

Genetic Divergence in Cotton (*Gossypium hirsutum* L.) for Yield and Yield Components

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ABSTRACT

Genetic divergence in cotton was carried out in 40 genotypes based on 15 characters using Mahalanobis D^2 statistic and principal component analysis. The pattern of grouping of genotypes revealed the presence of considerable diversity in the material studied for 15 characters viz., plant height (cm), days to 50% flowering, number of monopodia/plant, number of sympodia/plant, number of bolls/plant, boll weight (g), ginning out-turn (%), seed index (g), lint index (g), 2.5% span length (mm), micronaire (10^{-6} g/in), bundle strength (g/tex), uniformity ratio, seed cotton yield/plant (g) and lint yield/plant (g). The D^2 statistic indicated more percent contribution to divergence by 2.5% span length followed by bundle strength, micronaire, uniformity ratio, number of monopodia/plant and lint yield/plant. Principal component analysis identified six principal components (PCs), which contributed 86.76 per cent of cumulative variance. In both Tocher's and Ward's minimum variance methods the genotype were grouped into seven clusters but vary in clustering pattern. Divergence studies indicated scope of F-2522, TCH-1716, ARBH-1501, HS-296, CPD-1502 and GJHV-517 in the development of heterotic hybrids.

Keywords: Clusters, Genetic divergence, Mahalanobis D^2 statistic, Tocher's method, Ward's minimum variance method.

India is the leading country in terms of area under cotton cultivation and raw cotton production in the world. Cotton (*Gossypium hirsutum* L.) referred as "White gold" is a premier cash and fibre crop. It is also successful commercial crop with potential hybrids/varieties and provides opportunity to the scientists to exploit hybrid vigour commercially. The diversity of parents is of prime importance, to get desirable recombinants in the progenies. Multivariate analysis based on Mahalanobis D^2 statistic is widely used for estimating the genetic diversity. Therefore, the present investigation is an attempt to study genetic divergence in 40 genotypes of cotton using D^2 analysis and principal component analysis.

MATERIAL AND METHODS

The present study was carried out with 40 cotton genotypes obtained from different research centres across the country in randomized block design with three replications at Regional Agricultural Research Station, Lam, Guntur during *khari* 2016-17. The plot size adopted is three rows each of six meter length in each replication with a spacing of 105 cm x 60 cm. The observations were recorded on five randomly selected plants from each genotype in three replications for 15 characters viz., plant height (cm), days to 50% flowering, number of monopodia/plant, number of sympodia/plant, number of bolls/plant, boll weight (g), seed index (g), lint index (g), ginning out

turn (%), 2.5% span length (mm), micronaire value (10^{-6}), bundle strength (g/tex), uniformity ratio, lint yield/plant (g), seed cotton yield/plant (g). The data was statistically analyzed using Mahalanobis D^2 statistic as per Rao (1952), Principal Component Analysis (PCA) as described by Jackson (1991) and cluster analysis as given by Anderberg (1993).

RESULTS AND DISCUSSION

The D^2 statistic showed that, out of 15 characters studied, more percent contribution to diversity was from 2.5% span length (38.2), followed by bundle strength (32.3), micronaire (7.8), uniformity ratio (4.4), number of monopodia per plant (3.7) and lint yield per plant (3.3) indicating the possibility of genetic improvement of the characters. The other characters contributed less towards genetic diversity (Table 1).

Based on the six principal components, a cumulative of 86.76% of variation formed the basis for the divergence into different clusters. The contribution by first PC was maximum and is loaded with contribution viz., days to 50% flowering (0.4), number of bolls/plant (0.2), ginning out turn (3.0), seed index (0.3), lint index (0.1), 2.5% span length (0.1), micronaire (0.1), bundle strength (0.1), seed cotton yield/plant (0.3) and lint yield/plant (0.4) explained the maximum variance in the first principal component (PC_1) and signifying their importance in yield

Table 1. Contribution of different characters towards genetic divergence in 40 genotypes

S. No.	Source	Contribution towards divergence (%)	Times ranked first
1	Plant height (cm)	3	23
2	Days to 50% flowering	0.9	7
3	Monopodia/plant	3.7	29
4	Sympodia/plant	1.7	13
5	Bolls/plant	2.1	16
6	Boll weight (g)	1.4	11
7	Ginning out turn (%)	0.3	2
8	Seed index (g)	0.6	5
9	Lint index (g)	0.1	1
10	2.5% Span length (mm)	38.2	298
11	Micronaire (10-6g/inch)	7.8	61
12	Bundle strength (g/Tex)	32.3	252
13	Uniformity ratio	4.4	34
14	Seed cotton yield/plant	0.3	2
15	Lint yield/plant	3.3	26

Table 2. Eigen values, proportion of the total variance represented by first three principal components, cumulative per cent variance and component loading of different characters in cotton (*Gossypium hirsutum* L.)

	PC ₁	PC ₂	PC ₃	PC ₄	PC ₅	PC ₆
Eigene Value (Root)	4.2	3.3	2.4	1.2	1	0.9
% Var. Exp.	28.4	22.2	15.7	8	6.8	5.7
Cum. Var. Exp.	28.4	50.6	66.3	74.3	81.1	86.8
Plant height (cm)	0.3	0.1	0.4	0.2	0	0.4
Days to 50% flowering	0.3	0.1	0.1	-0.5	0.3	0.3
No. of monopodia/plant	0.3	0.2	0.3	-0.1	0	0.1
No. of sympodia/plant	0.4	-0.2	0	0.1	0	-0.3
No. of bolls/plant	0.2	-0.4	-0.3	0.2	0.2	0.3
Boll weight (g)	0.1	0.4	0.3	-0.2	-0.2	-0.4
Ginning out-turn (%)	0.3	-0.2	-0.1	0.2	0.4	-0.6
Seed index (g)	0.3	-0.2	-0.3	0	-0.2	0
Lint index (g)	0.1	-0.2	-0.3	-0.5	-0.5	0.1
2.5% span length (mm)	0.1	0.4	-0.3	0.2	-0.2	-0.2
Micronaire (10 ⁻⁶ g/inch)	0.1	-0.3	0.3	0.3	-0.5	0
Bundle strength (g/tex)	0.1	0.3	-0.2	0.4	-0.3	0.2
Uniformity ratio	0.2	-0.3	0.3	0	0	0.1
Seed cotton yield/ plant (g)	0.3	0.3	-0.2	0	0.2	0.3
Lint yield/plant (g)	0.4	0.1	-0.2	-0.1	-0.1	-0.1

PC= Principal Component

Table 3. Comparison between the Tocher's method and Ward's minimum variance methods for clustering of genotypes in cotton (*Gossypium hirsutum* L.)

Tocher's method			Ward's minimum variance method	
Cluster No.	No. of genotypes	Name of the genotype	No. of genotypes	Name of genotype
1	5	RS-2797, ARBH-1501, HS-296	7	F- 2522 , RS-2821, PBH29, CSH-5038, CCH15-1, BGDS-1055, GTHV 13/28
2	6	CNH126, GJHV-519, RS-2815, RAH-1271, SURAJ, CCH 15-6.	5	SURAJ, F-2532, TCH-1716, L-604, CCH15-5
3	2	GSHV-172, CSH-315.	9	TCH-1824, CSH-3158, CCH15-2, RAH-1069, H-1478, CSH-6109, ND LH-1938, TCH-1876, RAHC-1017
4	3	BGDS-1033, CPD-1502, GJHV	6	CNH126, RS-2797, RS-2815, PBH-19, ARBH-1501, HS-296
5	11	F-2522, PBH29, CCH15-1, TCH-1716, L-604, CSH-5038, CSH-6109, GTHV 13/28, CCH15-5, RS-2821, TCH-1876.	7	CSH-2932, CNH147-1, RAHC-1019, TSH-322, RAH-1271, CCH 15-6, GJHV-519
6	7	TCH-1824, CCH15-2, H-1478, RAH-1069, BGDS-1055, ND LH-1938, RAHC-1017.	5	HS-295, GJHV-517, CPD-1502, BGDS-1033, ARBC-1502
7	6	TSH-322, CSH-2932, HS-295, CNH147-1, ARBC-1502, RAHC-1019 .	1	GSHV-172

Table 4. Average intra-and inter-cluster D^2 and Euclidian² (Given in parenthesis) values among seven clusters in 40 cotton (*Gossypium hirsutum* L.) genotypes

Cluster No.	I	II	III	IV	V	VI	VII
I	10.0 (22.72)	20.8 (44.20)	20.0 (53.70)	39.0 (50.00)	57.4 (51.30)	53.1 (95.40)	38.3 (91.70)
II		12.4 (22.40)	29.0 (53.10)	18.9 (55.30)	25.1 (63.80)	24.2 (94.40)	23.4 (82.60)
III			18.2 (37.70)	53.6 (111.60)	72.9 (104.00)	53.8 (152.10)	46.7 (85.70)
IV				0.0 (32.20)	12.4 (50.60)	14.2 (62.20)	10.0 (110.00)
V					0.0 (28.10)	15.7 (62.40)	23.5 (90.90)
VI						0.0 (24.90)	13.7 (67.00)
VII							0.0 0.0

Values in parentners are the intra and inter cluster euclidian² values among the cluster formed by ward,s minimum variance method.

Table 5. Mean values of seven clusters estimated by Tocher's and Ward's (parenthesis) minimum variance methods from 40 genotypes of cotton (*Gossypium hirsutum* L.)

Cluster No.	Plant height (cm)	Days to 50% flowering	No. of Monopodia/plant	No. of Sympodia/plant	No. of bolls/plant	Boll weight (g)	Ginning out-turn (%)	Seed index (g)	Lint index (g)	2.5% span length (mm)	Micronaire (10-6g/inch)	Bundle strength (g/tex)	Uniformity ratio	Seed cotton yield /plant (g)	Lint yield/plant (g)
Cluster I	117.7	55.7	1.1	15.0	38.5	3.4	31.3	9.3	4.3	28.0	3.9	24.4	47.4	131.7	35.0
	(129.0)	(58.0)	(1.5)	(14.4)	(32.9)	(4.1)	(30.3)	(9.4)	(4.1)	(30.6)	(3.8)	(26.0)	(46.5)	(133.7)	(36.8)
Cluster II	123.6	57.7	1.4	15.4	34.5	3.9	31.1	9.6	4.4	31.4	3.6	25.7	46.5	134.3	36.2
	(121.1)	(58.0)	(1.3)	(16.7)	(38.6)	(3.7)	(32.3)	(10.1)	(4.8)	(32.1)	(3.5)	(25.2)	(46.6)	(138.7)	(37.3)
Cluster III	118.1	57.9	1.2	14.8	33.2	3.7	30.5	9.0	4.0	28.2	3.6	22.1	46.4	126.4	35.1
	(116.6)	(56.0)	(1.3)	(14.3)	(32.7)	(3.9)	(30.7)	(9.0)	(4.0)	(33.4)	(3.4)	(27.0)	(45.1)	(125.5)	(32.4)
Cluster IV	111.2	56.7	1.0	14.2	38.2	3.5	27.8	9.7	3.8	34.5	3.6	27.9	45.0	134.5	32.2
	(127.2)	(60.0)	(1.4)	(16.9)	(34.0)	(4.1)	(32.0)	(9.8)	(4.6)	(29.0)	(4.0)	(23.6)	(47.6)	(139.0)	(40.8)
Cluster V	121.2	58.0	1.6	15.3	30.3	4.4	32.6	9.7	4.7	35.4	3.8	29.0	45.7	137.3	39.4
	(117.7)	(56.0)	(1.1)	(15.0)	(40.0)	(3.3)	(31.5)	(9.3)	(4.3)	(28.0)	(3.9)	(24.6)	(47.2)	(131.4)	(34.7)
Cluster VI	124.9	54.7	1.2	14.3	32.1	4.0	32.8	7.9	3.9	36.1	3.2	26.1	44.3	121.2	33.3
	(115.7)	(57.0)	(1.2)	(14.2)	(33.9)	(3.7)	(30.5)	(8.4)	(3.7)	(27.6)	(3.4)	(21.2)	(46.6)	(124.4)	(32.6)
Cluster VII	111.6	52.3	1.1	12.2	32.1	3.2	29.2	8.1	3.3	33.6	3.7	26.5	42.2	96.6	28.3
	(99.4)	(54.0)	(1.0)	(12.4)	(28.1)	(3.2)	(25.1)	(9.1)	(3.0)	(30.2)	(3.1)	(23.2)	(43.5)	(98.7)	(29.4)

Values in parentheses are the mean values of seven clusters estimated by Ward's minimum variance method

Diagram illustrating the cluster pattern for the genotypes of cotton studied

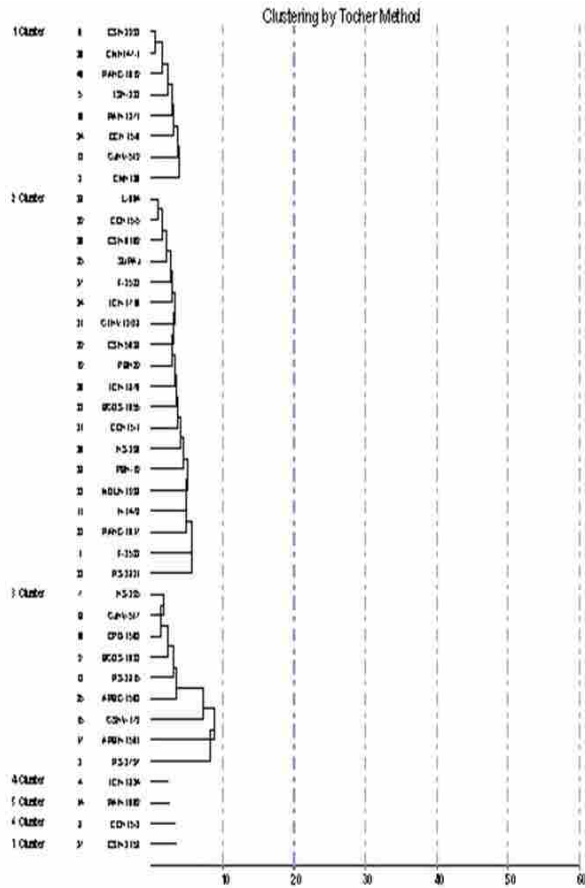


Fig. 1. Tocher's method

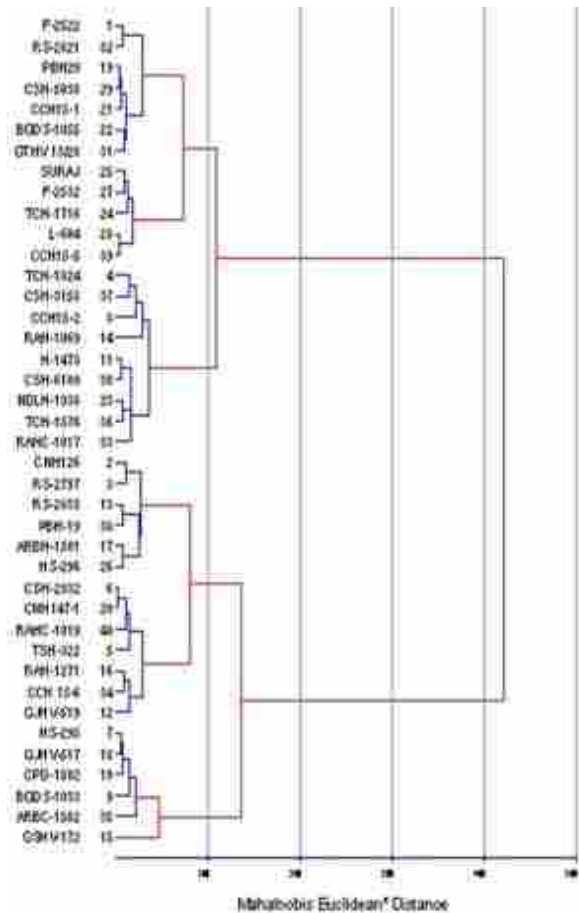


Fig. 2. Ward's minimum variance method

improvement. The principal component scores of genotypes were used as input for clustering procedures in order to group the genotypes into various clusters and confirm the results of principal component analysis. Main principal components are given in Table 2.

The results of multivariate analysis revealed the presence of considerable genetic variance among the 40 cotton genotypes and were grouped into seven clusters both in Tocher's and Ward's minimum variance methods. In Tocher's method, maximum genotypes were in cluster V (11) followed by cluster VI (7) while six genotypes each were grouped in cluster II and VII, followed by cluster I (5), cluster IV (3) and cluster III (2) (Table 3 and Fig. 1.) while in Ward's minimum variance method, maximum genotypes nine were grouped in cluster III followed by cluster I and V with seven genotype each. Six genotypes were grouped in cluster IV followed by cluster II and VI with five genotypes while one genotype in cluster VII. (Table 3 and Fig. 2)

Based on D^2 values, intra-cluster distances ranged from zero (cluster IV, V, VI and VII) to 18.2

(cluster III), while maximum inter-cluster distance was observed between cluster III and V followed by clusters I and V. The minimum inter-cluster distance was observed between cluster IV and V as shown in Table 4. On the basis of Euclidian² values, intra-cluster distances ranged from 0.0 (cluster VII) to 37.7 (cluster III) where as the maximum inter-cluster distance was observed between cluster III and VI followed by cluster III and IV while minimum inter-cluster distance in cluster I and II as shown in Table 4. In general, higher the divergence between the genotypes, higher will be the heterosis (Falconer, 1964). Therefore, it would be desirable to attempt crosses between the genotypes belonging to distant clusters for getting heterosis which may give rise to wide range of segregants.

In Tocher's method, low cluster means were observed in cluster VII for days to 50% flowering (52.3) which may be useful in evolving early types (Table 5). High cluster means were observed in cluster V for boll weight, lint index, bundle strength, seed cotton yield/plant and lint yield/plant; cluster IV for plant height and seed index; cluster I for bolls/plant, bolls/plant,

micronaire and Uniformity ratio; and cluster II for sympodia/plant; and cluster VI for plant height and ginning out turn. Low mean values for days to 50% flowering and high mean values for other characters is important to select the genotypes from the clusters. The results are in agreement with Mansingh *et al* (2016). The cluster mean values for all the 15 characters based on Ward's minimum variance method are presented in Table 5. Cluster IV has recorded high mean values for days to 50% flowering, number of sympodia, boll weight, micronaire, uniformity ratio, seed cotton yield/plant, lint yield/plant. These results are in agreement with Tulasi *et al* (2014).

CONCLUSION

The genotypes F-2522, TCH-1716, ARBH-1501, HS-296, CPD-1502 and GJHV-517 showed maximum inter-cluster distance in Mahalanobis' D^2 analysis, principal component analysis and cluster analysis and also have better *per se* performance for

number of sympodia/plant, number of bolls/plant, boll weight, seed index, lint index and quality characters. So, they can be exploited for the development of heterotic hybrids in future breeding programmes.

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Received on 21.06.2017 and revised on 04.12.2017