



## Genetic Variability, Heritability and Genetic Advance for Yield and Yield Contributing characters in inter-specific Cotton Hybrids (*G. hirsutum* L. × *G. barbadense* L.)

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### ABSTRACT

An investigation was carried out to assess the variability, heritability and genetic advance for sixteen characters *viz.*, days to 50% flowering, plant height (cm), number of monopodia plant<sup>-1</sup>, number of sympodia plant<sup>-1</sup>, number of bolls plant<sup>-1</sup>, boll weight (g), seed index (g), lint index (g), ginning out-turn (%), 2.5% span length (mm), micronaire value (10<sup>-6</sup> g/inch), bundle strength (g/tex), uniformity ratio, fibre elongation (%), lint yield plant<sup>-1</sup> (g) and seed cotton yield plant<sup>-1</sup> (g) in 40 hybrids and 13 parents. The results revealed that high PCV and GCV were observed for the characters number of monopodia per plant, lint yield per plant and seed cotton yield per plant. High heritability accompanied with high genetic advance was shown by the characters *viz.*, lint yield per plant and seed cotton yield per plant and micronaire value (10<sup>-6</sup> g/inch) indicating the preponderance of additive gene action which may be exploited through simple selection procedures.

**Key words :** Cotton, Genetic advance, Heritability, Variability.

The success of any breeding programme depends upon the quantum of genetic variability present in the population. Wider range of genetic variability helps in selecting desired genotypes. In addition to the genetic variability, knowledge on heritability and genetic advance helps the breeder to employ the suitable breeding strategy. Therefore, it is necessary to have knowledge of genetic variability, heritability and genetic advance present in the available genetic material.

### MATERIAL AND METHODS

Eight lines and five testers were crossed adopting Line x Tester mating scheme during *kharif* 2011 to obtain forty hybrids. These forty hybrids along with their parents were evaluated during *kharif* 2012-2013 at Regional Agricultural Research Station, Lam, Guntur in a Randomized Block Design with three replications. Observations were recorded on five randomly selected plants from each 40 hybrids and 13 parents per replication. The data were recorded on 16 economically important characters *viz.*, 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<sup>-6</sup>g/inch), bundle strength (g/tex), uniformity ratio, fibre elongation (%), lint yield per plant (g) and seed cotton yield per plant (g). The fibre quality characters were analyzed at CIRCOT, Regional Unit, Lam, Guntur. The mean values of all the biometrical traits were taken for statistical analysis. From the mean values variability parameters were computed using standard statistical procedures as per Johnson *et al.* (1955).

### RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among all the 40 hybrids and 13 parents under study for all the characters, indicating a high degree of variability in the material (Table 1). In the present study, the variation among genotypes was estimated as coefficient of variation (Table 2). The genotypic coefficient of variance (GCV) was slightly higher in magnitude than phenotypic coefficient of variance (PCV) for all the characters studied indicating that the material used in present study possessed sufficient variation which gives ample scope for improvement through selection procedures. Highest PCV and GCV (31.91 and 34.90) were exhibited by number of

Table 1. Analysis of variance for seed cotton yield and yield components in inter-specific cotton hybrids

Source	d.f.	Days to 50% flowering	Plant height (cm)	No. of monopodia/plant	No. of sympodia/plant	No. of bolls/plant	Boll weight (g)	Seed index (g)	Lint index (g)
Replication	2	0.79	18.59	0.008	0.75	69.80	0.001	0.06	0.11
Treatments	53	67.20**	754.93**	0.83**	15.47**	317.91**	0.98**	4.59**	1.16**
Error	106	1.73	47.10	0.051	2.03	26.18	0.03	0.42	0.17
Mean squares									
Source	d.f.	Ginning out-turn %	2.5% span length (mm)	Micronaire (10 <sup>-6</sup> g/inch)	Bundle strength (g/tex)	Uniformity ratio	Fibre elongation (%)	Lint yield/plant (g)	Seed yield/plant (g)
Replication	2	1.12	0.05	0.03	0.41	0.08	0.01	10.17	215.02
Treatments	53	6.10**	29.19**	0.44**	10.49**	6.33**	0.22**	805.62**	6807.00**
Error	106	0.90	0.39	0.02	0.58	0.53	0.004	39.68	350.81
Mean squares									

\*\* Significant at 1% level

Table 2. Estimates of variability, heritability ( $\%_{(ns)}^2$ ) and genetic advance as per cent of mean for seed cotton yield per plant and its component characters in inter-specific cotton hybrids.

Sl.	Character	Mean	Range		Coefficient of variation		Heritability (narrow sense) (%)	Genetic advance as percent of mean
			Minimum	Maximum	PCV(%)	GCV(%)		
1	Plant height (cm)	137.80	108.63	173.20	11.14	12.20	27.41	12.54
2	Days to 50 % Flowering	64.00	55.00	73.66	7.29	7.58	78.79	5.47
3	Number of monopodia/plant	1.60	0.60	2.73	31.91	34.90	31.32	23.05
4	Number of sympodia/plant	17.73	13.26	23.66	11.93	14.39	19.61	5.36
5	Number of bolls/plant	55.33	30.86	82.10	17.82	20.07	54.17	22.63
6	Boll weight (g)	3.55	2.46	4.70	15.87	16.63	45.69	13.24
7	Seed index (g)	9.38	6.80	12.56	12.56	14.33	30.83	9.71
8	Lint index (g)	4.55	3.06	6.03	12.59	15.61	31.21	10.49
9	Ginning out turn (%)	32.65	29.79	36.10	4.03	4.97	24.08	1.45
10	2.5% span length (mm)	32.10	27.20	37.20	9.64	9.84	86.38	19.94
11	Micronaire value ( $10^{-6}$ g/inch)	3.54	2.60	4.21	10.61	11.33	84.56	21.56
12	Bundle strength (g/tex)	25.26	21.79	30.56	7.19	7.80	65.52	8.96
13	Uniformity ratio	47.58	45.00	50.33	2.92	3.30	35.55	2.52
14	Fibre elongation (%)	5.83	5.26	6.26	4.67	4.79	16.51	1.75
15	Seed cotton yield/plant (g)	163.40	64.40	275.40	28.38	30.60	63.17	39.89
16	Lint yield/plant (g)	53.52	20.74	91.64	29.85	32.09	60.15	38.02

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

monopodia per plant, whereas lowest PCV and GCV (2.92 and 3.30) were recorded by uniformity ratio. These results were in accordance with the findings of Kishore *et al.* (2011) and Venkatesh (2012). High PCV and GCV were recorded for number of monopodia per plant, lint yield per plant and seed cotton yield per plant. Moderate PCV and GCV were recorded for plant height, number of sympodia per plant, boll weight, seed index, lint index and micronaire. While days to 50% flowering, ginning out turn, 2.5% span length, bundle strength and fibre elongation exhibited low PCV and GCV.

Heritability estimates were high for lint yield per plant, seed cotton yield per plant, days to 50% flowering, seed index, micronaire, and bundle strength. Heritability estimates along with genetic advance are more helpful in predicting the gain under selection than heritability estimates alone. The estimates of heritability and genetic advance as per cent of mean were high for lint yield per plant, seed cotton yield per plant and micronaire indicating that these characters were less influenced by environment and governed by additive gene action which may be exploited through simple selection procedures. These findings were in agreement with Iqbal *et al.* (2011), Venkatesh (2012) and Rao and Gopinath (2013).

High heritability coupled with low to moderate genetic advance as per cent of mean was observed for days to 50% flowering, 2.5% span length and bundle strength indicating the role of both additive and non-additive gene actions in the inheritance of these traits and improvement can be brought about using breeding methods like diallel selective mating or bi-parental mating followed by selection in advanced generation. Whereas low heritability and low genetic advance as percent of

mean were recorded in case of number of sympodia per plant, ginning out-turn and fibre elongation indicating preponderance of non additive gene action with little influence of environment in its inheritance. The traits controlled by non-additive gene action can be improved by selection and intermating among selected ones in early generation followed by reselection.

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(Received on 25.07.2013 and revised on 16.10.2014)