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Evaluation of Genetic Diversity in American Cotton (*Gossypium hirsutum L.*)

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A B S T R A C T

The improvement of any crop mainly depends upon the nature and magnitude of genetic variability present in the base population. The objective of this study was to assess the genetic diversity and relationship among the *G. hirsutum* genotypes using multivariate Mahalanobis D^2 statistics. Forty *G. hirsutum* genotypes of diverse origin were utilized in this study. Analysis of variances for dispersion showed significant differences among the genotypes and these genotypes were grouped into 7 clusters with maximum number of genotypes in cluster I (26 genotypes) from different locations. Cluster II was the second largest with 9 genotypes. Cluster III, IV, V, VI and VII were solitary clusters with nil intra-cluster D^2 values. Character, bundle strength (30.64) contributed maximum to genetic divergence followed by days to 50% flowering (20.38), number of monopodia per plant (10.64), 2.5% span length (8.97), boll weight (6.15), seed cotton yield per plant (6.03). Thus the present study identified divergent genotypes SCS 1061, CCH 14-2, TSH 0533-1, RS 2767, SCS 1207, L 1008, CCH 14-1, GJHV 510, BS 26 and BS 23 from distant clusters for their exploitation in the breeding programme.

Introduction

Cotton is an important cash crop grown all over world as well as in India. Cotton is the king of fibre crops and has large contribution in the Indian economy which continues to be the predominant fibre in the Indian textile scene, despite stiff competition from the man-

made synthetic fibres. India is pioneer country for cultivation of commercial hybrids of cotton. Hybrid vigor was successfully exploited in cotton with development of commercial hybrids. Extensive use of closely related cultivars/genotypes in cotton breeding has resulted in narrowing the genetic base. The genetic divergence among the parents is very important factor in selection of parents for hybridization. It has also been observed that greater the genetic variability among population greater will be the chance of obtaining the desirable gene combination.

Therefore, before initiating a breeding programme it is required to evaluate the genetic diversity of the genotypes desired to be taken as parents for broader genetic base as more heterosis is observed. Therefore the present study was carried out to understand the genetic diversity among the 40 genotypes of cotton and to identify the lines for further hybridization.

Material and Methods

The experiment was performed at Regional Agricultural Research Station, Lam, Guntur in *kharif* 2017. The experiment was laid in randomized block design with three replications and spacing of 105 x 60 cm. Forty genotypes of cotton were collected from different geographic locations.

Five plants from each genotype were selected and tagged randomly in all the three replications. The observations were recorded on for 14 quantitative characters *viz*., plant height (cm), days to 50% flowering, 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 outturn (%), 2.5% span length (mm), uniformity ratio, micronaire value (10^{-6} g/inch), bundle strength (g/tex) and seed cotton yield per plant (g).

Mahalanobis D^2 statistic is a powerful tool for quantifying genetic divergence in germplasm collections with respect to the characters considered together. Genetic divergence among the 40 genotypes was analyzed using the Mahalanobis D^2 statistics method (1928) and genotypes were grouped into clusters by following the Tocher's method described by Rao (1952).

Results and Discussion

Analysis of variances exhibited significant differences among the forty genotypes for all studied fourteen characters.

Test with Wilk's criterion '∧'

Significant differences among the genotypes for individual characters were determined at first and later the statistical significant differences between the genotypes based on the pooled effects of all the characters were carried out using the Wilk's criterion '∧'.

The Wilk's criterion obtained was used in calculations of 'V' statistic. The statistic was highly significant indicating that genotypes differ significantly when all the characters were considered simultaneously. The value of 'V' statistic was 1819.1 in the present investigation.

Mahalanobis D^2 values

To estimate the D^2 values, correlated mean of characters were transformed into standardized uncorrelated characters using pivotal condensation method. It measures the degree of diversification and determines the relative proportion of each component character to total divergence.

The statistical differences (D^2) between pairs of genotypes were obtained as the sum of squares of the differences between the pairs of

corresponding uncorrelated values of any two genotypes considered at a time.

The per cent contribution towards genetic divergence by all the 14 contributing characters is presented in Table 1 and Fig 1. The knowledge on characters influencing divergence is an important aspect to a breeder. Character wise rank has shown that no single character lonely had a greater contribution to total genetic divergence. The maximum contribution towards genetic divergence was by bundle strength (30.64) followed by days to 50% flowering (20.38), number of monopodia per plant (10.64), 2.5% span length (8.97), boll weight (6.15), seed cotton yield per plant (6.03), seed index (3.97), ginning out turn (3.97), micronaire value (3.21), number of sympodia per plant (2.31), lint index (2.18), plant height (0.77), uniformity ratio (0.64) and number of bolls per plant (0.13).

Grouping of genotypes into various clusters

The 40 genotypes were grouped into 7 clusters using the Tocher's method. The distribution off genotypes among the 7 clusters is presented in the table 2. Out of 7 clusters, 26 genotypes were grouped in to cluster I, cluster II has 9 genotypes and remaining clusters III, IV, V, VI, VII were solitary clusters with single genotype.

This 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 genotypes for hybridization should be based on genetic diversity rather than geographical diversity. Satish *et al.,* (2009), Haritha and Ahamed (2013), Asha *et al.,* (2013), Tulasi *et al.,* (2014), Kumar *et al.,* (2015), Sharma *et al.,* (2016), Naik *et al.,* (2016) and Anil *et al.,* (2017) also reported that there is no parallelism between genetic divergence and geographical divergence of genotypes.

The mutual relationships between the clusters were represented diagrammatically by taking average intra and inter cluster D^2 values. The tree like structure called dendrogram was constructed based on clustering by Tocher's method (Fig. 2.).

Average intra- and inter- cluster D^2 values

The average intra and inter-cluster D^2 values estimated as per the procedure given by Singh and Chaudhary (1977) are presented in the Table 4.13. The proximity and divergence among 7 clusters are indicated in Table 3.

The maximum intra-cluster distance was observed in the cluster II (41.96) followed by cluster I (21.90), while, it was zero for clusters III, IV, V, VI and VII.

The high intra-cluster distance in cluster II indicates the presence of wide genetic diversity among the genotypes present within this cluster. The inter-cluster distances were worked out considering 14 characters and these distances ranged from 19.30 (between clusters IV and III) to 121.29 (between clusters VI and II). The inter-cluster distance was maximum between clusters VI and II (121.29), followed by clusters VII and II (94.69), VII and III (89.21), VII and I (87.75), VII and VI (80.47) and IV and II (72.95). This suggested that there is wide genetic diversity between these clusters. Based on these studies crosses can be made between genotypes of these clusters to obtain desirable transgressive segregants. The intra- and inter-cluster distances revealed that inter-cluster distance values were greater than intra-cluster distance values. The hybrids between genotypes of different clusters will express high heterosis and throw more useful segregants.

Table 1 Contribution of different characters towards genetic divergence in 40 cotton (*Gossypium hirsutum* L.) genotypes

S.No.	Character	Contribution towards divergence %	Times Ranked 1st
1	Plant height (cm)	0.77	6
2	Days to 50% flowering	20.38	159
3	Number of monopodia per plant	10.64	83
4	Number of sympodia per plant	2.31	18
5	Bolls per plant	0.13	1
6	Boll weight (g)	6.15	48
7	Seed index (g)	3.97	31
8	Lint index (g)	2.18	17
9	GOT (%)	3.97	31
10	2.5% span length (mm)	8.97	70
11	Uniformity ratio (%)	0.64	5
12	Micronaire value (10^{-6} g/inch)	3.21	25
13	Bundle strength (g/tex)	30.64	239
14	Seed cotton yield per plant (g)	6.03	47

Table 2 Clustering pattern of 40 cotton (*Gossypium hirsutum* L.) genotypes by Tocher's method

Cluster No.	No of genotypes	Name of the genotype
I	26	LH 2256, F 2501, L 389, CNH 1118, L 799, CPD 1402, LH 2220, GJHV 497, H 1442, RAH 1033, RS 2765, SAKTI SULTAN, SURAJ, LRK 516, TCH 1741, F 2493, ARBH 1401, L 1060, H 1471, ARBH 1402, PBH 10, SCS 1214, HS 294, HS 292, CSH 2838, CNH 5
II	9	SCS 1061, CCH 14-2, TSH 0533-1. RS 2767, SCS 1207, L 1008, CCH 14-1, GJHV 510, BS 26
III	1	L 788
IV	1	RAH 1066
V	1	TSH 0499
VI	1	BS 23
VII	1	GISV 267

Table 3 Average intra- and inter-cluster D^2 values among 7 clusters in 40 genotypes of cotton (*Gossypium hirsutum* L.)

Cluster No.	I	II	III	IV	V	VI	VII
I	**21.90**	47.41	37.05	46.44	36.32	62.94	87.75
II		**41.96**	65.91	72.95	71.09	121.29	94.69
III			**0.00**	19.30	36.51	44.89	89.21
IV				**0.00**	53.14	28.41	60.85
V					**0.00**	55.42	61.42
VI						**0.00**	80.47
VII							**0.00**

Table 4 Mean values of 7 clusters estimated by Tocher's method from 40 genotypes of cotton (*Gossypium hirsutum* L.)

Cluster No.	Plant height (cm)	Days to 50% flowering	Monopodia per plant	Sympodia per plant	Bolls per plant	Boll weight (g)	Seed index (g)	Lint index (g)	GOT (%)	2.5% span length (mm)	Uniformity ratio (%)	Micronaire value (10^{-6} g/inch)	Bundle strength (g/tex)	Seed Cotton yield per plant (g)
I	144.42	60.01	**2.01**	16.22	39.98	3.57	8.73	6.34	**32.75**	27.55	48.76	4.12	23.03	94.53
II	148.80	60.92	2.74	16.15	39.53	**3.56**	**8.26**	5.87	32.38	**26.06**	48.40	**4.48**	**21.47**	95.51
III	142.53	**56.66**	2.46	17.33	35.93	**4.80**	10.00	6.22	30.15	29.13	47.66	4.03	23.03	95.46
IV	136.43	61.00	3.26	**12.80**	**33.13**	4.44	**10.22**	**7.00**	31.87	29.90	**49.33**	4.33	23.96	**61.73**
V	153.43	64.00	2.40	17.00	37.53	4.14	8.67	**4.52**	**27.42**	29.73	48.33	4.23	23.66	**115.05**
VI	**126.06**	62.33	3.80	13.46	**41.13**	3.79	9.26	6.56	32.38	**30.06**	48.00	**3.96**	**25.83**	88.37
VII	**171.30**	**73.00**	**4.63**	**17.46**	33.53	3.81	9.00	6.47	32.62	29.13	**47.33**	4.20	22.03	73.21

Note: Bold figures are minimum and maximum values

Fig. 1 Contribution of different characters towards genetic divergence in 40 cotton (*G. hirsutum* L.) genotypes

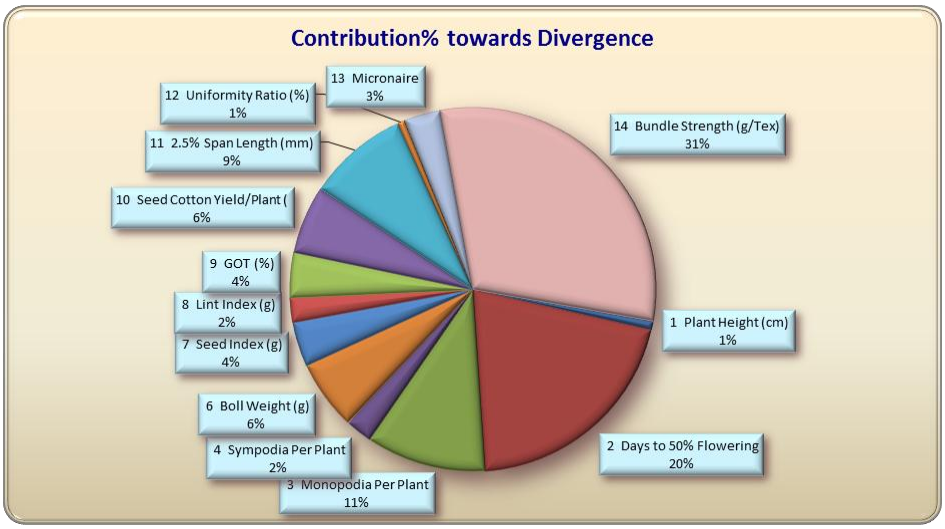
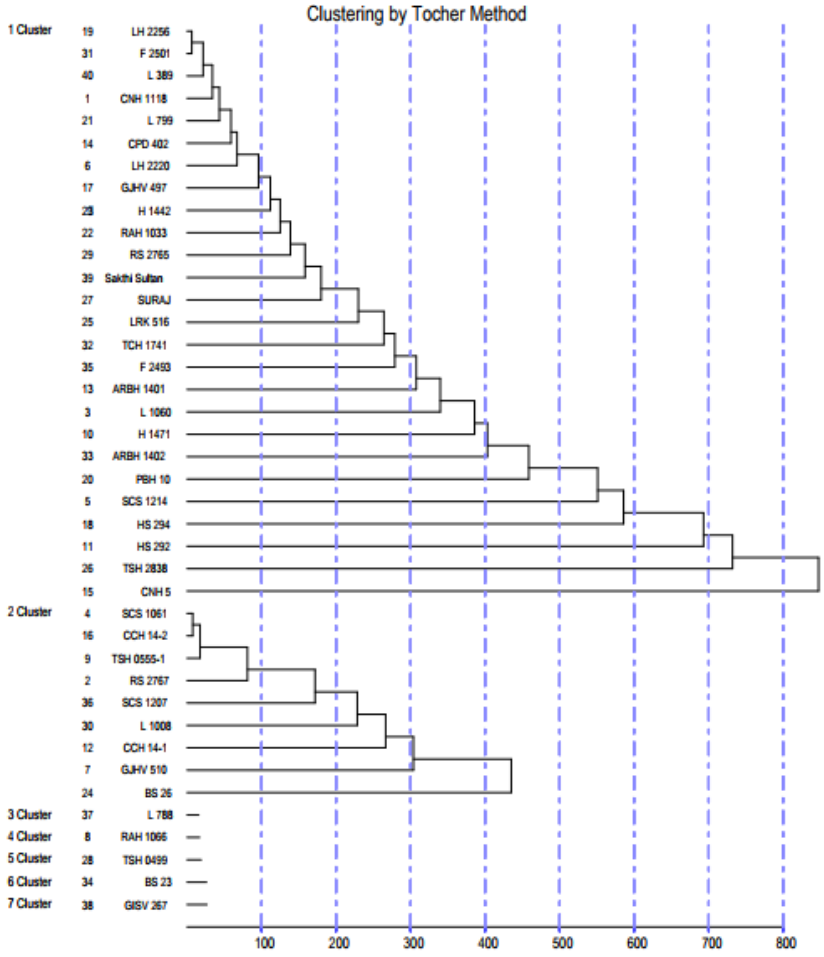


Fig. 2 Dendrogram showing relationship among 40 cotton (*G. hirsutum* L.) genotypes in seven clusters based on Mahalanobis D^2 values



Cluster mean values

The cluster mean values for 14 characters are presented in Table 4. The data indicated a wide range of mean values between the characters.

Higher mean values for boll weight were seen in cluster III and IV and higher means for number of boll per plant were observed in clusters VI and I which are major contributors in improving seed cotton yield per plant in cotton. Based on mean values, series of crosses in diallel fashion may prove highly successful.

The success and usefulness of Mahalanobis D^2 analysis in quantifying genetic divergence has been studied by Rajamani and Rao (2009), Satish *et al.,* (2009), Asha *et al.,* (2013), Sharma *et al.,* (2016) and Dahiphale and Deshmukh (2018)

Thus the present study identified divergent genotypes from clusters II and VI as they have high inter cluster distance SCS 1061, CCH 14-2, TSH 0533-1, RS 2767, SCS 1207, L 1008, CCH 14-1, GJHV 510, BS 26 and BS 23 and they should be used for further improvement in heterosis in yield targeted traits with creation of wider variability.

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