



Studies on Genetic Divergence in Upland Cotton (*Gossypium hirsutum* L.).

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ABSTRACT

Genetic divergence was studied among 63 genotypes of American cotton (*Gossypium hirsutum* L.) using D² technique for seventeen characters. The 63 genotypes were grouped into 8 clusters containing 1 to 23 genotypes. The random distribution of genotypes indicated absence of parallelism between geographical diversity and genetic diversity. Cluster VI is the largest with 23 genotypes and Clusters IV, V, VII and VIII were lowest with one genotype each. In D² analysis, lint index (24.99) followed by micronaire (21.76), seed index (21.51), days to 50% flowering (16.64) contributed maximum for the divergence. The inter-cluster distance was maximum between clusters V and VIII (329.865), followed by clusters IV and VII (329.019) and was minimum between cluster I and V (27.135). Based on these studies crosses can be made between genotypes of distant clusters to obtain desirable transgressive segregants.

Key words : Clusters, D² statistic, Genetic divergence, *Gossypium hirsutum*

Cotton (*Gossypium* spp.) is popularly called “White Gold” occupies the predominant position in the Indian textile industry, despite stiff competition from the man-made synthetic fibres. In India, cotton is cultivated in diverse situations ranging from irrigated situation characterized by intensive management to assured rainfed situation, where moisture is not a constraint to dry rainfed situation characterized by low rainfall (less than 500 mm) accompanied by high temperature.

For developing potential hybrids in cotton, it is necessary to exploit genetic diversity available in cotton. Mahalanobis D² statistic is a powerful tool for quantifying genetic divergence among germplasm collections with respect to characters considered together.

MATERIAL AND METHODS

The present study was conducted during *kharif*, 2012-13 in randomized block design with 63 genotypes obtained from all over India with three replications following 120 x 60 cm spacing at Regional Agricultural Research Station, Lam Farm, Andhra Pradesh. The soils are black cotton. Recommended doses of fertilizers 120 N, 60 P₂O₅ and 40 K₂O kg/ha were applied in split doses. Each plot consisted of three rows of 6 m length and observations were recorded on five randomly

selected plants from each genotype per replication for 17 characters viz., plant height (cm), no. of monopodia plant⁻¹, no. of sympodia plant⁻¹, no. of bolls plant⁻¹, boll weight (g), relative chlorophyll content, seed index (g), lint index (g), seed cotton yield plant⁻¹ (g) and lint yield plant⁻¹ (g). The data on days to 50% flowering, ginning out turn (%), 2.5% span length (mm), micronaire value (10⁻⁶g/inch), bundle strength (g/tex), uniformity ratio and elongation (%) were recorded on plot basis. The fibre quality parameters were studied at Central Institute for Research on Cotton Technology (CIRCOT), RARS, Lam, Guntur, Andhra Pradesh. The genetic diversity among the genotypes was computed by means of Mahalanobis (1928) D² statistic and the genotypes were grouped into clusters by following the Tochers's method.

RESULTS AND DISCUSSION

The analysis of variance (ANOVA) revealed highly significant differences among 63 genotypes for 17 characters (Table 1) indicating the existence of diversity among genotypes for characters studied. Wilk's criterion showed significant differences between the genotypes for pooled effect of 17 characters studied.

Character wise per cent contribution towards genetic divergence by all the 17 characters

Table 1. Analysis of variance for yield and yield components in cotton (*Gossypium hirsutum* L.).

Source	d.f.	Days to 50% flowering	Plant height (cm)	No. of monopodia/plant	No. of sympodia/plant	No. of bolls/plant	Boll weight (g)	Relative chlorophyll content	Seed index (g)	Lint index (g)
Replications	2	1.973	44.638	0.099	4.680	16.218	0.104	0.021	0.211	0.044
Treatments	62	55.084**	262.927**	0.238**	9.138**	118.018**	0.401**	0.048**	6.611**	2.146**
Error	124	0.785	15.858	0.047	1.633	6.492	0.073	0.008	0.074	0.021
Mean squares										
Source	d.f.	Ginning out-turn %	2.5% span length (mm)	Micronaire (10 ⁻⁶ g/inch)	Bundle strength (g/tex)	Uniformity ratio	Fibre elongation (%)	Seed yield / plant (g)	Lint yield / plant (g)	
Replications	2	3.352	1.989	0.058	4.180	8.638	0.057	252.02	37.600	
Treatments	62	36.132**	21.727**	1.255**	10.898**	10.438**	0.089**	3528.364**	482.594**	
Error	124	1.176	0.765	0.021	1.454	3.070	0.020	160.730	14.475	
Mean squares										

** Significance at 1% level,

d.f = Degrees of freedom

Table 2. Contribution of different characters towards genetic divergence in 63 genotypes of cotton (*Gossypiu hirsutum* L.).

S.No	Source	Times Ranked first	Contribution %
1	Days to 50 % flowering	325	16.64
2	Plant height (cm)	34	1.74
3	No. of monopodia plant ⁻¹	4	0.20
4	No. of sympodia plant ⁻¹	1	0.05
5	No. of bolls plant ⁻¹	33	1.69
6	Boll weight (g)	14	0.72
7	Relative chlorophyll content	9	0.46
8	Seed index (g)	420	21.51
9	Lint index (g)	488	24.99
10	Ginning out turn (%)	100	5.12
11	2.5% span length (mm)	82	4.20
12	Micronaire value (10 ⁻⁶ g/inch)	425	21.76
13	Budnle strength (g/tex)	0	0.00
14	Uniformity ratio	0	0.00
15	Elongation (%)	1	0.05
16	Seed cotton yield plant ⁻¹ (g)	5	0.26
17	Lint yield plant ⁻¹ (g)	12	0.61

Table 3. Clustering of 63 genotypes of cotton (*Gossypium hirsutum* L.) by Tocher's method.

Cluster No.	No. of genotypes	Name of genotype (s)
I	4	F 2296, LH 2256, CA 105, RS 2669
II	15	CCH 11-1, TSH 301, CPD 867, F 2310, CCH 2623, CNH 44, ARBH 2004, BS 27, ARBH 2411, RAH 103, SCS 1002, H 1442, L 770, GJHV 09/02, L 765, L 1011, L 801, L 1008, CCH 11-2, LH 2170, GJHV 440, TCH 1740, L 804, L 788, SURABHI, L 808, RHC 0811, L 762, GJHV 500, L 389, HYPS 152, NA 1325
III	17	TCH 1728
IV	1	GSHV 159
V	1	GSHV 162, BS 47, TCH 1741, RS 2670, CNH 50, GISV 272, BS 49, MR 786,
VI	23	SHS 2-4, BS 37, L 604, CSH 3088, GJHV 08/70, HS 289, L 755, KH 1101, RAH 1004, L 799, BS 59 SPI, TSH 0250, G COT 16, PUSA 5670, MCU 5
VII	1	L 761
VIII	1	NDLH 1938

is presented in Table 2. The maximum contribution towards genetic divergence was by lint index (24.99) followed by micronaire (21.76), seed index (21.51), days to 50% flowering (16.64), ginning out % (5.12) and 2.5% span length (4.20). Higher contribution to total divergence was reported by Pushpam *et al.*, (2004) for bolls plant⁻¹ and seed cotton yield plant⁻¹. Gopinath *et al.* (2009) also reported maximum contribution of boll weight, boll

number and 2.5% span length towards total divergence.

The 63 genotypes were grouped into 8 clusters using the Tocher's method (Fig.1), based on the criteria that the intra-cluster average D² values should be less than the inter-cluster D² values (Table 3).

In the present study, 63 genotypes were distributed into 8 clusters at random with maximum

Table 4. Average intra-and inter-cluster D² values among eight clusters in 63 cotton genotypes (*Gossypium hirsutum* L.).

Cluster No.	I	II	III	IV	V	VI	VII	VIII
I	12.195	49.403	102.381	27.479	27.135	104.344	210.005	253.391
II		42.038	73.818	82.673	81.827	122.751	146.876	205.347
III			70.256	144.226	157.578	169.272	152.742	200.777
IV				0.000	29.013	147.148	329.019	320.522
V					0.000	145.682	290.247	329.865
VI						98.731	233.069	249.855
VII							0.000	284.476
VIII								0.000

Note: Bold and diagonal values indicate intra-cluster D² distance

Fig 1. Dendrogram showing relationship of 63 cotton (*Gossypium hirsutum* L.) genotypes in eight clusters based on Mahalanobis' D² values.

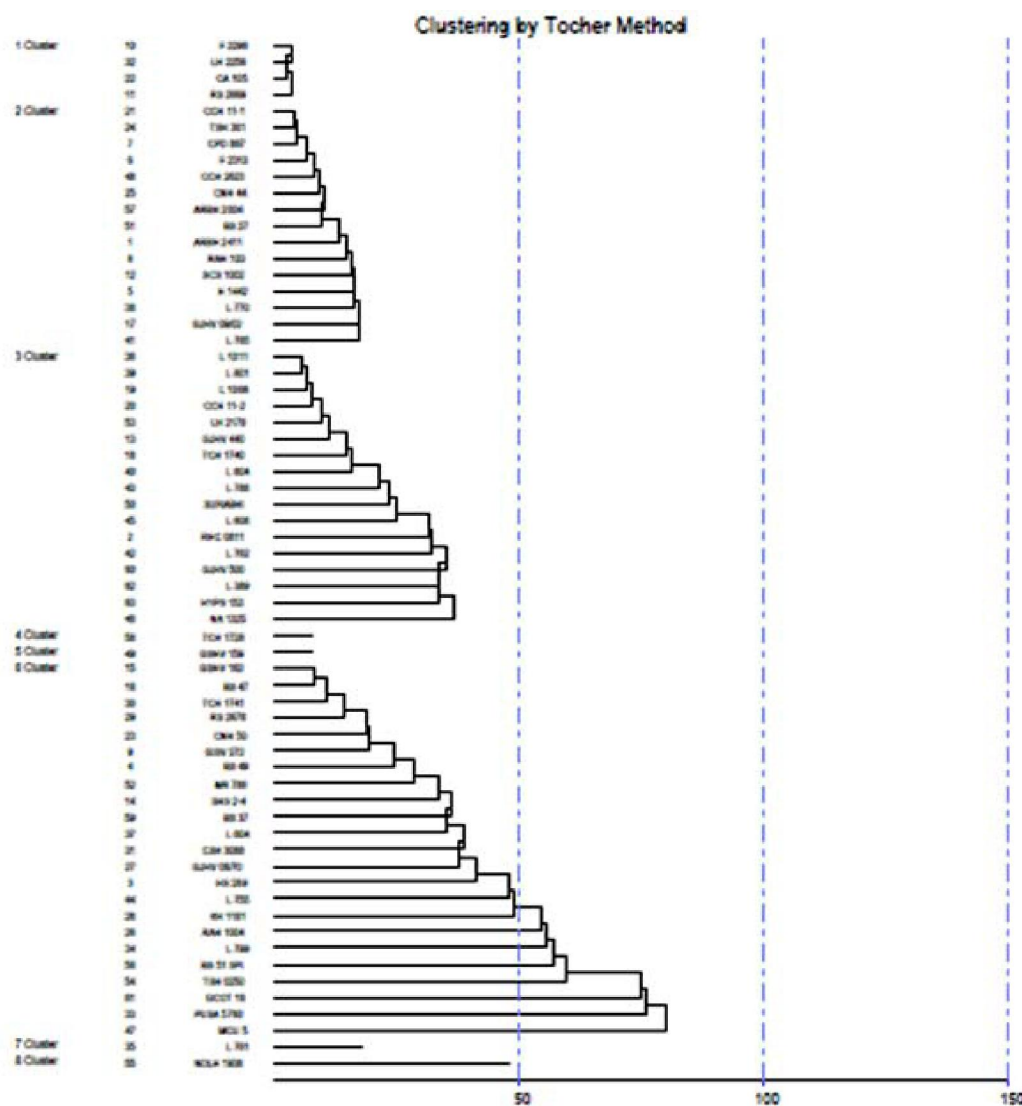


Table 5. Mean values of eight clusters estimated by Tocher's method from 63 genotypes of cotton (*Gossypium hirsutum* L.).

Cluster No	Days to 50% flowering	Plant height (cm)	No. of monopodia plant ⁻¹	No. of sympodia plant ⁻¹	No. of bolls plant ⁻¹	Boll weight (g)	Relative chlorophyll content	Seed index (g)	Lint index (g)	Ginning out turn (%)	2.5% span length (mm)	Micronaire value (10 ⁻⁶ g/inch)	Budhle strength (g/tex)	Uniformity ratio	Elongation (%)	Seed cotton yield plant ⁻¹ (g)	Lint yield plant ⁻¹ (g)
1 Cluster	57.667	98.333	1.328	16.624	31.719	4.562	1.058	8.173	3.225	29.935	25.123	4.520	20.200	49.339	5.267	145.714	43.767
2 Cluster	59.767	97.678	1.534	16.152	29.351	4.556	1.074	6.398	2.912	34.411	26.631	3.947	21.315	48.567	5.152	134.278	45.745
3 Cluster	58.048	101.396	1.469	16.711	31.190	4.396	1.006	9.179	4.248	32.337	26.150	4.545	20.959	48.829	5.270	137.008	44.499
4 Cluster	60.583	98.962	1.592	16.977	33.417	4.527	1.050	8.650	4.375	34.630	27.620	4.515	21.236	47.875	5.213	150.876	52.597
5 Cluster	61.167	89.556	1.781	17.543	47.208	4.893	1.203	9.106	4.188	33.293	30.882	2.793	23.787	46.289	5.013	228.623	77.808
6 Cluster	58.083	96.315	1.638	17.975	32.843	4.589	1.081	10.649	4.850	32.006	29.459	4.176	23.022	47.519	5.241	153.339	48.316
7 Cluster	57.167	92.055	1.297	15.860	32.502	3.947	0.880	7.942	3.223	29.302	24.045	5.308	19.948	48.938	5.407	130.060	38.655
8 Cluster	61.256	92.513	1.493	16.761	30.521	4.551	1.122	8.144	4.153	34.508	28.034	3.895	22.025	47.330	5.152	139.810	48.636

Note: Bold figures are minimum and maximum values

number of genotypes in cluster VI (23 genotypes) from different locations. Cluster III was the second largest with 17 genotypes followed by cluster II (15 genotypes), cluster I (4 genotypes). Clusters IV, V, VII and VIII were solitary clusters with nil intra-cluster D² values.

This pattern of grouping has indicated that the diversity need not be necessarily related to geographical diversity and it may be the outcome of several other factors like natural selection, exchange of breeding material, genetic drift and environmental variation. These results are in agreement with the findings of Asha *et al.* (2013), Kavithamani *et al.* (2013), Haritha *et al.* (2014) and Tulasi *et al.* (2014). Therefore, selection of varieties for hybridization should be based on genetic diversity rather than geographical diversity.

The average intra and inter-cluster D² values were estimated as per the procedure given by Singh and Chaudhary (1977) and were presented in the Table 4 and Fig.2.

The maximum intra cluster distance was 98.731 in cluster VI followed by 70.256 in cluster III, 42.038 in cluster II and 12.195 in cluster I, while, it was zero for IV, V, VII and VIII.

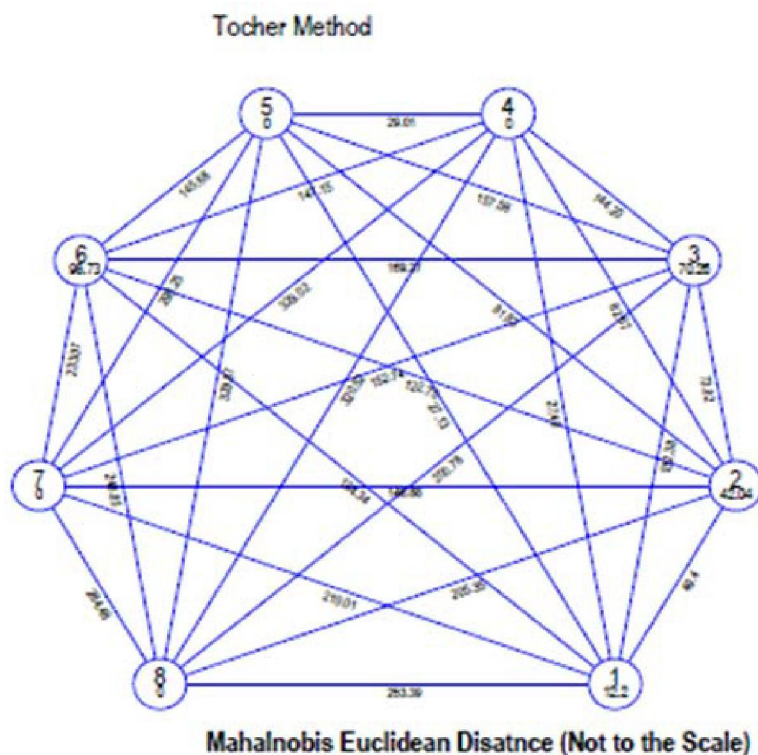
The inter-cluster distances were worked out considering 17 characters and these distances ranged from 27.135 (between cluster I and V) to 329.865 between cluster, V and VIII.

The inter-cluster distance was maximum between clusters V and VIII (329.865), followed by clusters IV and VII (329.019), clusters IV and VIII (320.522), clusters V and VII (290.247), clusters VII and VIII (284.476), clusters VI and VIII (249.855) and clusters VI and VII (233.069). 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 desirable transgressive segregants.

Choice of the particular cluster and selection of particular genotype from selected cluster are the two important points to be considered before initiating the crossing programme. The hybrids between varieties of diverse clusters will express high heterosis and give more useful segregants.

The cluster mean values for 17 characters are presented in Table 5. A considerable variation was observed in all the characters studied. Days to 50% flowering had a range from 57.167 (cluster VII) to 61.256 (cluster VIII), plant height had a range from 89.556 (cluster V) to 101.396 (cluster III), number of monopodia plant⁻¹ ranged from

Fig 2. Intra-and inter-cluster distance of 63 cotton (*Gossypium hirsutum* L.) genotypes in eight clusters based on Mahalanobis Euclidean distance.



1.297 for cluster VII to 1.781 for cluster V, number of sympodia plant⁻¹ ranged from 15.86 for cluster VII to 17.975 for cluster VI, number of bolls plant⁻¹ varied from 29.351 for cluster II to 47.208 for cluster V, boll weight ranged from 3.947 for cluster VII to 4.893 for cluster V, relative chlorophyll content ranged from 0.880 for cluster VII to 1.203 for cluster V, seed index varied from 6.398 for cluster II to 10.649 for cluster VI; lint index ranged from 2.912 for cluster II to 4.850 for cluster VI, ginning out-turn ranged from 29.302 for cluster VII to 34.63 for cluster IV, 2.5% span length varied from 24.045 for cluster VII to 30.882 for cluster V, micronaire ranged from 2.793 for cluster V to 5.308 for cluster VII, bundle strength varied from 19.448 for cluster VII to 23.787 for cluster V, uniformity ratio ranged from 46.289 for cluster V to 49.339 for cluster I, elongation varied from 5.013 for cluster V to 5.407 for cluster VII, seed cotton yield plant⁻¹ ranged from 130.060 for cluster VII to 228.623 for cluster V and lint yield plant⁻¹ ranged from 38.655 for cluster VII to 77.808 for cluster V.

The cluster V showed highest mean value for number of monopodia plant⁻¹ (1.781), number of bolls plant⁻¹ (47.208), boll weight (4.893), relative chlorophyll content (1.203), 2.5% span length (30.882), bundle strength (23.787), seed cotton yield plant⁻¹ (228.623) and lint yield plant⁻¹ (77.808).

The cluster VI showed highest mean value for number of sympodia plant⁻¹ (17.975), seed index (10.649) and lint index (4.850). Hence, the selection of genotype for hybridization should be more based on generic diversity rather than geographic diversity. Use of genetically distant genotypes as parents to get the most promising breeding material had also been suggested by Satish *et al.*, (2009).

Considering the intra and inter cluster distances, mean performance the following genotypes may be more effective for improvement of yield and yield contributing characters. These are NDLH 1938, GSHV 159, TCH 1728, L 761, L 604, RAH 1004, G COT 16, MCU 5, L 788, SURABHI, HYPS 152 and NA 1325.

LITERATURE CITED

- Asha R, Lal Ahamed M, Ratna Babu D and Anil Kumar P 2013** Multivariate analysis in upland cotton (*Gossypium hirsutum* L.). *Madras Agricultural Journal*, 100(4-6):333-335.
- Gopinath M, Rajamani S, Naik R K and Rao C M 2009** Genetic divergence for lint characters in upland cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*, 23(1): 46-48.
- Haritha T, Lal Ahamed M, Satyanarayanarao V and Ashoka Rani Y 2014** Genetic divergence for morpho physiological traits in upland cotton. *Journal of Cotton Research and Development*, 28(1): 34-36.
- Kavithamani D, Amala Balu P and Rajarathinam 2013** Assessment of genetic diversity in *Gossypium barbadense* L. *Journal of Cotton Research Development*, 27(1): 20-25.
- Mahalanobis P C 1928** A statistical study at Chinese head measurement. *Journal of Asiatic Society of Bengal*, 25: 301-307.
- Puspham R, Raveendran S, Devasena N and Ravikesavan R 2004** Studies on genetic diversity in upland cotton (*Gossypium hirsutum* L.) *Journal of Indian Society of Cotton Improvement*, 29 (1): 134-143.
- Satish Y, Jain P P and Chhabra B S 2009** Studies on genetic diversity in upland cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*, 23(1): 18-22.
- Singh R K and Chaudhary B D 1977** *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani Publishers, New Delhi. 215-218.
- Tulasi J, Lal Ahamed M, Samba Murthy J S V and Ashoka Rani Y 2014** Multivariate analysis in upland cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*, 28(2): 191-194.

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