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Research Article

Genetic Variability Studies for Quantitative and Qualitative Traits in Upland Cotton (*Gossypium hirsutum* L.)

K. V. Siva Reddy[1], Balakrishna, B.[2*] and Chenga Reddy, V.[3]

[1]Scientist, Agricultural Research Station, ANGRAU, Amaravathi, Guntur-522 020, Andhra Pradesh, India

[2]Teaching Associate, Dr Y S R Horticultural University, Venkataramannagudem-534101, Andhra Pradesh, India

[3]Principal Scientist (Cotton) (Rtd.), All India Co-ordinated Cotton Improvement Project, Regional Agricultural Research Station, ANGRAU, Lam, Guntur-522 034, Andhra Pradesh, India

*Corresponding Author E-mail: balubreeder@gmail.com

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ABSTRACT

The present experiment was conducted during kharif-2014-15 to know the genetic variability present among the upland cotton genotypes. The traits viz., boll weight, seed index, lint index and ginning out turn were recorded minimum difference between GCV and PCV values indicated less influence of environment on these traits phenotypic expression. Seed index and lint index exhibited high heritability coupled with high genetic advance as per cent of mean. It means these characters are may be controlled by additive gene action and more responsive to simple direct selection.

Key words: *Upland cotton, Genetic variability, Heritability and GAM.*

INTRODUCTION

The genus *gossypium* consists of four important cultivated species among them upland cotton (*Gossypium hirsutum* L.) is the mostly cultivated species. It occupies maximum area under rainfed area cotton cultivation. So that to select or develop premier hybrids in this species there is a lot of need of creation of variability and estimation of variability present in the already existing germplasm. Genetic improvement in any crop by largely depends on availability of genetic variability present in that particular crop[4]. Hence, the present investigation was carried out with 37 *hirsutum* genotypes collected from all over India to estimate genetic variability.

MATERIAL AND METHODS

The present investigation was conducted during *kharif*-2014-15 at Regional Agricultural Research Station, Lam. There 37 genotypes collected from different parts of country was planted in Randomized Block Design with three replication by adopting 105 cm x 60 cm regularly followed spacing. All recommended agronomic package of practices for cotton crop were followed for raising a good crop.

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The data was recorded on five randomly selected plants from each replication from each treatment. Data was analyzed for analysis of variance as per Cochran and Cox[3] and all genetic parameters were estimated as per Burton[2] and heritability and genetic advance as per cent of mean was estimated as per Lush[10] and Johnson *et al*.[7].

RESULTS AND DISCUSSION

The analysis of variance for 15 quantitative and qualitative characters indicated presence of significant genetic variability among the genotypes for all the characters studied. Analysis of variance for various traits presented in the Table 1.The main success of genetic improvement in any crop depends upon the quantum of genetic variability present in the available germplasm for various economic traits. Estimates of different genetic parameters for 15 characters were presented in the Table 2. The traits *viz*., days to 50% flowering (4.39, 6.86), plant height (6.95, 8.42), no. of sympodia per plant (5.83, 10.42), boll weight (7.61, 8.68), ginning out turn (7.23, 7.80), 2.5 % span length (4.28, 6.00) and uniformity ratio (1.31, 3.34) recorded low GCV and PCV values indicates presence low genetic variability among the genotypes studied. Similar reports were also reported by Erande *et al*.[6] and Vinodhana *et al*.[12]. The traits, no.of bolls per plant (12.24, 16.21), seed index (11.00, 11.72) and lint index (13.40, 14.52) exhibited medium range estimates for GCV and PCV and less difference between GCV and PCV estimates indicates less influence of environment on phenotypic of these characters. These results are in accordance with Vinodhana *et al*.[12] and Ahsan *et al*.[1].

Number of monopodia per plant exhibited high GCV and PCV values (25.78, 33.24) but the influence environment on this trait also very high as indicated by ECV value (21.00). It means considerable influence of environment on phenotypic expression of this character. Khan *et al*.[8], reported similar findings for this trait. The character micronaire value was also highly influence by environment because the difference between GCV and PCV is very high and influence of environment was more. Once there is a change in the environment automatically the micronaire value was also changes. High heritability and genetic advance as per cent was recorded by seed index (86.40, 20.87) and lint index (85.10, 25.46). These results are in accordance with Dhivya *et al*.[5]. It means that these characters may be controlled by additive type of gene action and may be direct selection is effective for improvement of these traits. Plant height (68.00, 11.83), boll weight (76.90, 13.74) and ginning out turn (87.10, 13.98) showed high heritability and medium genetic advance as per cent of mean indicates these traits influenced by both additive and non-additive type of gene actions. Similar findings were reported by Ahsan *et al*.[1], and Khan *et al*.[8]. Medium heritability and low genetic advance was exhibited by days to 50% flowering (41.00, 5.79), number of sympodia per plant (31.00, 6.73), 2.5 % span length (51.30, 6.32) and bundle strength (51.40, 7.04). Kulkarni *et al*.[9], Dhivya *et al*.[5], and Khan *et al*. (2015) also reported similar findings. It indicates phenotypic expression of these traits is as a result of both additive and non-additive type of gene actions.

No. of bolls per plant (57.00, 19.02), seed cotton yield/ ha (40.60, 13.62), lint yield/ha (52.10, 20.43) may controlled by both additive and non-additive type of gene actions as it indicated by medium heritability and genetic advance as per cent of mean. Low heritability and genetic advance as per cent of mean was exhibited by micronaire value (-4.00, -1.00) and uniformity ratio (15.30, 1.05). These results are in accordance with results of Rajamani and Rao[11]. It reveals that the inheritance of these traits may be regulated by non-additive type of gene action and heterosis breeding may be useful for better exploitation of these traits in future breeding programmes. There is a further need to study to know the detailed information on gene action involved in the phenotypic expression of different traits by using appropriate mating designs.

Table 1: Analysis of variance for various quantitative and qualitative characters in upland cotton (*Gossypium hirsutum* L.)

Source	**Df**	**DFF**	**PH**	**NMP**	**NSP**	**NB**	**BW**	**SI**	**LI**	**GOT**	**SCY**	**LY**	**2.5%SL**	**BS**	**MIC**	**UR**
Replications	2	20.57	2001.00*	1.64**	1.88	149.17	0.16	1.17	0.62	1.25	71.72	6.58	6.40	5.27	0.21	0.76
Treatments	36	35.75**	320.69**	0.56**	5.58**	78.74**	0.44**	3.80**	1.50**	18.98**	35.41**	6.24**	5.55**	4.16**	0.21	3.47
Error	72	11.61	43.08	0.10	2.35	15.84	0.04	0.19	0.08	0.89	11.59	1.46	1.33	1.00	0.24	2.25

* at 5% level of significance ** at 1% level of significance

Table 2: Estimates of genetic various genetic parameters for various quantitative and qualitative characters in upland cotton (*Gossypium hirsutum* L.)

Parameter	**Dyas to 50% flowering**	**Plant Height (cm)**	**No of Monopodia/ plant**	**No of Sympodia/ plant**	**No. of Bolls/ plant**	**Boll wt (g)**	**Seed Index (g)**	**Lint Index (g)**
ECV	5.27	4.745	20.99	8.64	10.64	4.17	4.33	5.61
GCV	4.39	6.95	25.78	5.83	12.24	7.61	10.90	13.40
PCV	6.86	8.42	33.24	10.42	16.21	8.68	11.72	14.52
h² (Broad Sense)	0.41	0.68	0.60	0.31	0.57	0.77	0.86	0.85
Genetic Advancement 5%	3.74	16.37	0.63	1.20	7.12	0.66	2.10	1.31
Gen.Adv as % of Mean 5%	5.79	11.83	41.19	6.73	19.02	13.74	20.87	25.46
General Mean	64.61	138.34	1.52	17.77	37.42	4.82	10.08	5.14

Parameter	**GOT (%)**	**Seed Cot Yield (q/ha)**	**Lint Yield (q/ha)**	**2.5% Span length (mm)**	**Bundle strength tex)**	**Micronaire (10^{-6} g/ inch)**	**Uniformity Ratio**
ECV	2.80	12.53	13.17	4.17	4.63	12.39	3.08
GCV	7.27	10.37	13.74	4.28	4.77	2.37	1.31
PCV	7.79	16.27	19.03	5.98	6.64	12.17	3.34
h² (Broad Sense)	0.87	0.41	0.52	0.51	0.51	-0.04	0.15
Genetic Advancement 5%	4.72	3.70	1.88	1.75	1.52	-0.04	0.51
Gen.Adv as % of Mean 5%	13.98	13.62	20.43	6.32	7.04	-0.95	1.05
General Mean	33.76	27.17	9.19	27.69	21.56	3.97	48.77

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