



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

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Abstract

Thirty three cotton genotypes were subjected to assess the extent of genetic variability, heritability and genetic advance for further crop improvement through breeding. Thirteen characters viz., days to fifty percent flowering, plant height, number of sympodial branches per plant, number of bolls per plant, single boll weight, seed index, Ginning out turn, lint index, biological yield, 2.5 percent span length, micronaire, bundle strength and seed cotton yield per plant were studied. The character *viz.*, biological yield, seed cotton yield, plant height and number of bolls per plant recorded high phenotypic and genotypic coefficient of variation. 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, number of sympodial branches per plant, number of bolls per plant, single boll weight, seed index, lint index, 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

Cotton is the ‘white gold’ and enjoys a pre-eminent status among all cash crops in the country. It is the principal raw material for a flourishing textile industry. It provides livelihood to about sixty million people and is an important agricultural commodity providing remunerative income to million of farmers both in developed and developing countries. In India, inspite of severe competition from synthetic fibres in recent years, it is occupying the Premier position with 70 per cent share in the textile industry.

Gossypium includes 50 species, four of which are cultivated, 44 are wild diploids and two are wild tetraploids. Out of the four cultivated species, *Gossypium hirsutum* L. and *Gossypium barbadense* L. are commonly called as new world cottons are tetraploids ($2n = 4x = 52$), whereas, *Gossypium herbaceum* L. and *Gossypium arboreum* L. are diploids ($2n = 2x = 26$) and are commonly called as old world cottons.

Breeding programmes are determined in the initial step by the variability existing in the base populations. Later, the success of the selected material depends upon

the stability of the characters under selection. Thus, understanding the genetic makeup of the crop and the architecture of character set up in that crop are basic to a plant breeder. Genotypic variability is the heritable component of the apparent variability and is expressed as the heritability. Heritability is a result of additive and non-additive effects and is defined as the proportion of phenotypic variability that is due to genotype.

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 33 cotton genotypes collected from various places. The details of the materials are presented in table 1.

These genotypes were sown in the second week of May. The experiment was laid out in a Randomized Block Design with three replications with a spacing of 75 cm between the rows and 30cm between plants within row. 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 per cent 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, biological yield per plant, 2.5 per cent span length, micronaire, bundle strength and seed cotton yield. 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).

Results and Discussion

The analysis of variance revealed significant differences among the accessions for all the characters studied. This indicated that the 33 genotypes differed genetically among themselves for all 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, plant height and number of bolls per plant recorded high PCV and GCV, while single boll weight, days to fifty percent flowering, lint index, number of sympodial branches per plant and seed index showed moderate PCV and GCV. Ginning out turn, 2.5 percent span length, micronaire showed low PCV and GCV, while

Table 1 : List of genotypes selected for variability studies.

Genotype code	Name of the genotype
G1	MR 786
G2	BS 27
G3	ARBH 2004
G4	GJHV 502
G5	GSHV 158
G6	LRA 5166
G7	H 1454
G8	CPD 2001
G9	MCU 13
G10	ARBH 2002
G11	BGDS 801
G12	HS 288
G13	GTHV 07/1
G14	RS 2620
G15	CSH 2810
G16	CNH 1094
G17	RHC 0717
G18	CCH 820
G19	ADB 531
G20	L 770
G21	SCS 793
G22	CPD 1002
G23	CNH 1106
G24	RAH 803
G25	Surabhi
G26	TSH 0250
G27	GJHV 503
G28	BS 39
G29	ADB 532
G30	SCS 792
G31	GSHV 157
G32	CCH 10-1
G33	F2337

the character bundle strength 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.

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

Table 2 : Magnitude of variability for various characters in 33 cotton genotypes.

S. no.	Characters	PCV (%)	GCV (%)
1	Days to 50% flowering	16.56	16.14
2	Plant height	23.71	23.70
3	Number of sympodial branches per plant	15.84	14.74
4	Number of bolls per plant	21.72	20.42
5	Single boll weight	16.72	16.61
6	Seed index	12.38	11.90
7	Ginning out turn	8.54	8.54
8	Lint index	16.47	15.82
9	Biological yield	31.18	31.08
10	2.5% span length	9.04	7.45
11	Micronaire	7.82	7.54
12	Bundle strength	16.7	2.49
13	Seed cotton yield	27.79	25.43

Table 3 : 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 50% flowering	94.96	32.40
2	Plant height (cm)	99.94	48.81
3	Number of sympodial branches per plant	86.56	28.25
4	Number of bolls per plant	88.44	39.57
5	Single boll weight	98.65	33.98
6	Seed index	92.36	23.56
7	Ginning out turn	99.96	17.60
8	Lint index	92.26	31.30
9	Biological yield	99.37	63.83
10	2.5% span length	67.99	12.66
11	Micronaire	92.88	14.97
12	Bundle strength	2.21	0.76
13	Seed cotton yield	83.69	47.92

High genetic advance as percent of mean was observed for biological yield followed by plant height, seed cotton yield, number of bolls per plant, single boll weight, days to fifty percent flowering, lint index, number of sympodial branches per plant and seed index. Moderate genetic advance as percent of mean was observed for ginning out turn followed by micronaire, 2.5 percent span length 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 sympodial branches per plant, number of bolls per plant, single boll weight, seed index, lint index, biological yield and seed cotton yield per plant. 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 ginning out turn, 2.5 percent span length and micronaire. This clearly indicated the existence of non-additive gene action in the expression of these traits. 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.

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