41.14	49.60	25.93	41.50	38.75	30.83	32.64	24.25	45.68	41.73	57.38
Gen.Adv as % of Mean 5%	24.64	16.37	10.47	13.75	9.74	13.93	13.79	7.74	7.71	8.43	18.19

Abbreviations: 1. Seed Cotton Yield (SCY), 2. Lint Yield (LY), 3. Number of Boll per Plant (NBP), 4. Boll Weight (BW), 5. Plant Height (PH), 6. Number of Monopodia per Plant (NMP), 7. Number of Synopodia per Plant (NSP), 8. Inter Boll Distance (IBD), 9. Ginning Outturn (GOT), 10. Seed Index (SI), 11. Lint Index (LN)

3.6 Number of Monopodia Per Plant

The variation for this trait among the lines in DCF₂ generation was from 0.98 (SG-14) to 2.34 (RGR-27) with an overall mean of 1.66. The lines in DCF₂ generation were recorded moderate GCV (12.18) and high PCV (21.93) coupled with moderate heritability (30.83) and GAM (13.93).

Besides, the bushy nature of the plant will make the intercultural and plant protection operations difficult. The GCV and PCV values were found to be moderate for this trait in DCF₂ generation. Vineela et al. [13], Dahiphale et al. [20] and Khokher et al. (2017), Gnanasekaran et al. [10] and Shruti [21] were also reported similar results.

3.7 Number of Sympodia Per Plant

The character ranged from 8.50 (RGR-27) to 24.50 (RGR-1) among the DCF₂ lines, with an overall mean of 11.67. The GCV (11.72) was moderate, while the PCV (20.52) was high. There was moderate heritability (32.64) and moderate GAM (13.9) observed. Observations indicating the existence of considerable variability in DCF₂ generation and same were reported earlier by Rao and Gopinath [12], Vineela et al. [13], Srinivas et al. [22] and Dahiphaleet al. [20], Eswari et al. [18] and Gnanasekaran et al. [10]. In DCF₂, the trait had moderate heritability and moderate GAM, indicating that additive gene action was dominant in influencing the trait. Ashok Kumar and Ravikesan [23], Patel et al. [24], and Vinodhana et al. [13] were also observed similar findings.

3.8 Inter-Boll Distance (cm)

Among the lines in DCF₂ generation value for this trait ranged from was from 7.09(SG-21) to 11.45 cm (RGR-6) with an overall mean of 9.13 cm. The estimated GCV (7.63) low and PCV (15.50) were moderate. Low heritability (24.25) coupled with low GAM (7.74) were recorded. The difference between the magnitude of GCV and PCV indicated the influence of the environment on the development of this character. The same result was also reported by Preetha and Raveendran [19].

3.9 Ginning Outturn (%)

Among the lines in DCF₂ generation value for this trait ranged from was from 26.00 (RGR-4) to 45.27 percent (RGR-6) with an overall mean of

34.79 percent. DCF₂ generation was estimated low GCV (6.70) and moderate PCV (12.00) coupled with moderate heritability (45.68) and GAM (7.71).

GCV and PCV have a considerable difference, indicating significant environmental interaction. Vinodhana et al. (2013) and Adsare and Salve (2017) reported low GCV and moderate heritability and GAM. Pujer et al. [25] reported a low GCV. Dhivya et al [14], Ahsan et al. [9] and Eswari et al. [18] also reported moderate PCV levels. Low GCV, moderate PCV and moderate heritability were also reported by Dhivya et al [14], Ahsan et al. [9] and Gnanasekaran et al. [10].

3.10 Seed Index (g)

This trait ranged from 6.80 (SG-39) to 9.80 (SG-6) among the DCF₂ lines, with an overall mean of 8.39 g. Low GCV (6.34) and PCV (9.81) were estimated among the lines in the DCF₂ generation, as well as moderate heritability (41.73) and low GAM (8.43). In DCF₂ generation, the trait had low genotypic and moderate phenotypic coefficients of variation. It had a high degree of heritability and a moderate GAM. Preetha and Raveendran (2007), Vinodhana et al. [13] and Dahiphaleet al. [20] also reported similar results.

3.11 Lint Index (g)

The variation for this trait among the lines in DCF₂ generation was from 3.08 (RGR-4) to 6.79 (RGR-40) with an overall mean of 4.52 g. The estimated GCV (13.32) moderate and PCV (20.10) were high. Moderate heritability (57.38) coupled with moderate GAM (18.19) were recorded. Moderate values for GCV and PCV were observed for both generations and the same results were reported by Vinodhana et al. [8], Dhivya et al. [14], and Ahsan et al., [18]. In DCF₂ generation, moderate heritability coupled with moderate GAM were recorded and the same results were recorded by Kumar et al. [11,26].

4. CONCLUSION

The present study revealed that DCF₂ lines showed significant genetic variability for the quantitative traits and which aids in the selection and identification of useful transgressive segregants. Information on heritability and genetic advance, in addition to genetic variability, evaluate the relative degree to which a trait is

transferred to its offspring, assisting the breeder in selecting a suitable breeding approach to meet the objectives.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Anonymous. All India coordinated cotton improvement project. Annu. Rep. 2022-23;1:1-5.
2. Hutchinson JB. The application of genetics to plant breeding-I. The genetic interpretation of plant breeding problems. J. Genet. 1940;40:271-282.
3. Meena AK, Patil SS, Verma LK. genetic variability and heritability study in double cross f3 lines of cotton (*G. hirsutum* L.). In Biological Forum—An International Journal. 2022;14(1):656-660.
4. Panse VG, Sukhatme PV, Statistical Methods for Agricultural Workers (II Edn.), ICAR, New Delhi; 1985.
5. Burton GW, Devane EW. Estimation heritability in tall fescue (*Festuca arundinaceae*) from eplicated clonal material. Agronomy Journal. 1953;45:478-481.
6. Johnson HW, Robinson H, Comstock RF. Estimates of genetic and environmental variability in soybean. Agronomy Journal. 1955;47:314-318.
7. Robinson HF, Comstock RE, Harley PH. Estimates of heritability and degrees of dominance in corn. Agron. J. 1949;43:353-359.
8. Vinodhana N, Gunasekharan M, Vindhiyavarman P. Genetic studies of variability, correlation and path coefficient analysis in cotton genotypes. Int. J. Pure. Appl. Biosci. 2013;1(5):6-10.
9. Ahsan MA, MajidanoMS, Bhutto H, Soomro AW, Panhwar FH, Channa AR, Sial KB. Genetic variability, coefficient of variance, heritability and genetic advance of some *Gossypium hirsutum*L. accessions. Journal of Agriculture Science. 2015;7(2):147-151.
10. Gnanasekaran M, Thiyyagu K, Gunasekaran M. Genetic variability, heritability and genetic advance studies in cotton (*Gossypium hirsutum* L.). Electronic Journal of Plant Breeding. 2018; 9(1):377-382.
11. Kumar CPS, Raju S, Rajan EB, MuraleedharanA, Suji DB. Studies on genetic variability, heritability and genetic advance in cotton (*Gossypium hirsutum*L.). Plant Archives. 2019;19: 934-937.
12. Rao PJM, Gopinath M. Variability and association studies for yield and yield components in upland cotton (*Gossypium hirsutum*L.) under red chalka soils. Electronic J. Plant Breed. 2012; 4(1):1093-1096.
13. Vineela N, Sambamurthy JSV, Ramakumar PV, Ratna KS. Variability studies for physio-morphological and yield components traits in American cotton (*Gossypium hirsutum*L.). J. Agric. and Vet. Sci. 2013;4(3):7-10.
14. Dhivya R, Amalabalu P, Pushpa R, Kavithamani D. Variability, heritability and genetic advance in upland cotton (*Gossypium hirsutum*L.). African Journal of Plant Science. 2014;8(1):1-5.
15. Khokhar ES, Shakeel A, MaqboolMA, Anwar MW, Tanveer Z, IrfanMF. Genetic study of cotton (*Gossypium hirsutum*L.) genotypes for different agronomic, yield and quality traits. Pakistan Journal Agriculture Research. 2017;30(4):363-372.
16. Ahuja SL, Tuteja OP. Variability and association analysis for chemical components imparting resistance to *Gossypium hirsutum* L. cotton. Journal of Cotton Research and Development. 2000;14(1): 19-22.
17. Rao GN, Reddy MSS. Studies on heritability and variability for yield and its components in *hirsutum* cottons. Journal of Cotton Research and Development. 2001;15: 84-86
18. Eswari KB, Sudheer KS, Gopinath, Rao MVB. Genetic variability, heritability and genetic advance studies in cotton. Int. J. Develop. Res. 2017;07(1):10902-10904.
19. Preetha S, Raveendran TS. Genetic variability and association analysis in three different morphological groupof cotton (*Gossypium hirsutum* L.). Asian J. Plant Sci.,2007;6 (1): 122-128.
20. Dahiphale KD, Deshmukh JD, Bagade AB, Jadhav AB. Studies on genetic variability, correlation and path coefficient analysis in cotton (*Gossypiumhirsutum*L.). International Journal of Tropical Agriculture.2015;33(1):23-29.
21. Shruti HC, Sowmya JM, Nidagundi R, Lokesha B, ArunkumarM, Shankar M.

- Genetic variability studies for yield, yield attributing and fibre quality traits in cotton (*Gossypium hirsutum L.*). Int. J. Curr. Microbiol. App. Sci. 2019;8(10):2677-2687
22. Srinivas B, Bhadru D, Brahmeswara RMV, Gopinath M. Genetic studies in yield and fibre quality traits in American cotton (*Gossypium hirsutumL.*). Agric.Sci. Dig. 2014;34(4):285–288.
23. Ashok KK, Ravikesavan R. Genetic studies of correlation and path coefficient analysis for seed oil, yield and fibre quality traits in cotton (*G. hirsutum L.*). Australian Journal of Basic and Applied Science. 2010;4(11):5496-5499.
24. Patel SM, Patel NA, Parmar MB, Patel MP, Patel JA. Studies on variability parameters, correlation and path coefficient analysis in *Bt*cotton hybrids (H x H). Crop Res. Hisar. 2013;46(1-3):212-216.
25. Pujer S, Siwach SS, Deshmukh J, Sangwan RS, Sangwan O. Genetic variability, correlation and path analysis in upland cotton (*Gossypium hirsutum.L.*). Electron. J. Plant. Breed. 2018;5(2):284-289.
26. Adsare AD, Salve AN. Study on genetic variability for the quantitative traits in some genotypes of upland cotton (*Gossypium hirsutum L.*). Bioscience Discovery. 2017;8 (3):365-368.

© Copyright (2024): Author(s). The licensee is the journal publisher. This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Peer-review history:

The peer review history for this paper can be accessed here:
<https://www.sdiarticle5.com/review-history/114581>