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Studies on genetic divergence in *Gossypium arboreum* L.

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ABSTRACT : On the basis of D^2 values, 60 genotypes were grouped into 8 clusters containing 1 to 14 genotypes. These clusters consisted of genotypes with different geographical origins and indicated no correlation between genetic divergence and geographical divergence. The genotypes of cluster VIII showed maximum genetic divergence with cluster I and V. The genotypes belonging to cluster VIII and I may be selected for hybridization for generating genetic variability. Cluster VI found 6 genotypes to be best performing for agronomic characters followed by cluster VIII with 1 genotype and cluster V with 8 genotypes. Thus, to generate desirable genetic variability the crossing between cluster VI, VIII and V genotypes would be useful. It was suggested that hybridization among the genotypes of above said clusters would produce segregants for more than 1 economic character which can serve as parents of hybrids. Days to first flower followed by seed cotton yield/plant, monopods and plant height contribute maximum toward divergence.

Key words: Cluster, genetic divergence, *G. arboreum*, D^2 statistic

Gossypium arboreum L. is a native of India. It is cultivated from Punjab in the north to Kanyakumari in the south and Assam in the east to Kutch in the west. *G. arboreum* genotypes matures between 150 to 180 days and is usually having coarse and short fibre and has high degree of resistance to disease and insect pests and is a very valuable germplasm resource having great export value.

It has also been well established that greater the genetic variability in the population, greater will be the chances of obtaining desirable gene combination. Genetic divergence is of considerable practical interest in any crop improvement programme. The wide range in genetic diversity available in India has not been fully exploited to improve the yield. Mahalanobis's D^2 statistic as a tool for estimating genetic divergence in crop plants can be used to choose the parents without making crosses before the initiation of hybridization programme. Therefore, the present investigation was undertaken to study the nature and magnitude of genetic divergence in 60 cotton genotypes.

The present investigation was carried out in Research Area of Cotton Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar during *kharif* 2011. Sixty diverse cotton genotypes from different cotton growing states were collected and raised in a randomized block design (RBD) in 3 replications. There were two rows of each genotype of 3 m length. Rows were spaced 67.5cm apart and plant to plant distance with in a row was 30 cm. The data were recorded on 5 competitive plants selected randomly from each replication. The mean of 5 plants was used for statistical analysis. Recommended package of practices were followed for raising the healthy crop. The data of the 9 parameters were recorded *viz*, days to first flower, plant h8 (cm), monopods, bolls/plant, boll w8 (g), seed cotton yield/plant (g), ginning outturn (%), seed index (g) and lint index (g). The genetic divergence was worked out by using Mahalanobis D^2 statistic. On the basis of D^2 values, these genotypes were grouped into different clusters by employing Euclidean cluster analysis.

The analysis of variance for different traits revealed highly significant differences among the genotypes for all the 9 characters suggested high degree of genetic variability in the material evaluated and specified existence of considerable genetic diversity among genotypes. Hence, further analysis was carried out for relative magnitude of D^2 values for all the characters and all genotypes were grouped into 8 clusters (Table 1 and Fig. 1). Among the clusters, maximum genotypes (14) were included in cluster II followed by Cluster I (10), III, IV and V accommodated 8 genotypes each, cluster VI accommodated 6 genotypes, cluster VII possessed 5 genotypes and cluster VIII contained solitary genotype. Generally, geographical diversity has been considered as a measure of genetic diversity. However, this is an inferential criterion and it may not be so effective in quantifying different populations. The present pattern of grouping of genotypes indicated that the genetic diversity was not fully related to the geographical diversity. These results are in agreement with the findings of Satish *et al.*, (2009) and Kulkarni *et al.,* (2011). There are forces other than geographical separation which are responsible for diversity such as natural and artificial selection, exchange of breeding material, genetic drift and environmental variation etc. Therefore, choice of the parents for hybridization should be decided on the basis of genetic diversity rather than geographic diversity.

The intra and inter cluster distances revealed that inter cluster distances were greater than intra cluster distances which suggested considerable amount of genetic diversity among genotypes (Table 2 and Fig 2). The maximum intra cluster distance was observed for cluster VII (3.546) followed by the cluster V (3.263), cluster II (3.096), cluster IV (2.745) and so on. Whereas, cluster VIII is solitary with single genotype, therefore, intra cluster distance would be minimum. The high intra cluster distance in cluster VII indicated the presence of wide genetic diversity among the genotypes *viz.*, PA 719, HD 508, PA 710, Das 1042, RAAS 1031. The nearest inter cluster distance was found between cluster III and IV (3.145) followed by cluster I and IV (3.437), cluster I and II (3.754) and so on. The widest inter cluster distance was found between cluster I and VIII (6.862) followed by cluster V and VIII (6.538), cluster IV and VIII (6.439) and so on. Maximum genetic divergence between the cluster points to the fact that hybridization among the genotypes included with them would produce potential and meaningful hybrids and desirable segregants. Use of genetically distant genotypes as parents to get the most promising breeding material had also been suggested by Jain and Yadav (2001), Gururajan and Manickam (2002), Sakhti *et al.*, (2009) and Kulkarni *et al.* (2011). However, Altaher and Singh (2003) proved that more number of heterotic combinations with high heterosis was from parents grouped into divergenent groups like clusters VIII and I. The results obtained from clustering pattern are in agreement with hypothesis of moderate divergence for the best heterotic combinations.

The contribution of individual characters to the divergence has been worked out in terms of number of times it appeared first (Table 3). This study helped to identify diversity in different proportion which ultimately helped to decide utilization of genetic material for improvement of specific characters. Among the 9 characters studied, the highest contribution to the divergence was days to first flower followed by seed cotton yield/plant. Lowest was from lint index. Higher contribution of days to first flower and seed cotton yield to total divergence was also

Table 1: Clustering pattern 60 genotypes of Asiatic cotton on D^2 analysis

Clusters	Number	Name of genotypes
I	10	LD 949, CCA A1, GAM 162, RAC 024, NDLA2977, HD 384, RG 600, HD 387, RG 585, HD 509.
II	14	HD 496, HD 383, HD 489, HD 386, LD 944, HD 511, RG 587, HD 510, RG 575P3, HD 385, RG 587, CAD 3, RG 542, SVA 1118.
III	8	FDK 178, CNA 1009, Arbas131, KWA 1001, NDLA 2981, CISA 105, CNA 1008, GBav 127.
IV	8	HD123, HD 418, HD 462-1 P1, CCA 1010, JLA 703, HD 507, HD 388, AKA 06-5.
V	8	RG 590, CISA 7R, GAM 147, AKA2005-3, HD 402, HD 499, HD 432, HD 462.
VI	6	LD 973, FDK 190, GBav 124, HD 499-1, HD 462-2, Das 1041.
VII	5	PA 719, HD 508, P A 710, Das 1042, RAAS 1031.
VIII	1	HD 324

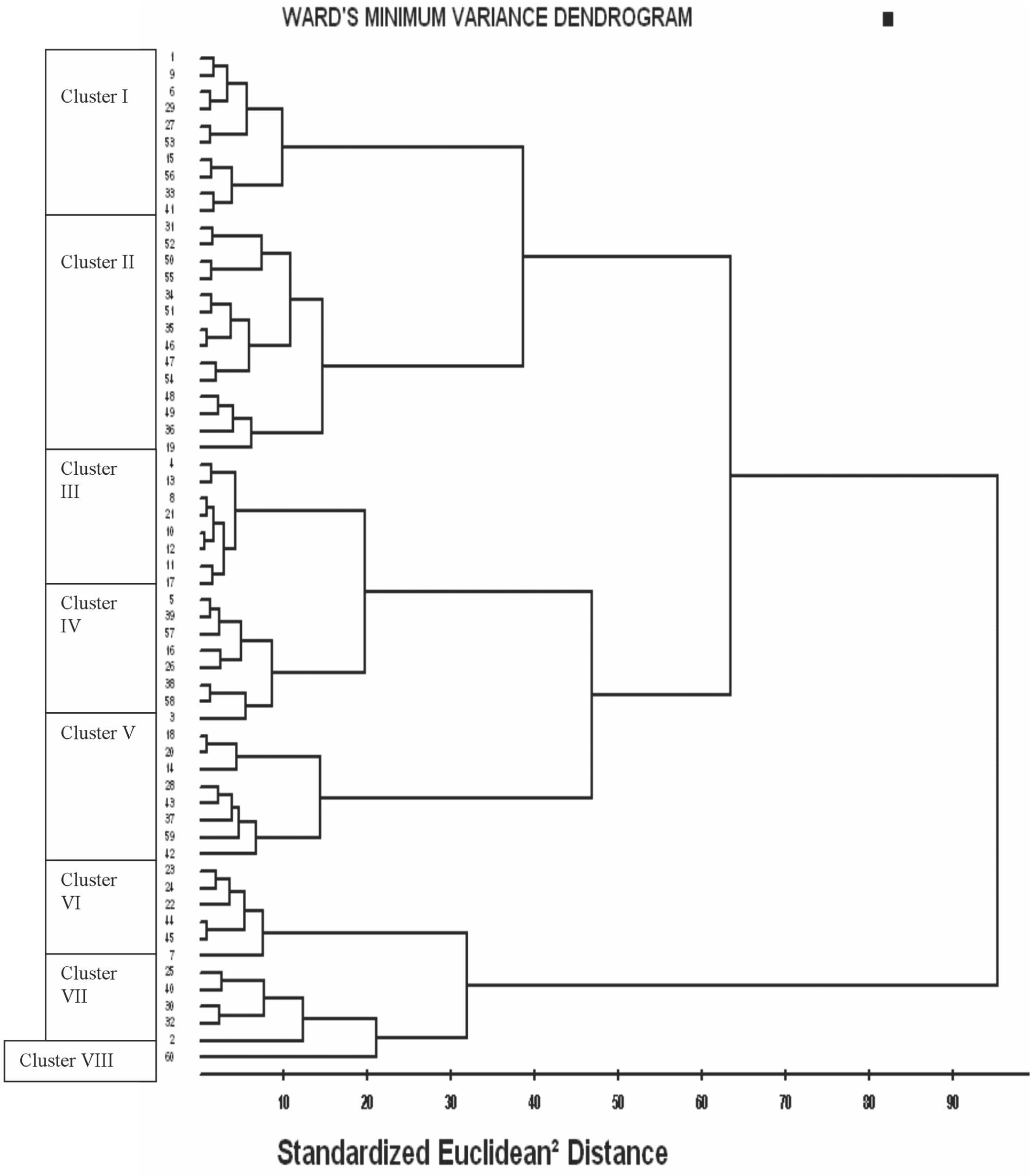

Fig. 1. Dendrogram based on Euclidean^2 distance illustrated the genetic relationship among sixty genotypes

Table 2. Average intra and inter cluster D^2 values of different clusters

Clusters	I	II	III	IV	V	VI	VII	VIII
I	**2.588**	3.754	3.806	3.437	4.687	5.342	5.302	6.862
II		**3.096**	4.216	3.935	4.279	4.480	4.669	5.923
III			**1.946**	3.145	3.972	4.908	3.859	5.201
IV				**2.745**	4.306	5.915	4.804	6.439
V					**3.263**	5.030	4.214	6.538
VI						**2.783**	4.424	5.624
VII							**3.546**	5.515
VIII								**0.000**

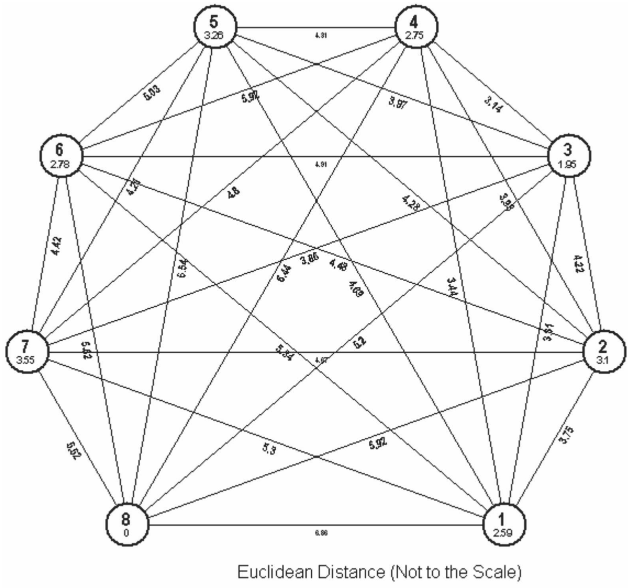

Fig. 2. Intra and inter cluster distances among VIII clusters

reported by Sakhti *et al.*, (2009) and Kulkarni *et al.*, (2011). The results imply that in order to select genetically diverse genotypes, the material should be screened for the important traits like days to first flower and seed cotton yield.

Cluster mean for various traits (Table 4) revealed that considerable differences were noticed between the cluster means for different characters. Maximum mean values for seed cotton yield were observed in cluster VII, V, VI and VIII; for bolls/plant in clusters VII, V and VI; for boll weight in clusters VI, VII, V and III and for ginning outturn in clusters VI, I and II. Thus, it was observed that genotype or genotypes grouped under cluster VI ranked first by having 8 characters (1-3 scores) at desirable direction followed by genotypes under cluster VIII with 5 character (1-3 scores), cluster V with 4 character (1-3 scores) and cluster VII with 5 characters (1-3 scores). Genotypes grouped under cluster IV (last rank) recorded 9 characters in negative direction (4-8 scores). Therefore, use of genotypes in cluster VI, VIII, V and VII would desirable to generate the variability in the desired direction.

Table 3. Percentage contribution of different characters toward divergence in *G. arboreum* (Tocher Method)

S. No.	Source	Time ranked first	Per cent contribution
1.	Days to first flower	800	45.20
2.	Plant height	220	12.43
3.	Bolls/ plant	64	3.62
4.	Monopods	235	13.28
5.	Boll weight	123	6.95
6.	Seed cotton yield/plant	273	15.42
7.	Ginning outturn	20	1.13
8.	Seed index	28	1.58
9.	Lint index	7	0.40

It is suggested that hybridization among the genotypes of above said clusters would produce segregants for more than 1 economic character which can served as parents of hybrids. These finding coincides with results of earlier studies (Gopinath *et al.*, 2009 and Kulkarni *et al.*, 2011).

Table 4. Cluster means of different traits

Clusters	Days to first flower	Plant height	Bolls/ plant	Monopods	Boll weight	Seed cotton yield/ plant	Ginning outturn	Seed index	Lint index	Total score	Rank
I	53.1(6)	171.2(6)	31.2(7)	3.8(5)	1.9(8)	56.1(8)	39.8(2)	4.8(8)	3.2(5)	55	**VI**
II	59.3(4)	151.2(8)	31.8(6)	5.6(2)	2.2(7)	68.2(6)	39.4(3)	5.1(5)	3.3(3)	44	**IV**
III	54.5(5)	198.0(1)	33.0(5)	3.2(8)	2.4(4)	70.8(5)	35.7(7)	5.3(4)	2.9(6)	45	**V**
IV	52.3(8)	159.1(7)	29.6(8)	3.7(6)	2.3(6)	62.5(7)	36.0(6)	4.9(6)	2.8(8)	62	**VII**
V	52.6(7)	178.4(4)	39.7(2)	5.9(1)	2.4(1)	87.1(2)	37.2(4)	4.9(7)	2.9(7)	35	**III**
VI	62.4(2)	193.6(2)	38.6(3)	4.9(4)	2.5(4)	85.0(3)	42.1(1)	5.4(3)	3.9(1)	23	**I**
VII	59.8(3)	171.8(5)	41.4(1)	3.4(7)	2.5(7)	94.5(1)	36.9(5)	5.4(2)	3.2(4)	35	**III**
VIII	64.6(1)	192.6(3)	33.3(4)	5.4(3)	2.3(3)	73.3(4)	33.8(8)	7.0(1)	3.6(2)	29	**II**

*Values in parentheses indicate relative score for each character across 8 cluster

On the basis of D^2 values, 60 genotypes were grouped into 8 clusters and the genotypes of Cluster VIII showed maximum genetic divergence with Cluster I and V, therefore genotypes of these clusters may be selected for hybridization for generating genetic variability. Cluster VI seemed to be most promising for agronomic traits followed by cluster VIII. Thus, selection and use of these genotypes be useful to generate desirable genetic variability.

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