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Identification of desirable genotypes by multivariate analysis in cotton (*Gossypium hirsutum* L.)

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ABSTRACT : Genetic divergence study was conducted with 37 upland cotton genotypes using Mahalanobis D^2 analysis. Total genotypes were grouped into nine clusters. The maximum inter cluster distance was recorded between cluster V and cluster IX. Maximum intra cluster distance was recorded in cluster I. Lint index contributed maximum per cent towards genetic divergence followed by seed index and boll weight. Cluster IX recorded maximum cluster mean value for quantitative characters and cluster VII recorded high cluster mean values for qualitative characters. Hybridization between CCH-14-1 and SCS 1207 may result in development of heterotic hybrid. The genotypes, HS 294, SCS 106, F 2501, CSH 3232, Suraj, CCH-14-1 and TSH 0533-2 may be utilized in future breeding programmes for exploitation of heterosis by using different mating designs.

Key words : Genetic divergence, mahalanobis D^2 analysis, principal component analysis, upland cotton

Cotton (*Gossypium hirsutum* L.) is the one among the major cash crops all over the world. In India the maximum cotton growing area is occupied by the hybrids than varieties. It further increased after introduction of *Bt* cotton hybrids. It was well proven that India is the pioneer country in development of cotton hybrids and their cultivation as it is evident by first intra *hirsutum* cotton hybrid was developed by India (Patel, 1971). Hybrids are superior than the varieties for seed cotton yield and fibre quality parameters as well as tolerance to some biotic and abiotic stresses. The superiority of hybrids over varieties is due to exploitation of heterosis. The heterosis breeding mainly depends on the availability of variability and presence of genetic divergence in any crop (Abd El-Moghny *et al.*, 2015). Genetic divergence studies play key role in selection of parents for hybridization program (Anil *et al.*, 2017). Shah, *et al.* (2018) reported that selection of parents from distant clusters indicates that they are genetically distinct and result in development of good heterotic hybrids or occurrence of superior transgressive seggregants in segregating generations. Hence, the present investigation was conducted to identify better parents for future hybridization program.

The present investigation was conducted during *kharif* 2014-2015 at Regional Agricultural Research Station, Lam. Thirty seven genotypes collected from different parts of country (Karnataka, Tamil Nadu, Haryana and Gujarat) were planted in randomized block design with three replications by adopting 105 x 60 cm spacing. All recommended agronomic package of practices for cotton crop were followed for raising a good crop. Observations were recorded on five randomly selected plants from each replication from each treatment. Data were analyzed for analysis of variance as per Cochran and Cox (1950) and genetic divergence was analyzed by Mahalanobi's D^2 statistic method (1936) and genotypes were grouped into different clusters by using Tocher's method described by Rao (1952). Principal Component Analysis (PCA) was carried out according to the procedure described by Banfield (1978).

The analysis of variance indicated significance of all the studied traits (Table 1). It indicated presence of considerable genetic variation among the genotypes and further analysis was conducted by using Mahalanobi's D^2 statistic for estimating genetic divergence present among the genotypes.

Total genotypes were grouped into nine clusters (Table 2). Cluster I consisted of maximum number of genotypes *viz.*, RS 2765, PBH 13, F 2501, SCS 1061, PBH 10, Shakti Sultana, F 2493, RS 2767, HS 294, CCH 14-2, RAH 1033, CPD 1401, TCH 1806, H 1471, CPD 1402, GJHV 510, GJHV 497, ARBH 1401, Suraj, RAH 1066, CNH 1118, BS 26 and CSH 3232 followed by cluster II viz., CNH 5, BS 23, L 1008, GSHV 177, L 1060, CSH 2838 and TSH 053-1 and cluster III (TSH 0533-2), cluster IV (GTHV 13/37), cluster V (GSHV 179), cluster VI (ARBH 1402), cluster VII (CCH 14-1), cluster VIII (L 604) and cluster IX (SCS 1207) consists one genotype each (Fig. 1). Similar kinds of results were also reported by Kanihal *et al.* (2018).

Table 1. Analysis of variance for quantitative and qualitative characters in cotton (*Gossypium hirsutum* L.)

Source	Df	DFF	PH	NMP	NSP	NB	BW	SI	LI	GOT	SCY	LY	2.5(%SL)	BS	MIC	UR
Replications	2	20.57	2001.00	1.64	1.88	149.17	0.16	1.17	0.62	1.25	71.72	6.58	6.40	5.27	0.21	0.76
Treatments	36	35.75**	320.69**	0.56**	5.58**	78.74**	0.44**	3.80**	1.50**	18.98**	35.41**	6.24**	5.55**	4.16**	0.21	3.47
Error	72	11.61	43.08	0.10	2.35	15.84	0.04	0.19	0.08	0.89	11.59	1.46	1.33	1.00	0.24	2.25

*Significant at 5% level **Significant at 1% level

Maximum inter cluster distance was recorded between cluster V and IX (78.86) followed by cluster VIII and cluster IX (77.81) and cluster VI and VIII (75.78). Minimum inter cluster distance exhibited between cluster IV and cluster VI (22.16) followed by cluster IV and cluster VII (22.20) and cluster I and cluster III (22.56). Hybridization between genotypes present in different clusters with high inter cluster distance may result in development of superior heterotic cross combinations or create greater genetic variability. Maximum intra cluster distance was observed in cluster I (15.07) (Table 3) (Fig.2). Hybridization programme performed among genotypes belongs to same clusters by using mating designs like diallel and partial diallel may result in producing good heterotic cross combinations or occurrence of desirable transgressive seggregants in segregating generations. The clustering pattern revealed that genetic divergence did not fully depend on geographical diversity and some other factors are also leading to presence of genetic diversity among the genotypes. These results are in association with Anil *et al.* (2017), Ranjan *et al.* (2014) and Anil *et al.* (2017)

Cluster II recorded minimum value for days to 50 per cent flowering and maximum mean values for no.of monopodia per plant and no.of bolls per plant. Cluster VI recorded maximum mean values for plant height, ginning

Table 2. Number of genotypes in different clusters

Cluster no.	Number of genotypes
I	RS 2765, PBH 13, F 2501, SCS 1061, PBH 10, Shakti Sultana, F 2493, RS 2767, HS 294, CCH 14-2, RAH 1033, CPD 1401, TCH 1806, H 1471, CPD 1402, GJHV 510, GJHV 497, ARBH 1401, Suraj, RAH 1066, CNH 1118, BS 26 and CSH 3232
II	5, BS 23, L 1008, GSHV 177, L 1060, CSH 2838 and TSH 053-1
III	TSH 0533-2
IV	GTHV 13/37
V	GSHV 179
VI	ARBH 1402
VII	CCH 14-1
VIII	L 604
IX	SCS 1207

Table 3. Intra and inter cluster distances

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9
Cluster 1	15.07	28.03	22.56	25.03	25.77	30.50	30.90	43.89	41.96
Cluster 2		13.98	31.82	31.24	47.24	52.99	27.10	29.78	47.55
Cluster 3			0.00	31.35	49.10	25.37	36.62	44.36	58.17
Cluster 4				0.00	34.64	22.16	22.20	59.99	38.27
Cluster 5					0.00	50.65	42.76	53.46	**78.86**
Cluster 6						0.00	37.95	**75.78**	42.97
Cluster 7							0.00	47.59	32.14
Cluster 8								0.00	**77.81**
Cluster 9									0.00

out turn and uniformity ratio. Cluster IX exhibited minimum mean value for monopodia/plant and maximum mean values for boll weight, seed index, lint index, seed cotton yield/plant, lint yield/plant and micronaire value (Table 4).

Lint index contributed maximum towards genetic divergence followed by seed index, boll weight, plant height, 2.5 per cent span length, bolls/plant, bundle strength, lint yield, sympodia/plant, monopodia/plant, micronaire value and negligible by days to 50 per cent flowering and uniformity ratio (Table 5).

The main purpose of principal component analysis in genetic divergence is to know the maximum contributing variable towards variability in principal component. Principal component analysis revealed that 37 genotypes were represented in the first six principal components. First principal component explained maximum variability (25.93) followed by remaining five principal components (Table 6).

Monopodia/plant (0.214), bolls/plant (-0.343), lint index (-0.306), seed cotton yield/ha (0.385), bundle strength (0.398), uniformity ratio (-0.389) in first principal component explained more variance. In the second principal component the traits *viz.*, monopodia/plant (-0.313), plant height (-0.450), sympodia/plant (0.303), seed index (-0.387) explained maximum

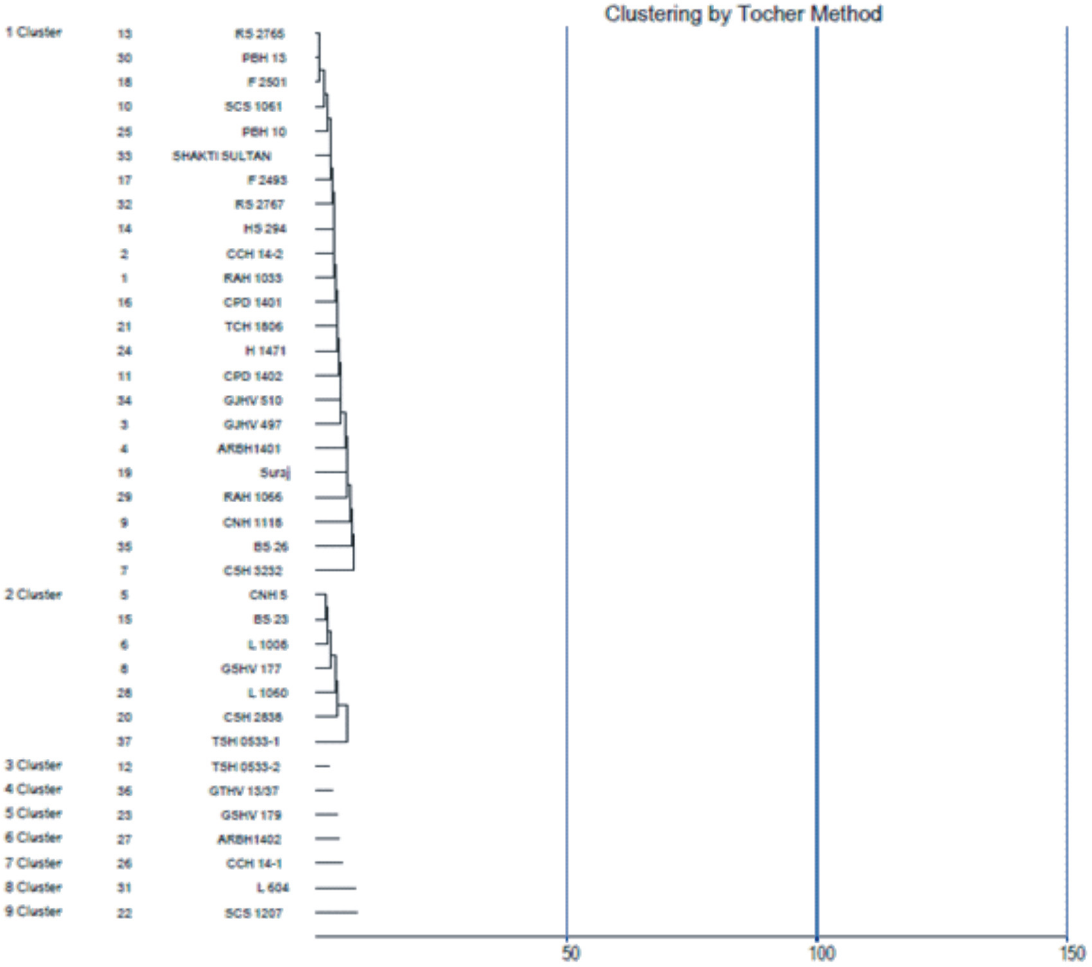

Fig 1. Dendrogram showing relationship of 37 cotton (*Gossypium hirsutum* L.) genotypes in seven clusters based on Mahalanobis' D^2 values

Table 4. Mean values of different clusters for various traits in cotton

	DFF	PH	NMP	NSP	NB	BW	SI	LI	GOT	SCY	LY	2.5(%SL)	BS	MIC	UR
Cluster 1	63.94	138.33	1.33	17.76	38.50	4.80	9.71	5.15	34.63	27.73	9.62	27.42	21.29	3.99	49.07
Cluster 2	65.00	133.24	2.02	17.63	37.08	4.93	10.91	4.70	30.10	27.73	8.34	28.05	21.95	4.04	48.68
Cluster 3	**58.33**	140.20	**2.07**	17.73	**38.53**	**3.97**	9.60	4.83	33.43	22.41	7.47	29.57	22.73	3.80	**46.13**
Cluster 4	63.00	162.80	**2.07**	17.67	34.33	5.30	10.33	5.77	35.80	27.07	9.71	28.57	22.23	3.87	47.30
Cluster 5	**72.67**	143.00	**1.20**	18.27	37.13	4.87	**7.93**	**4.60**	36.70	27.33	10.02	**25.33**	21.90	3.90	48.60
Cluster 6	70.00	**159.27**	1.60	16.93	37.53	4.23	11.07	6.37	**36.87**	23.36	8.62	26.80	**20.37**	3.73	**49.70**
Cluster 7	71.67	144.67	1.47	**21.07**	**28.13**	5.30	11.23	6.00	34.83	22.88	7.99	**31.77**	**24.57**	**4.07**	46.07
Cluster 8	67.67	**122.93**	1.87	**15.53**	28.77	4.30	9.70	3.90	**28.63**	**19.26**	**5.55**	27.60	21.73	3.50	49.17
Cluster 9	61.67	131.53	**1.20**	18.53	35.03	**5.70**	**13.30**	**7.43**	35.83	**31.16**	**11.16**	27.87	20.77	**4.07**	48.03

DFF: Days to 50% flowering, PH: Plant height, NMP: No.of monopodia/plant, NSP: No. of sympodia/plant NB: No.of bools/plant BW: Boll weight SI: Seed index, LI: Lint index GOT: Ginning out-turn SCY: Seed Cotton Yield/plant LY: Lint yield 2.5% Span length BS: Bundle strength MIC: Micronaire value

UR: Uniformity ratio

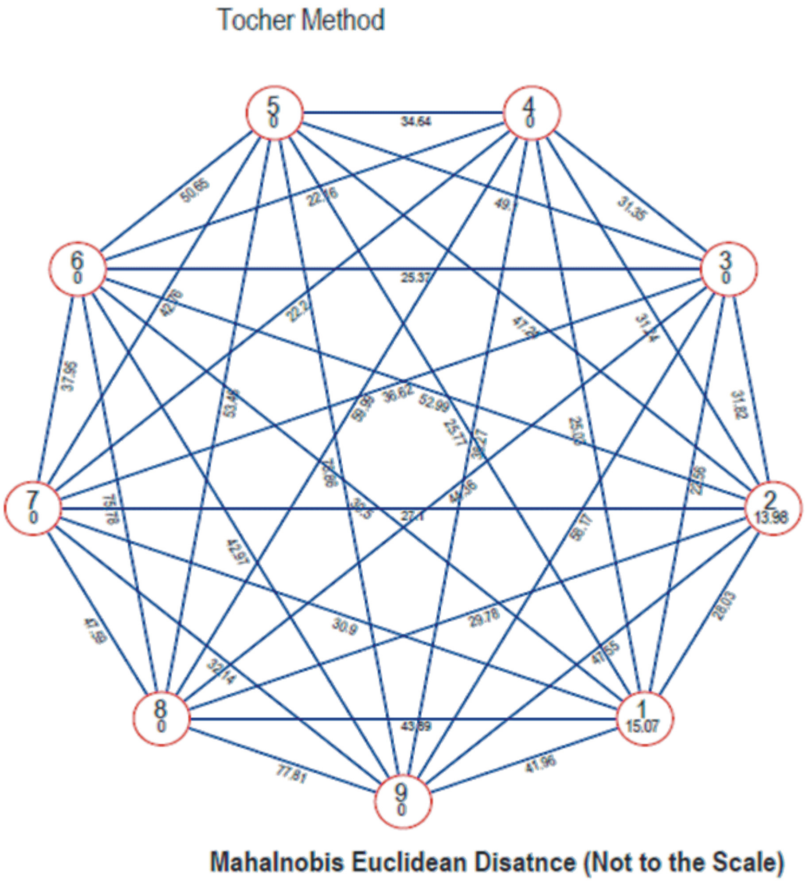

Fig 2. Intra-and inter-cluster distance of 37 cotton (*Gossypium hirsutum* L.) genotypes in seven clusters based on Mahalanobis Euclidean distance

Table 5. Contribution of different characters towards genetic divergence

1	Days to 50% flowering	4	0.60
2	Plant Height (cm)	46	6.91
3	No of Monopodia/plant	5	5.26
4	No of Sympodia/plant	13	1.95
5	No. of Bolls/plant	31	4.65
6	Boll wt (g)	80	12.01
7	Seed Index (g)	164	24.62
8	Lint Index (g)	201	30.18
9	GOT (%)	6	0.90
10	Seed Cotton Yield (q/ha)	0	0.00
11	Lint Yield (q/ha)	16	2.40
12	2.5% Span length (mm)	44	6.61
13	Bundle strength(g/tex)	17	2.55
14	Micronaire 10- 6 g/ inch	5	0.75
15	Uniformity Ratio	4	0.60

variance. Characters such as monopodia/plant (-0.443), sympodia/plant (0.387), boll weight (0.472), 2.5 per cent span length (-0.318), micronaire value (0.335) in principal component III, boll weight (0.301), ginning outturn (0.427), lint yield/ha (-0.637) in principal component IV, days to 50 per cent flowering (0.670), boll weight (-0.304), lint index (0.289) and ginning out turn (0.283) in principal component V, sympodia/plant (-0.427), seed index (-0.393), ginning outturn (-0.415) and 2.5 per cent span length (-0.386) explained the maximum variance in principal component VI, respectively. Haritha and Ahamed (2013) and Tulasi *et al.* (2014) studied the

Table 6. Principal component analysis

	Vector. 1	Vector. 2	Vector. 3	Vector. 4	Vector. 5	Vector. 6	Vector. 7
Eigene Value (Root)	3.89	2.40	1.78	1.42	1.29	1.06	0.78
Per cent Variation Exposession	25.93	16.05	11.89	9.49	8.59	7.07	5.20
Cumulative Variety Expenditures	25.93	41.98	53.87	63.37	71.96	79.04	84.25
Days to 50 per cent flowering	0.195	0.063	0.060	0.087	0.670	0.206	0.038
Plant Height (cm)	-0.160	-0.450	0.055	0.115	0.174	0.085	0.322
Monopodia/plant	0.214	-0.313	-0.443	0.114	-0.015	0.169	-0.112
Sympodia/plant	0.016	0.303	0.387	0.087	0.045	-0.427	-0.419
Bolls/plant	-0.343	0.085	-0.293	-0.124	-0.243	0.077	-0.031
Boll weight (g)	0.160	-0.153	0.472	0.301	-0.304	0.188	-0.029
Seed index (g)	0.201	-0.387	0.109	-0.237	-0.183	-0.393	0.347
Lint index (g)	-0.306	-0.232	0.219	-0.233	0.289	0.181	-0.338
GOT (%)	-0.210	0.078	-0.229	0.427	0.283	-0.415	0.133
Seed cotton yield (q/ha)	0.385	0.247	0.029	-0.130	-0.012	-0.226	0.335
Lint yield (q/ha)	0.146	0.164	-0.027	-0.637	0.274	0.047	0.105
2.5% Span length (mm)	0.177	-0.311	-0.318	-0.167	-0.009	-0.386	-0.518
Bundle strength(g/tex)	0.398	-0.189	-0.003	0.269	0.243	-0.064	-0.089
Micronaire 10- 6 g/ inch	-0.234	-0.370	0.335	-0.175	0.112	-0.226	0.033
Uniformity ratio	-0.389	0.053	-0.089	0.063	0.141	-0.280	0.220

utilization of principal component analysis in cotton. Thus the maximum contributing variables towards variability were monopodia/ plant, sympodia/plant, bolls/plant, boll weight, seed index, lint index, ginning out turn, 2.5 per cent span length, bundle strength and micronaire value.

It can be concluded that the genotypes, HS 294, SCS 106, F 2501, CSH 3232, Suraj, CCH-14-1 and TSH 0533-2 may be used as parents for getting better cross combinations. It also revealed that based on cluster mean values hybridization between CCH-14-1 and SCS 1207 may result in development of good intra hirsutum hybrid with high yield and better fibre quality traits.

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