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Genetic Variability,Heritability and Genetic Advance Studiesfor Yield and Fibre Quality Traits in American Cotton(*Gossypiumhirsutum*L.)

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ABSTRACT

Forty F_1's of American cotton were obtained by crossing 8 lines and 5 testers in Line × Tester design were evaluated along with parents during *Kharif,* 2016-2017 for genetic variability, heritability and genetic advance as per cent of mean based on 14 characters. High phenotypic coefficient of variation (PCV) was recorded for seed cotton yield per plant. Moderatephenotypic coefficient of variation (PCV) and Genotypic coefficient of variation (GCV) were recorded in number of monopodia per plant andnumber of sympodia per plant. High heritability coupled with high genetic advance as per cent of mean was recorded for characters *viz.,* number of bolls per plant, micronairevalue(10^{-6} g/inch) and seed cotton yield per plant indicating the preponderance of additivegene action making simple or direct selection effective.

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

Cotton (*GossypiumhirsutumL.*) is an important fibre crop and plays a vital role as a cash crop in commerce of many countries such as USA, China, India, Pakistan, Uzbekistan, Australia and Africa. It is an important commercial crop of India being used throughout the textile industry and plays a key role in the national economy by providing highest employment during production, processing, spinning, weaving and marketing. It also occupies the place of pride in Indian agriculture by earning valuable foreign exchange.

Knowledge on the nature and extent of genetic variability, heritability and genetic advance is an important pre-requisite in framing of any crop improvement programme. Genetic variability along with heritability of a character indicates the possibility and extent to which improvement was feasible through selection on phenotypic basis. Further, high heritability coupled with high genetic advance would bring out the progress expected from simple or direct selection. Therefore, the present study was undertaken to find out the genetic variability, heritability and genetic advance of various yield component and fiber properties to establish appropriate criterion for selection to improve the yield status of cotton.

MATERIAL AND METHODS

The present study was carried out with 54 genotypes of cotton (*GossypiumhirsutumL.*) in randomized complete block design (RCBD) with three replications at Regional Agricultural Research Station, Lam, Guntur during *kharif,* 2016-17. The material includes 8 lines i.e., L 1060, L1231, L 1384, L 1493, LH 2220, NDLH 1938, NDLH 2010 and SCS 1001 and 5 testers i.e., GTHV 13/32, HYPS 152, L 788, MCU 5 and SURAJ. The inter-row and intra-row spacing adapted was 105 cm x 60 cm. Each entry was sown in one row of 6 m length and observations were recorded on five randomly selected plants from each genotype per replication for characters *viz*., 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) and seed cotton yield plant per plant (g). The characters *viz.*, Days to 50% flowering, ginning out turn (%), 2.5% span length (mm), micronaire (10^{-6} g /inch), bundle strength (g /tex) and uniformity ratio were recorded on plot basis. The fibre quality characters were analysed at Central Institute for Research on Cotton Technology Regional Unit, Lam, Guntur. The data was statistically analysed to estimate phenotypic and genotypic coefficients of variation (PCV and GCV) as indicated by Burton (1952). Heritability in broad sense was estimated as per the formula given by Hanson *et al.* (1956) and the genetic advance as per cent of mean as suggested by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

The analysis of variance showed significant difference among the treatments (parents and crosses) for all the characters under study indicating existence of sufficient amount of variability in the material (Table 1). The value of phenotypic coefficient of variation (PCV) was slightly higher in magnitude than genotypic coefficient of variation (GCV) for all the characters (Table.2).

Among the different yield attributing and quality traits, the estimates of PCV and GCV were moderate for number of monopodia per plant (16.52 and 10.48) andnumber of bolls per plant (19.79 and 16.80).Both PCV and GCV were low for the traits *viz*., days to 50% flowering (7.12 and 4.67), plant height (7.71 and 5.81), boll weight (9.76 and 9.00), seed index (8.68 and 7.66), lint index (9.82 and 8.62), ginning out turn (3.27 and 2.92), bundle strength (9.03 and 8.23) and uniformity ratio (3.27 and 1.55) respectively.

The variation in the values of PCV and GCV was narrow for the characters *viz*., plant height, days to 50% flowering, boll weight, seed index, lint index, bundle strength, ginning out turn and uniformity ratio which indicates the less influence of the environment in the expression of thesetraits. These research finding are parallel to the findings of Rajamani *et al.* (2015) and Bayyapureddy*et al.*(2016) for plant height and days to 50% flowering,Ahsan*et al.* (2015) for boll weight, Venkatesh (2012) for seed index and ginning out turn, Bayyapureddy*et al.*(2016) for bundle strength and uniformity ratio.

Moderate heritability along with Low genetic advance as per cent of mean wasrecorded in days to 50% flowering (43.06 and 6.32), plant height (56.82 and 9.04) and number of sympodia per plant (32.50 and 7.97) indicating the operation of both additive and non-additive geneactions in the inheritance of these traits and offers the best possibility of improvement through progeny selection or any modified selection procedures aiming to exploit both additive and non additive gene effects. However, contrary results ofhigh heritability and low genetic advance as per cent of mean were reported byRajanna (2010) and Dhivya*et al.* (2014) for days to 50% flowering, Rajamani*et al.*(2015) and Bayyapureddy*et al.*(2016) for plant height.

High heritability with high genetic advance as per cent of mean was recorded in number of bolls per plant (72.12 and 29.40) and seed cotton yield per plant (85.56 and 45.37) indicated the role of additive gene action in the inheritance of this trait. Improvement of this trait can be aimed through simple selection. These results are in contrary with the findings of Haritha (2011), Vineela*et al.* (2013) and Bayyapu Reddy *et al.* (2016) for number of bolls per plant and seed cotton yield per plant.

High heritability coupled with moderate genetic advance as per cent of mean was observed for, boll weight, seed index, lint index, bundle strength and 2.5% span length indicating the operation of both additive and non-additive gene actions in the inheritance of these traits and further improvement of these trait would be possible through cyclic hybridization and biparental mating.

High heritability coupled with low genetic advance as per cent of mean was observed for ginning-out turn (79.95 and 5.39) indicating the role of non-additive gene action and this trait may be exploited through heterosis breeding.

Moderate heritability and low to moderate genetic advance as percent of mean were recorded in case of days to 50% flowering,plant height, number of monopodia per plant,number of sympodia per plant,these characters which are governed by non-additive gene action, it can be exploited by heterosis breeding.

Conclusion

Heritability and Genetic advance are important selection parameters.Estimation of heritability along with the genetic advance are more reliable and meaningful than individual consideration of the parameters. Assessing of heritability assists breeder to allocate resources necessary to effectively select for desired trait and to achieve maximum genetic gain with little time and resources.

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Table 4.1. Analysis of variance for yield and yield components in cotton (*GossypiumhirsutumL.*) during *kharif*, 2016-17

Source	d.f.	Plant height (cm)	Days to 20% flowering	Number of monopodia per plant	Number of sympodia per plant	Number of bolls per plant	Boll weight (g)	Seed index (g)
				Mean sum of squares				
Replications	2	63.26	7.30	0.26	4.79	26.47	0.07	0.39
Treatments	53	208.05**	33.67**	0.32**	4.11**	195.60**	0.50**	1.67**
Error	106	42.05	10.30	0.106	1.68	22.32	0.02	0.14

Source	d.f.	Lint index (g)	ginning outturn (%)	2.5 % span length (mm)	Micronaire value (10^{-6} g/inch)	Bundle strength (g/tex)	Uniformity ratio	Seed cotton yield per plant (g)
				Mean sum of squares				
Replications	2	0.16	0.35	0.11	0.01	0.61	0.22	169.57
Treatments	53	0.58**	3.27**	13.85**	0.44**	12.30**	3.47**	3907.07**
Error	106	0.05	0.25	0.58	0.02	0.77	1.85	208.09

** Significant at 1% level

Table 2. Estimates of mean, variability, heritability (broad sense) and genetic advance as per cent of mean for yield and its components in cotton (*Gossypiumhirsutum* L.) during *kharif*,2016-17

S.No.	Character	Mean	Range		Coefficient of		Heritability (broad sense) (%)	Genetic advances as per cent of mean
			Minimum	Maximum	PCV (%)	GCV(%)		
1	Plant height (cm)	127.83	113.33	149.46	7.71	5.81	56.82	9.04
2	Days to 50% flowering	59.73	54.33	69.33	7.12	4.67	43.06	6.32
3	Number of monopodia per plant	2.55	1.96	3.15	16.52	10.48	40.23	13.70
4	Number of sympodiaper plant	13.25	11.06	16.03	11.90	6.78	32.50	7.97
5	Number of bolls per plant	45.21	31.46	67.46	19.79	16.80	72.12	29.40
6	Boll weight (g)	4.44	3.53	5.62	9.76	9.00	85.10	17.11
7	Seed index (g)	9.32	7.84	11.14	8.68	7.66	77.86	13.93
8	Lint index (g)	4.86	3.95	5.92	9.82	8.62	77.14	15.61
9	Ginning outturn (%)	34.28	31.92	36.17	3.27	2.92	79.95	5.39
10	2.5% span length (mm)	29.18	24.43	32.93	7.66	7.20	88.36	13.95
11	Micronairevalue (10^{-6}g/inch)	3.83	3.03	4.83	10.58	9.71	84.25	18.37
12	Bundle strength (g/tex)	23.79	19.93	27.80	9.03	8.23	83.12	15.47
13	Uniformity ratio	47.26	45.00	49.33	3.27	1.55	22.52	1.52
14	Seed cotton yield per plant (g)	147.48	93.41	249.73	25.73	23.80	85.56	45.37

PCV = Phenotypic coefficient of variation GCV = Genotypic coefficient of variation

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