



Studies on Genetic Variability, Heritability and Genetic Advance for Seed Cotton Yield and Quality Traits in Upland Cotton

R Asha, Lal Ahamed M, D Ratna Babu and P Anil Kumar

Department of Genetics and Plant Breeding, Agricultural College, Bapatla 522 101

ABSTRACT

Forty genotypes of upland cotton of diverse origin were studied for genetic variability, heritability and genetic advance for yield, yield contributing traits including fibre quality characters. The analysis of variance revealed that sufficient variability was present in the material studied for all the 17 characters. The phenotypic coefficient of variation (PCV) was slightly higher in magnitude than genotypic coefficient of variation (GCV) for all the characters indicating the influence of environment. Higher heritability coupled with high genetic advance was observed for characters like number of monopodia plant⁻¹, number of sympodia plant⁻¹, number of bolls plant⁻¹, boll weight, seed index, lint index, micronaire, cellular membrane thermostability (RCI%), enzyme viability (EV) and seed cotton yield plant⁻¹ indicating the preponderance of additive gene action and simple selection may be effective for the improvement of these traits. Plant height, 2.5 % span length and bundle strength showed high heritability and moderate genetic advance indicating the presence of both additive and non-additive gene actions. The other traits *viz.*, days to 50% flowering, ginning out-turn (%), uniformity ratio and fibre elongation (%) showed moderate to high heritability and moderate to low genetic advance indicating the operation of non-additive gene action, making direct selection ineffective.

Key words : Cotton, GCV, Genetic advance, Heritability, PCV.

In the agro-based economy of the country, cotton is one of the most important commercial crops. By virtue of its wider adaptability it is grown in irrigated as well as rainfed conditions in India contributing 85 per cent to the national production. In any successful crop improvement programme, the availability of adequate variability in basic genetic stocks and their proper use through breeding for building up of improved strains are very necessary. The genetic improvement of plant population depends on the presence of magnitude of genetic variability and the extent to which the desirable traits are transmissible.

Thus, besides genetic variability, knowledge on heritability and genetic advance plays a predictive role in breeding, expressing the reliability of phenotype as a guide to its breeding value. The higher the heritability the greater would be the response to selection that is gained in yield as heritability is directly proportional to genetic advance making selection more effective (Burton, 1952 and Swarup and Chaugle, 1962). So, the magnitude of heritable variability is the most

important aspect of genetic contribution of the breeding material, which has close relationship on its response to selection (Panse, 1957).

MATERIAL AND METHODS

The experiment was conducted during *kharif* 2011-12 in randomized block design with 40 germplasm lines obtained from all over India with three replications following a spacing of 120 x 60 cm at Agricultural College Farm, Bapatla, Andhra Pradesh. The soils are black cotton type with clay texture. Each plot consisted of two rows of 6m length and observations were recorded on ten randomly selected plants from each genotype per replication for characters *viz.*, plant height (cm), number of monopodia plant⁻¹, number of sympodia plant⁻¹, number of bolls plant⁻¹, boll weight (g), seed index (g) and lint index (g) and seed cotton yield per plant. The data on days to 50% flowering, ginning out turn (%), bundle strength (g/tex), uniformity ratio, 2.5% span length (mm), micronaire (10⁻⁶g/in), fibre elongation (%), cellular membrane thermostability (RCI%) and enzyme viability (μ g/

Table 1. Analysis of variance for yield and yield components in cotton (*Gossypium hirsutum* L.).

Source of Variation	d.f.	Plant height (cm)	Days to 50% flowering	No. of monopodia plant ⁻¹	No. of sympodia plant ⁻¹	No. of bolls plant ⁻¹	Boll weight (g)	Ginning-out-turn (%)	Seed index (g)	Lint index (g)
Replications	2	222.1830	1.1083	0.0001	3.2480	20.4016	0.1341	1.7510	0.0731	0.0306
Treatments	39	646.1204**	10.5638**	0.3341**	17.2260**	162.6393*	1.0978**	14.5549**	3.4096**	1.0704**
Error	78	109.4772	0.3561	0.0053	3.0174	9.5989	0.0540	2.2439	0.0808	0.0631
Mean sum of squares										
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Source of Variation	d.f.	2.5% span length (mm)	Micronaire (10 ⁻⁶ g/in)	Bundle strength (g/tex)	Uniformity ratio	Elongation (%)	RCI (%)	Enzyme viability	Seed cotton yield plant ⁻¹ (g)
Replications	2	0.1874	0.0861	0.9836	5.5466	0.0432	0.0441	0.0018	51.2666
Treatments	39	16.8824**	1.0115**	10.4506**	23.2764**	0.1460**	446.6400**	0.0996**	1387.4840**
Error	78	0.9509	0.0613	0.5016	2.3496	0.0298	0.5236	0.0022	92.7402
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** = Significance at 1% level, d.f. = Degrees of freedom

ml) were recorded on plot basis. The phenotypic and genotypic coefficients of variability (PCV and GCV) were computed as per the methods of Burton and De Vane (1953). The method of Johnson *et al.* (1955) was followed for estimation of broad sense heritability (H^2) and genetic advance for all the traits recorded.

RESULTS AND DISCUSSION

Analysis of variance indicated the existence of sufficient variability in the material under study (Table-1). The mean, range, PCV, GCV, heritability and genetic advance as per cent of mean were presented in Table-2. The narrow difference between genotypic and phenotypic variance was observed for all the characters indicating that a major portion of phenotypic variation for these characters was contributed by genetic component. The estimates of PCV were slightly higher than corresponding GCVs for all the characters which may be due to interaction of genotypes with environment.

The PCV and GCV values are high for number of monopodia plant⁻¹ (23.09 and 22.55), number of bolls plant⁻¹ (28.17 and 25.84) and seed cotton yield plant⁻¹ (26.44 and 23.98). These results were in conformity with the findings of Vijaya Lakshmi *et al.* (2008) and Sarada *et al.* (2010). These values were moderate for plant height (14.79 and 11.65), number of sympodia plant⁻¹ (18.11 and 14.16), boll weight (19.48 and 18.13), seed index (12.68 and 12.24), lint index (14.41 and 13.22), micronaire (14.83 and 13.57), RCI (%) (15.43 and 15.41) and enzyme viability (19.17 and 18.54). Similar results were reported by Altaher and Singh (2003) and Vijaya Lakshmi *et al.* (2008). Low PCV and GCV values are observed for days to 50% flowering (3.41 and 3.24), ginning out-turn (7.46 and 6.00), 2.5% span length (9.00 and 8.29), bundle strength (9.30 and 8.67), uniformity ratio (6.44 and 5.57) and fibre elongation% (4.51 and 3.39). Similar results were reported by Vijaya Lakshmi *et al.* (2008) and Sarada *et al.* (2010).

High heritability coupled with high genetic advance as per cent of mean was observed for characters like number of monopodia plant⁻¹ (95.34 and 45.36), number of sympodia plant⁻¹ (61.08 and 22.79), number of bolls plant⁻¹ (84.16 and 48.84), boll weight (86.56 and 34.73), seed index (93.21

and 24.35), lint index (84.18 and 25.00), micronaire (83.77 and 25.60), RCI (%) (99.64 and 31.69), enzyme viability (93.55 and 36.95) and seed cotton yield plant⁻¹ (82.31 and 44.83) indicating the predominance of additive gene action and hence, direct phenotypic selection may be useful with respect to these traits. These results are in broad agreement with the results of Vijaya Lakshmi *et al.* (2008) and Sarada *et al.* (2010). High heritability coupled with moderate genetic advance was observed in case of plant height (62.03 and 18.91), 2.5 % span length (84.81 and 15.73) and bundle strength (86.86 and 16.64) revealing the role of additive and non-additive gene action. The other traits *viz.*, days to 50% flowering (90.52 and 6.36), ginning out-turn (%) (64.66 and 9.94), uniformity ratio (74.80 and 9.93) and fibre elongation% (56.84 and 5.25) showed moderate to high heritability and moderate to low genetic advance indicating the operation of non-additive gene action. Similar results were reported by Vijaya Lakshmi *et al.* (2008) and Sarada *et al.* (2010). These traits might be exploited through heterosis breeding, cyclic hybridization, biparental mating and diallele selective mating systems, rather than simple selection methods.

Taking into consideration the amount of variability, heritability and genetic advance as percent of mean in the present study it may be concluded that major emphasis should be laid out on selection process with more number of monopodia plant⁻¹, number of sympodia plant⁻¹, number of bolls plant⁻¹, seed index, lint index and micronaire for the improvement of seed cotton yield.

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Table 2. Mean, genetic variability, heritability (broad sense) and genetic advance as per cent of mean for seed cotton yield and morpho-physiological yield 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. Plant height (cm)	114.73	78.20	144.90	14.79	11.65	62.03	18.91
2. Days to 50% flowering	56.77	53.30	60.30	3.41	3.24	90.52	6.36
3. No. of monopodia plant ⁻¹	1.46	0.97	2.63	23.09	22.55	95.34	45.36
4. No. of sympodia plant ⁻¹	15.36	11.13	22.83	18.11	14.16	61.08	22.79
5. No. of bolls plant ⁻¹	27.64	18.97	52.13	28.17	25.84	84.16	48.84
6. Boll weight (g)	3.25	2.23	4.80	19.48	18.13	86.56	34.73
7. Ginning out-turn (%)	33.74	30.16	37.87	7.46	6.00	64.66	9.94
8. Seed index (g)	8.60	6.58	11.48	12.68	12.24	93.21	24.35
9. Lint index (g)	4.37	3.49	6.08	14.41	13.22	84.18	25.00
10. 2.5% span length (mm)	27.77	22.57	32.40	9.00	8.29	84.81	15.73
11. Micronaire (10 ⁻⁶ g/In)	4.14	2.85	5.57	14.83	13.57	83.77	25.60
12. Bundle strength (g/tex)	21.00	17.95	24.47	9.30	8.67	86.86	16.64
13. Uniformity ratio	47.37	40.97	52.09	6.44	5.57	74.80	9.93
14. Fibre elongation (%)	5.80	5.38	6.45	4.51	3.39	56.43	5.25
15. Relative cell injury (%)	79.12	52.80	100.00	15.43	15.41	99.64	31.69
16. Enzyme viability (µg/ml)	0.97	0.60	1.30	19.17	18.54	93.55	36.95
17. Seed cotton yield plant ⁻¹ (g)	86.60	58.36	150.07	26.44	23.98	82.31	44.83

PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation; Relative cell injury

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