

Assessment of Genetic Variability Parameters for Yield and Fibre Quality Traits of Cotton (*Gossypium Hirsutum* L.) in F₂ Population

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Abstract: The F₂ population of the crosses MCU 5 × KC 3 and MCU 5 × NDLH 1755 were taken for the investigation of variability and heritability studies to understand the gene action contributing to the each and every trait taken under study. The phenotypic coefficient of variation (PCV) in both the crosses were found to have environmental influence as it was greater than the genotypic coefficient of variation (GCV) for all the traits under study. The studies of heritability and genetic advance as percent of mean helps us to identify the trait is additive or epistatic in nature, therefore undergo suitable breeding programmes for the improvement of the population. 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 in the cross MCU 5 × KC 3. The cross MCU 5 × NDLH 1755 the traits namely, number of sympodial branches per plant, number of bolls per plant and seed cotton yield per plant 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. Other traits in both the crosses 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. Since traits are contributed by complex gene action.

Key words: Variability, Heritability, GCV, PCV, *G. hirsutum* L. and F₂ population

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1. Introduction

Cotton (*Gossypium spp.*) has been the world most important economic crop. Cotton has thrived in the face of rising artificial fibre manufacturing, which was formerly regarded to be a danger to its survival. As a natural fibre that is both environmentally beneficial and biodegradable, the globe has turned its attention to this crop (Mishra *et al.* 2015). Cotton has become the king of fibre crop until this day. It employs roughly 35 million people directly in India because to its worldwide value in agriculture and the industrial sector. Cotton accounts for 60% of the Indian textile sector, which accounts for 5% of the country's GDP (GDP). Providing employment to nearly 51 million people directly and 68 million people indirectly, it contributes 14% to industrial output and 11% to export revenues (Kumar *et al.* 2017). Understanding the extent and amount of genotypic and phenotypic variability in any crop

species is critical for developing effective breeding programmes that result in improved cultivars. In order to generate high yielding cultivars, breeders need genetic information on several qualitative and quantitative properties (Nadeem and Azhar 2004; Ali and Khan (2007). In a breeding programme, novel variability production and optimal exploitation, as well as genetic understanding, are critical. In fixed selection pressure, the quantity of genetic advance varied with the degree of the heritability, but heredity alone did not offer any indication of the genetic gain that would occur from selection. Heritability alone cannot determine genetic advancement in a population; instead, genetic gain under specific selection pressure must be calculated (Basal and Tuegut, 2005; Ali *et al.* 2008; Ali and Awan 2009). Plant breeders must first create genetic variability before they can undertake selection, as heredity is a source of continual change

(Ranganatha *et al.* 2013). Using genotypic and phenotypic variances, the phenotypic and genotypic coefficients of variation are calculated. The coefficient of variation informs you how much variation there is for certain characters, but it doesn't tell you how much of it is heritable. As a result, heritability is assessed together with estimations of genetic advance and genetic advance as a percent mean. The purpose of this study was to determine the degree of genetic variability, heritability, and genetic advance in cotton F₂ segregating populations for yield, yield characteristics, and fibre quality traits.

2. Materials and Methods

During the summer of 2022, the experiment was carried out on the research field of the Department of Cotton, Tamil Nadu Agricultural University, Coimbatore. Two F₂ populations of *G.hirsutum* segregants (MCU5 × KC3 and MCU5 × NDLH 1755) were used in the experiment. A Randomized Block Design with two replications was used to grow the two F₂ populations. Twenty rows of 90cm × 45cm spacing were sown for each population. Standard field care procedures were followed as were fundamental agronomic methods such as irrigation, fertilizer application, weed control and insect management. Days to first flowering, Plant height(cm), Number of sympodial per plant, Number of bolls per plant, Boll weight(g), Seed cotton yield per plant(kg/ha), Ginning outturn (%), Upper Half Mean Length(mm), Elongation percentage(%) and Micronaire value(μg/inch) were all recorded in each entry. The resulting lint was analyzed for fibre quality characteristics estimate using the High Volume Instrument 900 classic. 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.

Phenotypic variance (σ^2p) = Var F₂

Where,

Var F₂ = variance of F₂ population

Environmental variance

Because replication of the F₂ population is not feasible, 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

Genotypic variance (σ^2g) = $\sigma^2p - \sigma^2e$

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,

h^2 = 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)

GA

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

X

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).

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

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).

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

3. Result and Discussion

From table 1(fig. 1 &2), the crosses MCU 5 × KC 3 and MCU 5 × NDLH 1755 have low

PCV (9.11%, 7.64%), low GCV (8.63%, 6.96%), high heritability (89.68%, 82.93%) and moderate GAM (14.38%, 11.15%) for the trait days to first flowering respectively. Both the crosses exhibited moderate PCV (11.62%, 12.25%), moderate GCV (10.71%, 11.33%), high heritability (84.85%, 85.59%) and low GAM (17.36%, 18.45%) for the trait plant height respectively. High heritability for the trait plant height was also reported by Lokeshkumar *et al.* (2018).

The cross MCU 5 × NDLH 1755 found to have high PCV (27.94%), high GCV (23.58%), high heritability (71.25%) and high GAM (35.03%) for the trait number of sympodial branches per plant. Similar results of high GAM and high heritability for the same trait was reported by Gitte *et al.* (2007) but the cross MCU 5 × KC 3 was found to have moderate PCV (17.16%), moderate GCV (13.37%) and moderate GAM (18.34%) but with high heritability (60.75%) for the trait number of sympodial branches per plant. Similar results of high GCV, high PCV for the trait number of sympodial branches per plant was reported by Nandhini *et al.* (2018) and Lokeshkumar *et al.* (2018). Same trait with high GAM was reported by Lokeshkumar *et al.* (2018).

GCV was found to be moderate (11.96%, 19.96%) and heritability was found to be high (54.80%, 66.63%) in both the crosses respectively for the trait number of bolls per plant. The cross MCU 5 × KC 3 found to have moderate PCV (16.15%) and GAM (15.58%) and the cross MCU 5 × NDLH 1755 has high PCV (24.45%) and high GAM (28.68%) for the trait number of bolls per plant. Similar results of high GCV, high PCV for the trait number of bolls per plant was reported by Nandhini *et al.* (2018) and Lokeshkumar *et al.* (2018). Same trait with high GAM was reported by Lokeshkumar *et al.* (2018).

The trait boll weight was found to have moderate PCV (14.35%), moderate GCV (11.09%), high heritability (59.72%) and moderate GAM (15.09%) for the cross MCU 5 × KC 3. The MCU 5 × NDLH 1755 had moderate PCV (14.28%), moderate heritability (46.64%) and moderate GAM (11.72%). The same cross exhibited low GCV (9.75%) for the trait boll weight. Similar result of high heritability for the trait boll weight was reported by Gitte *et al.* (2007) and Lokeshkumar *et al.* (2018).

Lint index exhibited moderate PCV (13.60%), moderate GCV (10.11%), moderate heritability (55.20%) and low GAM (13.22%) for the cross MCU 5 × KC 3. MCU 5 × NDLH 1755 was observed to have moderate PCV (12.59%), low GCV (7.40%), moderate heritability (34.59%) and low GAM (7.66%).

The seed cotton yield per plant was found to have high PCV (21.71%, 28.22%), high GCV (21.16%, 27.57%), high heritability (95.03%, 95.42%) and high GAM (36.31%, 47.39%) for both the crosses respectively. 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).

The ginning outturn for both the crosses found to have low PCV (6.08%, 5.13%), low GCV (4.17%, 3.04%), moderate heritability (47.05%, 35.08%) and low GAM (5.03%, 3.16%) respectively. Similar results of low GAM for the same trait was reported by Gitte *et al.* (2007).

The upper half mean length had low PCV (8.50%), low GCV (3.55%), low heritability (17.40%) and low GAM (2.60%) for the cross MCU 5 × KC 3 and the MCU 5 × NDLH 1755 had low PCV (9.00%), low GCV (5.02%), low GAM (4.92%) with moderate heritability (31.05%) for the same trait. The trait elongation percent and micronaire value had low GCV and GAM for both the crosses. The cross MCU 5 × KC 3 had moderate heritability (33.97%) for the trait elongation percent and the cross MCU 5 × NDLH 1755 had low heritability (28.27%) for the same trait under study. Both the crosses had moderate PCV and low heritability for the trait micronaire value. 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).

Due to 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 variance 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 are possibilities for improvement through breeding as suggested by Johnson *et al.* (1955). Selection criteria such as heritability and genetic advance are significant. Heritability estimates combined with genetic advance are usually more useful in projecting selection gain than heritability estimates alone as reported by Lokeshkumar *et al.* (2018).

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 in both the crosses MCU 5 × KC 3 and MCU 5 × NDLH 1755. The cross MCU 5 × NDLH 1755 the traits, number of sympodial branches per plant and number of bolls 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). 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 as suggested by Pujer *et al.* (2014).

Application of research: Study of environmental coefficient of variation, heritability, genetic advancement, genotypic and phenotypic coefficient of variation were estimated in this study to understand the variability present in the population.

Research Category: Genetics and Plant Breeding

Abbreviations: PCV-Phenotypic variations, GCV-genotypic variations

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Traits	Crosses	Variance		PCV	GCV	h ² (bs)	GAM
		σ_p^2	σ_g^2				
DAYS TO FIRST FLOWERING	MCU5 × KC3	24.23	21.73	9.11	8.63	89.68	14.38
	MCU5 × NDLH 1755	16.99	14.09	7.64	6.96	82.93	11.15
PLANT HEIGHT (cm)	MCU5 × KC3	134.42	114.05	11.62	10.71	84.85	11.62
	MCU5 × NDLH 1755	159.65	136.64	12.25	11.33	85.59	12.25
NUMBER OF SYMPODIAL BRANCHES	MCU5 × KC3	21.31	12.95	17.16	13.37	60.75	18.34
	MCU5 × NDLH 1755	29.35	20.91	27.94	23.58	71.25	35.03
NUMBER OF BOLLS PER PLANT	MCU5 × KC3	22.53	12.35	16.15	11.96	54.80	15.58
	MCU5 × NDLH 1755	31.17	20.77	24.45	19.96	66.63	28.68
BOLL WEIGHT (g)	MCU5 × KC3	0.32	0.19	14.35	11.09	59.72	15.09
	MCU5 × NDLH 1755	0.33	0.15	14.28	9.75	46.64	11.72
LINT INDEX (g)	MCU5 × KC3	0.73	0.40	13.60	10.11	55.20	13.22
	MCU5 × NDLH 1755	0.57	0.20	12.59	7.40	34.59	7.66
GINNING OUTTURN (%)	MCU5 × KC3	5.11	2.40	6.08	4.17	47.05	5.03
	MCU5 × NDLH 1755	3.77	1.32	5.13	3.04	35.08	3.16
SEED COTTON YIELD PER PLANT (g)	MCU5 × KC3	642.22	610.32	21.71	21.16	95.03	36.31
	MCU5 × NDLH 1755	665.92	635.39	28.22	27.57	95.42	47.39
UPPER HALF MEAN LENGTH (mm)	MCU5 × KC3	5.38	0.94	8.50	3.55	17.40	2.60
	MCU5 × NDLH 1755	5.57	1.73	9.00	5.02	31.05	4.92
ELONGATION PERCENT (%)	MCU5 × KC3	0.07	0.02	4.69	2.73	33.97	2.80
	MCU5 × NDLH 1755	0.06	0.02	4.38	2.33	28.27	2.18
MICRONAIRE VALUE (µg/inch)	MCU5 × KC3	0.29	0.02	13.37	3.33	6.21	1.46
	MCU5 × NDLH 1755	0.29	0.03	12.75	4.19	10.80	2.42

Table 1. Variances, coefficient of variation for phenotype and genotype followed by heritability and genetic advance as percent of mean

