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Genetic Variability and Heritability Study in Double Cross F_3 Lines of Cotton (*G. hirsutum* L.)

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ABSTRACT: In any crop improvement programme, understanding the amount of genetic variability in the population, mechanism of gene action and inheritance of traits is essential for selecting an appropriate breeding methodology. Information on heritability and genetic advance, in addition to genetic variability, evaluate the relative degree to which a trait is transferred to its offspring, allowing the breeder in selecting a suitable breeding approach to meet the objectives. As a result, using genetic variables like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h2), and genetic advance as a percent of mean (GAM). It becomes essential to divide total variability into heritable and non-heritable components. Through the present study, efforts were made to exploit the variability present in segregating generation of cotton. For the study, 80 Double Cross F_3 lines from stay green (SG) and high relative growth rate (high RGR) heterotic groups with one commercial check of cotton were evaluated in Randomized Block Design with two replications during *Kharif* 2017 at Botany Garden UAS, Dharwad. In RBD analysis lines in DCF_3 generation showed significant differences for all the characters and also showed significant variability for genetic parameters like GCV, PCV, heritability and GAM. DCF_3 segregating generation was showing significant variability for most the character which facilities for selecting desired lines.

Keywords: Genetic variability, DCF_3 generation, GCV, PCV, heritability, GAM.

INTRODUCTION

It is very known that cotton is a very important fibre and cash crop of India, which plays an important role in the industrial and agricultural economy of the country. It provides basic raw material to cotton textile industry. Cotton has played a very important role in social and cultural evolution of mankind in the country. It is known fact that India is native of old world cultivated cotton. The scenario of Indian cotton cultivation has several distinct features, such as cultivation of all the four cultivated species, largest cotton growing area, diversity in agro-climatic zones in which cotton is cultivated and leading country in the world to grow hybrid cotton. All these features give India a unique place in global cotton scenario.

Cotton is grown on 33.3 million hectares around the world, yielding 118.93 million bales with a productivity of 779 kg ha^{-1}. On a total area of 12.2 million hectares, India produces 36.1 million bales of cotton. Cotton productivity in India, however, is 501 kg ha^{-1}, which is lower than the global average. Gujarat, Maharashtra and Telangana are India's largest cotton producing states. It is grown on 0.575 million hectares in Karnataka, with a production of 1.8 million bales and a productivity of 532 kg ha^{-1} (Anon., 2019).

The availability of genetic variability is without a question the most necessary attribute for any crop development initiative. The determination of the level of variation present in genetic material is a necessary step in determining the scale of improvement that can be achieved for specific traits and the methods to achieve it. The efficiency of selection is determined by the amount of genetic variability present in a given trait. Variability in quantitative characters relating to genetic parameters such as genotypic variance, phenotypic variance, heritability, and genetic advance as a percent of mean must be investigated. A greater range of variability will improve your chances of finding the genotype you want. Knowledge of heritability and genetic advance, in addition to genetic variability, quantifies the relative degree to which a character is transferred to progeny and allowing the breeder to adopt a proper breeding strategy to fast attains the goal. A percentage of means comparison of heritability values and projected genetic advance gives an insight of the nature of gene activity influencing a given character. As a result, a detailed understanding of the variability present in the available breeding material is required for the successful improvement of any crop.

The basic formula of heterosis ($HF_1 = \sum dy^2$) indicates that, magnitude of heterosis depends on the extent of dominance existing at different yield influencing loci and genetic diversity between the parents (Falconer, 1981). The efficiency of selection is determined by the amount of genetic variability present in a given character. 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.

MATERIAL AND METHODS

The present investigation on variability measurement includes 80 Double Cross F2 lines, 40 DCF2 lines from the stay green (SG) group and 40 DCF2 lines from the relative growth rate (high RGR) group, as well as one commercial check. During Kharif 2017, selected lines were tested in a Randomized Block Design with two replications at Botany Garden UAS, Dharwad. Quantitative traits such as seed cotton yield (SCY), lint yield (LY), number of bolls per plant, boll weight (NBP), plant height (PH), number of monopodia per plant (NMP), number of sympodia per plant (NSP), sympodia length at 50% height (SL), inter boll distance (IBD), ginning outturn (GOT), seed index (SI), lint index (LI) were observed and the data was analyzed by the procedures and formulas suggested by different scientists as following heads.

A. Analysis of variance

Analysis of variance was done separately for each character for all the treatments. The model of the analysis of variance is given by Panse and Sukhatme (1985) as below.

Source	d.f.	SS	MS	F-ratio
Replications	r-1	SS_r	M_r	M_r/M_e
Treatments	t-1	SS_t	M_t	M_t/M_e
Error	(r-1) (t-1)	SS_e	M_e	

Where,
r = Number of replications
t = Number of treatments

Significance of treatment means squares and replications mean squares were tested by comparing with error mean squares and referring to 'F' Table at 5 and 1 percent level probabilities.

Phenotypic coefficient of variance (PCV): PCV was calculated by the following formula by Burton and Devane (1953).

$$PCV = \frac{\sigma_p}{\bar{X}} \times 100$$

Where,
σ_p = Phenotypic variance
$\bar{X}$ = General mean of the character

Genotypic coefficient of variance (GCV): GCV was calculated by the following formula by Burton and Devane (1953).

$$GCV = \frac{\sigma_g}{\bar{X}} \times 100$$

Where,
σ_g = Genotypic variance
$\bar{X}$ = General mean of the character

GCV and PCV were classified as follows (Robinson *et al*., 1949).

Low	0-10 percent
Moderate	10-20 percent
High	> 20 percent

B. Heritability

Heritability in the broad sense, which is the heritable variation, was computed using the following formula

$$\text{Heritability } (h^2_{bs}) = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,
σ^2_g = Genotypic variance
σ^2_p = Phenotypic variance

Heritability was classified as follows (Robinson *et al.*, 1949).

Low	0-30 percent
Moderate	30-60 percent
High	> 60 percent

Genetic advance as a percentage over mean (GAM)

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

Where,
$\bar{X}$ = General mean of the character

The range of genetic advance as percent of mean was classified as suggested by Johnson *et al.* (1955).

Low	0-10 percent
Moderate	10-20 percent
High	> 20 percent

RESULTS AND DISCUSSION

The evaluation of the genetic material for degree of variation becomes a necessary step in determining the magnitude of improvement. The efficiency of selection is determined by the amount of genetic variability in a given character. In segregating generation (DCF_3) of four parental populations, the GCV, PCV, Heritability, and GAM were measured. For the most parameters, significant variability was observed in the DCF_3 generation. Table 1 shows the results of an analysis of variance for DCF_3 generation for twelve characters. For all of the characters, RBD analysis lines in DCF_3 generation exhibited significant variation. The coefficients of variation expressed in percent at phenotypic and genotypic levels have been used to compare the variability observed for different characters.

Estimates of genetic parameters revealed that for all of the characters tested, the phenotypic coefficient of variance was larger than the genotypic coefficient of variance, indicating that they all interacted with the environment to some extent. The outcome was explained in detail below, along with supporting references for each character.

Table 1: Analysis of variance for different quantitative characters in involving DCF_3 lines of SG Population and RGR Population.

Source of variation	**df**	**SCY (kg ha^{-1})**	**LY (kg ha^{-1})**	**NBP**	**BW (g)**	**PH (cm)**	**NMP**	**NSP**	**SL (cm)**	**IBD (cm)**	**GOT (%)**	**SI (g)**	**LI (g)**
Replication	1	333870.00**	23701.69*	2.94	0.98	1675.17*	0.07	189.41**	557.01**	21.14**	17.88	7.15**	0.30
Treatments	79	148802.13**	19988.06**	35.30**	0.72*	596.23**	0.37**	55.28**	177.53**	5.46**	15.40*	1.18**	0.76**
Error	79	23370.62	3621.38	10.87	0.46	208.69	0.17	10.77	30.23	1.42	9.60	0.48	0.34

A. Seed cotton yield (kg ha^{-1})

In DCF_3 segregating generation, mean values ranged from 647 (RGR-3) to 1919 kg ha^{-1} (RGR-10) with an overall mean of 1043kg ha^{-1}. The DCF_3 generation was estimated moderate GCV (17.05) coupled with high PCV (24.30) and moderate heritability (41.14) couples with high GAM (24.64).

In DCF_3 segregating generation, a high range of GCV and PCV were recorded for seed cotton yield which indicates that direct selection that this contributes much to total variability and there is good scope for improvement through direct selection for this trait. Same result was also reported by Ahsan *et al.*, (2015); Vinodhana, *et al.* (2013); Gnanasekaran *et al.* (2018); Kumar *et al.* (2019).

Seed cotton yield in DCF_3 generation had a moderate heritability. GAM, when combined with moderate heritability, provides a more accurate representation of the amount of progress that may be expected by selection (Johnson *et al.*, 1955). As a result, the genotypes in the present investigation have a good chance of improving seed cotton yield through selection. Rao and Gopinath (2012); Vinodhana *et al.* (2013); Dhivya *et al.* (2014); Pujer *et al.* (2014); Khokher *et al.* (2017) all reported intermediate heritability and high GAM.

B. Lint yield (kg ha^{-1})

In DCF_3 lines mean value was ranged from 215 (RGR-3) to 688 kg ha^{-1} (RGR-10 and SG -5) with an overall mean of 370 kg ha^{-1}. The DCF_3 lines were estimated high GCV (24.48) and PCV (29.40) with high heritability (69.32) couples with high GAM (41.98) for lint yield. Same GCV, PCV heritability and GAM response were also reported by Kumar *et al.* (2019).

C. Number of bolls per plant

The DCF_3 lines mean value ranged from 13.92 (RGR-36) to 36.13 (RGR-8) with an overall mean of 21.73. These DCF_3 lines were estimated moderate GCV (16.08) coupled with high PCV (22.11) and moderate heritability (52.93) couples with high GAM (24.10) were also recorded for this trait. These findings corroborate those of Ahuja and Tuteja (2000); Rao and Reddy (2001); Vinodhana *et al.* (2013); Eswari *et al.* (2017); Gnanasekaran *et al.* (2018).

D. Boll weight (g)

In DCF_3 lines mean values ranged from 3.61 (RGR-3) to 6.44 g (SG-10) with an overall mean of 4.81 g. DCF_3 lines estimated low GCV (7.53) moderate PCV (15.93) coupled with low heritability (22.32) and moderate GAM (15.93) for the trait. For DCF_3 generation, the boll weight expressed low genotypic and moderate phenotypic coefficients of variation. Pujer *et al.* (2014); Preetha and Raveendran (2007); Vinodhana *et al.* (2013); Eswari *et al.* (2017); Kumar *et al.* (2019) all came to similar conclusions. Vinodhana *et al.* (2013) reported the same heritability and GAM response.

E. Plant height (cm)

In DCF_3 lines mean value ranged 117.25 (RGR-35) to 201.25 cm (RGR-39) with an overall mean of 149.25 cm. DCF_3 lines were estimated low GCV (9.33) and moderate PCV (13.44) coupled with moderate heritability (48.15) and moderate GAM (13.33) recorded for plant height.

In the DCF_3 generation, moderate GCV and PCV value were reported, and the little difference between them showed that the majority of the variability observed was attributable to genotype dominance in the ultimate expression of the phenotype. Vinodhana *et al.* (2013); Pujer *et al.* (2014); Ahsan *et al.* (2015); Dahiphale *et al.* (2015); Shruti *et al.* (2019) also published the same reports. In the DCF3 generation, moderate heritability pairs with moderate GAM were seen, and comparable results for plant height were reported by Gnanasekaran *et al.* (2018).

F. Number of monopodia per plant

In DCF_3 lines the mean values ranged from 1.13 (SG-13 and RGR-16) to 3.25 (RGR-1) with an overall mean of 1.92. DCF_3 lines were estimated moderate GCV (16.19) and high PCV (26.94) coupled with moderate heritability (36.12) and high GAM (20.05) for number of monopodia per plant.

Besides, the bushy nature of the plant will make the intercultural and plant protection operations difficult. The moderate GCV and high PCV values were observed for this trait in DCF_3 generation. Vineela *et al.* (2013); Dahiphale *et al.* (2015); Khokher *et al.* (2017); Gnanasekaran *et al.* (2018); Shruti *et al.* (2019) all reported similar findings.

G. Number of sympodia per plant

In DCF_3 lines mean value ranged from 12.25 (RGR-12) to 38.00 (RGR-38) with an overall mean of 22.71. DCF_3 lines were estimated high GCV (20.77) and high PCV (25.30) coupled with high heritability (67.38) and high GAM (35.12) for this trait.

Rao and Gopinath (2012); Vineela *et al.* (2013); Srinivas *et al.* (2014); Dahiphale *et al.* (2015); Eswari *et al.* (2017); Gnanasekaran *et al.* (2018) also reported similar observations revealing the existence of large diversity in DCF_3 generation. The variable had a high heritability estimate and a high GAM in DCF_3 generation, indicating that additive gene action was the dominant mode of regulation. Ashok Kumar and Ravikesaran (2010); Patel *et al.* (2013); Vinodhana *et al.* (2013); Dhivya *et al.* (2014); Ahsan *et al.* (2015); Khokher *et al.* (2017) all reported similar findings.

H. Sympodial length at 50 percent height (cm)

In DCF_3 lines mean value ranged 22.75 (RGR-17 and RGR-5) to 68.50 cm (SG-34) with an overall mean of 37.10 cm. DCF_3 lines were estimated as high GCV (23.13), PCV (27.47), heritability (70.90) couples with high GAM (40.12).

In DCF_3 generation, the trait had significant GCV and PCV, as well as high heritability and GAM, showing the efficacy of selection for this trait in crop development. The findings contradicted those of Patankar (2001); Gururaj (2006).

I. Inter-boll distance (cm)

In DCF_3 lines mean value ranged 4.79 (RGR-17) to 16.01 cm (SG-28) with an overall mean of 8.79 cm. In DCF_3 lines were estimated moderate GCV (16.17) and high PCV (21.09) coupled with moderate heritability (58.80) and high GAM (25.54). The difference between the magnitude of GCV and PCV indicated the influence of the environment on the development of this character. The trait exhibited moderate heritability and high GAM. The same result was also reported by Preetha and Raveendran (2007).

J. Ginning outturn (%)

In DCF_3 lines, the mean value ranged from 30.21 (RGR-1) to 43.12 percent (RGR-13) with an overall mean of 35.51 percent. In the case of DCF_3 lines estimated low GCV (4.79), PCV (9.96), heritability (23.18) couples with low GAM (4.76). Similar results were also observed by Vinodhana *et al.* (2013); Dhivya *et al.* (2014); Pujer *et al.* (2014); Ahsan *et al.* (2015); Adsare and Salve (2017); Eswari *et al.* (2017); Gnanasekaran *et al.* (2018).

K. Seed index (g)

In DCF_3 lines the mean value ranged from 7.09 (RGR-7) to 10.25 g (SG-24) with an overall mean of 8.66 g. DCF_3 lines were estimated low GCV (6.83) and moderate PCV (10.23) and moderate heritability (42.23) couples with low GAM (9.15). The trait depicted low genotypic and moderate phenotypic coefficients of variation in DCF_3 generation. It had a high degree of heritability and a moderate genetic advance as a percentage of the mean. Preetha and Raveendran (2007); Vinodhana *et al.* (2013); Dahiphale *et al.* (2015) all reported similar results. Dhivya *et al.* (2014) and Khokher *et al.* (2017) alos reported same heritability response for this trait.

L. Lint index (g)

The mean value for DCF_3 lines ranged from 3.53 g (RGR-33) to 6.59 g (SG-25), with an average of 4.78 g for lint index. For the lint index, DCF3 lines revealed a low GCV (9.54), moderate PCV (15.55), moderate heritability (37.63), and moderate GAM (12.05). Vinodhana *et al.* (2013); Dhivya *et al.* (2014); Ahsan *et al.* (2015) all reported similar findings. Moderate heritability coupled with moderate GAM were found in the DCF_3 generation, Kumar *et al.* (2019) also reported same results for this trait.

Table 2: Mean value, GCV, PCV, Heritability and Genetic Advance for fourteen different Quantitative characters of DCF_3.

DCF_3	SCY (kg ha^{-1})	LY (kg ha^{-1})	NBP	BW (g)	PH (cm)	NMP	NSP	SL (cm)	IBD (cm)	GOT (%)	SI (g)	LI (g)
Mean	1043	370	21.73	4.81	149.25	1.92	22.71	37.10	8.79	35.51	8.66	4.78
GCV	24.02	24.48	16.08	7.528	9.33	16.19	20.77	23.13	16.17	4.79	6.83	9.54
PCV	28.14	29.40	22.11	15.934	13.44	26.94	25.30	27.47	21.09	9.96	10.52	15.55
h^2 (Broad sense)	72.85	69.32	52.93	22.32	48.15	36.12	67.38	70.90	58.80	23.18	42.23	37.63
Genetic advance as % of mean 5%	42.22	41.98	24.10	15.93	13.33	20.05	35.12	40.12	25.54	4.76	9.15	12.05

CONCLUSION

The present study revealed that DCF_3 lines showed significant genetic variability for the quantitative traits and which aids in the selection and identification of useful transgressive segregants.

FUTURE SCOPE

Identified high yielding transgressive segregants can be used for further crossing programme with suitable parents and high yielding hybrid can be developed.

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Conflict of Interests. None.

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