Genetic Variability and HeritabilityStudy in Double Cross F_2Linesof Cotton (*G. hirsutum* L.)

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 F_1 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 (h2), and genetic advance as a percent of mean (GAM). It becomes important to divide total variability into heritable and non-heritable components.Throughthe present study, efforts were made to exploit the variability present in segregating generation of cotton. For the study, 80 Double Cross F_2lines from staygreen (SG) and high relative growth rate (high RGR) heterotic groups of cotton were evaluated in Randomized Block Design with two replications during *Kharif* 2016 at Botany Garden UAS, Dharwad.In RBD analysis lines in DCF_2 generation showed significant differences for all the characters except for inter boll distance.

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Keywords:DCF_2 generation, GCV, GAM, Genetic Variability, Heritability, PCV,

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~~world, cotton occupies an area of 323.61 lakh hectares and production of 242.59 million bales of 170 kgwith average productivity of 749 kg lint/ha(Anon., 2022)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 (Anon., 2022). 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 (1940) 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 F_2lines 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).

Material and Methods

The present study on measurement of variability consists of 80 Double Cross F_2 which consists of 40 DCF_2 lines from stay green (SG) group and 40 DCF_2 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.

The analysis of variance was carried out according to Panse and Sukhatme (1985) recommendations. Burton and Devane (1953) formula was used to determine genotypic and phenotypic coefficients of variation, while Johnson *et al*. (1955),formula's was used to calculate heritability and GAM. According to Robinson *et al*. (1949) GCV, PCV, and heritability were divided into three categories: low, moderate, and high.

Results and Discussion

Analysis of variance DCF_2 segregating generation for eleven characters was presented in Table 1. In RBD analysis lines in DCF_2 generation showed significant differences for all the characters except for inter boll distance. In the present study mean, GCV, PCV, heritability and GAM of DCF_2 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.

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 DCF_2 lines, with an overall mean of 1174 kg ha^{-1}.The Lines of DCF_2generation was estimated moderate GCV (17.05) coupled with high PCV (24.30) and moderate heritability (41.14) coupled with high GAM (24.64).

The GCV and PCV ranges in the DCF_2 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*. (2013), Ahsan *et al*. (2015), Gnanasekaran *et al*. (2018), Kumar *et al*. (2019) also reported the same result for this trait.

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Seed cotton yield was estimated to have a ~~high~~ moderateheritability. GAM, when coupled with heritability, provides a more accurate view 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 to improve seed cotton yield through selection. Rao and Gopinath (2012), Vinodhana*et al*. (2013), Dhivya *et al*. (2014), Pujer *et al*. (2014), and Khokher *et al*. (2017) were also reported ~~high~~ moderateheritability and GAM.

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

This trait ranged from 218 kg ha^{-1} (RGR-15) to 674 kg ha^{-1} (SG-31) among DCF_2 lines, with an overall mean of 405 kg ha^{-1}. The lines in DCF_2 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~~accordance of Ahuja and Tuteja (2000), Rao and Reddy (2001), Vinodhana*et al*. (2013), Eswari *et al*. (2017~~) and~~) andGnanasekaran*et al*. (2018).

3. Number of bolls per plant

This trait ranged from 14.38 (SG-13) to 30.25 (SG-18) among DCF_2 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 (2001), Vinodhana*et al*. (2013), Eswari *et al*. (2017), and Gnanasekaran *et al*. (2018).

4. Boll weight (g)

The variation for this trait among the lines in DCF_2 generation was from 3.05 (RGR-31) to 6.08 (RGR-3) with an overall mean of 3.96 g. The moderateGCV (10.36) and~~high~~moderatePCV (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 DCF_2 generation. This was in agreement with the findings of Pujer *et al.* (2014), Preetha and Raveendran (2007), Vinodhana, *et al.* (2013), Eswari *et al.* (2017) and Kumar *et al.* (2019). The same heritability and GAM response were reported by Vinodhana*et al.* (2013).

5. Plant height (cm)

The variation for this trait among the lines in DCF_2 generation was from 108.40 (SG-2 and SG- 21) to 195.50 cm (RGR-1) with an overall mean of 139.70 cm**.** DCF_2 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*. (2013), Pujer *et al*. (2014), Ahsan *et al*. (2015), Dahiphale*et al*. (2015), and Shruti *et al*. (2019) all provided similar reports. In DCF_2 generation, moderate heritability was seen along with moderate GAM, while Gnanasekaran *et al*. (2018) were also reported similar results for plant height.

6. Number of monopodia per plant

The variation for this trait among the lines in DCF_2 generation was from 0.98 (SG-14) to 2.34 (RGR-27) with an overall mean of 1.66.The lines in DCF_2 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 DCF_2 generation. Vineela *et al.* (2013), Dahiphale *et al.* (2015)and Khokher *et al.* (2017), Gnanasekaran *et al.*(2018) and Shruti (2019) were also reported similar results.

7. Number of sympodia per plant

The character ranged from 8.50 (RGR-27) to 24.50 (RGR-1) among the DCF$_2$ 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 (13.79) observed. Observations indicating the existence of considerable variability in DCF$_2$ generation and same were reported earlier by Rao and Gopinath (2012), Vineela *et al.* (2013), Srinivas *et al.* (2014) and Dahiphale*et al.* (2015), Eswari *et al.*(2017) and Gnanasekaran *et al.* (2018). In DCF2, the trait had moderate heritability and moderate GAM, indicating that additive gene action was dominant in influencing the trait. Ashok Kumar and Ravikesaran (2010), Patel *et al*. (2013), and Vinodhana*et al*. (2013) were also observed similar findings.

8. Inter-boll distance (cm)

Among the lines in DCF$_2$ generation value for this trait ranged from was from7.09(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 (2007).

9. Ginning outturn (%)

Among the lines in DCF$_2$ 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**.** DCF$_2$ generation was estimated low GCV (6.70) and moderate PCV (12.00) coupled with moderate heritability (45.68) and low 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*. (2014) reported a low GCV. Dhivya *et al* (2014) Ahsan *et al*. (2015) and Eswari *et al*. (2017) also reported moderate PCV levels. Low GCV, moderate PCV and moderate heritability were also reported by Dhivya *et al* (2014), Ahsan *et al*. (2015) and Gnanasekaran*et al*. (2018).

10. Seed index (g)

This trait ranged from 6.80 (SG-39) to 9.80 (SG-6) among the DCF$_2$ lines, with an overall mean of 8.39 g. Low GCV (6.34) and PCV (9.81) were estimated among the lines in the DCF$_2$ generation, as well as moderate heritability (41.73) and low GAM (8.43). In DCF$_2$ 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*. (2013) and Dahiphale*et al*. (2015) also reported similar results.

11. Lint index (g)

The variation for this trait among the lines in DCF$_2$ 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.* (2013), Dhivya *et al*. (2014), and Ahsan *et al.*, (2015). In DCF$_2$ generation, moderate heritability coupled with moderate GAM were recorded and the same results were recorded by Kumar *et al.* (2019).

Conclusion

The present study revealed that DCF$_2$ lines showed significant genetic variability for the quantitative traits and which aids in the selection and identification of useful transgressive segregants.

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Table 1 : ANOVA of DCF$_2$ lines for different quantitative characters

Source of variation	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

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Table 2: Mean value, GCV, PCV, Heritability and Genetic Advance for eleven different Quantitative characters of DCF$_2$ lines

DCF$_2$	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
h^2 (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