



Genetic Variability in Upland Cotton (*Gossypium hirsutum* L.)

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ABSTRACT

The analysis of variance revealed significant differences for all the 15 characters studied indicating presence of sufficient variability among the 53 genotypes. The genetic parameters revealed that moderate to high variability was observed for number of monopodia per plant, seed index, number of bolls per plant, boll weight, seed cotton yield per plant and lint yield per plant. High heritability and high genetic advance as percent of mean was observed for number of monopodia per plant, boll weight, seed index, lint yield per plant and seed cotton yield per plant. Hence selection for these traits would be quite effective to improve the seed cotton yield in upland cotton.

Key words: *Genetic advance, Heritability, Upland cotton, Variability.*

Cotton (*Gossypium* spp.) is one of the most important commercial crops and is popularly known as “white gold”. It is a precious gift of nature to mankind contributed by the genus *Gossypium* to clothe the people all over the world. It is primarily used in textile industries providing highest employment during production, processing, spinning, weaving and marketing throughout the world. It also occupies the place of pride in Indian agriculture and economy by earning valuable foreign exchange. In India, cotton is being grown in an area of 126.55 lakh ha with an annual production of 400 lakh bales (1 bale = 170 kg) with a productivity of 537 kg lint ha⁻¹ (AICCIP Annual Report, 2014-15). Breeding programs continue to develop new cotton varieties to meet the requirements of both producers and consumers. High fiber quality is important for the textile industry since fiber quality directly affects processing performance, productivity, yarn quality, and the marketing of textile properties. New spinning and weaving technologies in the textile industry mandate that plant breeders and geneticists develop hybrids of cotton with improved fiber quality, especially fiber strength, fiber length, and uniformity length without sacrificing yield potential. Development of an effective breeding programme depends on the existence of genetic variability for various economic characters in the gene pool. Study of variability, heritability and genetic advance in the germplasm will help to ascertain the real potential

value of the genotype. Hence, the present investigation was carried out during *kharif*, 2013-14 at Regional Agricultural Research Station, Lam Farm with an aim to know the variability among the cotton genotypes.

MATERIAL AND METHODS

The experimental material for this study consisted of 40 intra-specific crosses of cotton along with their 13 parents. The crosses were generated by crossing 8 lines with 5 testers in a line × tester fashion (Kempthorne, 1957) during *kharif*, 2012-2013 at Regional Agricultural Research Station, Lam Farm, Guntur. The evaluation of these hybrids has been undertaken during *kharif*, 2013-2014. Observations were recorded on days to 50% flowering, plant height (cm), number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight (g), seed index (g), lint index (g), ginning out-turn (%), 2.5% span length (mm), micronaire value (10⁻⁶g/inch), bundle strength (g/tex), uniformity ratio, seed cotton yield per plant (g) and lint yield per plant (g) from five randomly selected plants which were subjected to the statistical analysis. The data were analyzed by using ANOVA (Panse and Sukhatme, 1978) and the genetic parameters such as PCV and GCV were calculated by the formula given by Burton (1952), heritability broad sense (h²) by Allard (1960) and genetic advance in percent of mean (genetic gain) were work out as suggested by Johnson *et al.* (1955).

Table 1. Analysis of variance for seed cotton yield and yield components of 40 crosses and 13 parents of cotton (*Gossypium hirsutum* L.).

Source	d.f.	Days to 50% flowering	Plant height (cm)	Number of monopodia per plant	Number of sympodia per plant	Number of bolls per plant	Boll weight (g)	Seed index (g)	Lint index (g)
Mean squares									
Replications	2	1.376	67.684	0.076	4.342	28.574	0.022	0.009	0.098
Treatments	52	46.293**	539.923**	1.119**	9.033**	145.648**	0.775**	24.605**	0.785**
Error	104	4.024	51.354	0.050	1.951	35.826	0.029	0.491	0.117

Source	d.f.	Ginning out-turn %	2.5% span length (mm)	Micronaire value (10 ⁻⁶ g/inch)	Bundle strength (g/tex)	Seed cotton yield per plant (g)	Uniformity ratio	Lint yield per plant (g)
Mean squares								
Replications	2	0.459	0.254	0.005	0.527	512.668	2.668	80.363
Treatments	52	4.407**	8.050**	0.258**	1.546**	4311.464**	2.677**	597.775**
Error	104	0.938	0.231	0.041	0.176	583.981	0.940	72.301

** Significant at 1% level

RESULTS AND DISCUSSION

Analysis of variance recently revealed significant differences among the genotypes for all the characters, indicating presence of sufficient amount of variability among the varieties (Table 1). Thus, there is ample scope for selection of different quantitative and qualitative characters for cotton improvement. Variability, heritability and genetic advance as per cent mean for 15 characters were presented in Table 2. The estimates of genetic variability revealed that phenotypic coefficient of variation (PCV) ranged from 2.62 (uniformity ratio) to 40.73 (number of monopodia per plant) and the corresponding values for genotypic coefficient of variation (GCV) were 1.62 and 38.15, respectively. Number of monopodia per plant showed highest coefficients for both phenotypic and genotypic variation. Similar results were reported by Neelima *et al.* (2008) and Rajamani *et al.* (2015). Seed index also showed higher values of coefficients of variation. Number of bolls per plant, boll weight, seed cotton yield per plant and lint yield per plant showed moderate estimates of phenotypic and genotypic coefficient of variation indicating variability among the material studied depicting the possibility of improvement in the yield by further selection in segregating generations. These results are in agreement with the findings of Rajamani *et al.* (2015). Low values of phenotypic and genotypic coefficient of variation were observed for days to 50% flowering, ginning out-turn, 2.5% span length, micronaire value, bundle strength and uniformity ratio indicating narrow range of variability for these traits, thereby restricting the scope for selection. These results are in

agreement with the findings of Srinivasulu *et al.* (2010). The estimates of heritability and genetic advance can be utilized for the prediction of inheritance of traits, which indicates the genetic improvement that would result from the selection of best individuals. High heritability in conjunction with high genetic advance as per cent of mean were recorded in case of number of monopodia per plant (87.70 and 73.59%), boll weight (89.51 and 20.35%), seed index (94.24 and 64.57%), seed cotton yield per plant (68.03 and 25.89%) and lint yield per plant (70.78 and 28.50%) indicating the preponderance of additive gene action in the inheritance of these traits and offers the scope for further improvement through simple selection procedures. High heritability coupled with low genetic advance as per cent of mean was observed for bundle strength (72.11 and 5.25%) indicating the role of non-additive gene action and further improvement of these traits would be possible through cyclic hybridization, diallel selective mating and biparental mating.

Present investigation suggested the presence of adequate variability in the material studied. Moderate to high GCV, PCV coupled with high heritability and moderate to high genetic advance as percent of mean were observed for number of monopodia per plant, boll weight, seed index, seed cotton yield per plant and lint yield per plant suggesting the predominance of additive type of gene action in controlling these traits. These results indicating the operation of additive gene action in the inheritance of these traits and improvement of these characters is possible through simple selection. High heritability coupled

Table 2. Estimates of variability, heritability (broad sense) and genetic advance as per cent of mean for Seed cotton yield per plant and its components in cotton (*Gossypium hirsutum* L.).

S. No.	Character	Mean	Range		Coefficient of variation		Heritability (broad sense) (%)	Genetic advance as per cent of mean
			Minimum	Maximum	PCV (%)	GCV (%)		
1	Days to 50% flowering	61.03	53.67	69.33	6.97	6.15	77.78	11.17
2	Plant height (cm)	129.44	99.20	157.23	11.31	9.86	76.03	17.71
3	Number of monopodia per plant	1.56	0.30	2.66	40.73	38.15	87.70	73.59
4	Number of sympodia per plant	17.11	14.63	20.87	12.13	8.98	54.75	13.69
5	Number of bolls per plant	54.67	37.67	71.33	15.57	11.07	50.54	16.21
6	Boll weight (g)	4.77	3.60	5.77	11.04	10.44	89.51	20.35
7	Seed index (g)	8.78	3.60	12.00	33.26	32.29	94.24	64.57
8	Lint index (g)	5.55	4.39	6.90	10.51	8.50	65.48	14.17
9	Ginning out-turn (%)	34.53	30.57	36.17	4.20	3.11	55.20	4.76
10	2.5% span length (mm)	30.64	26.30	33.43	5.50	5.27	91.87	10.40
11	Micronaire value (10^{-6} g/inch)	4.06	3.40	4.63	8.30	6.61	63.42	10.84
12	Bundle strength (g/tex)	22.51	20.47	23.87	3.53	3.00	72.11	5.25
13	Uniformity ratio	47.02	45.00	49.00	2.62	1.62	38.11	2.06
14	Seed cotton yield per plant (g)	231.35	154.67	334.67	18.47	15.24	68.03	25.89
15	Lint yield per plant (g)	80.48	48.74	119.19	19.55	16.44	70.78	28.50

PCV = Phenotypic coefficient of variation

with low genetic advance as per cent of mean was observed for bundle strength indicating the role of non-additive gene action and further improvement of these traits would be possible through cyclic hybridization, diallel selective mating and biparental mating.

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GCV = Genotypic coefficient of variation

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