Genetic Divergence in Upland Cotton

D Krishna Kishore, M Gopinath, V Satyanarayana Rao and V Srinivasa Rao
Department of Genetics and Plant Breeding, Agricultural College, Bapatla 522 101, Andhra Pradesh

ABSTRACT

Genetic divergence as measured by Mahalanobis D^2 statistic was assessed among 60 genotypes of Upland cotton for eleven characters. The pattern of distribution of genotypes into different clusters was at random. The seed index contributed maximum towards genetic divergence followed by seed cotton yield per plant, plant height, boll weight and number of bolls per plant. The maximum inter-cluster distance was observed between clusters 3 and 6 (1671.909) followed by clusters 2 and 6 (1291.112) and clusters 6 and 8 (1241.931). The genotypes from these clusters can be utilized in cotton improvement programmes.

Key words : Cluster analysis, Cotton, Divergences, D^2 Analysis, Principal component analysis.

Cotton is a major crop of global economic importance and has high commercial value. Upland cotton (*Gossypium hirsutum* L.) is a predominant species of cotton cultivated in more than 60 countries in the world. The first problem that often concerns a breeder in formulating a breeding programme for the improvement of any crop is the presence or absence of variation in the germplasm. Precise information on the nature and degree of genetic divergence would help the plant breeder in choosing the right type of parents for different breeding programmes. Therefore the present investigation was undertaken to study the nature and magnitude of genetic divergence in 60 genotypes of upland cotton.

MATERIAL AND METHODS

Sixty genotypes having different geographical origins were sown during kharif 2007 in a randomized block design with three replications. Each genotype was raised in a row of 6 m length. The row to row and plant to plant spacings were 120 cm and 60 cm, respectively. Five randomly selected plants were used for recording observations on eleven characters viz., plant height (cm), number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight (g), seed index (g), lint index (g), ginning (%), 2.5% span length (mm), uniformity ratio, seed cotton yield per plant (g). The data were subjected to analysis of variance and then multivariate analysis using statistic (Mahalanobis, 1928). Based on genetic distance (D^2 values), the genotypes were grouped into clusters of genetically closer related groups following the Tocher's method (Rao, 1952). PCA and cluster analyses were also exploited to know the direvsity among the genotypes.

RESULTS AND DISCUSSION

The significant treatment mean squres indicated the presence of wide variability among the genotypes for all the traits studied. The 60 genotypes were grouped into VIII clusters in cluster analysis and 10 clusters in D^2 analysis.

In D^2 analysis method 40 genotypes were randomly distiributed into 10 clusters (Table 1). The intra- and inter-cluster distances revealed that inter-cluster distance values were greater than intra-cluster distance values. Cluster 10 had maximum intra-cluster distance followed by clusters 4, 3, 2 and 1. Five clusters (Clusters 5,6,7,8 and 9) were solitary and had no inter-cluster distances. The high intra-cluster distance in cluster 10 indicates the presence of wide genetic diversity among the genotypes present within this cluster. It was suggested to attempt crosses among the genotypes with in clusters 10 and 4 to exploit the vaiability to produce transgressive segregants. Similar results were obtained by Kalsy and Garg (1995) and Sambamurthy *et al.* (1995).

The contribution of various characters to the total genetic divergence, seed index (36.50), seed cotton yield per plant (g) (20.45) followed by plant height (cm) (18.64), boll weight (g) (11.02), and bolls per plant (g) (9.44) contributed more to the total divergence out of eleven characters studied (Table 2). These characters should be given importance while selecting parents from the clusters. There is no contribution towards genetic divergence from the characters number of monopodia per plant and 2.5% span length.

Intra (bold) and inter cluster distances were presented in Table 3. The maximum inter cluster distance observed between clusters VIII and IX and minimum inter cluster distance ranged between clusters VI and VII.

Table 1. Clustering of 60 cotton genotypes by Tocher's method.

Cluster No.	Number of genotypes	Name of the genotypes
I	13	ICMF-230, NDLH-1754, TSH-9727, CPD-787, RS-2169, SES-21, Abhadita, BUSP-13, HLS-271, ARB-9009, SCS-95, L-768, LK-861.
II	11	CCH-5104, HD-328, NDLH-1678, L-765, L-763, RHH-7553, Surabhi, TCH-1542, SCS-101, CNH-3003, LRK-5166.
III	21	SCS-51, L-769, ARB-2005, RAH-3, RS-2141, NA-1325, ARB-760, RCH-1594, ICMF-1452, HAG-785, NH-100, MCU-5, ACP-738, MCU-9, SRT-1, L-603, GMP-5, ARB-8906, PKV-Rajat, L-761, Khandwa.
IV	7	CCH-18, MCU-2, ADB-39, Krishna, GJHV-392, MCU-7, MCU-12.
V	1	CWROK-165.
VI	1	L-864.
VII	1	ARB-784.
VIII	1	H-1246.
IX	1	L-604.
X	3	GIHV-53, GJHV-99 / 307, KH-140.

Table2. Contribution of different characters towards genetic divergence in 60 genotypes of cotton.

Sl. No.	Character	Per cent contribution towards divergence	Times ranked 1st
1	Plant height (cm)	18.64	330
2	Number of monopodia/ plant	0.00	0
3	Number of sympodia/ plant	0.17	3
4	Number of bolls/ plant	9.44	167
5	Boll weight (g)	11.02	195
6	Ginning out-turn (%)	2.99	53
7	Seed index (g)	36.50	646
8	Lint index (g)	0.62	11
9	2.5% span length (mm)	0.00	0
10	Uniformity ratio	0.17	3
11	Seed cotton yield/ plant (g)	20.45	362

Table 3. Average intra (Bold values) and inter cluster D^2 values of 10 clusters for 60 genotypes of cotton (*Gossypium hirsutum* L.).

Clusters	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster	7 Cluster	8 Cluster	9 Cluster	10 Cluster
				Inter & Intra- cluster distances						
1 Cluster	**61.130**	157.599	145.664	211.179	107.418	109.452	137.982	91.206	129.090	450.365
2 Cluster		**82.306**	221.993	254.295	216.804	165.346	146.748	323.816	258.136	224.989
3 Cluster			**95.272**	218.835	275.771	321.673	364.127	187.228	182.675	479.329
4 Cluster				**161.599**	420.093	290.809	338.489	278.522	362.338	409.855
5 Cluster					**0.000**	128.533	91.552	120.553	167.474	584.264
6 Cluster						**0.000**	37.302	190.458	258.602	411.508
7 Cluster							**0.000**	235.101	287.456	385.248
8 Cluster								**0.000**	198.794	702.395
9 Cluster									**0.000**	655.924
10 Cluster										**275.158**

In principal component analysis the first four principal components with eigen values more than one contributed 91.690 per cent towards total variability. The principal component with eigen values less than one were considered as non-significant. It was therefore inferred that the essential features of data set had been represented in the first four principal components (Table 5).

The first principal component (PC_1) contributed maximum towards variability (35.175%) and it reflected significant positive loading of seed index (0.774), plant height (0.362), boll weight (0.284), lint index (0.281) and seed cotton yield per plant (0.265). The second principal component (PC_2) contributed 30.844 per cent of total variance. The characters *viz.,* seed cotton yield per plant (0.750), number of bolls per plant (0.428), seed index (-0.340) and plant height (0.282) explained the maximum variance in the second principal component (PC_2) and signifying their importance in this principal component. The third principal component (PC_3) was characterized by 17.468 per cent contribution towards the total variability. Character *viz.,* boll weight (0.585), plant height (0.494), number of bolls per plant (-0.504) and seed index (-0.297) contributed maximum variance in this principal component. The fourth principal component (PC_4) was characterized by 8.202 per cent contribution towards the total variability. Characters *viz.,* plant height (0.711), boll weight (-0.477) and seed cotton yield per plant (-0.398) showed maximum variance in this component.

In cluster analysis, the genotypes were grouped into 8 clusters (Table 6). Maximum genotypes (14) were grouped under cluster II, followed by cluster V and VII with 9 genotypes. The cluster III had 8 genotypes cluster I with 7 genotypes and cluster IV with 6 genotypes, followed by cluster VIII with 4 genotypes and cluster VI with 3 genotypes. The clustering pattern of different genotypes from different geographical regions into different clusters was at random. This suggests that geographical diversity does not necessarily relate to genetic diversity.

The inter cluster Euclidean 2 distance varied from 346.895 (between cluster 1 and cluster 2) to 1671.909 (cluster 3 and cluster 6). All the inter-cluster Euclidean 2 values were lying between these values.

Cluster 1 had 7 genotypes. It was nearest to cluster 2 (346.895) followed by cluster 5 (361.039) and farthest from cluster 8 (1209.205) followed by cluster 7 (985.312). Cluster 2 comprised of 14 genotypes (Table 7). It was nearest to cluster 1 (346.895) followed by cluster 5 (371.340) and

Table 4. The nearest and the farthest cluster from each cluster based on D^2 values.

Cluster No.	Nearest cluster with D^2 values	Farthest cluster with D^2 values
I	VIII (91.206)	X (450.365)
II	VII (146.748)	VIII (323.816)
III	I (145.664)	X (479.329)
IV	I (211.179)	V (420.093)
V	VII (91.552)	X (584.264)
VI	VII (37.302)	X (411.508)
VII	V (91.552)	X (385.248)
VIII	I (91.206)	X (702.395)
IX	I (129.090)	X (655.924)
X	II (224.989)	VIII (702.395)

Fig 1. Three dimensional graph showing relative position of 60 cotton genotypes based on PCA scores
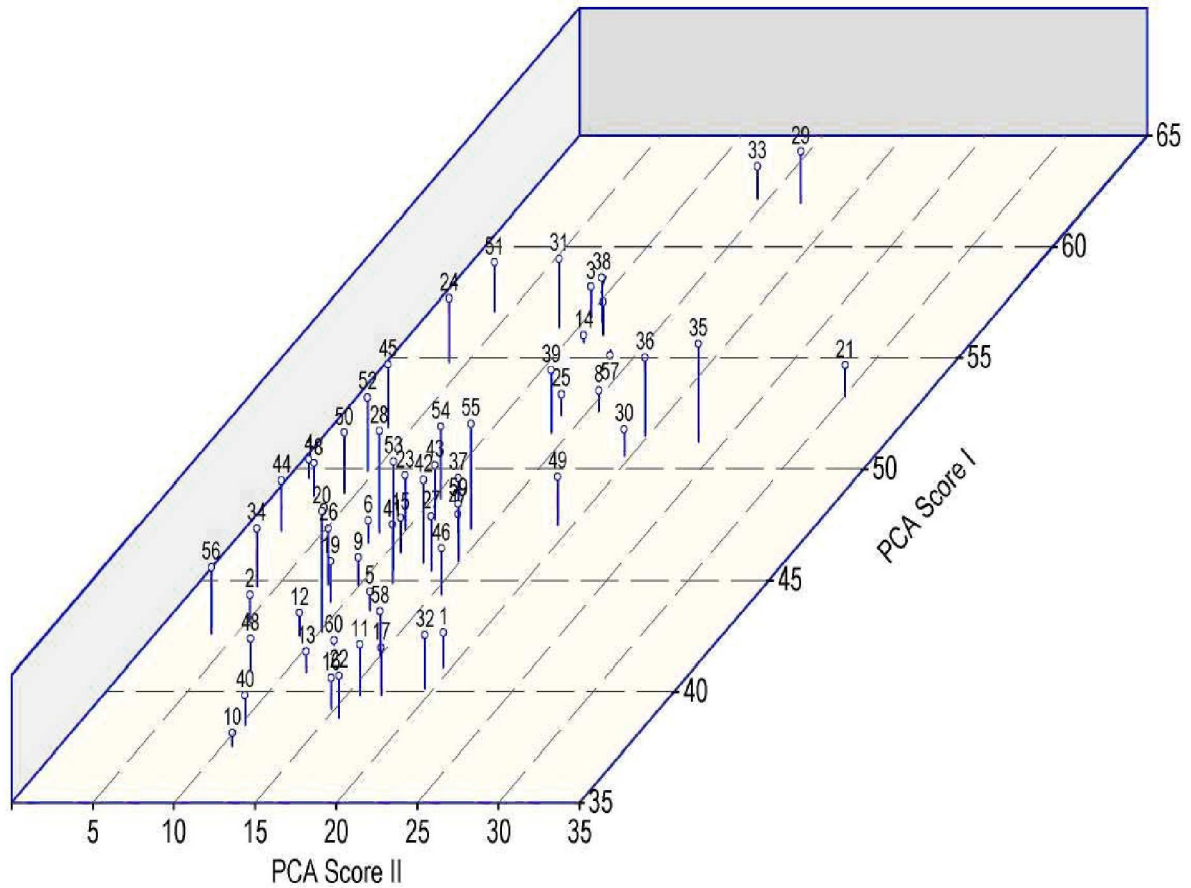
Fig 2. Wards minimum variance dendrogram showing relationship of 60 upland cotton genotypes in 8 clusters.
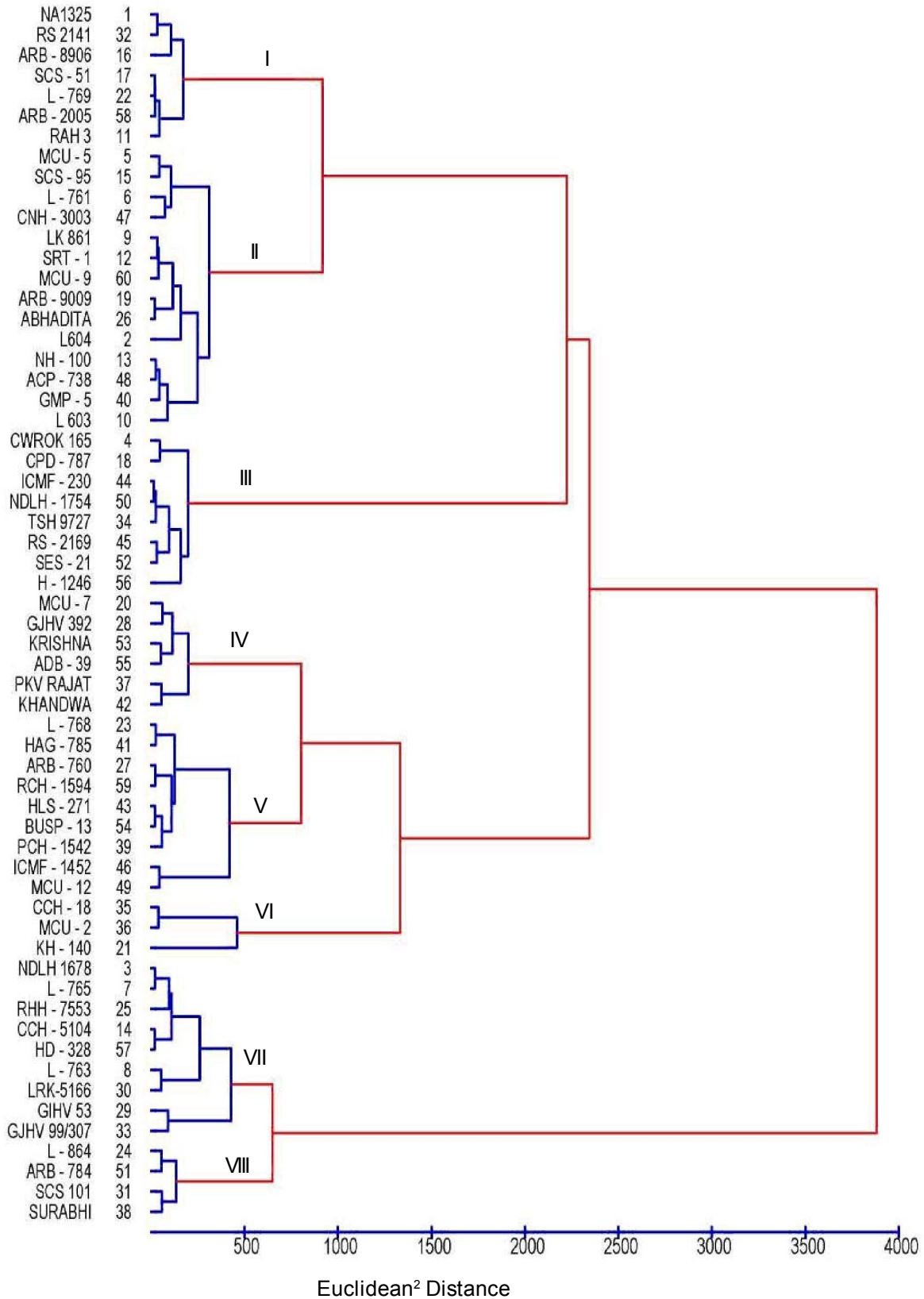

Euclidean² Distance

Table 5. Eigen values, proportion of the total variability, cumulative per cent variability and component loading of different characters.

	PC_1	PC_2	PC_3	PC_4
Eigen Value (Root)	2059.432	1805.840	1022.742	480.227
% Var. Exp.	35.175	30.844	17.468	8.202
Cum. Var. Exp.	35.175	66.019	83.487	91.690
Plant height	0.362	0.282	0.494	0.711
Monopodia / plant	-0.002	0.010	-0.021	0.009
Sympodia/ plant	-0.035	0.014	-0.008	0.001
Bolls/ plant	0.010	0.428	-0.504	0.231
Boll weight (g)	0.284	0.076	0.585	-0.477
Ginning out/turn (%)	-0.174	0.001	0.113	-0.190
Seed index (g)	0.774	-0.340	-0.297	-0.057
Lint index (g)	0.281	-0.207	-0.165	-0.032
2.5% span length (mm)	0.094	-0.069	-0.069	-0.009
Uniformity ratio	-0.018	-0.076	0.086	-0.124
Seed cotton yield/ plant (g)	0.265	0.750	-0.136	-0.398

Table 6. Clustering of 60 genotypes of cotton by Ward's minimum variance method.

Cluster No.	Number of Genotypes	Name of the Genotypes
I	7	NA 1325, RS 2141, ARB 8906, SCS-51, L-769, ARB-2005, RAH-3.
II	14	MCU-5, SCS-95, L-761, CNH-3003, LK-861, SRT-1, MCU-9, ARB-9009, Abhadita, L-604, NH-100, ACP-738, GMP-5, L-603.
III	8	CWROK-165, CPD-787, ICMF-230, NDLH-1754, TSH-9727, RS-2169, SES-21, H-1246.
IV	6	MCU-7, GJHV-392, Krishna, ADB-39, PKV Rajat, Khandwa.
V	9	L-768, HAG-785, ARB-760, RCH-1594, HLS-271, BUSP-13, TCH-1542, ICMF-1452, MCU-12.
VI	3	CCH-18, MCU-2, KH-140.
VII	9	NDLH-1678, L-765, RHH-7553, CCH-5104, HD-328, L-763, LRK-5166, GJHV-53, GJHV-99/307.
VIII	4	L-864, ARB-784, SCS-101, Surabhi.

Table 7. Intra (Bold values) -and inter-cluster squared Euclidian^2 distance between eight clusters formed by Ward's minimum variance method.

				Euclidean^2 : Cluster Distances				
Clusters	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster	7 Cluster	8 Cluster
1 Cluster	**131.78**	346.895	880.030	556.547	361.039	903.163	985.312	1209.205
2 Cluster		**202.055**	429.835	615.509	371.34	1291.112	767.442	771.988
3 Cluster			**162.241**	584.58	501.134	1671.909	806.818	396.225
4 Cluster				**193.039**	395.411	923.151	959.224	706.813
5 Cluster					**206.285**	784.706	561.042	557.508
6 Cluster						**498.419**	821.444	1241.931
7 Cluster							**269.426**	417.024
8 Cluster								**166.394**

Bold and diagonal values are intra - cluster distances

farthest from cluster 6 (1291.112) followed by cluster 8 (771.988). Cluster 3 had 8 genotypes. It was nearest to cluster 8 (396.225) followed by cluster 2 (429.835) and farthest from cluster 6 (1671.909) followed by cluster 7 (806.818). Cluster 4 was comprised of 6 genotypes. It was nearest to cluster 5 (395.411) followed by cluster 1 (556.547) and farthest from cluster 7 (959.224) followed by cluster 6 (923.151).

Cluster 5 had 9 genotypes. It was nearest to cluster 1 (361.039) followed by cluster 2 (371.340) and farthest from cluster 6 (784.706) followed by cluster 7 (561.042). Cluster 6 was comprised of 3 genotypes. It was nearest to cluster 5 (784.706) followed by cluster 8 (1241.931). Cluster 7 had 9 genotypes. It was nearest to cluster 8 (417.024) followed by cluster 5 (561.042) and farthest from cluster 1 (985.312) followed by cluster 4 (959.224). Cluster 8 was comprised of 4 genotypes. It was nearest to cluster 3 (396.225) followed by cluster 7 (417.024) and farthest from cluster 6 (1241.931) followed by cluster 1 (1209.205).

The genotypes from the diversified cluster can be applaited in plant breeding programmes to produce transgressire sgresants for the desired traits.

LITERATURE CITED

Kalsy H S and Garg H R 1995. Genetic divergence and heterosis in American cotton. Crop Improvement 22(2): 232-236

Mahalanobis P C 1928. A statistical study at Chinese head measurement. Journal of Asiatic Society of Bengal 25:301-307

S**ambamurthy J S V, Reddy D M and Reddy K H G 1995.** Genetic variability correlation and path analysis in upland cotton (Gossypium hirsutum L.) Journal Indian Society for Cotton Improvement 20 (2):133-138.

Singh R K and Choudhary B D 1977. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi pp: 215-219.

Rao C R 1952. Advanced statistical methods in biometrical research. John Wiley and Sons, New York pp: 236-272.