Plant Archives Vol. 18 No. 2, 2018 pp. 1341-1344 **e-ISSN:2581-6063 (online), ISSN:0972-5210**

A STUDY ON GENETIC DIVERSITY AMONG COTTON GENOTYPES (*GOSSYPIUM HIRSUTUM* L.)

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Abstract

Thirty three genotypes of Cotton (*Gossypium hirsutum* L.) representing different geographic regions were evaluated to assess the extent of genetic diversity by employing Mahalanobis' D^2 statistic. The genotypes were classified into five discrete clusters and the entire collection was allocated to different clusters. There was no parallelism between genetic and geographic divergence was observed. Substantial variation in cluster means was observed for all the characters studied. Considering extent of diversity among the genotypes and cluster means for various characters, crosses among the genotypes of Clusters *viz.*, III, IV and V may give rise to heterotic hybrids and wide spectrum of variability in subsequent segregating generations. Genotypes CSH 2810 and GJHV 503 were observed to be potential parents for future cotton breeding programme.

Key words: *Gossypium hirsutum* L., Mahalanobis' D^2 statistic

Introduction

Cotton belongs to genus Gossypium of Malvaceae family and is extensively grown for its fibre and seed oil. The genus Gossypium includes about 50 species split across to two ploidy levels, *viz.*, diploid (2n=2×=26) and tetraploid (2n=4×=52). Of the 50 Gossypium species, four namely G. hirsutum, G. barbadense (both amphidiploids) are cultivated. Globally, G. hirsutum is the predominantly cultivated cotton species. It is cultivated on about 90% area worldwide, followed by G. barbadense (8%): G. arboreum and G. herbaceum occupy rest of the area. In India, cotton occupies an area of 10.2 million hectares with a total production and productivity of 295 lakh bales and 494 kg lint per hectare, respectively. Cotton contributes nearly 75 per cent of the total raw material needs of the textile industry and provides livelihood to about 60 million people directly or indirectly related to its farming, trade and textile industry in the country. Both cotton and textile exports account for nearly one-third of total foreign exchange earnings of the country. It is expected that the requirement of natural fibres spearheaded by cotton is likely to enhance from 36 to 45 per cent during the coming decade. The genetic diversity of different fibre quality parameters has been studied only a limited extent. To attain sustainability in quality aspects, access is made for diversity present in the private and public sector varieties as well as hybrids both for morphological and fibre quality traits. The diverse genotypes thus selected may be exploited in cotton breeding programme.

Materials and method

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 names 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 following 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 and the mean of five plants were taken. The data were recorded for the following yield and yield components and quality paraments *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. These data were subjected to D^2 analysis as per the standard method of Mahalanobis (1936). The genotypes were grouped on the basis of minimum generalized distance using Torcher's method as described by Rao (1952).

Table 1: List of genotypes selected for D^2 analysis.

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	F 2337

Results and discussion

The analysis of variance revealed significant differences among the accessions for all the characters studied. Based on the relative magnitude of D^2 values, 33 genotypes were grouped into as many as five clusters (table 2). Cluster I was the largest as it comprised 12 genotypes closely followed by cluster V had 9 genotypes. Cluster III consist of 8 genotypes whereas Cluster II and IV had two genotypes each. This indicated that geographical diversity is not always related to genetic diversity. The genotypes included in cluster I were from different geographical regions indicating that there was no parallelism between clustering pattern and geographic distribution of genotypes (Khan *et al.*, 2007). The distribution of genotypes also indicated that the genotypes from one region were distributed in different clusters. Therefore the kind of genetic diversity found among the genotypes belonging to same geographic origin might be due to differences in adoption, selection criteria and selection pressure in environmental conditions (Sambamurthy *et al.*, 2004). This further explains that forces other than eco-geographical differentiation such as natural and human selection pressure would exert considerable influence on the genetic divergence. Therefore, selection of cultivars for breeding programme should be based on genetic diversity rather than geographical diversity.

Table 2: Composition of D^2 clusters for 33 cotton genotypes.

Cluster	No of genotypes	Name of genotypes
I	12	MR 786, BS27, ARBH 2004, GJHV 502, GSHV 158, LRA 5166, H 1454, CPD 2001, MCU 13, ARBH 2002, CCH 820, GSHV 159
II	2	CCH 10-1, F 2337
III	8	BGDS 801, HS 288, GTHV 07/1, RS 2620, CSH 2810, CNH 1094, RHC 0717, L 770
IV	2	GJHV 503, BS 39
V	9	ADB 531, SCS 793, CPD 1002, CNH 1106, RAH 803, Surabhi, TSH 0250, ADB 532, SCS 792

D^2 values computed among 33 genotypes ranged from 1841.70 to 29,306.96 (table 3). Maximum inter cluster distance was observed between clusters III and IV (171.19) followed by Cluster I and III (161.87),

Table 3: Average inter and intra cluster D^2 and D values for 33 cotton genotypes.

Cluster Number	I	II	III	IV	V
I	9685.58 **(98.41)**	8070.25 (89.83)	26201.81 (161.87)	10258.63 (101.28)	12184.93 (110.38)
II		374.22 **(19.34)**	19190.89 (138.53)	1841.70 (42.91)	10139.64 (100.69)
III			11223.87 **(105.94)**	29306.96 (171.19)	24789.09 (157.44)
IV				1007.30 **(31.73)**	13362.45 (115.59)
V					16536.51 **(128.59)**

Table 4: Cluster means of 33 cotton genotypes for various characters.

S. No.	Characters	I	II	III	IV	V
1	Days to 50% flowering	64.41	55.66	85.92	64.66	68.88
2	Plant height	133.45	102.95	97.42	101.0	125.92
3	No. of sympodial branches/plant	17.91	20.50	16.37	18.50	18.11
4	Number of bolls per plant	48.77	51.66	37.58	50.66	51.22
5	Single boll weight	3.60	3.10	3.10	3.12	3.11
6	Seed index	8.85	8.72	7.64	8.38	8.44
7	Ginning out turn	35.02	33.61	38.91	31.88	35.32
8	Lint index	4.80	4.42	4.82	3.92	4.60
9	Biological yield	14.93	14.21	12.42	18.10	14.14
10	2.5 per cent span length	27.50	27.00	28.40	29.40	27.67
11	Micronaire	4.40	4.45	4.70	4.35	4.80
12	Bundle strength	20.14	14.23	20.66	20.86	21.77
13	Seed cotton yield	2584.5	2387.0	1731.9	2342.8	2397.5

whereas minimum inter cluster distance was observed between cluster II and IV (42.91) followed by between clusters I and II (89.83) and so on. The intra cluster distance was maximum in cluster V (128.59) followed by cluster II (105.94) and Cluster I (98.41) and so on.

Out of these Clusters, the minimum intra cluster distance was recorded for the cluster II (19.34) followed by cluster IV (31.73). Thus, the hybridization between genotypes from distant clusters may result in heterotic hybrids and transgressive segregants.

Cluster mean values for yield and its component traits have been presented in table 4. Cluster I recorded maximum average values for plant height, single boll weight, seed index and seed cotton yield whereas cluster III recorded maximum for days to fifty per cent flowering, ginning out turn and lint index.

The contribution of different characters towards total divergence has been presented in table 5. It revealed that with 39.58 per cent contribution by ginning outturn with 28.03 per cent contribution by the seed cotton yield and 23.67 per cent contribution by plant height were the major forces of discrimination among the genotypes tested. Similar findings were made by Sakthi *et al*., 2009; Preetha and Raveendran (2008); Sambamurthy *et al.,* 2005.

Table 5: Contribution of each character to genetic divergence.

S.No.	Characters	Contribution (%) of each character
1.	Days to 50% flowering	0.00
2.	Plant height	26.67
3.	Number of sympodial branches per plant	0.00
4.	Number of bolls per plant	0.00
5.	Single boll weight	1.13
6.	Seed index	0.37
7.	Ginning out turn	39.58
8.	Lint index	0.18
9.	Biological yield	3.78
10.	2.5 per cent span length	1.13
11.	Micronaire	1.51
12.	Bundle Strength	0.56
13.	Seed cotton yield	28.03

The major traits contributing to total divergence may be utilized as parameters in selecting genetically diverse parents. It is necessary to carefully analyse the selection of a particular cluster from which genotypes are to be chosen in crossing programme as well as selection of a particular genotype from a selected cluster. While selecting genotypes from distinct cluster for hybridization programme their *per se* performance of different traits should also be given due importance depending upon the traits to be combined.

On the basis of above results, it is clear that CSH 2810 from cluster III and GJHV 503 from cluster IV were superior for major yield contributing characters. These lines therefore can be considered as potential parents for cotton breeding programmes aimed at the development of high yielding cultivars with high performance.

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