



Research Article

GENETIC DIVERGENCE STUDIES FOR YIELD AND FIBRE QUALITY TRAITS IN UPLAND COTTON (*Gossypium hirsutum* L.)

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Abstract- Genetic diversity in 70 upland cotton genotypes for 16 yield attributes and quality characters was studied using Mahalanobis D² statistic. The 70 genotypes were grouped into 13 clusters. The pattern of grouping of genotypes revealed the presence of considerable diversity in the material studied. The forces other than geographical separation may be responsible for genetic divergence among the genotypes and this was further confirmed by the distribution of genotypes into different clusters. The distance between genotypes placed in same cluster was less when compared with genotypes belongs to different clusters. This clearly indicates that exploitation of heterosis may be possible when hybrids produced by crossing parents from different and distant clusters.

Keywords- Genetic divergence, Mahalanobi's D² statistic, Clusters, Upland cotton

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Introduction

Cotton (*Gossypium* spp.) is one of the most important crop among the natural fibre crops and back bone of Indian textile industry. It provides rural livelihood to a large number of people through cultivation, industry and textile. It is also successful commercial crop with potential hybrids/varieties and provides opportunity to the scientists to exploit hybrid vigour commercially. In any crop commercial exploitation of heterosis is more successful when parents involved in hybridisation programme are genetically distant. Genetic diversity plays a crucial role in analyzing the general distance among the genotypes selected as parents. Within a certain limit, hybridisation of more diverged parents is expected to enhance the level of hybrid vigour in hybrids and chance to appearance of new plant types with different character combinations in segregating generations [1]. Hence, the present study was undertaken to elucidate the nature and magnitude of genetic diversity in 70 upland cotton genotypes.

Materials and Methods

The experimental material for the present investigation comprised of 70 American cotton genotypes. All the 70 accessions were evaluated during *khairif* 2013-14 at Regional Agricultural Research Station (RARS), Lam Farm, Guntur, Andhra Pradesh, India. The entries were raised in randomised complete block design with three replications by adopting 105 cm × 60 cm. The data was recorded for plant height (cm), no. of monopodia per plant, no. of sympodia plant⁻¹, no. of bolls per plant, boll weight (g), lint index (g), seed index (g), ginning out-turn (%), seed cotton yield per plant and lint yield per plant (g) on five randomly selected competent plants from each genotype per replication. Whereas, days to 50% flowering, 2.5% span length (mm), micronaire value (10⁻⁶g/inch), bundle strength (g/tex), uniformity ratio, fibre elongation (%) were recorded on plot basis. Fibre quality traits recorded by using HVT Expert 1201 high volume fibre tester instrument. The genetic divergence was worked out by using Mahalanobis D²

statistic described by [2]. On the basis of D² values, the genotypes were grouped into different clusters by employing Tochers's method as outlined by [2].

Results and Discussion

The analysis of variance indicated significant differences among all the genotypes for all the characters studied and specified existence of considerable genetic diversity among genotypes [Table-1]. Hence, further analysis was done to estimate the D² values; all the 70 genotypes were grouped into 13 clusters [Table-2] and [Fig-1]. The distribution of 70 genotypes into 13 clusters was at random with maximum number of genotypes in cluster I (33 genotypes). Cluster IV was the second largest with 11 genotypes followed by cluster VII (7 genotypes), cluster III (6 genotypes), cluster X (5 genotypes). Clusters II, V, VI, VIII, IX, XI, XII and XIII were solitary clusters with nil intra- cluster D² values. These findings are in agreement with the results of [3-10]. The average intra- and inter- cluster D² values estimated as per the procedure given by [11] are presented in [Table-3]. The proximity and divergence among 13 clusters are indicated in [Table-4] and [Fig-2].

The maximum intra cluster distance was 124.02 for cluster X followed by 110.20 for cluster IV, 92.49 for cluster VII and 67.03 for cluster III, 48.38 for cluster I while, it was zero for clusters II, V, VI, VIII, IX, XI, XII and XIII. Cluster I, with 33 genotypes, was the largest of all clusters. It was closest to cluster II (71.68) followed by Cluster V (72.11) and it was farthest from cluster X (180.17) followed by cluster XI (146.47). Cluster II had only one genotype (RAH 1004). It was nearest to cluster IV (59.91) followed by cluster V (96.51) and it was farthest from cluster XI (155.92) followed by cluster XII (141.21). Six genotypes were grouped in cluster III. It was nearest to cluster VIII (87.59) followed by cluster VI (92.43) and it was farthest from cluster XI (297.04) followed by XII (250.85). Cluster IV comprised of 11 genotypes. It was nearest to the cluster II (59.91) followed by cluster I (84.43) and it was farthest from cluster X (185.31) followed by cluster VIII (155.86).

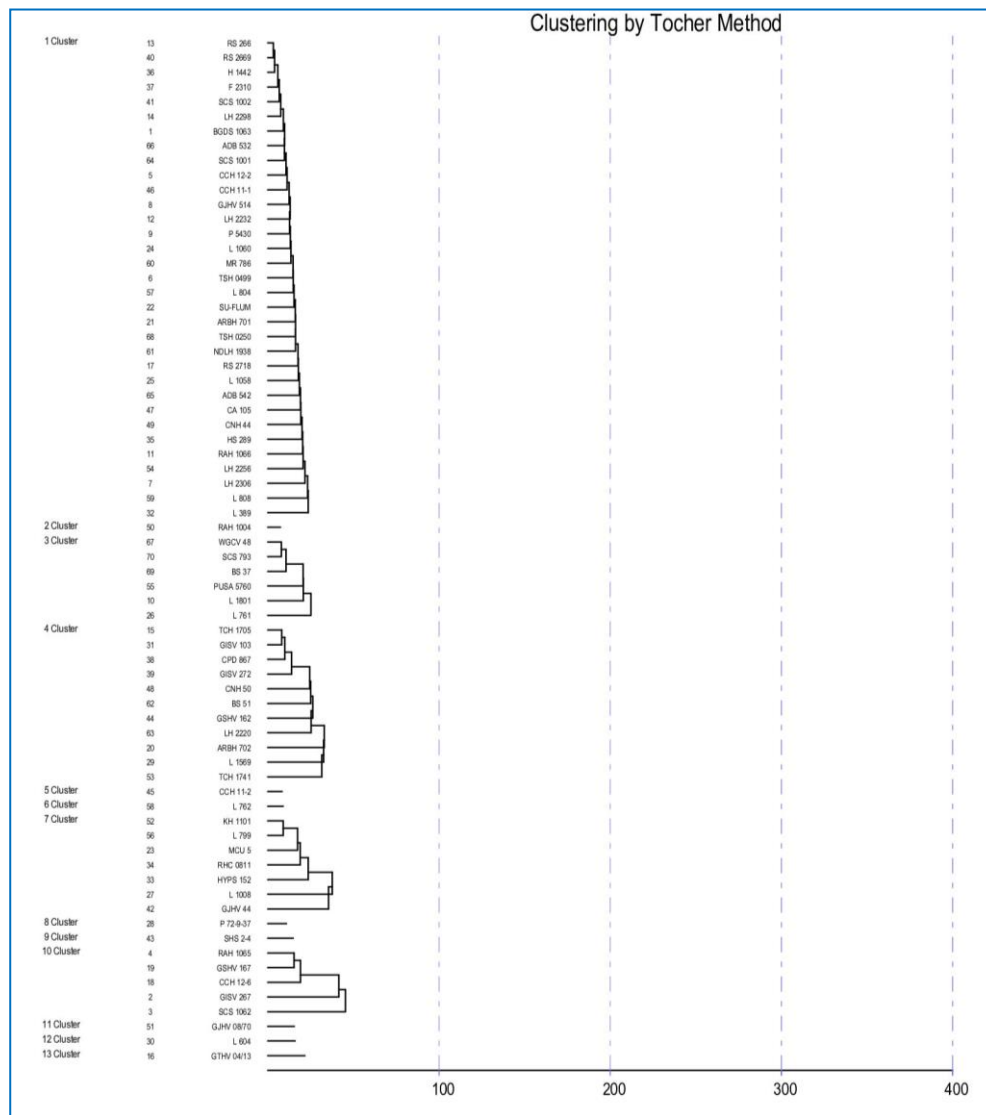


Fig-1 Dendrogram showing relationship of 70 American cotton (*Gossypium hirsutum* L.) genotypes in thirteen clusters based on Mahalanobis' D² values

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

Source	d.f	Days to 50 % flowering	Plant height (cm)	No. of monopodia plant ¹	No. of sympodia per plant	No. of boll s per plant	Boll weight (g)	Lint index (g)	Seed index (g)
Mean squares									
Replications	2	1.60	0.10	0.01	0.78	2.64	0.03	0.03	0.00
Treatments	69	50.78**	209.11**	0.61**	7.79**	126.58**	0.51**	1.69**	4.18**
Error	138	0.94	42.49	0.01	0.85	4.16	0.03	0.02	0.09

Source	d.f	Ginning out turn (%)	2.5% span length (mm)	Uniformity ratio	Micronaire value (10 ⁻⁶ g/ich)	Bundle strength (g/tex)	Fibre elongation %	Seed cotton yield per plant (g)	Lint yield per plant (g)
Mean squares									
Replications	2	1.57	0.31	2.83	0.02	0.24	0.02	48.62	12.62
Treatments	62	33.04**	11.92**	14.32**	0.93**	4.54**	0.15**	1036.02**	181.14**
Error	124	1.50	0.54	2.27	0.01	0.36	0.02	97.04	14.44

** Significance at 1% level, d.f = Degrees of freedom

Cluster V was monogenotypic (CCH 11-2). It was nearest to I (72.11) followed by cluster VII (83.14) while it was farthest from cluster XI (260.37) followed by cluster IX (197.35). Cluster VI had only one genotype (L 762). It was nearest to cluster I (72.38) followed by cluster III (92.43) and it was farthest from X (235.53) followed by XI (215.52). Cluster VII comprised of 7 genotypes. It was nearest to the cluster V (83.14) followed by cluster VI (99.21) and it was farthest from cluster XI (273.72) followed by cluster X (225.14). Cluster VIII was monogenotypic (P 72-9-37). It was closest to XIII (57.85) followed by cluster V (85.62) and was farthest from XI

(266.12) followed by cluster XII (217.22). Cluster IX was monogenotypic (SHS 2-4). It was nearest to XI (41.00) followed by cluster I (106.69) and was farthest from cluster X (315.66) followed by cluster XIII (236.30).

Cluster X consisted of five genotypes. It was closest to II (107.25) followed by cluster VIII (143.64) and was farthest from cluster XII (317.26) followed by cluster IX (315.66). Cluster XI was solitary (GJHV 08/70). It nearest to cluster IX (41.00) followed by cluster IV (130.33) and was farthest from cluster X (315.32) followed by cluster III (297.04). Cluster XII was monogenotypic (L 604). It was closest to

cluster IX (112.31) followed by cluster I (113.55) and was farthest from cluster X (317.26) followed by cluster III (250.85). Cluster XIII was solitary (GTHV 04/13). It was nearest to VIII (57.85) followed by cluster V (101.08) and was farthest from XI (254.97) followed by cluster IX (236.30). The intra-inter cluster distance values revealed that inter-cluster distance values were greater than intra-cluster distance values. Cluster X (124.02) has maximum intra-cluster distance followed by cluster IV (110.20), cluster VII (92.49), cluster III (67.03) and cluster I (48.38). Eight

clusters (cluster II, V, VI, VIII, IX, XI, XII and XIII) were solitary had no intra-cluster distances. The high intra-cluster distance in cluster X indicates the presence of wide genetic diversity among the genotypes present within this cluster. These results are in accordance with findings of [12-16]. In the present investigation, inter-cluster distances were worked out considering 16 characters and these distances ranged from 41.00 (between cluster IX and XI) to 317.26 (between X and XII).

Table-2 Clustering of 70 genotypes of American cotton (*Gossypium hirsutum* L.) by Tocher's method.

Cluster No.	No. of genotypes	Name of genotype(s)
I	33	RS 2669, RS266, H 1442, F 2310, SCS 1002, LH 2296, BGDS 1063, ADB 532, SCS 1001, CCH 12-2, CCH 11-1, GJHV 514, LH 2232, P 5430, L 1060, MR 786, TSH 0499, L 804, SUFLUM, ARBH 701, TSH 0250, NDLH 1938, RS 2718, L 1058, ADB 542, CA 105, CNH 44, HS 289, RAH 1066, LH 2256, LH 2306, L 808, L 389
II	1	RAH 1004
III	6	WGCV 48, SCS 793, BS 37, PUSA 5760, L 1801, L 761
IV	11	TCH 1705, GISV 103, CPD 867, GISV 272, CNH 40, BS 51, GSHV 162, LH 2220, ARBH 702, L 1569, TCH 1741
V	1	CCH 11-2
VI	1	L 762
VII	7	KH 1101, L 799, MCU 5, RHC 0811, HYPS 152, L 1008, GJHV 44,
VIII	1	P 72-9-37
IX	1	SHS 2-4,
X	5	RAH 1065, GSHV 167, CCH 12-6, GISV 267, SCS 1062
XI	1	GJHV 08/70
XII	1	L 604
XIII	1	GTHV 04/13

Table-3 Average intra-and inter-cluster D^2 values among thirteen clusters in 70 American cotton (*Gossypium hirsutum* L.) genotypes

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	48.38	71.68	95.53	84.43	72.11	72.38	100.22	90.42	106.69	180.17	146.47	113.55	113.76
II		0.00	109.33	59.91	96.51	124.71	102.80	116.49	132.64	107.25	155.92	141.21	120.86
III			67.03	153.31	110.20	92.43	120.80	87.59	226.62	165.79	297.04	250.85	162.61
IV				110.20	141.70	116.61	142.46	155.86	110.17	185.31	130.33	126.03	149.78
V					0.00	126.20	83.14	85.62	197.35	196.46	260.37	129.11	101.08
VI						0.00	99.21	111.77	130.50	235.53	215.52	198.98	166.59
VII							92.49	128.74	176.58	225.14	273.72	169.86	156.19
VIII								0.00	212.74	143.64	266.12	217.22	57.85
IX									0.00	315.66	41.00	112.31	236.30
X										124.02	315.32	317.26	164.71
XI											0.00	134.68	254.97
XII												0.00	139.23
XIII													0.00

Note: Bold and diagonal values indicate intra-cluster D^2 distance

Table-4 The nearest and the farthest cluster from each cluster based on D^2 values using Tocher's method in 70 American cotton (*Gossypium hirsutum* L.) genotypes

Cluster No.	Nearest cluster with D^2 values	Farthest cluster with D^2 values
I	II (71.68)	X (180.17)
II	IV (59.91)	XI (155.92)
III	VIII (87.59)	XI (297.04)
IV	II (59.91)	X (185.31)
V	I (72.11)	XI (260.37)
VI	I (72.38)	X (235.53)
VII	V (83.14)	XI (273.72)
VIII	XIII (57.85)	XI (266.12)
IX	XI (41.00)	X (315.66)
X	II (107.25)	XII (317.26)
XI	IX (41.00)	X (315.32)
XII	IX (112.31)	X (317.26)
XIII	VIII (57.85)	XI (254.97)

Note: Values in parentheses indicate D^2 values

The inter cluster-distance was maximum between cluster X and XII (317.26) followed by cluster IX and X (315.66), cluster X and XI (315.32), cluster III and XI (297.04), cluster VII and XI (273.72), cluster VIII and XI (266.12), cluster V and XI (260.37), cluster XI and XIII (254.97), cluster III and XII (250.85), cluster IX and XIII (236.60), cluster VI and X (235.53), cluster VII and X (225.14), cluster VIII and XII (217.22) and cluster VI and XI (215.52).

Divergence reflecting in the material was also evidenced by an appreciable amount of desirable variation among cluster means for different characters. The cluster mean values for 16 characters are presented in [Table-5]. The data indicated a wide range of mean values between the clusters. Days to 50 % flowering had a range of 53.00 for cluster XIII to 68.33 for cluster VI; plant height had a range of 107.11 for cluster IX to 135.55 for cluster II; number of monopodia plant⁻¹ ranged from 1.00 for cluster VI to 2.00 for cluster XIII; number of sympodia plant⁻¹ varied from 12.07 for cluster I to 17.11 for cluster II; number of bolls plant⁻¹ ranged from 28.11 for cluster IX to 45.32 for cluster III; boll weight varied from 3.45 for cluster VI to 4.74 for cluster VII; lint index ranged from 2.37 for cluster XI to

5.86 for cluster VIII; seed index varied from 5.80 for cluster XI to 10.77 for cluster V; ginning out-turn ranged from 28.07 for cluster IX to 39.75 for cluster XIII; 2.5 % span length varied from 19.01 for cluster VI to 22.99 for cluster XII ; micronaire value ranged from 3.03 for cluster XII to 4.09 for cluster II; uniformity ratio varied from 46.22 for cluster XII to 51.03 for cluster VIII; fibre elongation ranged from 4.53 for cluster XIII to 5.29 for cluster X; seed cotton yield plant⁻¹ varied from 99.59 for cluster XIII to 159.83 for cluster III; lint yield plant⁻¹ ranged from 30.76 for cluster XI to 54.79 for cluster III. Higher mean values for number of bolls plant⁻¹ were seen in cluster III and VI and higher means for boll weight were observed in clusters VII, V, II and IX which are major contributors in improving seed cotton yield plant⁻¹ in cotton. Based on mean values genotypes from these clusters can be used in seed cotton yield improvement programmes.

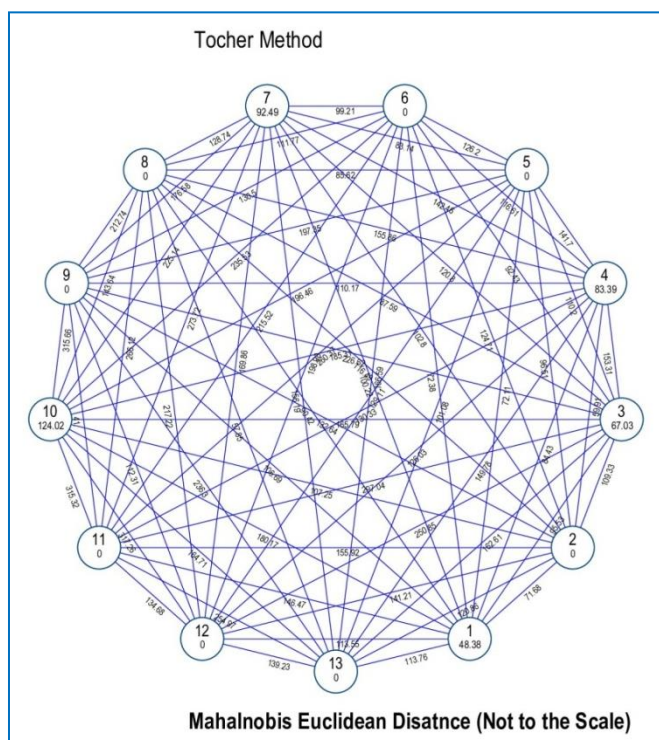


Fig-2 Intra-and inter-cluster distance of 70 American cotton (*Gossypium hirsutum* L.) genotypes in eight clusters based on Mahalanobis Euclidean distance

Discussion

In the present investigation formation of distinct solitary clusters may be due to the fact that geographic barriers prevent gene flow or intensive natural and human selection for diverse and adoptable gene complexes. The 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. Therefore, selection of varieties for hybridization should be based on genetic diversity rather than geographical diversity. The mutual relationships between the clusters were represented diagrammatically by taking average intra and inter cluster D values. Genotypes grouped into the same cluster presumably differ little from one another as the aggregate of characters measured. General notion exists that the larger is the divergence between the genotypes, the higher will be the heterosis [17].

Conclusion

Therefore, it would be desirable to attempt crosses between genotypes belonging to distant clusters for getting high heterotic cross combinations which are likely to yield a wide range of segregants on which selection can be practiced. 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.

Conflict of Interest: None declared

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Table-5 Mean values of thirteen clusters estimated by Tocher's method from 70 American cotton (*Gossypium hirsutum* L.) genotypes.

Cluster No	Days to 50 % flowering	Plant height (cm)	No. of monopodia per plant	No. of sympodia per plant	No. of bolls per plant	Boll weight (g)	Lint index (g)	Seed index (g)	Ginning out turn (%)	2.5% span length (mm)	Uniformity ratio	Micronaire value (10 ⁻⁶ g/inch)	Bundle strength (g/tex)	Fibre longation (%)	Seed cotton yield per plant (g)	Lint yield per plant (g)
1 Cluster	59.41	128.13	1.12	15.06	38.07	4.11	4.27	8.51	33.36	26.87	48.24	3.42	20.34	5.01	131.74	44.01
2 Cluster	61.33	135.55	2.00	17.11	35.78	4.64	4.34	7.95	35.31	25.84	49.14	4.09	19.93	5.27	140.87	49.72
3 Cluster	62.00	130.99	1.09	16.23	45.32	4.18	5.17	9.86	34.39	27.35	48.60	3.84	21.32	5.05	159.83	54.79
4 Cluster	61.39	127.90	1.66	14.99	38.49	4.07	3.93	7.15	35.36	26.02	49.37	3.77	19.76	5.08	128.68	45.50
5 Cluster	56.00	129.00	1.33	15.33	32.17	4.65	4.70	10.77	30.39	27.67	49.79	3.07	21.59	5.25	128.17	38.99
6 Cluster	68.33	124.33	1.00	12.67	42.89	3.45	4.31	8.97	32.47	26.00	47.03	3.36	19.01	5.05	135.93	44.17
7 Cluster	64.57	127.59	1.60	14.81	31.13	4.74	4.46	9.87	31.02	28.97	47.35	3.50	21.29	4.89	124.02	38.27
8 Cluster	58.00	122.78	1.00	14.22	28.99	4.43	5.86	8.85	39.85	25.99	51.03	3.59	20.40	5.12	108.95	43.42
9 Cluster	63.00	107.11	1.00	14.22	28.11	4.60	2.60	6.67	28.07	26.92	50.72	3.39	21.16	5.04	109.79	30.86
10 Cluster	57.07	129.07	1.91	14.13	35.38	4.30	5.29	8.83	37.54	25.21	48.21	4.89	19.39	5.29	124.75	47.34
11 Cluster	57.00	131.22	1.00	15.67	32.45	3.84	2.37	5.80	28.95	26.27	50.04	3.75	20.29	5.25	105.95	30.76
12 Cluster	54.00	116.55	1.67	12.67	30.45	4.35	3.60	6.59	35.35	33.06	46.22	3.03	22.99	4.77	112.34	39.71
13 Cluster	53.00	117.77	2.00	12.07	30.67	3.83	5.53	8.39	39.75	27.82	48.05	3.42	19.51	4.53	99.59	39.57

Note: Bold figures are minimum and maximum values