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GENETIC DIVERSITY ANALYSIS FOR FIBRE QUALITY, BIOCHEMICAL AND YIELD RELATED TRAITS IN COTTON *(Gossypium hirsutum L.)*

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ABSTRACT

On the basis of D^2 values, forty genotypes were grouped into three clusters. Cluster II (C 1579, EL 174C, BP 52 and G 3637 IP) genotypes are potential donor for fiber quality traits and Cluster III (K 3259-EC-9, PD 9363, DS 28, Ibadem allon, SDN 24 and Co American 8-29) genotypes are potential donor for seed cotton yield and its component traits. The genotype of cluster III showed maximum genetic divergence with cluster II and genotypes of these clusters may be selected for hybridization for generating genetic variability. Cluster III seems to be most promising for agronomic traits followed by cluster II and I. Genetic divergence studies revealed that genotypes of cluster III and cluster II may be used for intercrossing to produce higher seed cotton yielding plant with better fiber quality characters.

KEY WORDS: Bio-chemical, Cotton, D^2 Statistics, Fibre quality, Genetic diversity

INTRODUCTION

Cotton is one of the most important commercial crop and popularly known as the "White Gold". Cotton belongs to genus *Gossypium* under tribe *Gossypieae* of *Malvaceae* family, which comprises 50 species. Out of these, four species are under commercial cultivation *G. herbaceum* (2n=26), *G. arboreum* (2n=26), *G. hirsutum* (2n=52) and *G. barbandense* (2n=52). Cotton is a fiber, oil and protein yielding crop of global significance. Cotton is a multipurpose crop that supplies five basic products i.e. seed, lint, oil, hulls and linters.

India is the only country where all the four cultivated species being grown commercially. Gujarat, Maharashtra and Telangana are the major cotton growing states contributing around 70 per cent of the area and 67 per cent of cotton production in India. During the year 2016-17 in Gujarat cotton was grown in 24.00 lakh ha area with production of 91.80 lakh bales and productivity of 673 kg/ha (Anonymous, 2017).

Genetic variation is a prerequisite for any crop improvement programme. Assessment of the extent and distribution of genetic variation in a crop species and its relatives is essential in understanding pattern of diversity and evolutionary relationships between accessions that help to sample genetic resources in a more systematic fashion for conservation and plant improvement. Traditionally, genetic diversity is assessed based on morphological features, which exhibit enormous variation for the particular use of the crop. Since plant breeding is the utilization of crop variability for economic end uses, analysis of genetic divergence would help in better parent selection, particularly for hybridization purpose. The wide range of genetic diversity present in India has to be exploited to improve yield and more importantly, the fibre quality, which is of prime concern in this era of economic liberalization and globalization.

MATERIALS AND METHODS

The present investigation was carried out during 2016-17 at Main Cotton Research Station, Navsari Agricultural University, Surat. The material consisted of forty cotton *Gossypium hirsutum* L. genotypes from Main Cotton Research Station, Navsari Agricultural University, Surat. The material was evaluated in the field in a randomized block design with three replications. The observations were recorded for seventeen characters *viz*., days to 50 per cent flowering, number of sympodia per plant, number of bolls per plant, plant height (cm), boll weight (g), seed index (g), seed cotton yield per plant (g), ginning percentage, 2.5 per cent span length (mm), fibre strength (g/tex). fibre fineness (mv), oil percentage (%), gossypol content (%), phenol content (%), leaves protein content (%) and reducing sugar content (%). The fibre quality parameters were analyzed at Central Institute for Research on Cotton Technology (CIRCOT), Mumbai.

The genetic divergence was worked out by using Mahalanobis D^2 statistic as described by Rao (1952). Intra and inter cluster distance (D) between all possible pairs of three clusters were computed with the help of method given by Singh and Chaudhary (1997). Genotypes of cotton were grouped into different clusters on the basis of relative magnitude of D^2 values following Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

Forty genotypes of cotton were grouped into three clusters on the basis of relative magnitude of D^2 values following Tocher's method (Rao, 1952) (Table 1 and Figure 1). Thirty genotypes were grouped in cluster I, while six genotypes weregrouped in cluster III and cluster II having four genotypes. Mahalanobis's D^2 statistic as a tool for estimating genetic divergence in crop plants that can be used to choose the parents without making crosses before the initiation of hybridization programme(Bhatt,1970).

The intra cluster distance ranged from 26.75 to 29.92. The cluster I exhibited maximums intra cluster distance (29.92) followed by the cluster II (29.00) and cluster III (26.75). The high intra-cluster distance in cluster I indicated the presence of wide genetic diversity among the genotypes present within this cluster. The suggestion was made to attempt crossing amongst the genotypes within cluster I in all possible combinations. The maximum inter cluster distance observed between cluster II and cluster III (72.92) followed by cluster I and cluster II (47.37), whereas the minimum inter cluster distance was observed between I and III (44.55) (Table 2). 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 Kulkarni *et al*. (2011).

Cluster III exhibited high mean value for almost all the characters, except plant height, ginning percentage, phenol content, seed protein and reducing sugar. Cluster II exhibited high mean value for plant height (148.67 cm), ginning percentage (35.93 %), phenol content (2.07 %), seed protein content (15.59 %) and reducing sugar (2.42 %) (Table 3). Cluster I exhibited moderate mean value for number of sympodia per plant (15.18), boll weight (3.65 g), seed index (8.23 g), ginning percentage (33.88 %), fibre fineness (4.31 mv), oil percentage (17.40 %), gossypol content (0.31 %), phenol content (1.68 %), leaf protein content (13.56 %) and seed protein content (17.91 %).

The component of D^2 due to each character variable was ranked in descending order of magnitude, rank-I being assigned to the highest value. This per cent contribution of different characters to diversity is presented in Table 4. This study helps to identify diversity in different proportion which ultimately helps to decide utilization of genetic material for improvement of specific characters. The present study revealed oil percentage (47.18 %) and reducing sugar (37.69 %) was the main contributors to the total divergence. These two characters accounted for 84.87 per cent of total divergence. The contribution gossypol content (5.90 %), seed protein content (4.36 %), leaf protein content (3.08 %), phenol content (1.54 %), seed index (0.13 %) and fibre fineness (0.13 %) was negligible.

CONCLUSION

Cluster III recorded higher mean values for almost all the characters except plant height, ginning percentage, phenol content, seed protein and reducing sugar. Cluster II exhibited high mean value for plant height, ginning percentage, phenol content, seed protein content and reducing sugar. Cluster III was farthest from cluster II having D value 72.92. Therefore, crosses can be made among desirable genotypes to obtain desirable segregants for the important economic attributes

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Table 1: Composition of cluster based on D^2 values

Cluster	Number of Genotypes	Name of Genotypes
I.	30	134-CO2-M-21-6-2, 16105-K, 23F, 68-4-B, Acala 63-75, BC 761, BC-68, BTE 22, DHY 286, EC 12062, EC 1318568, EC 165659, EC 1777, G.Cot 12, Girja, GS 34, GS M-3, H 144, IAN 1327, IAN 6361-5306, ISC 77, JLH 59, JR 5, K 3299, KOP 236, KOP 8, LL 54, MUCU 2, NH 239, RG 1
II	4	C 1579, EL-174C, BP52, G 3637 IP
III	6	K-3259-EC-9, PD 9363, DS 28, lbadem allon, SDN-24, Co American 8-29

Table 2: Intra and inter-cluster distances (D) between forty genotypes of cotton (D = $\sqrt{D}$2)

Cluster	I	II	III
I	29.92	47.37	44.55
II	47.37	29.00	72.92
III	44.55	72.92	26.75

Table 3: Cluster mean for seventeen characters in cotton (*G. hirsutum* L.)

Clusters	Days to 50 Per Cent Flowering	Number Sympodia Per Plant	Number of Bolls Per Plant	Plant Height (cm)	Boll Weight (g)	Seed Index (g)	Seed Cotton Yield Per Plant (g)	Ginning Percentage
I	56.60	15.18	22.96	144.00	3.65	8.23	81.94	33.88
II	56.67	13.08	25.00	148.67	3.48	6.77	86.75	35.93
III	56.94	17.89	27.22	147.54	3.73	8.93	101.56	32.15

Clusters	2.5 % Span Length (mm)	Fibre Strength (g/tex)	Fibre Fineness (mv)	Oil (%)	Gossypol Content (%)	Phenol Content (%)	Leaf Protein Content (%)	Seed Protein Content (%)	Reducing Sugar Content (%)
I	26.63	25.53	4.31	17.40	0.31	1.68	13.56	17.91	4.97
II	26.67	26.04	3.92	16.39	0.18	2.07	15.59	15.57	2.42
III	27.37	26.38	4.49	18.11	0.42	1.08	12.84	20.47	1.67

Table 4: Contribution of different characters towards total divergence in cotton (*G. hirsutum* L.)

Sr. No.	Characters	Times Ranked First	Contribution (%)
1	Days to 50 per cent flowering	0	0
2	Number of sympodia per plant	0	0
3	Number of bolls per plant	0	0
4	Plant height (cm)	0	0
5	Boll weight (g)	0	0
6	Seed index (g)	1	0.13
7	Seed cotton yield per plant (g)	0	0
8	Ginning percentage (%)	0	0
9	2.5 per cent span length (mm)	0	0
10	Fibre strength (g/tex)	0	0
11	Fibre fineness (mv)	1	0.13
12	Oil percentage (%)	368	47.18
13	Gossypol content (%)	46	5.90
14	Phenol content (%)	12	1.54
15	Leaf protein content (%)	24	3.08
16	Seed protein content (%)	34	4.36
17	Reducing sugar content (%)	294	37.69

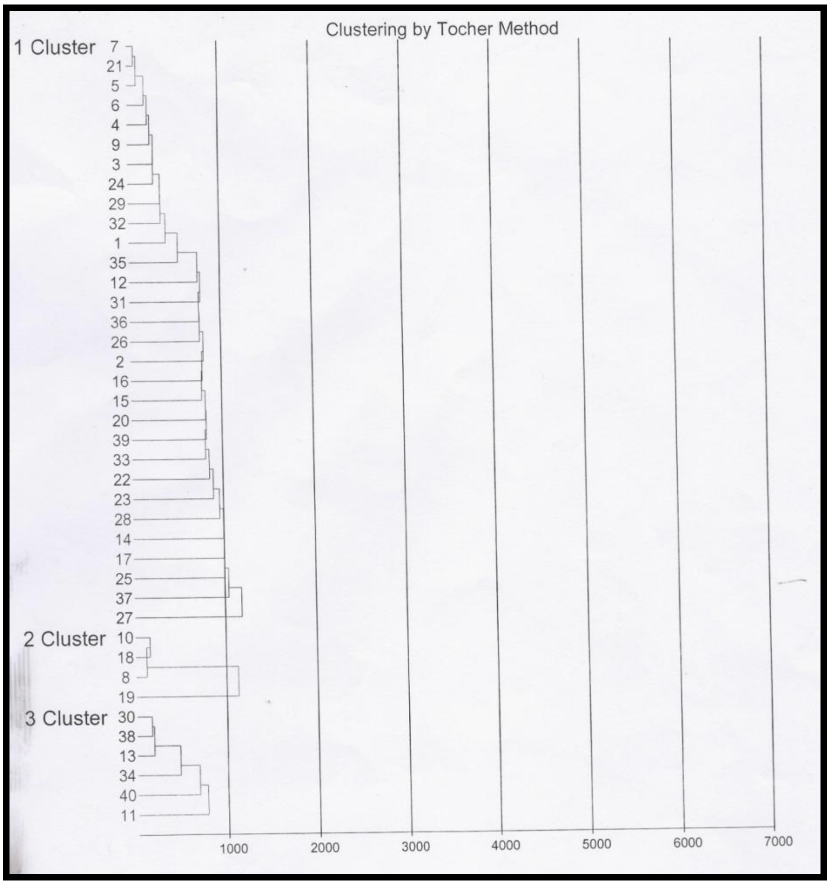

Figure 1: Clustering of genotype by Tocher method

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