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Research Article

Genetic variability, correlation and path analysis of upland cotton (*Gossypium hirsutum* L.) germplasm for seed cotton yield

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Abstract

One hundred upland cotton germplasm accessions were evaluated for eight traits to evaluate the *per se* performance, genetic variability, heritability, genetic advance as a per cent of mean, correlation and path analysis. The estimation of variability indicated that the number of monopodia per plant had high GCV and PCV. High heritability along with high GAM was found in plant height, internode length, the number of monopodia per plant, the number of sympodia per plant, the number of bolls per plant and seed cotton yield per plant which suggested that additive gene activity had a significant influence in the inheritance of these traits. Correlation analysis showed that the number of sympodia per plant, the number of bolls per plant and boll weight have a significant high positive correlation on the seed cotton yield. Path analysis showed that the number of bolls per plant and boll weight had the highest positive direct effect on seed cotton yield per plant.

Keywords: Cotton, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, genetic advance, correlation, path analysis.

INTRODUCTION

Cotton is the world's most important fibre producing crop and is referred to as the "King of Fibre Crops" or "White Gold". It serves as the main raw material for the textile industry, accounting for 60 - 70% of the Indian textile industry. It contributes significantly to the Indian economy in terms of income and foreign exchange. It offers a variety of useful products and is a vital agricultural product that supports the livelihoods of millions of farmers in both developed and developing nations (Qaim *et al*., 2006). Globally, it is cultivated in about 33 million hectares in which India alone shares about 37% of the world's cultivated area (12.35 million hectares) accounting for 22% of the world's cotton production (5.79 million tonnes). Despite having the largest cotton growing area, India's productivity (469 kg/ha) remains lower than the global average (787 kg/ha) (ICAC, 2022). Therefore, in order to raise the production of seed cotton, it is necessary to enhance high-yielding and high-quality cotton varieties (Balci *et al*., 2020). One strategy is genetic improvement through the use of germplasm resources and the development of prospective cultivars (Rathinavel, 2019).

Germplasm is a basic material for any breeding programme, which serves as vital source material as it provides scope for the development of genetic variability (Pujer *et al.,* 2014). In order to determine the genotype's true potential, studies on heritability, variability and genetic advance should be done and it serves as the foundation for successful selection

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(Ahmad *et al.,* 2008; Batool *et al.,* 2010; Khan *et al*., 2010). Knowledge on the genotypic, phenotypic and environment variability measured in terms of their coefficient of variation is critical to the breeding programme for establishing successful selection (Gnanasekaran *et al.,* 2018). However, it does not provide a precise estimate of the overall heritable variation. Magadum *et al.* (2012) suggested that heritability accompanied by the estimation of genetic advance and genetic advance over a mean (GAM) may be used to measure the degree of heritable variation and for the effective selection of genotypes. According to Johnson *et al.* (1955) heritability estimations and GAM provide a comparatively better image of the degree of advancement that may be anticipated through selection. Furthermore, understanding how the traits are associated is a key factor in determining how effective selection is in any breeding effort.

Keeping the above facts into consideration, a study was conducted to determine the real genetic potential value of the genotypes. Such information may be useful in creating an effective selection programme for creating novel cotton genotypes with increased yield and the traits that contribute to it.

MATERIALS AND METHODS

The present experiment was conducted at the Department of Cotton, Tamil Nadu Agricultural University, Coimbatore. One hundred upland cotton germplasm along with five checks (KC3, MCU 5, SVPR 6, CO 14 and CO 17) were raised in Augmented Block Design during the summer, 2022. The recommended agronomic practices were followed throughout the whole study. The observations were recorded on five selected plants in each entry for eight characters *viz*., days to 50% flowering (DFF), internode length (cm) (IL), plant height (cm) (PH), the number of monopodia per plant (NMP/P), the number of sympodia per plant (NSP/P), the number of bolls per plant (BN/P), boll weight (g) (BW) and seed cotton yield per plant (g) (SCY/P).

The mean for each trait under study trait was worked out and was further subjected to analysis of variance (ANOVA). The phenotypic and genotypic coefficient of variation was determined by the formula given by Burton (1952). The phenotypic and genotypic coefficients of variation were classified as low (10%), moderate (10-20%) and high (20%) as described by Sivasubramanian and Madhavamenon (1973). Heritability (h^2) in a broad sense was worked out by the method given by Lush (1949). According to Johnson *et al.* (1955), heritability values were classified as low (30%), moderate (30-60%) and high (> 60%). Using the approach described by Johnson *et al*. (1955) the genetic advance was computed. The genetic advance is frequently expressed as a percentage of the mean and according to Johnson *et al*. (1955) the range of genetic advance as a percentage of the mean was classified as low (10%), moderate (10 - 20%) and high (> 20%). Utilizing the technique outlined by Singh and Chaudhary (1979), correlation coefficients for each attribute under study were examined. The simple correlation was used to create a path coefficient analysis to determine the direct and indirect impacts of the yield components on seed cotton yield as suggested by Dewey and Lu (1959).

RESULTS AND DISCUSSION

Analysis of variance (ANOVA) showed significant for all the traits under study suggesting the existence of an adequate amount of variability in the research material (**Table 1**). Based on the mean performance, the genotypes KK 1543, Stardel, 5\44, Stone Ville, D4, D16, RS 277, RS 267, FSB 3, TCH 1742, RU 4\4, AR 9, Acala-1577-D, B 50, KC 2 and Pelimond Cleveland showed high yield and a high number of bolls per plant and thus it can be used as a potential donor for breeding programs in the future (**Table 2**). Among the different genotypes, Acala-1577-D (4.67 g boll weight), D 16 (20.3 sympodia per plant) and Stardel (23.67 bolls per plant) showed the highest performance for a specific character. Hence, these genotypes can be used in the crop improvement programme to enhance the particular characteristics.

The number of monopodia per plant recorded high PCV and GCV (48.40 and 42.46) (**Table 3**). Similar results were also reported by Joshi *et al.* (2018), Gnanasekaran *et al.* (2018) and Anjani *et al.* (2020). PCV and GCV were

Table 1. Range and mean of different traits

Traits	Minimum	Maximum	Mean
Days to 50% flowering	50.00	65.00	54.42
Plant height (cm)	56.00	103.00	81.88
Internode length (cm)	3.00	6.33	4.25
Number of monopodia per plant	0.33	2.33	1.23
Number of sympodia per plant	9.67	20.30	15.11
Number of bolls per plant	11.67	23.67	17.28
Boll weight (g)	2.60	4.67	3.55
Seed cotton yield per plant (g)	44.25	92.22	64.88

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Table 2. ANOVA for the different traits

Traits	Mean sum of squares	
	Genotypes	Error
Days to 50% flowering	8.26**	1.32
Plant height	70.04**	1.38
Internode length	0.36**	0.11
Number of monopodia per plant	0.35**	0.08
Number of sympodia per plant	4.88**	0.53
Number of bolls per plant	6.17**	0.67
Boll weight	0.14**	0.05
Seed cotton yield per plant	108.28**	13.05

** significant at 1 % level

Table 3. Genetic parameters for different traits

Traits	PCV (%)	GCV (%)	h^2 (%)	GA	GAM (%)
Days to 50% flowering	5.28	4.84	84.01	4.97	9.14
Plant height	10.22	10.12	98.03	16.90	20.64
Internode length	14.20	11.82	69.23	0.86	20.25
Number of Monopodia per plant	48.40	42.46	76.98	0.94	76.75
Number of sympodia per plant	14.62	13.80	89.15	4.06	26.85
Number of bolls per plant	14.38	13.57	89.07	4.56	26.38
Boll weight	10.59	8.42	63.27	0.49	13.80
Seed cotton yield per plant	16.04	15.04	87.95	18.85	29.06

moderate for plant height (10.22 and 10.12), internode length (14.20 and 11.82), the number of sympodia per plant (14.62 and 13.80), the number of bolls per plant (14.38 and 13.57) and seed cotton yield per plant (16.04 and 15.04). Aarthi *et al.* (2018), Jarwar *et al.* (2018), Naik *et al.* (2019) and Shruti *et al.* (2019) also reported a moderate number of sympodia per plant, the number of bolls per plant, the number of sympodia per plant and seed cotton yield per plant. Boll weight showed moderate PCV and low GCV (10.59 and 8.42) which is in agreement with Naik *et al.* (2019) and Sowmya *et al.* (2021). Days to 50% flowering showed low PCV and GCV (5.28 and 4.84, respectively) which showed that the studied material had this trait in low levels of variability. Jarwar *et al.* (2018) and Anjani *et al.* (2020) also reported low PCV and GCV for days to 50% flowering.

Estimation of heritability showed high for all the traits under study *viz.,* days to 50% flowering, plant height, internode length, the number of monopodia per plant, the number of sympodia per plant, the number of bolls per plant, boll weight and single plant yield with plant height showing the highest heritability (98%). This indicates that the selection and improvement for these characters would be more effective in upcoming breeding programmes given that the genetic variance is primarily caused by the additive gene action. Gnanasekaran *et al.* (2018), reported high heritability for days to 50% flowering, plant height, seed cotton yield. Elango *et al.* (2012), Aarthi *et al.* (2018), Komala *et al.* (2018) and Naik *et al.* (2019) also reported high heritability for the number of monopodia, number of sympodia, boll weight, the number of bolls per plant and seed cotton yield. Similar results were also reported by Shruti *et al.* (2019) and Sowmya *et al.* (2021).

Estimation of heritability along with genetic advance is often more effective in projecting the gain under selection (Johnson *et al.,* 1955). In the present study, high heritability along with high genetic advance as a percentage of mean was found in plant height, internode length, the number of monopodia per plant, the number of sympodia per plant, number of bolls per plant and seed cotton yield per plant. This showed that the environment has less of an impact, heredity is most likely caused by additive genetic effects, and selection may be beneficial. Similar results were also found with those of Reddy *et al.* (2015), Nikhil *et al.* (2018), Kumar *et al.* (2019) and Shruti *et al.* (2019). Boll weight showed high heritability but moderate GAM, indicating that it is likely governed by additive gene action and such a trait might be rewarding for selection. The same results were also reported by Naik *et al.* (2019) and Sowmya *et al.* (2021). Days to 50% flowering showed high heritability, whereas low in genetic advance

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indicating that the trait is controlled by non-additive gene action and such trait might not be rewarding for selection. This result is in concordance with Aarthi *et al.* (2018), Gnanasekaran *et al.* (2018) and Jarwar *et al.* (2018).

Correlation studies (**Table 4**) revealed that all the traits under study are positively associated to seed cotton yield. Among the studied traits, the number of sympodia per plant (r = 0.45**), the number of bolls per plant (r = 0.81**) and boll weight (r = 0.61**) recorded significant a high positive correlation on the seed cotton yield. Therefore, selection for these characters will aid in choosing genotypes with better seed cotton output per plant. Such features were also observed by Gnanasekaran *et al.* (2018), Nawaz *et al.* (2019) and Chapepa *et al.* (2020). Internode length (r = 0.025) and the number of monopodia per plant (r = 0.078) showed non-significant positive correlation to seed cotton yield. The same outcomes on the monopodia were also attained by Nawaz *et al.* (2019), Nikhil *et al.* (2018) and Rai and Sangwan (2020).

Studies on path analysis revealing the direct and indirect effects on the seed cotton yield are displayed in **Table 5**. The path analysis revealed that plant height (0.058), the number of monopodia per plant (0.027), the number of bolls per plant (0.649) and boll weight (0.299) have high positive direct effects on the seed cotton yield, whereas days to 50% flowering (0.004) displayed negligible positive direct effect on seed cotton yield. Therefore, direct selection for traits *viz.,* the number of bolls per plant and boll weight is advised to increase yield. Rauf *et al.* (2004) also recorded similar observations. Nawaz *et al.* (2019) observed positive direct effects of plant height, the number of bolls per plant and boll weight but a negative direct effect of the number of monopodia per plant on seed cotton yield. In this study, boll weight (0.307) showed high positive indirect effects on seed cotton yield via the number of bolls per plant which is in agreement with Reddy *et al.* (2015) and Nikhil *et al.* (2018), however, it is conflicting with the results of Rauf *et al.* (2004). The number of sympodia per plant displayed negative direct effects on seed cotton

Table 4. Correlation between seed cotton yield and its component traits

	DFF	PH	IL	NMP/P	NSP/P	BN/P	BW	SCY/P
DFF	1.000**	0.155	-0.117	0.104	0.010	0.178	0.205*	0.204*
PH		1.000**	0.124	0.021	0.277**	0.237*	0.142	0.251**
IL			1.000**	0.015	0.160	0.079	0.050	0.025
NMP/P				1.000**	0.333**	0.066	0.049	0.078
NSP/P					1.000**	0.602**	0.158	0.450**
BN/P						1.000**	0.448**	0.815**
BW							1.000**	0.610**
SCY/P								1.000**

* Significance at 5%; ** Significance at 1% level

DFF- Days to 50% flowering; IL- Internode length; PH- Plant height; NMP/P - Number of monopodia per plant; NSP/P- Number of sympodia per plant; BN/P- Number of bolls per plant; W- Boll weight; SCY/P- Seed cotton yield per plant

Table 5. Direct and indirect effects of various traits on seed cotton yield

	DFF	PH	IL	NMP/P	NSP/P	BN/P	BW	Correlation co-efficient for SCY/P
DFF	**0.004**	0.009	0.005	0.003	0.000	0.122	0.061	0.204
PH	0.001	**0.058**	-0.006	0.001	-0.008	0.162	0.043	0.251
IL	-0.001	0.007	**-0.046**	0.000	-0.004	0.054	0.015	0.025
NMP/P	0.000	0.001	-0.001	**0.027**	-0.009	0.045	0.015	0.078
NSP/P	0.000	0.016	-0.007	0.009	**-0.027**	0.412	0.047	0.450
BN/P	0.001	0.014	-0.004	0.002	-0.016	**0.649**	0.134	0.815
BW	0.001	0.008	-0.002	0.001	-0.004	0.307	**0.299**	0.610

Residual effect = 0.5057

DFF- Days to 50% flowering; IL- Internode length; PH- Plant height; NMP/P - Number of monopodia per plant; NSP/P- Number of sympodia per plant; BN/P- Number of bolls per plant; BW- Boll weight; SCY/P- Seed cotton yield per plant yield whereas it displayed high positive indirect effects on seed cotton yield via the number of bolls per plant. Rauf *et al.* (2004) also displayed the number of sympodia per plant to have high positive indirect effects on seed cotton yield *via* the number of bolls per plant.

In conclusion, the current experiment presents the study of the genetic parameters of upland cotton along with the direct and indirect effects of the various traits on the yield. It also highlighted that selection would be beneficial by accounting for the degree of variability heritability, and genetic advance as per cent of mean for the number of monopodia, the number of sympodia, the number of bolls per plant apart from seed cotton yield to develop high yielding cotton cultivars. Association analysis suggested that selection focussed on plant height, the number of sympodia per plant, the number of monopodia per plant, the number of bolls per plant and boll weight will help in crop improvement for increasing cotton yield.

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