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Research Article

Estimation of genetic diversity in upland cotton (*Gossypium hirsutum* L.) genotypes

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Abstract

Genetic divergence of sixty genotypes of upland cotton for 15 characters was estimated using D^2 statistic. The genotypes were grouped into 11 clusters based on D^2 values and PCA identified seven principal components which explained 78.6 per cent of the total variability. Divergence results indicated that geographical diversity is not necessarily associated with the genetic diversity. Multivariate analysis revealed maximum divergence among genotypes HYPS 152, GISV 267, MCU 5, L 389 and TCH 1741 signifying their role in possible exploitation of heterosis.

Key words

Genetic divergence, D^2 statistic, Principal Component Analysis, *Gossypium hirsutum* L.

Introduction

Cotton alone accounts for 70 per cent of total fibre consumption in textile sector with approximately 38 per cent of the country's export. The diversity of parents is of prime importance, since the crosses made between the genetically divergent parents are likely to throw desirable recombinants in the progenies. The present study was carried out to study genetic divergence in 60 genotypes of upland cotton with two methods of clustering based on D^2 analysis and principal component analysis. Mahalanobis' D^2 statistic is an effective tool in quantifying the degree of genetic divergence at genotypic level and provides quantitative measure of association between geographic distribution and genetic diversity based on generalized distance (Mahalanobis, 1928) and Principal Component Analysis was carried out to transform the inter dependent traits into a set of independent traits as well as to reduce the dimensionality of the data structure (Banfield, 1978).

Material and Methods

The present study was carried out with 60 genotypes of cotton (*Gossypium hirsutum* L.) obtained from different research centres across the country which were evaluated using randomized complete block design with three replications at Regional Agricultural Research Station, Lam Farm, Guntur, Andhra Pradesh during *kharif* 2014-15. The inter- and intra-row spacing adopted was 105 cm x 60 cm. Each plot consisted of 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, lint yield per plant (g) and seed cotton yield per plant(g), while, days to 50% flowering, boll weight (g), seed index (g), lint index (g), micronaire (10^{-6}g/in), bundle strength (g/tex), ginning out-turn (%), 2.5% span length (mm) and uniformity ratio were also recorded. The fibre quality characters were analyzed at CIRCOT regional unit Lam, Guntur. The data were statistically analyzed to study diversity by Mahalanobis' D^2 statistic as per Rao (1952) and principal component analysis (PCA) as described by Jackson (1991).

Results and Discussion

On the basis of D^2 values, the sixty genotypes were grouped into 11 clusters (Fig. 1), out of which cluster I was the biggest cluster with 34 genotypes followed by clusters II and III which consisted of nine genotypes each while, the remaining clusters IV, V, VI, VII, VIII, IX, X and XI consisted of single genotype as shown in Table 1.

The per cent contribution towards genetic divergence was maximum by 2.5% span length (18.14 %) followed by seed index (17.57 %), days to 50% flowering (13.62 %), micronaire (10.56 %), number of monopodia per plant (10.45 %), bundle strength (8.02 %), number of bolls per plant (6.1 %), seed cotton yield per plant (5.48 %), plant height (4.41 %), boll weight (1.86 %), lint index (1.41 %), lint yield per plant (1.19 %), uniformity ratio (0.68 %), ginning out-turn (0.34 %) and number of sympodia per plant (0.17 %) as shown in Table 2.

The maximum intra cluster distance was observed for cluster III (35.23) followed by cluster II (31.03) and cluster I (24.95), while, it was zero for clusters IV, V, VI, VII, VIII, IX, X and XI as they were mono genotypic (Table 3). The high intra-cluster distance in cluster III indicated the presence of wide genetic diversity among the genotypes present within this cluster.

The inter-cluster distance was maximum between cluster IX and X (185.35), followed by cluster X and XI (177.20), cluster VII and XI (122.06), cluster VIII and X (115.83), cluster V and IX (110.20), cluster V and XI

(104.69), cluster III and VII (101.74) and cluster IV and VIII (100.36). This suggested that there is wide genetic diversity between these clusters. Based on these studies crosses can be made between genotypes of these clusters to obtain heterotic hybrids.

A general notion exists that the larger the divergence between the genotypes, the higher will be the heterosis (Falconer, 1964). Therefore, it would be desirable to attempt crosses between the genotypes belonging to distant clusters for getting highly heterotic crosses which are likely to yield a wide range of segregants on which selection can be practiced. By Mahalanobis' D^2 statistic, it could be inferred that based on intra-and inter-cluster distance among the groups, it is suggested to make crosses between the genotypes of cluster IX (HYPS 152) and cluster X (IH 65), between genotypes of cluster X (IH 65) and cluster XI (L 389), between the genotypes of cluster VII (TCH 1705) and cluster XI (L 389), between the genotypes of cluster VIII (GISV 267) and cluster X (IH 65) after confirming their combining ability.

Principal component analysis identified seven principal components (PCs), which contributed 78.6 per cent of cumulative variance. The first principal component (PC_1) contributed maximum towards variability (19.33) followed by PC_2 (16.04), PC_3 (11.48), PC_4 (10.62), PC_5 (8.96), PC_6 (7.09) and PC_7 (5.18) as shown in Table 4. The significant factors loaded in PC1 towards maximum genetic divergence were plant height, ginning out turn, lint yield per plant, number of bolls per plant, 2.5% span length, seed index, lint index, number of monopodia per plant, days to 50% flowering, seed cotton yield per plant, number of sympodia per plant and boll weight. 2D graphs (Fig. 2) showed wide divergence between GISV 267, MCU 5, HYPS 152, TCH 1741, CNH 120 M/B, LH 2256 and IH 65 signifying their usefulness in cotton breeding to develop high heterotic hybrids.

The genotypes HYPS 152, GISV 267, MCU 5, L 389 and TCH 1741 showed maximum inter-cluster distance in Mahalanobis' D^2 analysis, principal component analysis and also had better *per se* performance in sympodia per plant, number of bolls per plant, boll weight, seed index, lint index and quality characters. So these genotypes may be exploited for the development of heterotic hybrids in future breeding programmes.

Selection of parents for hybrid breeding programme is of prime importance in the utilization of heterosis. For obtaining hybrids with high level of heterosis is a question generally arises regarding the ideal distance (degree of divergence) at phenotypic level. Arunachalam and Bandopadhyay (1984) have proved experimentally that more number of heterotic combinations with higher level of heterosis was from the parents grouped into moderate divergent groups. Hence, along with the above mentioned 5 genotypes two other genotypes viz., LH 2256 and HS 292 which belong to moderately divergent groups can also be included in producing heterotic combinations using crossing patterns like diallel or partial diallel.geographical diversity in the present study. Hence, selection of varieties should be more dependent on genetic diversity than the geographical diversity. Similar findings were also reported by Asha *et al*. (2013), Kavithamani *et al.* (2013) and Tulasi *et al.* (2014). In a broad sense, all the three methods of classifying genotypes into different groups is equally useful but hierarchical cluster analysis gave an additional advantage of identifying sub-clusters of the major groups so that these small groups can be critically analysed.

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Table 1. Clustering pattern of 60 cotton (*Gossypium hirsutum* L.) genotypes by Tocher's method

Cluster No.	No. of genotypes	Name of the genotype
I	34	SCS 1002, CNH 120 M/B, BS-3, GJHV 511, CCH 11-2, ARBH 701, RAH 1066, PRAMUK, GJHV 375, GJHV 02145, L 808, CCH 1831, RB 57, AKALA 15-77 D, CNH 19, CCH 11-1, P 5629, H 1300, SCS 1211, ARBA 271, KH 1101, TSH 04/115, CNH 44, HS 293, L 1058, RHC 0811, CNH 1116, NDLH 1938, NH 644, 241-2-4, L 804, DS 56, GJHV 516, BJA 592
II	9	SCS 1001, HS 292, KH 1301, SCS 1210, ARBH 1301, CPD 1301, L 1801, SCS 1214, HAG 1055
III	9	RSA 2455, H 7, TSH 0499, H 1442, TCH 1741, MCU 5, LH 2256, CPD 1302, L 1011
IV	1	CNH 50
V	1	IH 615
VI	1	L 604
VII	1	TCH 1705
VIII	1	GISV 267
IX	1	HYPS 152
X	1	IH 65
XI	1	L 389

Table 2. Contribution of different characters towards genetic divergence in 60 cotton (*Gossypium hirsutum* L.) genotypes.

S. No.	**Character**	**Contribution towards divergence (%)**	**Times ranked first**
1	Plant height (cm)	4.41	78
2	Days to 50% flowering	13.62	241
3	Number of monopodia per plant	10.45	185
4	Number of sympodia per plant	0.17	3
5	Number of bolls per plant	6.1	108
6	Boll weight (g)	1.86	33
7	Ginning out-turn (%)	0.34	6
8	Seed index (g)	17.57	311
9	Lint index (g)	1.41	25
10	2.5% Span length (mm)	18.14	321
11	Micronaire (10^{-6}g/in)	10.56	187
12	Bundle strength (g/tex)	8.02	142
13	Uniformity ratio	0.68	12
14	Seed cotton yield per plant (g)	5.48	97
15	Lint yield per plant (g)	1.19	21

Table 3. Average intra-and inter-cluster D^2 values among 11 clusters in 60 cotton (*Gossypium hirsutum* L.) genotypes.

Cluster No	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	**24.95**	36.11	44.31	35.50	39.20	32.89	54.01	60.22	55.00	71.39	67.87
II		**31.03**	59.14	47.71	41.25	56.21	47.40	46.12	66.54	67.14	96.02
III			**35.23**	72.00	61.17	51.30	101.74	55.47	69.07	96.15	69.18
IV				**0.00**	14.84	32.80	32.58	100.36	99.37	39.77	95.15
V					**0.00**	53.87	41.62	83.04	110.20	25.77	104.69
VI						**0.00**	64.72	91.44	63.98	99.52	73.68
VII							**0.00**	91.50	90.11	70.71	122.06
VIII								**0.00**	59.03	115.83	87.48
IX									**0.00**	185.35	27.69
X										**0.00**	177.20
XI											**0.00**

Table 4. Eigen values, proportion of the total variance represented by first seven 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**	**PC_7**
Eigen Value (Root)	2.90	2.41	1.72	1.59	1.34	1.06	0.78
% Var. Exp.	19.33	16.04	11.48	10.62	8.96	7.10	5.18
Cum. Var. Exp.	19.33	35.37	46.85	57.46	66.42	73.52	78.70
Plant height (cm)	0.38	0.11	0.17	0.18	0.31	0.24	0.37
Days to 50% flowering	0.10	-0.33	0.26	-0.43	-0.07	0.18	0.19
No. of monopodia/ plant	0.22	0.28	-0.34	-0.31	-0.20	0.22	0.11
No. of sympodia/ plant	0.05	-0.04	0.12	-0.52	0.31	0.05	-0.43
No. of bolls/ plant	0.27	0.34	0.05	0.07	0.53	-0.02	0.10
Boll weight (g)	0.03	-0.15	-0.15	0.50	-0.10	0.41	-0.02
Ginning out-turn (%)	0.31	-0.35	-0.18	0.03	0.05	0.27	-0.12
Seed index (g)	0.26	-0.34	-0.37	0.05	0.19	-0.03	-0.24
Lint index (g)	0.26	-0.22	-0.14	0.11	0.24	-0.63	-0.10
2.5% Span length (mm)	0.27	-0.16	0.35	0.27	-0.35	-0.13	-0.22
Micronaire (10g/Inch)	-0.47	-0.12	-0.29	0.02	0.11	0.07	-0.17
Bundle strength (g/tex)	-0.14	-0.34	-0.35	-0.09	0.18	0.04	0.46
Uniformity ratio	-0.29	-0.23	0.23	0.08	0.15	-0.26	0.39
Seed cotton yield/ plant(g)	0.09	-0.40	0.32	-0.12	-0.03	0.15	0.06
Lint yield/ plant (g)	0.30	0.03	-0.28	-0.19	-0.43	-0.33	0.29

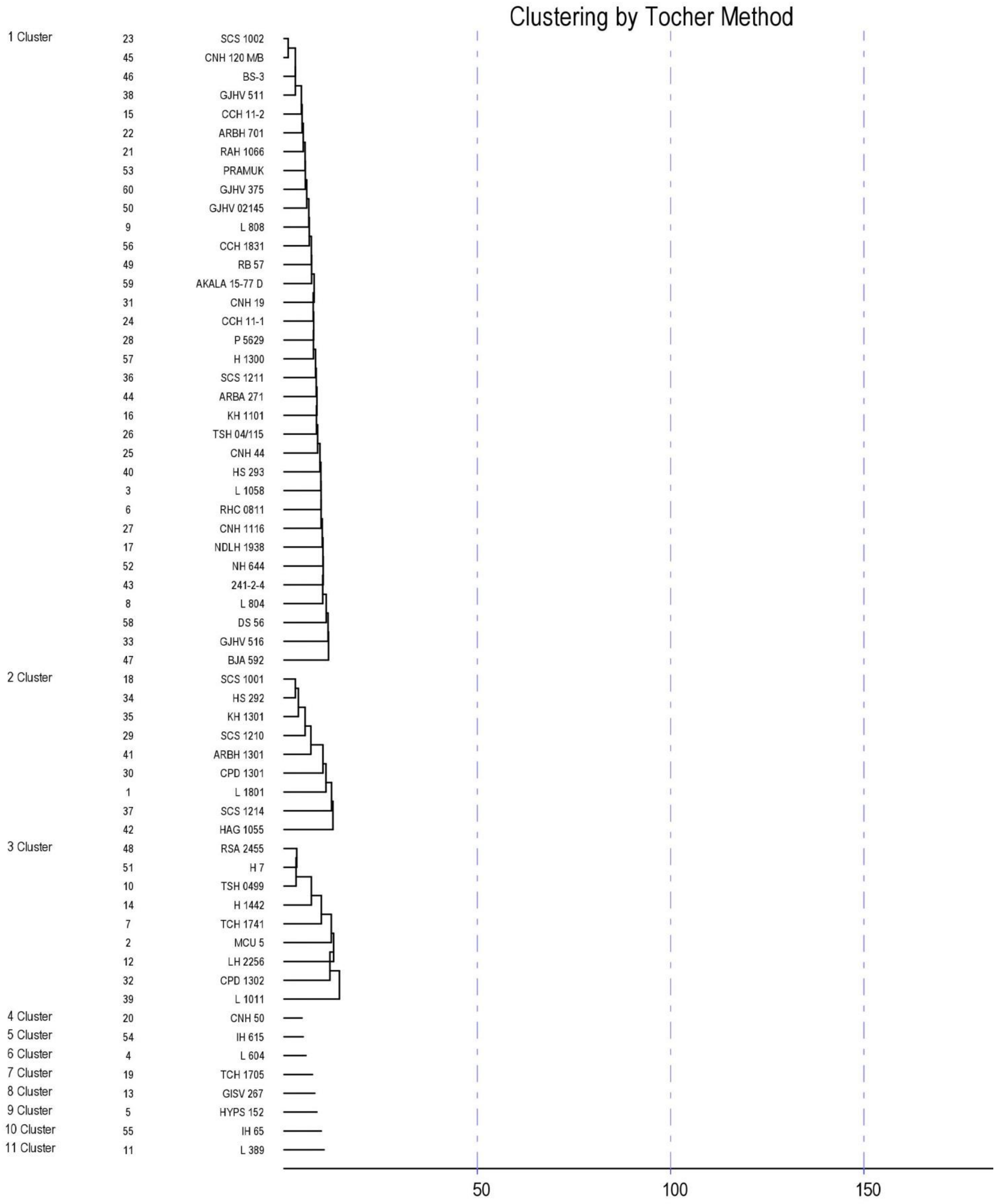

Fig.1. Dendrogram showing relationship among 60 cotton (*Gossypium hirsutum* L.) genotypes in eight clusters based on Mahalanobis' D^2 values.

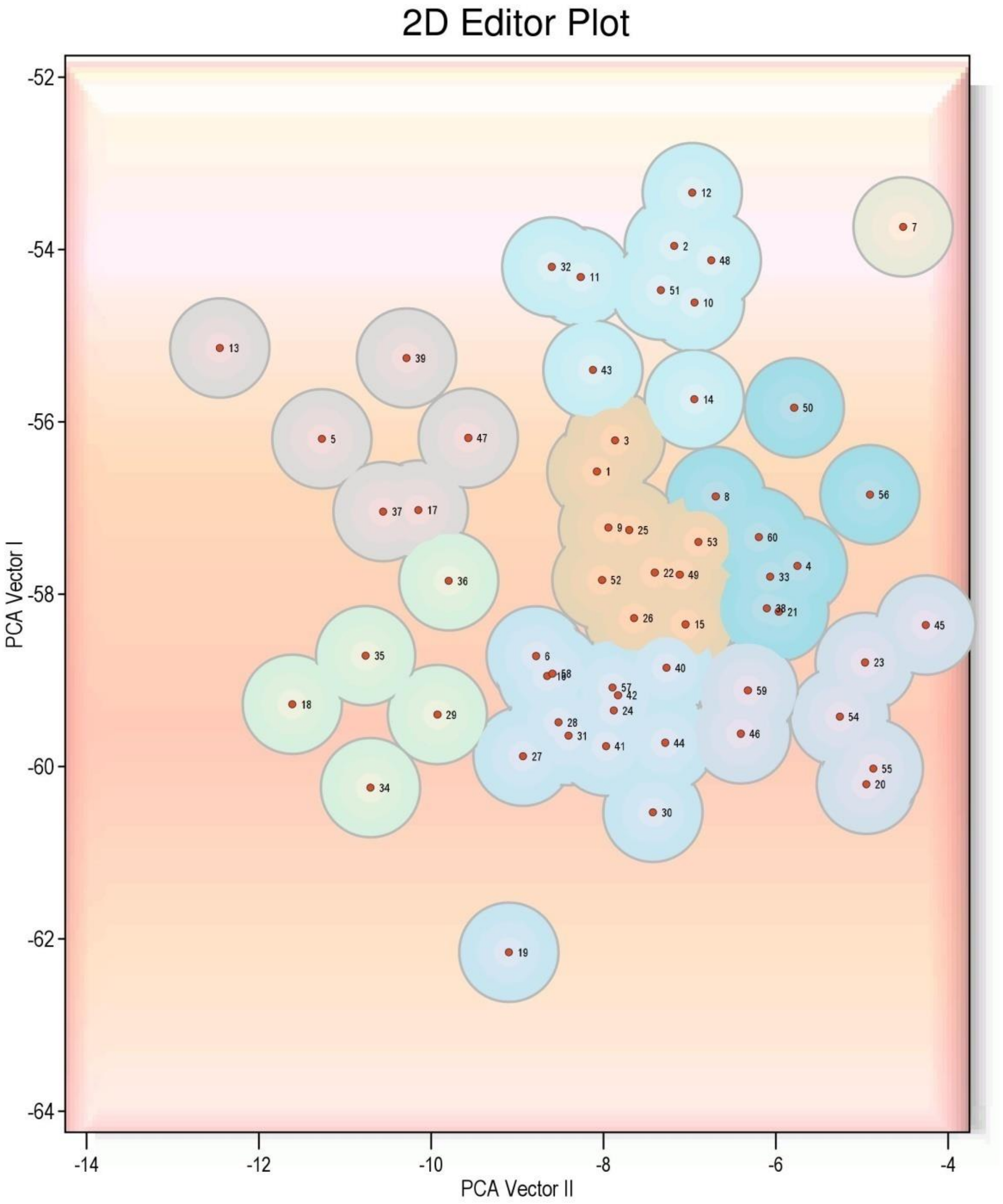

Fig. 2 . Two dimensional graph showing relative position of 60 cotton (*Gossypium hirsutum* L.) **genotypes based on PCA scores.**