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Assessment of genetic diversity in *Gossypium hirsutum* L. germplasm following Mahalanobis D^2 analysis

PANKAJ SHARMA*, R S SOHU AND DHARMINDER PATHAK
Department of Plant Breeding and Genetics, Punjab Agricultural University Ludhiana 141 004
**E-mail: pankaj01972@gmail.com*

ABSTRACT: The present study was undertaken to assess the genetic diversity present in the 81 American cotton (*Gossypium hirsutum* L.) germplasm lines representing the collection from various eco geographical regions of the country. Mahalanobis D^2 analysis grouped all 81 genotypes into 10 clusters. Cluster V (21 genotypes) and cluster III (1 genotype) were the largest and the smallest clusters respectively amongst all. The mean for boll weight (4.13g) and seed index (8.55g) was highest in cluster III, where as cluster VII had highest mean for lint index (3.99g). Cluster V and X had highest mean values for ginning outturn (34%) and seed cotton yield (132g), respectively. The inter cluster distance was highest between III and X cluster pair (2726.1) followed by I and X (1652.7) suggesting significant high genetic diversity among genotypes of these clusters. The present study has been useful for the identification of genotypes possessing higher seed cotton yield, boll weight and ginning outturn.

Key words : *Gossypium hirsutum*, Mahalanobis D^2 analysis, yield and yield component traits

Cotton plays an important role in Indian economy. Among the major cotton producing countries, China has the highest production followed by India and USA. In India, cotton occupied an area of 11.55 million ha in the country during 2013 with a total production of 375.0 lakh bales and productivity of 552.00 kg lint/ha (Anonymous, 2014). High productivity is still the primary goal of breeding programme. Identification of diverse strains and their use in hybridization with elite cultivars plays an important role. Therefore, attempts were made to differentiate *Gossypium hirsutum* accessions using plant morphological differences combined with geographic origins.

MATERIALS AND METHODS

Eighty one eco geographically different genotypes of *G. hirsutum* were taken for genetic diversity study. These were raised in a partially balanced lattice design with two replications at the experimental area of Cotton Section, Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana. Each genotype was grown with row to row and plant to plant spacing of 67.5 and 60 cm, respectively. Observations on seed cotton yield/plant, boll weight, ginning outturn, lint yield/plant, lint index and seed index were recorded in 5 randomly selected plants in each genotype in each replication. Replicated data recorded was used for Mahalanobis D^2 statistics. The grouping of different genotypes into different clusters was done.

RESULTS AND DISCUSSION

Mean squares due to genotypes were found to be significant for all the characters studied indicating diversity in the plant material under investigation.

Categorization of the germplasm lines : Based on the mean values for the morphological traits germplasm lines were categorized for some of the important quantitative characters namely, seed cotton yield/plant, boll weight, ginning outturn and seed index (Table 1).

Diversity analysis of the genotypes based on quantitative traits : The 81 accessions (79 test genotypes and 2 checks) were grouped into various clusters depending on their genetic similarities/differences. Lines within a cluster were more similar than lines in the other groups. The accessions were grouped into 10 clusters (Table 2). The critical examination of clusters indicated the presence of high level of genetic diversity in the material studied. High level of genetic diversity was also observed by Basavaraddi and Katageri (2011) while grouping 24 derivatives of F_8 generation into 8 clusters. In the present study the cluster V consisting of 21 genotypes was the largest amongst all and was closely followed by cluster VI with 14 genotypes and IV with 10 genotypes. Cluster III was the smallest one with a single genotype and none of the other clusters was monotypic, whereas cluster VII and VIII had 7 genotypes each. Cluster I, II, IX and X included 3, 9, 6 and 3 genotypes, respectively. The check cultivars LH 2076 and F 1861 used in the present study fell in cluster IV and II, respectively. Greater number of genotypes in a single cluster manifests that these genotypes were more closely related and had less genetic variation among them. It further implies that hybridization programme involving genotypes from same cluster will be of little use in cotton improvement programme.

Cluster II included genotypes originating from Ludhiana (Punjab), Khandwa (Madhya Pradesh), Bhawanipatna (Orissa), Hisar (Haryana), Junagadh (Gujrat) etc. The results were in accordance with the findings of Satish *et al.,* (2009) and Kulkarni *et al.,* (2011) who observed that genotypes belonging to different geographic origin can be grouped into same cluster The pattern of distribution of genotypes occurring in clusters cutting across geographical boundaries demonstrated that geographical isolation was not the only factor causing genetic diversity (Satish *et al.,* 2009). Similarly, in cluster V entries originating from Ludhiana, Faridkot and Sirsa etc were grouped together. Thus, grouping of genotypes into different clusters did not follow any specific pattern. There was no parallelism between the genetic background and the geographical diversity of the genotypes as also observed by Tulasi *et al.,* (2014). This can be attributed either due to free exchange of the breeding material from one center to another center across the country or due to the unidirectional selection pressure followed at several locations.

Identification of diverse and desirable germplasm lines : In addition to grouping of lines into different clusters, D^2 analysis was also used to identify the diverse and desirable lines in terms of inter cluster distance and mean performance of characters, respectively. The important points considered while selecting genotypes were: (1) Choice of the clusters which are separated by maximum inter cluster distance. (2) Selection of particular accessions that showed good performance in the selected clusters. For this purpose intra and inter cluster distance (Table 3) and characterwise clusters means (Table 4) were considered.

The minimum inter cluster distance value (334.1) was observed between clusters IV and VIII, whereas, maximum inter cluster distance value (2726.1) was recorded between clusters III and X (Table 3) indicating that genotypes in these clusters were distant to each other. Maximum intra cluster distance value, as shown in Table 3, was recorded in cluster I (327.4) followed by clusters VI (312.4) and X (254.3) indicating that genotypes in cluster I were relatively more diverse. The intra cluster distance for cluster III was zero because it had

Table 1. Categorization of the germplasm lines

Character	Frequency	Accession name
Seed cotton yield/plant (g)		
Upto 75.0	3	BS 37,GJHV 500 and HS 283
75.1 - 95.0	40	RS 2013, LH 2331, H 1246, LH 2376, H 1226, CSH 3114, LH 2355, LH 2107, F 1861, LH 2309, LH 2139, F 1054, LH 2232, F 2276, LH 2108, TCH 1728, LH 900, LH 2367, PIL 8, F 2427, KH 1001, PIL 43, CSH 3129, LRA 5166, F 2164, LH 2280, LRK 516, LH 2380, F 2440, HS 286, LH 2358, F 846, LH 2332, LH 2170, LH 2349, Bihani 251, F 1378, LH 2378, H 1454 and F 2397
95.1 - 115	26	LH 2372, LH 2369, LH 2370, LH 2277, LH 2076, F 2437, CSH 3158, LH 2381, LH 2315, P 2150, LH 2357, F 2228, LH 2307, LH 2377, LH 2334, CSH 10, LH 2342, LH 2347, LH 2382, LH 2306, LH 2298, LH 2384, LH 2353, LH 2348, LH 2379 and LH 2255
115.1-135	10	LH 2338, F 2177, MR 68, LH 2368, LH 2360, LH 2374, LH 2386, LH 2312, F 2170 and LH 2258
Above 135	2	MR 786 and F 505
Boll weight (g)		
Upto 3.50	8	F 2276, TCH 1728, LH 2355, CSH 3114, LRA 5166, F 2427, CSH 3158 and LRK 516
3.51 - 3.80	21	F 2440, H 1246, LH 2368, F 2228, LH 2232, HS 286, LH 900, LH 2108, LH 2382, LH 2298, CSH 3129, GJHV 500, LH 2342, LH 2076, H 1454, F 1054, BS 37, LH 2360, PIL 43, LH 2348 and H 1226
3.81 – 4.10	35	LH 2309, LH 2369, LH 2280, LH 2358, LH 2347, F 2170, PIL 8, LH 2372, KH 1001, LH 2349, LH 2306, LH 2367, LH 2377, LH 2331, F 2437, LH 2277, P 2150, F 1378, LH 2380, LH 2312, LH 2332, LH 2378, CSH 10, LH 2370, F 1861, LH 2384, LH 2357, LH 2381, F 505, LH 2139, F 2177, LH 2255, MR 68, LH 2386 and LH 2353
4.11 – 4.40	14	RS 2013, HS 283, LH 2170, LH 2107, F 846, H 2374, LH 2258, MR 786, F 2164, LH 2338, LH 2307, LH 2376, Bihani 251 and F 2397
Above 4.40	3	LH 2379, LH 2315 and LH 2334
Ginning outturn (%)		
Upto 32.0	4	HS 283, LH 2331, PIL 43 and LH 2334
32.01 – 33.00	16	LH 2367, LH 2232, F 2437, TCH 1728, H 1226, LH 2380, F 2228, F 505, F 2170, LH 2255, RS 2013, CSH 3129, LH 2372, F 2427, LH 2353 and LH 2338
33.01 – 34.00	16	F 2164, GJHV 500, LRK 516, LH 2358, LH 2374, LH 2370, F 1861, KH 1001, LH 2277, LH 2360, LRA 5166, LH 2368, LH 2342, LH 2348, H 1454 and F 1054
34.01 – 35.00	26	F 2397, CSH 3158, LH 2139, BS 37, LH 2384, LH 2377, CSH 10, LH 2309, LH 2332, F 846, LH 2386, MR 68, F 2276, LH 2379, LH 2381, LH 2315, F 1378, H 1246, F 2177, LH 2382, LH 2307, HS 286, LH 2298, LH 2312, F 2440 and LH 2369
Above 35.00	19	LH 2108, LH 900, LH 2378, Bihani 251, LH 2349, MR 786, PIL 8, P 2150, LH 2076, LH 2280, LH 2258, CSH 3114, LH 2347, LH 2355, LH 2107, LH 2357, LH 2306, LH 2376 and LH 2170
Seed index (g)		
Upto 7.00	15	LH 2360, F 2440, LRA 5166, LH 2331, LH 2358, H 1246, CSH 10, CSH 3158, LH 2170, LH 2312, CSH 3129, LH 2349, RS 2013, F 2177 and P 2150
7.01 – 7.50	25	LH 2306, F 1378, LH 2372, LH 900, LH 2378 KH 1001, LH 2298, TCH 1728, LH 2367, LH 2381, F 2170, PIL 8, LH 2076, LH 2369, F 1054, MR 68, F 846, HS 286, LH 2277, H 1454, F 1861, LH 2357, CSH 3114, LH 2309 and LH 2108
7.51 – 8.00	29	LH 2348, LH 2374, LH 2280, F 2427, LRK 516, GJHV 500, F 2228, LH 2384, LH 2258, F 505, LH 2368, LH 2107, LH 2353, H 1226, LH 2342, LH 2380, LH 2382, LH 2332, LH 2355, LH 2307, LH 2315, MR 786, LH 2347, LH 2376, LH 2232, LH 2386, LH 2334, LH 2377 and F 2276
8.01 – 8.50	8	Bihani 251, BS 37, LH 2379, LH 2255, LH 2139, LH 2370, LH 2338 and PIL 43
Above 8.50	4	HS 283, F 2164, F 2437 and F 2397

Table 2. Clustering pattern obtained by Mahalanobis D^2 analysis

Cluster	Frequency	Genotypes
I	3	RS 2013, LH 2232 and LH 2331
II	9	F 2427, H 1226, KH 1001, TCH 1728, LH 2367, LH 2380, GJHV 500, F 1861 and BS 37
III	1	HS 283
IV	10	F 2228, LRK 516, F 846, LH 2307, CSH 10, F 1378, LH 2076, LH 900, P 2150 and LH 2357
V	21	F 1054, LH 2309, H 1246, LH 2355, LH 2376, LH 2108, LH 2107, Bihani 251, LH 2349, F 2440, PIL 8, HS 286, LH2381, H 1454, LH 2369, LH 2280, LH 2332, LH 2170, CSH 3114, F 2276 and LH 2378
VI	14	CSH 3129, LRA 5166, LH 2358, CSH 3158, LH 2384, LH 2372, LH 2277, LH 2334, LH 2139, F 2397, LH 2370, F 2164, PIL 43 and F 2437
VII	7	LH 2255, LH 2338, LH 2353, LH 2368, LH 2374, LH 2379 and LH 2377
VIII	7	LH 2382, LH 2342, LH 2315, LH 2348, LH 2347, LH 2306 and F 2177
IX	6	LH 2258, MR 786, LH 2386, LH 2312, MR 68 and LH 2298
X	3	F 2170, F 505 and LH 2360

only one genotype. The inter cluster distances were larger than the intra cluster distances indicating wider genetic diversity between genotypes of the clusters with respect to the traits considered. This diversity suggested that the breeding programme with selected genotypes belonging to different clusters having greater inter cluster distance may produce high magnitude of heterosis or desirable segregants which will out yield the parental lines involved. The results are in accordance with the findings of Satish *et al.,* (2009), Shakthi *et al.,* (2009) and Kulkarni *et al.,* (2011) who also reported greater inter cluster distances as compared to intra cluster distances. The hybridization programme with the selected genotypes by considering inter cluster distances may produce high magnitude of heterosis or desirable segregants. Low levels of intra cluster distances were pinpointing of narrow genetic variation within a cluster.

The cluster mean value for the quantitative characters in Table 5 indicated considerable differences for all the characters between the clusters. The cluster III had the lowest mean values for seed cotton yield, ginning outturn and lint yield; cluster I had lowest mean value for lint index and seed index, while minimum mean value for boll weight was found in cluster II. The mean value of two characters viz. boll weight and seed index, was highest in cluster III whereas Sundar *et al.,* (2014) observed highest mean values for three characters *viz.*, seed cotton yield, number of bolls/plant and number of sympodia/plant, in one cluster (cluster

Table 3. Mahalanobis D^2 cluster distance matrix

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	**327.4**	513.6	915.1	618.7	893.7	686.6	1159.7	849.5	1463.6	1652.7
II		**214.7**	585.3	597.3	449.8	385.6	641.4	730.2	996.8	1483.4
III			**0.00**	1489.1	1310.3	955.9	1383.3	1525.8	1646.4	2726.1
IV				**211.6**	417.3	457.7	606.9	334.1	894.1	838.8
V					**238.4**	403.8	514.3	482.1	813.8	1129.1
VI						**312.4**	407.7	453.0	729.9	958.3
VII							**179.2**	415.9	413.4	569.0
VIII								**174.2**	451.3	663.3
IX									**218.9**	953.1
X										**254.3**

Table 4. Mean values of different clusters for some economic characters of cotton

Character/ Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
Seed cotton yield/plant (g)	78.1	80.8	73.7	95.8	86.8	93.6	116	109	127	132
Boll weight (g)	3.87	3.72	4.13	3.86	3.78	3.91	4.05	3.90	4.02	3.87
Ginning outturn (%)	32.1	32.9	31.3	34.5	34.9	33.1	33.4	34.6	34.8	32.9
Lint yield /plant (g)	25.1	26.5	23.1	33.0	30.3	31.0	38.8	37.7	44.3	43.5
Lint index (g)	3.35	3.70	3.90	3.82	3.94	3.80	3.99	3.96	3.96	3.46
Seed index (g)	7.08	7.54	8.55	7.26	7.36	7.66	7.94	7.50	7.43	7.09

Table 5. Nearest cluster and farthest cluster from each other based on D^2 value

Cluster Number	Nearest cluster with D^2 value	Farthest cluster with D^2 value
I	II (513.6)	X (1652.7)
II	VI (385.6)	X (1483.4)
III	II (585.3)	X (2726.1)
IV	VIII (334.1)	III (1489.1)
V	VI (403.8)	III (1310.3)
VI	II (385.6)	X (958.3)
VII	VI (407.7)	III (1383.3)
VIII	IV (334.1)	III (1525.8)
IX	VII (413.4)	III (1646.4)
X	VII (569.0)	III (2726.1)

X). Cluster IX had highest mean value for lint yield and cluster VII had highest mean value for lint index. The mean value for seed cotton yield was highest in cluster X and the highest mean value for ginning outturn was found in cluster V.

On the basis of mean values of different clusters desirable lines for a particular trait may be selected from a specific cluster such as seed cotton yield (IX, X), boll weight (III), ginning outturn (V, IX), seed index (III), lint index (VII, VIII, IX). By combining the genotypes with high seed cotton yield (cluster X) with genotypes having high ginning outturn (cluster V), the genotypes with maximum lint yield potential can be developed either in the form of hybrids or as transgressive segregants. The hybrids with even better yield potential can be developed by crossing such lines from cluster X with the lines of cluster III

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