



Research Article

VARIABILITY STUDIES IN F₂ POPULATION OF UPLAND COTTON (*GOSSYPIMUM HIRSUTUM* L.) FOR YIELD AND FIBRE QUALITY TRAITS

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Abstract: The present experiment on F₂ population of MCU 5 x KC 3, CO 14 x KC 3, CO 14 x KC 2 and TCH 1828 x KC 2 was investigated for the variability studies thereby identifying the phenotypic (PCV), genotypic variations (GCV), heritability (h²) and genetic advance as percent of mean (GAM) present in the population. These estimates provide the knowledge of genes that are additive or non-additive in nature. Predicting the nature of gene action would help in formulating the successful breeding programmes for the respective populations under study. For majority of the characteristics, PCV and GCV had a high level of agreement, indicating that the observed variance might be mostly genetic. High heritability along with high genetic advance as percent of mean might be viewed as positive qualities that indicate additive gene activity which was found in the trait seed cotton yield per plant in all the four crosses taken under study and as a result, simple selection method is effective for improvement of such trait. For seed cotton yield associated and fibre quality parameters, moderate to high GCV, PCV, heritability, and genetic advance percent of mean values were found, indicating that these qualities could be passed to the progeny when hybridization was undertaken and phenotypic based selection was effective.

Keywords: GCV, PCV, heritability, GAM, *G. hirsutum* L., Variability studies, F₂ population

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Introduction

Cotton is extremely important cash crop and plays a key part in the economy. Excavations at Mohen Jo Daro revealed that cotton was produced in Sindh Pakistan before 2500 B.C [1]. Cotton is cultivated in more than 60 countries across the world and is a major source of natural fibre. Cotton retains its title as "queen of the fibre plants" despite threats from synthetic or artificial fibre. Cotton is also known as "white gold" because to the numerous applications of lint and byproducts. Cotton provides the majority of our foreign exchange reserves, either directly or indirectly. As a result, not only has sustainable cotton production become critical, but we must also figure out how to increase per-acre yields in order to boost the cotton-based economy. For improved cotton production, the discovery and usage of genotype with higher genetic potential is a constant demand. Efforts are being made to improve both the yield and the fibre quality. Comprehensive investigations to understand the genetic mechanisms that govern plant traits under various environmental situations are also required to attain these goals. Understanding the gene action and inheritance pattern of characteristics is critical for selecting an appropriate breeding process and crop enhancement [2]. When the level of heterogeneity in the breeding population is large enough, selection is effective. The current study programme was modelled after in order to better understand the gene action in yield and associated variables among various upland cotton accessions. 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.

Materials and methods

The present study was carried out in Department of cotton, Tamil Nadu Agricultural University, Coimbatore-03. The F₂ population were obtained from the crosses namely, MCU 5 x KC 3, CO 14 x KC 3, CO 14 x KC 2 and TCH 1828 x KC 2. The thinning, one plant per hill was maintained. All agronomic and cultural operations were followed as per recommended and completed on schedule.

The data was collected from the F₂ population for the observation of the following characters namely, days to first flowering (days), plant height (cm), number of monopodial branches per plant, number of sympodial branches per plant, the number of bolls per plant, boll weight (g), number of locules per boll, seed index (g), lint index (g), 100 seed weight (g), single cotton yield per plant (g), ginning outturn (%), upper half mean length (cm), uniformity index (%), bundle strength (g/tex), elongation percent (%) and micronaire value (µg per inch). The genetic variance was split from the overall variance using the Fisher *et al.* approach (1932) [3]. According to Weber *et al.* (1952) [4], the environmental variation was calculated from the non-segregating population. The genotypic variance was calculated as suggested by Empig *et al.* (1970) [5]. Heritability (h²) estimated in the broad sense method devised by Lush (1940) [6] was used in this experiment. The genetic advance and genetic advance as percent of mean was estimated by the method formulated by Johnson *et al.* (1955)[7].

Results and Discussion

Crop improvement is mostly determined by the amount of genetic variation existing among the traits in question. Genetic variability studies offer fundamental information on the genetic features of a population, which is used to develop field crop breeding approaches. From [Table-1] and [Fig-1], the phenotypic coefficient of variation was found to be moderate for the traits namely, plant height, boll weight, lint index and micronaire value in all the crosses taken under study. Low PCV, GCV and genetic advance as percent of mean was observed in all the crosses for the trait days to first flowering. High heritability was observed for the same trait in all the crosses except the cross CO 14 x KC 3 which had moderate heritability (35.77%). Moderate GCV value of plant height was observed in all the crosses under study. The high heritability value was observed in all the crosses for the same trait. The trait plant height showed high GAM value in the cross MCU 5 x KC 3 (21.63%).

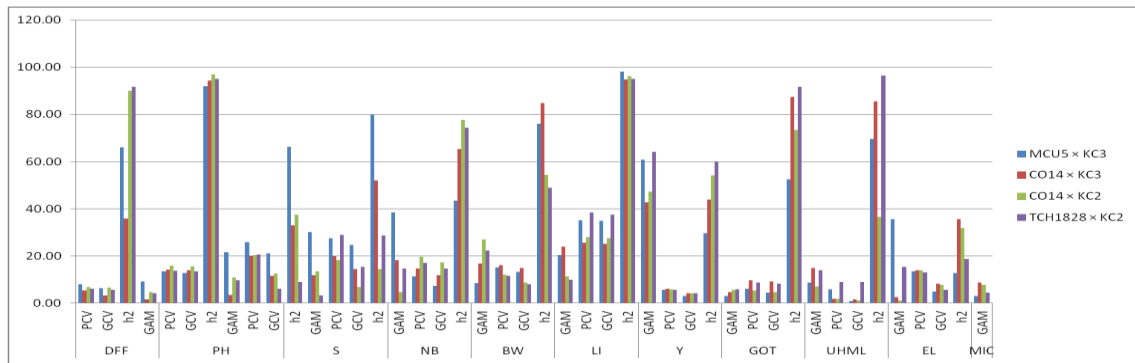


Fig-1 Variances, and coefficient of variation for phenotype and genotype followed by heritability and genetic advance as percent of mean

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)	MCU5 × KC3	17.93	11.85	7.88	6.41	66.09	9.17
	CO14 × KC3	8.97	3.21	5.41	3.24	35.77	1.47
	CO14 × KC2	13.67	12.31	6.8	6.45	90.05	4.65
	TCH1828 × KC2	11.61	10.65	5.98	5.72	91.73	4.17
Plant Height (cm)	MCU5 × KC3	186.4	171.6	13.35	12.81	92.06	21.63
	CO14 × KC3	188.08	177.44	14.27	13.86	94.34	3.41
	CO14 × KC2	312.92	303.2	15.77	15.52	96.89	10.78
	TCH1828 × KC2	171.26	162.94	13.72	13.39	95.14	9.65
Number Of Sympodial Branches Per Plant (nos.)	MCU5 × KC3	20.23	13.43	25.72	20.96	66.38	30.06
	CO14 × KC3	8.97	2.97	20.12	11.57	33.08	11.71
	CO14 × KC2	11.37	4.25	20.31	12.42	37.39	13.37
	TCH1828 × KC2	10.23	0.91	20.53	6.13	8.91	3.22
Number Of Bolls Per Plant (nos.)	MCU5 × KC3	37.7	30.06	27.47	24.53	79.73	38.55
	CO14 × KC3	12.31	6.39	19.95	14.38	51.92	18.23
	CO14 × KC2	11.35	1.63	18.12	6.87	14.35	4.58
	TCH1828 × KC2	17.47	5.03	28.81	15.46	28.8	14.6
Boll Weight (g)	MCU5 × KC3	0.23	0.1	11.2	7.38	43.37	8.55
	CO14 × KC3	0.32	0.21	14.53	11.75	65.41	16.73
	CO14 × KC2	0.59	0.46	19.67	17.35	77.73	26.91
	TCH1828 × KC2	0.38	0.28	17.07	14.72	74.31	22.33
Lint Index (g)	MCU5 × KC3	0.84	0.64	15.2	13.26	76.05	20.35
	CO14 × KC3	0.79	0.67	16.09	14.81	84.73	23.99
	CO14 × KC2	0.44	0.24	11.92	8.8	54.5	11.43
	TCH1828 × KC2	0.39	0.19	11.455	8.018	49.003	9.879
Ginning Outturn (%)	MCU5 × KC3	4.22	1.25	5.55	3.02	29.63	2.89
	CO14 × KC3	4.84	2.13	6.14	4.07	43.99	4.75
	CO14 × KC2	4.51	2.44	5.8	4.26	54.06	5.51
	TCH1828 × KC2	4.14	2.48	5.54	4.28	59.91	5.84
Seed Cotton Yield Per Plant (g)	MCU5 × KC3	903.56	886.36	35.16	34.82	98.1	60.7
	CO14 × KC3	307.88	291.68	25.69	25.01	94.74	42.84
	CO14 × KC2	410.58	395.62	27.9	27.38	96.36	47.31
	TCH1828 × KC2	306.64	291.16	38.37	37.39	94.95	64.12
Traits	Crosses	Variance		PCV	GCV	h ² (bs)	GAM
		σ^2_p	σ^2_g				
Upper Half Mean Length (mm)	MCU5 × KC3	3.4	1.78	6.08	4.4	52.47	8.81
	CO14 × KC3	7.59	6.65	9.73	9.11	87.57	15
	CO14 × KC2	2.14	1.57	5.43	4.65	73.43	7.02
	TCH1828 × KC2	5.94	5.44	8.69	8.32	91.66	14.03
Elongation Percent (%)	MCU5 × KC3	0.07	0.05	5.88	0.79	69.67	35.68
	CO14 × KC3	0.01	0.01	1.73	1.6	85.46	2.6
	CO14 × KC2	0.01	0	1.73	1.04	36.45	1.11
	TCH1828 × KC2	0.28	0.27	8.99	8.83	96.46	15.26
Micronaire Value (µg/inch)	MCU5 × KC3	0.29	0.04	13.46	4.82	12.81	3.04
	CO14 × KC3	0.31	0.11	13.96	8.33	35.62	8.75
	CO14 × KC2	0.29	0.09	13.83	7.79	31.75	7.73
	TCH1828 × KC2	0.3	0.06	13.08	5.67	18.78	4.32

The same trait exhibited moderate GAM for the cross CO 14 x KC 2 (10.78 %) ; low GAM for the cross CO 14 x KC 3 (3.41%) and TCH 1828 x KC 2 (9.65%). High PCV value was observed in all crosses for the trait number of sympodial branches per plant similarly as reported by Rathinavel *et al.* (2017) [8]. The cross MCU 5 x KC 3 exhibited high GCV (20.96%), heritability (66.38%) and GAM (30.06%) for

the trait, number of sympodial branches per plant. Similar results for the same trait with high heritability and high GAM was reported by Khokhar *et al.* (2017) [9]. The crosses CO14 x KC3 and CO14 x KC 2 have moderate GCV, heritability and GAM values for the sympodial branches per plant. The same trait showed low GCV (6.13%), heritability (8.91%) and GAM (3.22%) for the cross TCH 1828 x KC2.

High PCV (27.47%), GCV (24.53%), heritability (79.73%) and GAM (38.55%) was observed for the trait number of bolls per plant only in the cross MCU 5 x KC 3. High heritability and high GAM for the same trait was reported by Khokhar *et al.* (2017). The cross CO 14 x KC 3 exhibited moderate PCV (19.95%), GCV (14.38%), heritability (51.92%) and GAM (18.23%) for the same trait. The cross CO 14 x KC 2 revealed moderate PCV value (18.12%) for the trait number of bolls per plant, low GCV (6.87%), low heritability (14.35%) and low GAM (4.58%). TCH 1828 x KC 2 had high PCV (28.81%), moderate GCV (15.46%), low GAM (14.60%) and low heritability (28.80%) for number of bolls per plant. Boll weight trait was found to have moderate GCV and PCV values and high heritability for all the crosses except MCU 5 x KC 3. Similar result for boll weight with moderate PCV was observed by Srinivas *et al.* (2014) [10]. The cross MCU 5 x KC 3 had moderate PCV (11.20%), low GCV (7.38%), moderate heritability (43.37%) and low GAM (8.55%) for the trait boll weight. Lint index contributed moderate GCV (15.20%, 16.09%), moderate PCV (13.26%, 14.81%), high heritability (74.31%, 84.73%) and high GAM (20.35%, 23.99%) in the crosses MCU 5 x KC 3 and CO 14 x KC 3 respectively.

The crosses CO 14 x KC3 and x CO 14 x KC 2 exhibited moderate PCV, heritability, low GCV for lint index. Except the cross MCU 5 x KC 3, which all other crosses exhibited moderate heritability for the trait ginning outturn. All crosses showed low PCV, GCV and GAM for ginning outturn. Similar results of low PCV, GCV for ginning outturn was reported Pujer *et al.* (2014) [11] by indicating that the trait was highly influenced by environmental factors. All the crosses under study have high GCV, PCV, heritability and GAM for the trait seed cotton yield per plant. Similar results for seed cotton yield per plant was reported by Hampannavar *et al.* (2020) [12] and Jarwar *et al.* (2018) [13]. Similar results for seed cotton yield per plant with high heritability and high GAM was reported by Pujer *et al.* (2014) and Khan *et al.* (2015) [14]. They suggested that improvement of these traits could be made through direct phenotypic selection. Similar results of high PCV, GCV values for seed cotton yield were reported by Rathinavel *et al.* (2017) and Joshi *et al.* (2018) [15]. High heritability for seed cotton yield was also reported by Khan *et al.* (2010) [16], Ahmad *et al.* (2011)[17]. All the crosses had low PCV, GCV values for upper half mean length as reported by Khokhar *et al.* (2017) and elongation percent which depicts that these traits were greatly influenced by environment. The crosses CO 14 x KC 3 and TCH 1828 x KC 2 had high heritability (87.57%, 91.66%) and moderate GAM (15%, 14.03%) while the crosses MCU 5 x KC 3 and CO 14 x KC 2 had low GAM with moderate heritability and high heritability for upper half mean length respectively. The trait elongation length had high heritability (69.67) and high GAM (35.68%) for the cross MCU 5 x KC 3. The same trait had low PCV and GCV for all the crosses taken under study as reported by Srinivas *et al.* (2014). The same trait exhibited high heritability (85.46%) with low GAM (2.60%) in the cross CO14 x KC 3, this character was under the control of non additive gene action and heterosis breeding may be used to improve the character because of its high heritability and low genetic advance as a percent of mean as suggested by Srinivas *et al.* (2014) and Pujer *et al.* (2014). Elongation length was found to be moderate heritability (36.45%) with low GAM (1.11%) in the cross CO 14 x KC 2 and high heritability (96.46%) with moderate GAM (15.26%) in the cross TCH 1828 x KC 2. The trait micronaire value exhibited moderate PCV, low GCV and low GAM values in all four crosses. The same trait had low heritability in the cross MCU 5 XKC 3 (12.81%) and TCH 1828 x KC 2 (18.78%) and moderate heritability in the cross CO 14 x KC 3 (35.62%) and CO 14 x KC 2 (31.75%). All quality traits showed low PCV and GCV except micronaire value same as reported by Hampannavar *et al.* (2020).

For majority of the characteristics, PCV and GCV had a high level of agreement, indicating that the observed variance might be mostly genetic as reported by Kumar *et al.* (2019) [18], Khan *et al.* (2015). Environmental influences have a lesser overall impact as reported by Baloch *et al.* (2015) [19]. This demonstrates the consistency with which phenotypic performance is used to make selections. High heritability along with high genetic advance as percent of mean might be viewed as positive qualities that indicate additive gene activity and as a result, simple selection method is effective for improvement of such traits as reported by Srinivas *et al.* (2014), which was observed in all crosses for the trait seed cotton yield per plant. For seed cotton yield associated and fibre quality parameters,

moderate to high GCV, PCV, heritability, and genetic advance percent of mean values were found, indicating that these qualities could be passed to the progeny when hybridization was undertaken and phenotypic based selection was effective as suggested by Srinivas *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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Study area / Sample Collection: Cotton (*Gossypium hirsutum* L.)

Cultivar / Variety / Breed name: Department of Cotton, Tamil Nadu Agricultural University, Coimbatore, 641003, Tamil Nadu, India

Conflict of Interest: None declared

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.

Ethical Committee Approval Number: Nil

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