Variability studies in F_2 population of upland cotton (*Gossypium hirsutum* L.) for quantitative and qualitative traits

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Abstract

The present investigation on F_2 population of TCH 1828 X GTHV 15-34, CO 14 X GISV 323, CO 14 X RHC 1409 and CO 17 X KC 3 were used for the variability studies thereby identifying the phenotypic (PCV), genotypic variations (GCV), heritability (h^2) and genetic advance as percent of mean (GAM) present in the population. Heritability and genetic advance are crucial selection criteria. Heritability estimates combined with genetic advance are usually more accurate in forecasting gain under selection than heritability estimates. Seed cotton yield per plant was observed to have additive gene action, high heritability, and high genetic advance as a percent of mean, therefore it may be chosen as the essential feature for population growth among all the traits evaluated in all the crosses under study. The crosses TCH 1828 X GTHV 15-34 and CO 14 X RHC 1409 for the trait, number of bolls per plant and the cross TCH 1828 X GTHV 15-34 for the trait, boll weight per plant also had high heritability and high genetic advance as percent of mean hence additive in nature hence could be taken for direct selection for the improvement of the population. All other traits studied were found to contribute non-additive or epistatic gene action, hence heterosis breeding could be performed for the enhancement of the population for these traits.

Key words: GCV, PCV, heritability, GAM, *G. hirsutum* L., variability studies, F_2 population

INTRODUCTION

Cotton (*Gossypium* spp.), the white gold, has been the world's main economic crop from the dawn of humanity. Cotton has succeeded despite increased manufacturing of artificial fibres, which was deemed to be a danger to its existence a few years ago. Due to its worldwide relevance in agriculture and the industrial sector, it employs over 35 million people directly in India (Kumar *et al.* 2017). Understanding the extent and amount of genotypic and phenotypic variability in any crop species is essential for developing effective genetic improvement that will result in improved cultivars. Because heredity is an aspect of continuous variation, plant breeders must generate genetic variability before they can practice selection (Ranganatha et al., 2013). Using genotypic and phenotypic variances, the phenotypic and genotypic coefficients of variation are calculated. The coefficient of variation just reveals how much variation is present in different traits, but it doesn't inform you how much of that variability is heritable. As a result, heritability is calculated in conjunction with estimates of genetic advance and genetic advance as a percentage mean reported by Khan et al. (2010) who investigated adaptability of *G. hirsutum* cultivars and found a large variation for agronomic, morphological, and yield-related traits. In *G. hirsutum*, genetic variability was identified for yield and yield components (Preetha *et al*. 2004). In upland cotton, Dhivya et al. (2014) reported the upland cotton used yield attributing characteristics to test heritability and genetic advance of yield. Upland cotton genotypes were researched by Pujer et al. (2014), who discovered considerable genetic diversity for yield and yield attributing traits. The study's main goals were to assess the genetic potential and variability, as well as heritability in the broad sense (bs) and genetic advance in upland cotton cultivars in the form of their expressions for various attributes. Such knowledge may be used to formulate an effective selection strategy for the synthesis and development of novel cotton genotypes with better yield and fibre quality attributes and a wide genetic base.

Materials and Methods

The experiment was carried out in the research field of the Department of Cotton, Tamil Nadu Agricultural University, Coimbatore. Four F_2 populations of *G.hirsutum* segregants (TCH 1828 X GTHV 15-34, CO 14 X GISV 323, CO 14 X RHC 1409 and CO 17 X KC 3) were used in the experiment. Twenty rows of 90 cm x 45cm spacing were seeded for each population. Standard field care procedures were followed, as well as fundamental agronomic measures such as irrigation, fertiliser management, weed control, and insect management. Biometrical data *viz.*, days to first flowering, plant height (cm), number of sympodial per plant, number of bolls per plant, boll weight (g), ginning outturn (percent), upper half mean length (mm), elongation percentage (percent), and micronaire value (µg/inch) were all recorded. Singh and Chaudhary (1977) used statistical analysis to determine the mean and variances.

Phenotypic variance

Individual observations were obtained for each characteristic on the F_2 population in order to calculate the phenotypic variance.

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

Where,

$$\text{Var } F_2 = \text{variance of } F_2 \text{ population}$$

Environmental variance

The average variance of the parents is utilised to calculate environmental variance.

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

Where,

σ^2p_1 = Variance of parent P_1

σ^2p_2 = Variance of parent P_2

Genotypic variance

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

σ^2p = Phenotypic variance

σ^2e = Environmental variance

Genetic advance as per cent of mean (GAM)

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

Where,

GA = Genetic advance

x = General mean of the character

Coefficient of Variability (CV)

Burton and Devane (1953) proposed measuring genotypic (GCV) and phenotypic (PCV) coefficients of variations.

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

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

Heritability (h^2) (Broad Sense)

According to Lush (1949) and Henson (1950), the heritability percentage was calculated for all of the variables studied.

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

Results

From Table 1, the following crosses *viz.*, TCH 1828 x GTHV 15-34, CO 14 x GISV 323, CO 14 x RHC 1409 and CO 17 x KC 3 showed low PCV, GCV and GAM with high heritability for all four crosses for the traits namely, days to first flowering and plant height. High heritability for the trait plant height was also reported by Lokeshkumar *et al.*(2018).

All the crosses had high PCV, moderate GCV for the trait number of sympodial branches per plant. The cross TCH 1828 x GTHV 15-34 had moderate heritability (26.52%) and high GAM (23.42%); CO 14 x GISV 323 had moderate heritability (40.84%) and moderate GAM (17.74%) and the crosses, CO 14 x RHC 1409 and CO 17 x KC 3 had low heritability (27.03%, 20.99%) and moderate GAM (11.87%, 10.35%) respectively for the trait number of sympodial branches per plant. Similar results of high GCV, high PCV, high GAM and moderate heritability for the trait number of sympodial branches per plant was reported by Nandhini *et al.* (2018). Same trait with high GAM was reported by Lokeshkumar *et al.* (2018).

The crosses, TCH 1828x GTHV 15-34 and CO 14 X GISV 323 had high PCV (40.40%, 35.85%), high GCV (37.12%, 31.49%), high heritability (84.44%, 77.19%) and high GAM (60.04%, 48.70%) while the cross CO 14 x RHC 1409 exhibited high PCV (34.32%), moderate GCV (17.62%), low heritability (26.37%) and moderate GAM (15.93%) for the trait number of bolls per plant. CO 17 X KC 3 showed high PCV (25.80%) with low GCV (2.90%), low heritability (1.27%) and low GAM (0.58%) for the trait number of bolls per plant. Similar results of high GCV, high PCV, high GAM and high heritability for the trait number of bolls per plant was reported by Nandhini *et al.* (2018). Same trait with high GAM was reported by Lokeshkumar *et al.* (2018).

The trait boll weight was found to have low PCV in all the four crosses. The cross TCH 1828 X GTHV 15-34 reported moderate GCV (15.07%), high heritability (81.41%) and high GAM (23.93%) while the cross CO 17 x KC 3 showed moderate PCV (14.93%), moderate GCV (11.23%), moderate heritabiilty (56.58%) and moderate GAM (14.87%) for the trait boll weight. The crosses, CO 14 X GISV 323 and CO 14 x RHC 1409 had low GCV (9.36%, 9.40%), moderate heritability (45.45%, 40.23%) and moderate GAM (11.11%, 10.50%) respectively. Similar results of high GCV, high PCV, high GAM and moderate heritability for the trait boll weight was reported by Nandhini *et al.* (2018). Similar results of high GAM and high heritability for the trait boll weight was reported by Gitte *et al.* (2007) and Lokeshkumar *et al.* (2018).

The trait lint index in the cross TCH 1828 X GTHV 15-34 had moderate PCV (13.38%), moderate GCV (11.60%), high heritability (75.10%) and moderate GAM (17.69%). The cross CO 14 X GISV 323 had moderate PCV (14.50%), low GCV (7.57%), low heritability (27.26%) and low GAM (6.96%) for the same trait while the cross CO 14 x RHC 1409 had moderate PCV (11.55%), low GCV (7.74%), moderate heritability (44.94%) and low GAM (9.14%). The cross CO 17 x KC 3 was observed to have low PCV (9.69%), low GCV (7.61%), low heritability (6.40%) and moderate GAM (10.51%) for the trait lint index.

All the four crosses showed high PCV, high GCV, high heritability and high GAM for the trait seed cotton yield per plant. Similar results of high GCV, high PCV for the trait seed cotton yield per plant was reported by Lokeshkumar *et al.* (2018), Jarwar *et al.* (2018) and Hampannavar *et al.* (2020). The trait ginning outturn had low PCV, GCV, heritability and GAM for all the crosses but the crosses TCH 1828 X GTHV 15-34, CO 14 x RHC 1409 and CO 17 x KC 3 have moderate heritability. Similar results of low GAM for the same trait was reported by Gitte *et al.* (2007).

The qualitative trait upper half mean length was observed to have low PCV, low GCV, high heritability and low GAM for all the crosses except for the crosses, TCH 1828 x GTHV 15-34 and CO 17 X KC 3 with moderate GAM. The trait elongation percent was reported to have low PCV, low GCV, low heritability and low GAM for all the crosses except for the cross, CO 14 x RHC 1409 with high heritability (42.18%). Similar results of low GCV, low PCV and high heritability for the qualitative traits namely, upper half mean length and elongation percent was reported by Lokeshkumar *et al.* (2018). Similar results for the same trait with low GCV, low PCV was reported by Srinivas *et al.* (2014), Kumar *et al.* (2017). The trait micronaire value was noted to have moderate PCV, low GCV, moderate heritability for all the crosses except for the cross, TCH 1828 x GTHV 15-34 with low heritability (28.57%), CO 17 x KC 3 with high heritability (60.50%). TCH 1828 x GTHV 15-34 and CO 14 X GISV 323 had low GAM for the trait micronaire value (7.32%, 7.70%) respectively.

Discussion

Despite the fact that the magnitude of the phenotypic coefficient of variation was greater than the genotypic coefficient of variation in the current study, the PCV and GCV values for all of the traits analysed showed a narrow variation as reported by Gitte *et al.* (2007). These findings suggested that the environment had less of an impact on the expression of these traits and that there was plenty of potential for improvement through breeding suggested by Johnson *et al.* (1955). Heritability and genetic advance are crucial selection criteria. Heritability estimates combined with genetic advance are usually more accurate in forecasting gain under selection than heritability estimates alone as suggested by Lokeshkumar *et al.* (2018). Seed cotton yield per plant was observed to have additive gene action, high heritability, and high genetic advance as a percent of mean, therefore it may be chosen as the essential feature for population growth among all the variables evaluated in all the crosses under study. The crosses TCH 1828 x GTHV 15-34 and CO 14 x RHC 1409 for the trait, number of bolls per plant and the cross TCH 1828 x GTHV 15-34 for the trait, boll weight per plant also had high heritability and high genetic advance as percent of mean hence additive in nature hence could be taken for direct selection for the improvement of the population as reported by Khan *et al.* (2015). All other traits studied were found to contribute non-additive or epistatic gene action, high heritability with low or medium genetic advance as a percent of mean, and heterosis breeding programmes, according to Pujer *et al*. (2014).

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Conflicts of Interest

Conflicts of interest are none

Ethical Standards

Not applicable

Author contribution

SS is the corresponding author of this manuscript and KK helped in writing the manuscript. RS and PN had corrected the article; KT, MMS and JP had supervised the overall work.

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Table 1. 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^2_p	σ^2_g				
DAYS TO FIRST FLOWERING (days)	**TCH1828 × GTHV15-34**	16.03	15.23	7.22	7.03	95.01	5.21
	CO14 × GISV323	23.17	21.81	8.75	8.49	94.13	6.26
	CO14 × RHC1409	27.40	25.72	9.59	9.29	93.87	6.84
	CO17 × KC3	26.07	18.67	9.52	8.05	71.61	5.18
PLANT HEIGHT (cm)	**TCH1828 × GTHV15-34**	193.92	187.38	14.46	14.22	96.62	12.07
	CO14 × GISV323	227.10	220.86	15.27	15.06	97.25	14.49
	CO14 × RHC1409	212.96	207.35	14.90	14.71	97.37	15.84
	CO17 × KC3	290.26	275.14	17.58	17.12	94.79	12.00
NUMBER OF SYMPODIAL BRANCHES PER PLANT (nos.)	**TCH1828 × GTHV15-34**	15.40	7.73	26.52	18.79	50.18	23.42
	CO14 × GISV323	14.20	5.80	24.67	15.77	40.84	17.74
	CO14 × RHC1409	13.70	3.70	24.96	12.98	27.03	11.87
	CO17 × KC3	17.72	3.72	28.02	12.84	20.99	10.35
NUMBER OF BOLLS PER PLANT (nos.)	**TCH1828 × GTHV15-34**	59.85	50.54	40.40	37.12	84.44	60.04
	CO14 × GISV323	27.18	20.98	35.85	31.49	77.19	48.70
	CO14 × RHC1409	15.75	4.15	34.32	17.62	26.37	15.93
	CO17 × KC3	16.12	0.20	25.80	2.90	1.27	0.58

Traits	Crosses	Variance		PCV	GCV	h^2 (bs)	GAM
		σ^2_p	σ^2_g				
BOLL WEIGHT (g)	TCH1828 × GTHV15-34	0.40	0.32	16.70	15.07	81.41	23.93
	CO14 × GISV323	0.30	0.14	13.89	9.36	45.45	11.11
	CO14 × RHC1409	0.24	0.10	14.82	9.40	40.23	10.50
	CO17 × KC3	0.24	0.14	14.93	11.23	56.58	14.87
LINT INDEX (g)	TCH1828 × GTHV15-34	0.48	0.36	13.38	11.60	75.10	17.69
	CO14 × GISV323	0.55	0.15	14.50	7.57	27.26	6.95
	CO14 × RHC1409	0.36	0.16	11.55	7.74	44.94	9.14
	CO17 × KC3	0.34	0.21	9.69	7.61	6.40	10.51
GINNING OUTTURN (%)	TCH1828 × GTHV15-34	4.95	2.34	6.02	4.14	47.34	5.01
	CO14 × GISV323	5.50	1.58	6.41	3.43	28.63	3.23
	CO14 × RHC1409	3.95	1.83	5.33	3.63	46.45	4.36
	CO17 × KC3	4.36	0.92	5.72	2.63	48.49	2.13
SEED COTTON YIELD PER PLANT (g)	TCH1828 × GTHV15-34	902.83	877.28	55.67	54.87	97.17	95.20
	CO14 × GISV323	468.46	451.06	37.93	37.22	96.29	64.27
	CO14 × RHC1409	106.69	87.21	35.14	31.77	81.74	50.56
	CO17 × KC3	213.90	200.18	34.49	33.36	93.59	56.80

Traits	**Crosses**	**Variance**		**PCV**	**GCV**	**h^2 (bs)**	**GAM**
		σ^2_p	**σ^2_g**				
UPPER HALF MEAN LENGTH (mm)	**TCH1828 × GTHV15-34**	3.90	3.40	6.74	6.28	86.99	16.17
	CO14 × GISV323	3.51	2.90	5.92	5.38	82.47	8.60
	CO14 × RHC1409	1.84	1.38	4.25	3.68	74.97	5.61
	CO17 × KC3	5.21	4.18	7.50	6.72	80.25	10.60
ELONGATION PERCENT (%)	**TCH1828 × GTHV15-34**	0.02	0.01	2.39	0.33	0.25	0.01
	CO14 × GISV323	0.01	0.00	1.98	0.75	14.35	0.50
	CO14 × RHC1409	0.02	0.01	2.23	1.45	42.18	1.65
	CO17 × KC3	0.01	0.00	2.10	0.44	4.38	0.16
MICRONAIRE VALUE (µg/inch)	**TCH1828 × GTHV15-34**	0.34	0.10	14.56	7.78	28.57	7.32
	CO14 × GISV323	0.30	0.10	13.51	7.69	32.38	7.70
	CO14 × RHC1409	0.34	0.14	19.40	9.31	40.97	13.99
	CO17 × KC3	0.33	0.13	14.59	9.25	60.50	10.33