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Full Length Research Article

GENETIC VARIABILITY HERITABILITY AND GENETIC ADVANCE STUDIES IN COTTON

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ABSTRACT

The experiment was carried out at college farm, college of Agriculture, Rajendranagar, Hyderabad, to determine genetic variability, heritability and genetic advance estimates in upland cotton. The analysis of variance involving a set of 11 genotypes for eleven characters viz., Days to 50 % flowering, Number of monopodia/plant, Number of sympodia/plant, Number of bolls/plant, Boll weight, Ginning percentage, 2.5 % span length, Uniformity ratio, Bundle strength, Micronaire value and Seed cotton vield/plant, revealed highly significant mean sum of squares for all the characters indicating greater diversity among the genotypes. The value of phenotypic coefficient of variation (PCV) is greater than genotypic coefficient of variation (GCV); it means that the apparent variation is not only due to genotypes but also due to influence of environment. High GCV and PCV were observed for number of monopodia per plant. The difference between the estimates of PCV and GCV were low for all the characters except number of monopodia per plant thereby indicating that lesser role played by the environment in the expression of these characters. The characters Number of bolls/plant, Bundle Strength, Ginning percentage, Boll Weight, 2.5 % span length, Seed cotton yield/plant and Days to 50 % flowering exhibited high estimates of heritability. High heritability coupled with high genetic advance as percent of mean was observed for Number of bolls/plant, Boll Weight and Seed cotton yield/plant.

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INTRODUCTION

Cotton (Gossypium species), is the world's most utilized natural textile fibre. It is also one of the most important cash crops of India, which accounts for 60% of total foreign exchange earnings through export of lint and value added cotton products. India is one of the important cotton growing countries in world and occupies an area of 110 lakh hectares, production of 325 lakh bales and productivity of 503 kg per hectare. Improving cotton fibre quality and lint yield remains challenging for cotton breeders. Many of the current high yielding, commercial upland cotton cultivars do not possess the fibre quality desired by the textile industry. One of the ways to improve fibre quality and cotton yield is to transfer genes into high yielding G.hirsutum cultivar from G.barbadense (Mc Carty et al., 2004). The success of any breeding programme depends on the spectrum of genetic variability present in the population. A wider spectrum of variability will enhance the chances of selecting a desired genotype. In the presence of high amount of genetic variability, knowledge on heritability and genetic advance

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Department of Genetics and Plant Breeding, PJTSAU, Rajendranagar, Hyderabad (500030) Telangana, India helps the breeder to exercise section on the desired characters to achieve the objective quickly. Therefore, for improvement of target trait in any crop, it is necessary to have full information on the variability, heritability and genetic advance (Burton, 1952 and Swarup and Chaugle, 1962). Keeping in view the importance of these aspects a study was conducted to ascertain the real potential value of the genotypes.

MATERIALS AND METHODS

The present investigation was carried out at college farm, college of Agriculture, Rajendranagar, Hyderabad. In the present study, genetic parameters were worked out for 11 genotypes (includes seven *Gossypium hirsutum* lines *viz.*, Narasimha, Galama, L 604, L 389, LK 861, CPD 420 and AKH 9331, four testers out of which two (2) are *G.barbadense viz.*, Suvin, Pima and the rest two (2) *viz.*, HAG 1055 and MCU 17) and 28 hybrids derived from 7 x 4; line x tester programme. The material was sown in Randomized Block Design replicated thrice. Parents and hybrids were sown in two rows with spacing of 90 x 60 cm for parents and 120 x 60 cm for hybrids.

Table 1. Analysis of variance (mean squares) for quality, yield and yield component characters in cotton

Source of variation	Degrees of	Days to 50 %	No. of mono-	No. of	No. of	Boll	Ginning	2.5 % span	Uniformity	Micro-naire	Bundle	SeedCotton
	freedom	flowering	podia/	sympodia/	Bolls/	weight	Percent-tage	length	ratio	value	strength	Yield/ plant (g)
			plant	plant	plant	(g)		(mm)			(g/tag)	
Replications	2	6.01	0.38	25.35**	58.78	1.58**	3.77	10.65**	0.57	0.14	6.86*	277.52
Treatments	38	17.79**	0.53**	18.90**	292.22^{**}	2.18**	23.66**	25.85**	10.48^{**}	0.72^{**}	18.11**	754.50**
Error	76	2.68	0.19	5.80	22.11	0.29	3.00	3.29	4.48	0.17	1.87	97.77

** Significant at 1 % level

* Significant at 5 % level

Table 2. Mean, range, genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance as per cent of mean for eleven characters in cotton

Character	Mean	Rang	e GCV	7 PCV	7 h ²	GA	GA in %	
		Min	Max				over mean	
Days to 50 % flowering	54.19	50.33	64.00	4.25	5.20	66.47	7.12	
Number of monopodia/plant	1.79	1.20	2.73	18.82	30.55	37.93	23.88	
Number of sympodia/plant	19.80	14.67	25.67	11.14	16.46	45.76	15.52	
Number of bolls/plant	43.41	27.07	63.47	21.68	24.20	80.25	40.01	
Boll weight	6.13	4.52	8.61	12.92	15.61	68.47	22.02	
Ginning percentage	32.15	25.29	37.16	8.18	9.76	70.20	14.11	
2.5 % span length	30.92	24.98	36.88	8.74	10.55	68.65	14.92	
Uniformity ratio	45.82	42.50	51.43	3.05	5.59	29.69	3.42	
Micronaire value	3.64	2.70	4.87	11.61	16.23	51.10	17.10	
Bundle strength	24.86	20.53	29.67	9.33	10.82	74.30	16.56	
Seed cotton yield/plant	113.65	83.8	146.63	12.82	15.57	67.83	21.75	

Fifty randomly selected plants in F_2 and five randomly selected plants from other generations from each plot in each replication were chosen and labeled for recording observations and the means were taken into consideration for statistical analysis. The data on fiber quality, yield and yield components were recorded. The genotypic and phenotypic coefficients of variation were calculated according to the formula given by Falconer (1981). Heritability (h²) in the broad sense was calculated according to the formula given by Allard (1960). From the heritability estimates the genetic advance was estimated by the following formula given by Burton (1952).

RESULTS AND DISCUSSION

The mean data on eleven characters *viz.*, days to 50 % flowering, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight, ginning percentage, 2.5 % span length, uniformity ratio, micronaire value, bundle strength and seed cotton yield per plant were collected and analyzed. The analysis of variance showed significant difference among the treatments (parents and crosses) for all the characters studied. The results of analysis of variance for eleven characters are presented in Table 1.





The results pertaining to genetic parameters viz., phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability (h_{bs}^2) and genetic advance as percent of mean (GAM) for all the twelve characters are furnished in Table 2 and Figure 1. The Highest magnitude of both PCV (24.20%) and GCV (21.68%) were observed for number of bolls per plant followed by number of monopodia per plant (30.55% - 18.82%) for High PCV and moderate GCV suggesting that these characters were under the influence of genetic control. The characters number of sympodia per plant (16.46%-11.14%), micronaire value (16.23%-11.61%), boll weight (15.61%-12.92%) and seed cotton yield per plant (15.57%-12.82%) recorded for moderate magnitudes of both PCV and GCV respectively. The traits ginning percentage (9.76%-8.18%), 2.5% span length (10.55%-8.74%) and uniformity ratio (5.59%-3.04%) recorded for low magnitudes of both PCV and GCV respectively. The trait bundle strength (10.82%-9.33%) recorded for low GCV and moderate magnitudes of PCV.

The results are in agreement with the findings of earlier workers for days to 50 % flowering by Sangeetha (1998), Narisireddy and Ratnakumari (2004); no of sympodia per plant by Rao and Reddy (2001) and Kale et al. (2006); no of bolls per plant by Murthy and Rao (1998), Sangeetha (1998), Preetha and Raveendran (2007) ; boll weight as reported earlier by Ahmad et al. (2003), Narisireddy and Ratnakumari (2004) and Preetha and Raveendran (2007); ginning percentage by Sangeetha (1998), Sankarapandian et al. (1998), Rao and Reddy (2001); 2.5 % span length by Ahmad et al. (2003); uniformity ratio by Preetha and Raveendran (2007); micronaire value by Kumar et al. (2000); bundle strength by Rajarathinam et al. (1993); seed cotton yield per plant by Narisireddy and Ratnakumari (2004), Kumari and Chamundeshwari (2005). Heritability estimates were high for the characters Number of bolls/plant, Bundle Strength, Ginning percentage, Boll Weight, 2.5 % span length, Seed cotton yield/plant and Days to 50 % flowering. This suggested the greater effectiveness of selection and improvement to be expected for these characters in future breeding programmes as the genetic variance is mostly due to the additive gene action. High heritability coupled with high genetic advance as percent of mean was observed for Number of bolls/plant, Boll Weight and Seed cotton yield/plant indicating the preponderance of additive gene action. Hence pedigree method

of breeding would be rewarding one to improve the traits under investigation. These findings are in agreement with the results reported by Kumari and Chamundeshwari (2005), Kale *et al.* (2006) and Preetha and Raveendran (2007) for seed cotton yield per plant, Narisireddy and Ratnakumari (2004) for boll weight,

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