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STUDIES ON GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE IN COTTON (*GOSSYPIUM HIRSUTUM L.*)

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Abstract

Thirty cotton genotypes were subjected to assess the extent of genetic variability, heritability and genetic advance for further crop improvement through breeding. Fourteen characters viz., days to fifty percent flowering, plant height at maturity, number of sympodial branches per plant, number of bolls per plant, single boll weight, seed index, ginning out turn, lint index, lint yield, biological yield, 2.5 percent span length, micronaire, bundle strength and seed cotton yield per plant were studied. The character *viz.*, seed cotton yield, lint yield, biological yield, plant height at maturity, number of bolls per plant and lint index recorded high phenotypic and genotypic coefficient of variation. High heritability was observed for seed cotton yield followed by number of bolls per plant, lint yield, days to fifty per cent flowering, biological yield number of sympodial branches per plant, plant height at maturity, ginning out turn, 2.5 percent span length, bundle strength, seed index and single boll weight. High genetic advance as perent of mean was observed in seed cotton yield followed by lint yield, biological yield, number of bolls per plant, plant height at maturity. High heritability coupled with high genetic advance as percent of mean was observed for most of the characters *viz.,* days to fifty percent flowering, plant height at maturity, number of sympodial branches per plant, number of bolls per plant, single boll weight, seed index, ginning out turn, lint yield, biological yield and seed cotton yield per plant. These characters could well be improved by resorting to simple pureline selection.

***Key words*:** Cotton, variability, heritability and genetic advance

Introduction

India is the only country in the world where in all the four cultivated species, *viz.*, *Gossypium herbaceum*, *Gossypium arboreum, Gossypium hirsutum* and *Gossypium barbadense* are grown on commercial scale. In India, diploid cotton is grown from time immemorial. During pre-independence era, about 97 per cent of the cotton area was under Asiatic cotton and only 3 per cent area was under American cotton (*Gossypium hirsutum*). Now upland cotton and its hybrids (both intra and inter specific) cover about 76 per cent area in the country and the remaining 20 per cent of area is under Asiatic cotton (Singh, 1981). India is the second largest producer of cotton in the world after China accounting for about 18% of the world cotton production. It has the distinction of having the largest area under cotton cultivation in the world ranging around 12.2 million hectares and constituting about 25% of the world area under cotton cultivation. India has the harvested area of 12.19 lakh hectares among the total area of worldwide 36.1 lakh hectares. In the total production of 26.88 million MT India has the share of 6.05 million MT.

Cotton Mills Federation has projected the cotton requirement for 2025 at 60 million bales (Deshpande *et al.*, 2008). Therefore, one of the main objectives of cotton improvement program is to breed varieties and hybrid cultivars with high seed cotton yield and superior quality of fibre. Cotton hybrids are always being utilized to give an extra push to yield and quality potential.

In the state of Tamil Nadu, cotton is cultivated both under irrigated and rainfed condition. The textile industry of the state is mainly based on extra long staple with high bundle strength of cotton to the extent of 89%. All the four cultivated species of cotton, namely *Gossypium hirsutum, Gossypium barbadense, Gossypium arboreum* and *Gossypium herbaceum* are grown in this state along with their intra and inter-specific hybrids. Among the southern states of India which grow *Gossypium barbadense* genotypes, the climate of Tamil Nadu is conductive for *Gossypium barbadense* hybrids and varieties. Tamil Nadu produces only one sixth of its cotton requirements and the balance is met by purchases from up-country markets.

Cultivation of cotton in both assured rainfall and irrigated situations has so far been dominated by *hirsutum* based cottons, while cotton in rainfed or rather low rainfall areas is dominated by *desi* cotton. After decades of intensive cultivation of *hirusutum* cottons, today cotton ecosystem is characterized by a hostile pest complex. This is insufficient to obtain a good crop of *hirsutum* hybrids because of the cost of the seed and especially plant protection in the hostile pest background which would discourage farmers from cultivating *hirsutum* hybrids.

Pure breeding variety would prove to be highly desirable in a country like India because unlike in some cereal crops; the utilization of male sterility system in hybrid seed production is limited, because it is costly and time consuming job. Because of handicaps in commercial production of hybrid seeds, it is urgently necessary to step up production in India by evolving high yielding varieties. Selection of superior varieties would be effective only when genetic variability exists in the material selected for improvement.

Since several economic characters including yield in cotton are polygenically controlled, it is necessary to partition the observed overall phenotypic variability into heritable (genetic) and non-heritable (environment) components with the help of genetic coefficient of variation and heritability. Thus, estimation of expected genetic advance may help to select particular population for further selection and improvement.

Hanson *et al.* (1956) proposed heritability in broad sense as the ratio of genotypic variance of a particular character to its phenotypic variance is a function of its heritability, selection pressure and variance existing in the base population. Though the heritability is the relative value of the selection based on phenotypic expression of a character, the genetic advance is more useful in judging the actual value of selection as shown by Johnson *et al.* (1955).

Estimation of co-efficient of variation helps to assess the extent of genetic variability in a population and to compare among the traits. Heritable variation could well be effectively used with greater degree of accuracy when heritability is studied in conjunction with genetic advance.

Materials and Methods

The present investigation was carried out in the Plant Breeding farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University. The experimental material comprised of 30 cotton genotypes collected from Central Institute for Cotton Research, Coimbatore. The details of the materials are presented in Table 1.

These genotypes were sown in the second week of June. The experiment was laid out in a Randomized Block Design with three replications following spacing of 75 cm between the rows and 30cm between plants within row and 6m X 1.5m plot size. Recommended agronomic practices and need based plant protection measures were adopted.

Five plants at random in each replication were chosen and labeled for recording observations. The mean of five plants were used for statistical analyses. The data on the following yield and yield components and quality parameters were recorded. The characters *viz.,* days to fifty percent flowering, plant height at maturity, number of sympodial branches per plant, number of bolls per plant, single boll weight, seed index, ginning out turn, lint index, lint yield, biological yield, 2.5 percent span length, micronaire, bundle strength and seed cotton yield per plant. Genotypic co-efficient of variation (GCV) and phenotypic (PCV) co-efficient of variation were calculated based on the formula advocated by Burton (1952). Heritability in broad sense was calculated according to Hanson *et al.* (1956) and expressed in percentage. The GA as per cent of mean was classified according to Robinson *et al.* (1949).

Table 1 : List of genotypes selected for variability studies

Genotype Code	Name of the Genotype
G1	KH-1301
G2	ARBH-1301
G3	L-804
G4	TSH-04/115
G5	L-1011
G6	TCH-1777
G7	SCS-1211
G8	CPD-1301
G9	LH 2307
G10	SCS 1210
G11	CSH-3175
G12	GLHV-511
G13	H-1476
G14	LH 2255
G15	GJHV 516
G16	RS 2728
G17	GSHV 169
G18	BPHI 537
G19	NDLH 1975
G20	CNH 1116
G21	F 2451
G22	CCH 13-2
G23	TCH 1742
G24	ARBH-1302
G25	BS 1
G26	NDLH 1976
G27	HS 292
G28	CCH 13-1
G29	RS 2733
G30	SCS 1214

Results and Discussion

The analysis of variance revealed significant differences among the 30 genotypes for all the characters except studied. This indicated that the thirty genotypes differed genetically among themselves for most of the characters studied. This implied that there is good scope for further improvement in cotton genotypes. In the present investigation, estimates of genetic parameters revealed that phenotypic coefficient of variability was higher than the genotypic coefficient of variability for all the characters studied which indicated that they are all interacted with the environments to a considerable extent. Similar observations were made by Hussain *et al.* (2010); Rasheed *et al.* (2009) and Kaushik *et al.* (2006).

In the present study, the traits *viz.,* biological yield, seed cotton yield, lint yield, plant height and number of bolls per plant recorded high PCV and GCV, While single boll weight, days to fifty percent flowering, number of sympodial branches per plant, ginning out turn and seed index showed moderate PCV and GCV. High PCV coupled with moderate GCV was recorded by the trait lint index. Bundle strength and 2.5 percent span length showed low PCV and GCV, whereas the character micronaire showed moderate PCV with low GCV. There existed a close agreement between PCV and GCV for most of the traits indicating that the observed variation could largely be due to genetic. There was only less influence of environmental effects in general. This reflects on the reliability of the selection based on the phenotypic performance.

Table 1 : Magnitude of variability for various characters in 30 cotton genotypes

S. No.	Characters	PCV (%)	GCV (%)
1	Days to fifty percent flowering	12.01	11.94
2	Plant height	29.99	28.89
3	Number of sympodial branches per plant	17.10	16.63
4	Number of bolls per plant	28.56	28.54
5	Single boll weight	19.82	15.96
6	Seed index	17.94	14.57
7	Ginning out turn	10.84	10.32
8	Lint index	23.95	13.80
9	Lint yield	33.25	33.09
10	Biological yield	32.84	32.38
11	2.5 percent span length	9.44	8.98
12	Micronaire	14.43	6.19
13	Bundle strength	7.94	7.20
14	Seed cotton yield	34.28	33.86

The heritability estimates were always high for most of the traits except lint index and micronaire. High heritability estimates were observed for seed cotton yield followed by number of bolls per plant, lint yield, days to fifty percent flowering, biological yield, number of sympodial branches per plant, plant height, ginning out turn, 2.5 percent span length, bundle strength, seed index and single boll weight.

High genetic advance as percent of mean was observed for seed cotton yield followed by lint yield, biological yield, number of bolls per plant, number of sympodial branches per plant, single boll weight, days to fifty percent flowering and ginning out turn. Moderate genetic advance as percent of mean was observed for 2.5 percent span length followed by lint index and bundle strength indicating the predominance of additive gene action for these traits, enabling ease of selection. These findings are in agreement with Rasheed *et al.* (2009) and Dhamayanathi *et al.* (2010).

Johnson *et al.* (1955) suggested that heritability estimates in conjunction with the high genetic advance were usually helpful in predicting its resultant effects for selecting the best individuals. High heritability estimates coupled with high genetic advance as percent of mean was recorded for most of the traits namely, days to fifty percent flowering, plant height, number of bolls per plant, number of sympodial branches per plant, single boll weight, seed index, ginning out turn, lint yield, biological yield, and seed cotton yield per plant.

Table 2 : Estimation of heritability and genetic advance for various characters in cotton

S. No.	Characters	h^2 (%)	Genetic advance as per cent of mean
1	Days to fifty percent flowering	98.74	24.44
2	Plant height	92.81	57.33
3	Number of sympodial branches per plant	94.50	33.30
4	Number of bolls per plant	99.81	58.73
5	Single boll weight	64.87	26.49
6	Seed index	65.98	24.39
7	Ginning out turn	90.65	20.24
8	Lint index	33.18	16.37
9	Lint yield	99.04	67.85
10	Biological yield	97.19	65.76
11	2.5 percent span length	90.55	17.61
12	Micronaire	18.44	5.48
13	Bundle strength	82.12	13.44
14	Seed cotton yield	99.86	70.63

This clearly indicated the existence of additive genetic control in the expression of these traits. This suggested that quick improvement could well be expected in a short time for these characters by following simple pureline selection. High heritability coupled with low to moderate genetic advance as percent of mean was observed for bundle strength, 2.5 percent span length and lint index. This clearly indicated the characters are mainly under the control of non-additive types of genes. This suggested that the improvement cannot be expected by resorting to simple selection procedures for these characters. These characters could well be exploited by resorting to hybrid breeding. Low heritability coupled with low genetic advance was observed in micronaire which showed that although there was some improvement in the characters, they are still to a greater extent influenced by the environment and controlled by a non-additive type of genes, hence they need further confirmation and evaluation for their fixation and that could be possible through recurrent selection in the succeeding generations.

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