Studies on diversity analysis of upland cotton genotypes (*Gossypium hirsutum* L.) based on morphological traits

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ABSTRACT : On the basis of D^2 values, sixty eight genotypes of various geographical origins were grouped into eight clusters containing one to fifty five genotypes. For fibre quality traits genotypes grouped in to six cluster indicating non significant correlation between genetic and geographical diversity. The traits days to first flower, seed cotton yield and bolls / plant, monopods contributed maximum toward the divergence. The genotypes of cluster VIII showed maximum genetic divergence with cluster VI, III and VII and genotypes of these clusters may be selected for hybridization for generating genetic variability. Maximum divergence for fibre quality traits was observed between genotype of cluster III with genotypes of cluster VI indicating the fact that the genotypes found in one cluster differed entirely from the genotypes present in other clusters. Cluster VI seems to be most promising for agronomic traits followed by cluster VII, IV and II. Thus, selection and use of these genotypes be useful to generate desirable genetic variability.

Key words: cluster mean analysis, genetic diversity, *Gossypium hirsutum*, seed cotton yield

Cotton is the most important natural fiber in the world for textile manufacture, accounting for about 50 per cent of all fibers used in the textile industry. It is the member of *Malvaceae* family and genus *Gossypium*. There are four species in the genus *Gossypium* — *G. hirsutum* L., *G. barbadense* L., *G. arboreum* L. and *G. herbaceum* L. that were domesticated independently as source of textile fibre. *Gossypium hirsutum* L. is known as New World or upland cotton having tetraploid (2n = 4x = 52) with the genome AADD. The place of origin of the genus is not known, however, the primary centres of diversity for the genus are west-central and southern Mexico (18 species), north-east Africa and Arabia (14 species) and Australia (17 species). Cotton is currently the leading fibre crop worldwide and is grown commercially in the temperate and tropical regions of more than 50 countries.

Characterization and quantification of genetic diversity has long been a major goal in evolutionary biology. Information on genetic diversity within and among closely related crop varieties is essential for a rational use of genetic resources. The analysis of genetic variation both within and among elite breeding materials is of fundamental interest of plant breeders. Diversity based on phenological and morphological characters usually varies with environments and evaluation of these traits requires growing the plants to full maturity prior to identification.

In the present study, promising cotton genotypes possessing high yield coupled with good fibre quality traits was undertaken to assess genetic diversity. Our objective was firstly to

assess the genetic diversity of large collection of hirsutum genotypes based on the morphological traits and secondly to identify the suitable parents for hybrid breeding programme.

MATERIALS AND METHODS

The experimental material for present investigation comprised of sixty eight diverse genotypes from different cotton research stations of India. All the sixty eight genotypes were grown at two locations *viz.*, Hisar and Sirsa. The crop is taken in two seasons at both locations, thereby creating four environments. All the genotypes were raised in a randomized block design (RBD) with three replications. There were two rows of each genotype of three meter length, row was spaced at 67.5cm apart and plant to plant distance was kept 30 cm. All the recommended agronomical package of practices ware followed to raise the good crop. The data was recorded on

five competitive plants selected randomly from each replication. The mean of the five plants was used for statistical analysis. Recommended package of practices were followed for raising the crop. The data on the following parameters were recorded *viz.*, days to first flower, plant height (cm), monopods and bolls / plant, boll weight (g), seed cotton yield / plant (g), ginning outturn (%), seed index (g), lint index (g), 2.5 per cent span length (mm), fibre strength (g/tex), fibre fineness (mg/inch) and Uniformity ratio (%).

RESULTS AND DISCUSSION

Creation of variability and selection within, leading to diverse genotypes is the common protocol a conventional plant breeder follows. Genetic relationship among genotypes thus generated can be measured by similarity or dissimilarity of any seed cotton yield and important yield components characters

Table 1. Grouping of 68 upland cotton genotypes for seed cotton yield and important yield components in to different clusters

Cluster	Genotypes	Number of genotypes
I	MR68 , TCH 1728, KH 1001,BS 37, F 1861, ARBH 1001, P 2150, GJHV 500, F 2276, CSH 3114, CA 107, H 1117, H 1462, GCHV 160, RS 2596, CPD 1001, BGDS 801, HS 288, RS 2620, CNH 1094, RHC 0717, CCH 820, CPD 1002, CNH 1106, RAH 803, RS 2013, TSH 0250, GJHV 503, BS 39, ADB 532, SCS 792, CCH 10-1, F 2337, SR 1, H 1300, H 1422, FYT/09-14, FYT/09-17, FYT/09-19, H 1435, H 1462, FYT/09-12, H 1442, H 1454, PRT/09-3, PRT/09-4, PRT/09-6, PRT/09-8, MR 68-1, F 1861-1, F 2337-1, F 2177, F 2228, Bihani 251, LH 2107	55
II	ADB 531, L 770, SCS 793, LH 2170	4
III	GSHV 159	1
IV	GTHV 07/1	1
V	H 1316, H 1428, LH 2152, H 1451	4
VI	H 1439	1
VII	TCH 1717	1
VIII	CSH 2810	1

assuming that the differences between characters of genotypes ultimately reflect in the divergence of genotypes. In heterosis breeding programs the diversity of parents is always emphasized upon. More diverse the parents within a reasonable range, better the chances of improving economic traits under consideration in the resulting offspring. However, it is a difficult task for the breeder to select the most suitable and genetically divergence parents, unless one is provided with necessary information about genetic variability and genetic diversity present in the available germplasm.

Generally, geographical diversity was considered as a measure of genetic diversity when no scientific tools were available. However, this is an inferential criterion and may not be used for discrimination among the populations occupying ecologically marginal habits.

The multivariate D^2 analysis using Mahalanobis's D^2 statistic provides a useful statistical tool for measuring the genetic diversity in a given population with respect to the characters considered together. Further the problem of selecting diverse parents for hybridization programme can be narrowed, if one can identify the characters responsible for the discrimination between populations.

The data collected on different traits from sixty eight genotypes were subjected to multivariate analysis and genetic divergence was estimated using Mahalanobis's D^2 statistic. The magnitude of D^2 values suggested that there was considerable variability in the material studied, which leads to genetic diversity.

Gopinath *et al.*, (2009), Satish *et al.*, (2009), Shakthi *et al.*, (2009), Kulkarni *et al.,* (2011), Pujer *et al.*, (2015) successfully used the Mahalanobis's D^2 analysis for quantifying the genetic divergence in cotton.

On the basis of D^2 values, 68 genotypes were grouped into eight clusters indicating the presence of appreciable amount of genetic diversity among the genotypes under study. The maximum s of genotypes (55) were grouped in to

Table 2. Grouping of 68 upland cotton genotypes of fibre quality traits in to different clusters

Cluster	Genotypes	Number of genotypes
I	MR68 , KH 1001, F 1861, ARBH 1001, P 2150, GJHV 500, F 2276, CSH 3114, CA 107, GCHV 160, CPD 1001, BGDS 801, HS 288, RS 2620, CNH 1094, RHC 0717, RAH 803, RS 2013, TSH 0250, ADB 532, SCS 792, CCH 10-1, F 2337, H 1422, FYT/09-14, FYT/09-17, FYT/09-19, FYT/09-12, H 1442, PRT/09-4, MR 68-1, F 1861-1, F 2337-1, F 2177, F 2228, Bihani 251, LH 2107, H 1439 ,GTHV 07/1, H 1316, H 1428, LH 2152, H 1451, CSH 2810, GSHV 159, ADB 531, SCS 793, LH 2170	47
II	CPD 1002, GJHV 503, F 2228, TCH 1728, CCH 820, H 1454, TCH 1717 , PRT/09-3, CNH 1106, H 1435, BS 37	11
III	H 1462, PRT/09-8, SR 1, H 1117, H 1300, RS 2596, H 1462	7
IV	L 770	1
V	PRT/09-6	1
VI	BS 39	1

Table 3. Intra (diagonal) and inter (off diagonal) cluster distance based on seed cotton yield and important yield components

Clusters	I	II	III	IV	V	VI	VII	VIII
I	**4.56**	6.80	6.36	6.56	7.03	7.54	6.41	8.29
II	6.80	**4.58**	8.47	7.35	9.38	7.84	7.24	7.67
III	6.36	8.47	**0.00**	6.05	10.63	4.46	7.42	12.01
IV	6.56	7.35	6.05	**0.00**	9.96	4.98	5.97	10.99
V	7.03	9.38	10.63	9.96	**5.61**	11.77	8.64	7.59
VI	7.54	7.84	4.46	4.98	11.77	**0.00**	5.77	12.53
VII	6.41	7.24	7.42	5.97	8.64	5.77	**0.00**	11.11
VIII	8.29	7.67	12.01	10.99	7.59	12.53	11.11	**0.00**

cluster I, followed by cluster II and V with 4 genotypes, clusters III, IV, VI, VII and VIII contained solitary genotype respectively (Table.1). For fibre quality traits 68 genotypes were grouped into six clusters indicating the presence of diversity for different traits. The cluster I had highest genotypes (47) followed by cluster II (11), cluster III (7). The clusters IV, V and VI were monogenotypic (Table 2).

This study revealed that genetic diversity has nothing to do with geographical diversity as the genotypes from the different parts of the country were accommodated in the same clusters. There were forces other than geographical separation which were responsible for diversity such as natural and artificial selection, exchange of breeding material, genetic drift and environmental variation. Magnitudes of divergence among parents determine the inherent potential of a cross and therefore, selection of the parent based on the genetic divergence would be desirable for creating the maximum variability. Similar result were reported by Pushpam *et al.,* (2004), Pathak *et al.*, (2007), Satish *et al.*, (2009) Kulkarni *et al.*, (2011) and Pujer *et al.*, (2015).

The intra and inter cluster distances revealed that inter cluster distance values were greater than intra cluster distance values. The maximum intra-cluster distance was observed for cluster V (5.61) followed by cluster II (4.58), cluster I (4.56). Whereas, clusters III, IV, VI, VII and VIII contained solitary with single genotype so intra cluster distance would be minimum (Table 3). The high intra cluster distance in cluster V indicated the presence of wide genetic diversity among the genotypes in this cluster *viz* H 1316, H 1428, LH 2152 and H 1451. The nearest inter cluster distance is found between cluster III and VI (4.46) followed by cluster IV and VI (4.98), cluster VII and VI (5.77) and so on. The widest inter cluster distance was found between cluster VI and VIII (12.53) followed by cluster III and VIII (12.01), cluster V and VI (11.77) and so on. In this study, the genotypes of cluster VIII showed maximum genetic divergence with

Table 4. Intra (diagonal) and inter (off diagonal) cluster distances based on D^2 values of fibre quality traits

Clusters	I	II	III	IV	V	VI
I	**4.37**	9.80	7.93	6.67	13.47	18.24
II	9.80	**4.44**	16.08	6.74	6.33	9.78
III	7.39	16.08	**3.42**	12.64	19.42	24.81
IV	6.67	6.74	12.64	**0.00**	11.56	14.13
V	13.47	6.33	19.42	11.56	**0.00**	7.34
VI	18.24	9.78	24.81	14.13	7.34	**0.00**

cluster III and VI. Based upon these studies, crosses may be attempted between the genotypes of cluster VIII (CSH 2810) and cluster VI (H 1439) followed by III (GSHV 159) and VIII (CSH 2810), cluster VI (H 1439) and cluster V *viz*, H 1316, H 1428, LH 2152 and H 1451 to obtain better recombinants in cotton.

Intra and inter cluster distance of fibre quality traits (Table 4) the maximum intra cluster distance was recorded within cluster II (4.44) followed by cluster I (4.37) and clusters III (3.42), Whereas, clusters IV, V and VI contained solitary with single genotype so intra cluster distance would be minimum. The high intra cluster distance in cluster II indicated the presence of wide genetic diversity among the genotypes in this cluster *viz.,* CPD 1002, GJHV 503, F 2228, TCH 1728, CCH 820, H 1454, TCH 1717, PRT/09-3, CNH 1106, H 1435 and BS 37. The nearest inter cluster distance is found between cluster II and V (6.33) followed by cluster I and IV (6.67), cluster II and IV (6.74), cluster VI and V (7.34) and so on. The widest inter cluster distance was found between cluster III and VI (24.81) followed by cluster IV and III (19.42), cluster I and VI (18.24) and cluster II and III (16.08).

Based upon these studies, crosses may be attempted between the genotypes of Cluster III (H 1462, PRT/09-8, SR 1, H 1117, H 1300, RS 2596, H 1462) and VI (BS 39,) followed by cluster IV (L 770) and III (H 1462, PRT/09-8, SR 1, H 1117, H 1300, RS 2596, H 1462), Cluster I and VI and cluster II and III to obtain better recombinants in cotton.

For successful breeding programme, selection of genetically diverse parents is an important prerequisite so as to obtain better and desirable recombinants Gururajan (2002), Kumar *et al.*, (2000), Jain and Yadav (2001),Chovatia *et al.,* (2006), Pathak *et al.*, (2007), Shakthi *et al.,* (2009) and Kulkarni *et al.*, (2011).

Contribution of characters towards divergence : The contribution of individual characters to the divergence (table. 5) has been worked out in terms of times it appeared first. This study helps to identify diversity in different proportion which ultimately helps to decide utilization of genetic material for improvement of specific characters. Among the nine characters studied the highest contribution to the divergence was from days to first flower followed by seed cotton yield, monopods and bolls / plant (Table 5). Lowest was from ginning out

Table 5. Percentage contribution of each trait toward divergence (Tocher Method).

S.N	Characters	Time ranked first	Contribution (%)
1.	Days to first flower	559	24.54
2.	Plant height(cm)	266	11.68
3.	Monopods/plant	427	18.74
4.	Bolls/plant	356	15.63
5.	Boll weight (g)	33	1.45
6.	Seed index (g)	129	5.66
7.	Lint index (g)	39	1.71
8.	Ginning outturn (%)	26	1.14
9.	Seed cotton yield/plant (g)	443	19.45

Table 6. Cluster mean of different seed cotton yield and important yield components

Clusters	Days to first flower	Plant height (cm)	Monopod/ plant	Bolls/ plant	Boll weight (g)	Seed index (g)	Lint index (g)	Ginning outturn (%)	Seed cotton yield/ plant (g)	**Total score**	Rank
I	52.44(6)	122.43(5)	2.07(6)	41.40(6)	3.13(4)	7.53(6)	4.23(4)	35.02(3)	138.12(6)	**46**	V
II	53.67(2)	136.25(3)	2.14(5)	42.40(5)	3.38(3)	7.75(4)	4.18(6)	34.43(6)	146.06(5)	**39**	IV
III	42.00(8)	125.71(6)	0.19(8)	53.92(3)	3.37(4)	8.17(3)	4.25(4)	33.45(8)	164.07(2)	**46**	V
IV	53.29(3)	137.66(2)	2.78(2)	58.08(1)	2.94(6)	6.82(8)	3.97(7)	36.84(1)	161.44(3)	**33**	III
V	53.02(5)	122.04(7)	2.73 (3)	33.23(7)	2.65(7)	7.43(7)	3.77(8)	34.23(7)	128.19(7)	**58**	VII
VI	53.22(4)	125.71(4)	2.26(4)	56.67(2)	3.54(2)	8.64(1)	4.68(1)	34.52(4)	168.15(1)	**23**	I
VII	48.33(7)	154.51(1)	3.45(1)	44.00(4)	3.64(1)	8.28(2)	4.52(2)	34.48(5)	153.16(4)	**27**	II
VIII	54.28(1)	121.04(8)	1.81(7)	32.25(8)	2.34(8)	7.64(5)	4.32(3)	35.95(2)	121.08(8)	**50**	VI

*Values in parentheses indicate rank for each trait across eight clusters

tern, boll weight and lint index. Higher contribution of days to first flower and seed cotton yield to total divergence was also reported by Shakthi *et al.*, (2009) and Kulkarni *et al.*, (2011). The above 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.

Analysis of cluster means : In fact genotypes forming single genotype cluster were extra ordinary for one or more characters, which made them so divergent from others. This fact also reflected in cluster means. Analysis of cluster means indicated substantial variation among clusters grouped according to D^2 analysis. Based on the range of means it is possible to know the characters influencing divergence. The cluster having single or less genotypes revealed highest or lowest mean values for different characters as evident from mean Table. Although, the distance between various clusters was reflected in cluster means but it was not proportional for few characters. It seems that there are some other factors responsible for divergence.

In the present investigation, it was observed that genotype or genotypes grouped under cluster VI ranked first by having three characters (1-3 scores) in desirable direction followed by genotypes under cluster VII with five character (1-3 scores), cluster IV with six character (1-3 scores) and cluster II with five characters (1-3 scores). Genotypes grouped under cluster V (last rank) recorded eight characters in negative direction (4-8 scores) (Table. 6). Therefore selection of genotypes following in cluster VI, VII, IV and II would be useful to generate desirable genetic resource by crossing the genotypes under these clusters. Among fibre quality traits (Table. 7) genotypes grouped under cluster V ranked first by having two characters (1-3 scores) at desirable direction followed by genotypes under cluster II with four character (1-3 scores), cluster I, III and VI with six character (1-3 scores). Genotypes grouped under cluster IV (last rank) recorded five characters in negative direction (4-5 scores). Therefore, selection of genotypes following in cluster V and II would be useful to generate desirable genetic resource by crossing the genotypes under these clusters. It is suggested that hybridization among the genotypes of above said clusters would produce segregants for more than one economic character which can serve as parents of hybrids. The same has been

Table 7. Cluster mean values of different fibre quality traits

Clusters	2.5 per cent span length (mm)	Fibre fineness (micronaire value)	Bundle strength (g/tex)	Uniformity ratio (%)	**Total score**	Rank
I	26.57(5)	4.54(3)	20.53(4)	48.49(3)	**15**	III
II	28.92(3)	4.46(4)	22.47(3)	46.64(4)	**14**	II
III	24.54(6)	4.84(2)	19.60(6)	49.43(1)	**15**	III
IV	28.20(4)	3.90(5)	20.43(5)	45.00(5)	**19**	IV
V	29.33(2)	4.90(1)	24.87(1)	49.00(2)	**6**	I
VI	31.17(1)	3.87(6)	24.70(2)	45.00(6)	**15**	III

*Values in parentheses indicate rank for each trait across six clusters

suggested by several authors Pushpam *et al.,* (2004), Gopinath *et al.,* (2009) and Kulkarni *et al.,* (2011).

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