

Original Research Article

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Genetic Diversity Studies on Parental and Interspecific Hybrids (*Gossypium hirsutum* L. × *Gossypium barbadense* L.) of Cotton

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Genetic diversity analysis was conducted at Main Agricultural Research Station, University of Agricultural Sciences, Dharwad during *Kharif*, 2017. In this study, 35 genotypes were evaluated for 11 yield and yield attributing traits and grouped into four clusters through Mahalanobis D² statistic. Cluster I was the biggest with 23 genotypes followed by cluster II, III and IV. Among eleven characters studied, seed cotton yield (25.38 %) and days to 50 per cent flowering (22.86 %), contributed high for divergence while other characters like boll weight (0.34 %), number of sympodia per plant (0.5 %) and lint index (0.67 %) contributed very little for divergence. Cluster IV with solitary genotype secured 1st rank with an overall score of 20 across 13 characters and the cluster III obtained 4th rank with an overall score of 34. As high inter-cluster distance is shown by cluster III and IV, hence is desirable to select genotypes from these clusters to develop triple cross hybrids for further crop improvement programs.

Introduction

Cotton the king of fibre reside one of the momentous and important cash crop exercising profound influence on economics and social affairs of the world. The word “cotton” derived from the Arabic word “al qatan” and popularly known as “White Gold”. Cotton plays vital role in Indian economy as it is the backbone of textile industry. The *Gossypium* species were domesticated in both the old and new world. It supplies products such as lint, oil, seed meal, hulls and linters. The genus *Gossypium*, a member of the Malvaceae family, consists of 50 species, four

of which are generally cultivated species. Out of the four cultivated species, *Gossypium hirsutum* L. and *Gossypium barbadense* L. are tetraploids (2n=4x=52) and are commonly called as new world cottons. Whereas, *Gossypium arboreum* L. and *Gossypium herbaceum* L. are diploids (2n=2x=26) and known as old world cottons. India is the only country, where all four cultivated species of cotton viz., *G. herbaceum*, *G. arboreum*, *G. hirsutum* and *G. barbadense* are grown. In India, the crop is being grown in area of 12.3 million hectares, producing 28.50 million bales with a productivity of 504 kg ha⁻¹. In Karnataka, cotton is being grown in area of

5.65 lakh hectares with production and productivity of 19.0 lakh bales and 572 kg ha⁻¹ respectively (Anon., 2018). For an outstanding breeding program in the crop improvement, diversity analysis greatly helps the breeder in the identification and proper choice of parents for specific breeding objectives. The present study was to assess the genetic diversity among genotypes of cotton.

Materials and Methods

The experimental material consisted of 35 genotypes comprising of eight lines, three testers (Table 1) and their resultant twenty four hybrids produced by line x tester mating design. The experimental material was sown in Randomised Block Design with three replications during *Kharif*, 2017-18 at Agricultural Research Station Dharwad. Three rows of each 4.2 m length was assigned to each genotype with plants having 60 cm intra spacing and 90 cm inter row spacing.

Five plants were randomly selected from each replication for each genotype and the average value for each plot was computed for plant height, number of monopodia, number of sympodia, boll weight, number of bolls per plant, ginning outturn, seed index and seed cotton yield whereas lint index was calculated on formula basis. The development of potential hybrids depends on selecting superior parents possessing higher directional dominance, genetic diversity and allelic differences for most of the traits. Of these, the genetic divergence can be estimated by an effective statistical tool, Mahalanobis D² statistic that gives an estimate about the diverse nature of the parents.

In this experiment genetic diversity was assessed among genotypes consisting of both hybrids and parents, to determine the best possible triple cross hybrids and double cross

hybrids as reported by Antonio *et al.*(2016) in tomato.

Results and Discussion

The genetic diversity among 35 genotypes was measured by employing D² statistics and grouped into four clusters using Tocher's method as given by Rao (1952). Distribution of genotypes in each cluster is presented in Table 2 and Figure 1. Similar genetic diversity works were carried out on this crop by Sambamurthy *et al.* (2004), Satish *et al.* (2009), Shakthi *et al.* (2009) and Kulkarni *et al.* (2011). Cluster I was found largest with 23 genotypes followed by cluster II comprising six genotypes, while cluster III comprised of five genotypes and cluster IV includes a solitary hybrid. The inter-cluster and intra-cluster D² values were estimated and have been presented in Table 3. The maximum intra cluster distance was recorded within cluster III (13.91) which had only parents, while it was lowest in cluster IV as it included only one hybrid (CPD-462×SB-YF-425), indicating that the genotypes of these respective clusters might be differing marginally in their genetic architecture.

The maximum inter cluster distance was observed between cluster III and cluster IV (76.21) followed by cluster I and cluster III (42.67). The genotypes belonging to clusters III and cluster IV possess highest inter cluster distance, suggesting that hybridization between the parents of these respective divergent clusters may lead to higher magnitude of heterosis for the characters concerned. Significant level of desired heterosis is achieved whenever parents with moderate divergence are used for crossing. (Arunachalam *et al.*, 1984)

From this exercise it was clear that the lines which were selected for experiment got included in two different clusters, cluster II

and cluster III, where as all the testers were under the single cluster, i.e cluster III. The inter cluster distance between clusters II and III was considerably high, hence the high yielding hybrids such as CPD-462×SB-YF-425, FLT-36×SB-YF-425, FLT-31×SB-YF-425, FLT-31×BCS 23-18-7, CPD-462×BCS 23-18-7 resulted from the parental genotypes from cluster II and III. Similar results were found by Pushpam *et al.* (2004), Gopinath *et al.*, (2009), and Xian Tao *et al.*, (2011).

Cluster means of 11 yield and yield contributing characters were assessed and are presented in Table 4. The mean comparison of the different characters indicated considerable differences among the clusters for all the characters. The genotypes in cluster II had minimum days to 50 per cent flowering and maximum days to 50 per cent flowering was found in genotypes falling under cluster III. With respect to the trait boll weight, the genotypes possessing highest boll weight fell under cluster II (4.34 g) and genotypes with lowest boll weight fell under cluster III (3.10 g). Tall types were found in cluster II (138.42 cm) and dwarf types in cluster III (120.60 cm). The parental lines possessing less number of monopodia per plant were included under cluster III (1.12) while highest number in cluster II (1.68). The genotypes in cluster I (23.89) had the highest number of sympodia while cluster III (20.53) genotypes had the lowest number. Cluster II (16.91) and cluster

III (6.66) recorded highest and lowest means for the trait total number of bolls per plant, respectively. Genotypes of highest lint index were found to be under cluster III (6.04 g) and lowest under cluster II (10.62 g). The ginning outturn mean values were highest for genotypes falling under cluster II (35.38 %) and lowest in cluster III (33.31 %). Cluster I (42.22 cm) and cluster II (38.88 cm) had highest and lowest sympodial length at 50 per cent plant height, respectively. The low seed index genotypes were categorised under cluster II (10.62 g), while highest were under cluster III (11.97 g). The cluster II (948.83 kg/ha) mean for the seed cotton yield is highest where as the genotypes of cluster III (194.24 kg/ha) had lowest mean value. Among 11 characters studied, the genotypes in cluster II had maximum values for boll weight, plant height, number of monopodia per plant, number of bolls per plant, ginning outturn and seed cotton yield. Cluster I had maximum values for number of sympodia per plant, sympodial length at 50 per cent plant height and cluster III had highest mean values for days to 50 per cent flowering, seed index and lint index. Analysis of cluster means indicated substantial variation among the four clusters formed. In the present study clusters I and IV included high yielding hybrids, whereas cluster II and cluster III included parental genotypes. The different genetic make up of parents and hybrids has shown up in differential clustering.

Table.1 Experimental material used in the study

Lines (<i>G. hirsutum</i> L.)	Testers (<i>G. barbadense</i> L.)
1. FLT-36	1. BCS-23-18-7
2. FLT-44	2. GIZA-70
3. FLT-31	3. SBYF-425
4. FLT-28	
5. SG-1	
6. SG-2	
7. EL-4	
8. CPD-462	

Table.2 Distribution of genotypes into clusters considering both hybrids and parents together

Sl. No.	Cluster	Number of genotypes	Name of genotype
1	I	23	FLT-36 × BCS-23-18-7, FLT-36 × GIZA-70, FLT-36 × SB-YF-425, FLT-44 × BCS-23-18-7, FLT-44 × GIZA-70, FLT-44 × SB-YF-425 , FLT-31 × BCS-23-18-7, FLT-31 × GIZA-70, FLT-31 × SB-YF-425, FLT-28 × BCS-23-18-7, FLT-28 × GIZA-70, FLT-28 × SB-YF-425, SG-1 × BCS-23-18-7, SG-1 × GIZA-70, SG-1 × SB-YF-425, SG-2 × BCS-23-18-7, SG-2 × GIZA-70, SG-2 × SB-YF-425, CPD-462 × BCS-23-18-7, CPD-462 × GIZA-70
2	II	6	FLT-36,FLT-31, FLT-28, FLT-33, EL-4, CPD-462
3	III	5	BCS-23-18-7,GIZA-70,SB-YF-425, SG-1, SG-2
4	IV	1	CPD-462 × SB-YF-425

Table.3 Average intra and inter cluster distance values considering both hybrids and parents together

Clusters	I	II	III	IV
I	7.38	24.69	42.67	22.47
II		8.07	39.75	33.49
III			13.91	76.21
IV				0.00

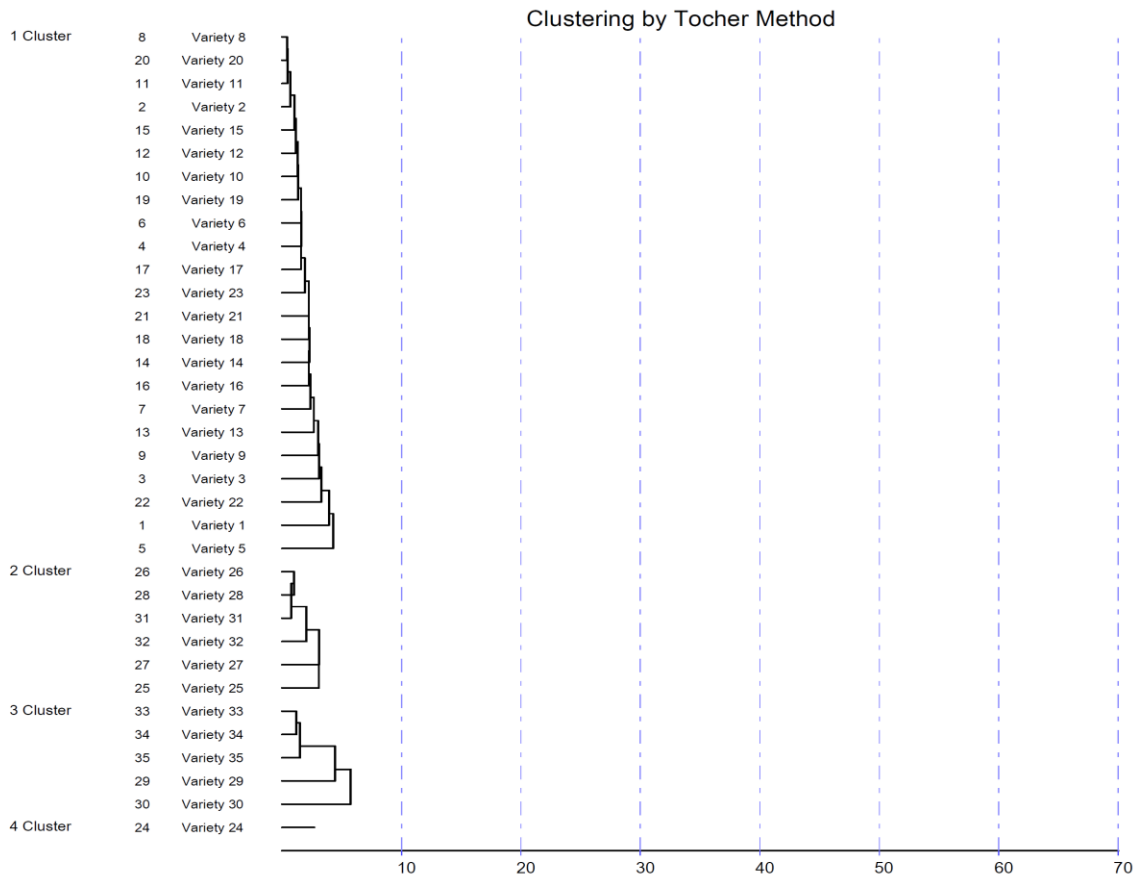
Table.4 Cluster means considering both hybrids and parents together

Cluster	Days to 50 % flowering	Boll weight (g)	Plant height (cm)	Number of monopodia per plant	Number of sympodia per plant	Number of bolls per plant	Sympodial length at 50 % plant height (cm)	Ginning outturn (%)	Seed index (g)	Lint index (g)	Seed cotton yield (kg/ha)	Cluster score	Cluster rank
I	77.54 (3)	3.75 (3)	162.20 (1)	1.97 (2)	22.92 (2)	25.15 (2)	50.89 (1)	30.50 (4)	12.88 (2)	5.68 (3)	582.05 (3)	26	II
II	78.67 (2)	4.24 (1)	132.79 (3)	1.39 (3)	22.72 (4)	13.89 (3)	41.48 (3)	34.60 (1)	10.52 (4)	5.58 (4)	825.66 (2)	30	III
III	96.00 (1)	3.43 (4)	127.23 (4)	1.14 (4)	22.91 (3)	8.80 (4)	40.89 (4)	34.49 (2)	11.63 (3)	6.16 (1)	289.66 (4)	34	IV
IV	77.33 (4)	4.07 (2)	158.07 (2)	2.36 (1)	24.13 (1)	34.00 (1)	48.55 (2)	31.70 (3)	12.95 (1)	6.01 (2)	1239.38 (1)	20	I

Table.5 Per cent contribution of characters towards divergence

Sl. No.	Characters	Characters contribution (%) considering both parents and hybrids
1	Days to 50 % flowering	22.86
2	Plant height	7.23
3	Boll weight	0.34
4	Number of monopodia per plant	8.24
5	Number of sympodia per plant	0.50
6	Number of bolls per plant	12.10
7	Sympodial length at 50 % plant height	2.69
8	Ginning outturn	2.18
9	Lint index	17.82
10	Seed index	0.67
11	Seed cotton yield	25.38

Fig.1 Cluster grouping considering parents and hybrids using Tocher method



All 36 genotypes spread over 6 clusters were scored based on their means across the clusters for all the 13 characters, as given in Table 4. The highest cluster mean with respect to particular character was given the first rank and next cluster possessing next best means were given 2nd, 3rd and so on up to 6th rank for all the traits. Finally, the clusters are ranked based on the overall score obtained from 13 characters. The lowest scoring cluster was given the first rank, and next cluster possessing the score above the previous ones were given 2nd, 3rd and so on up to 6th rank. Accordingly, cluster IV with an overall score of 20 across the 13 characters elected the first rank followed by cluster I, II and III, indicating presence of most promising genotypes in them and further breeding programme to generate new material. Cluster III stood highest with an overall score of 34. Similar work was reported by Bhaganna *et al.*, (2017) in French bean.

The contribution of various characters towards diversity is given in Table 5. Among eleven characters studied, seed cotton yield (25.38 %) and days to 50 per cent flowering (22.86 %), contributed high for divergence while other characters like boll weight (0.34 %), number of sympodia per plant (0.5 %) and lint index (0.67 %) contributed very little for divergence. The contribution of other traits include plant height (7.23 %), number of monopodia per plant (8.24 %), number of bolls per plant (12.10 %), sympodial length at 50 per cent plant height (2.69 %), ginning outturn (2.18 %) and lint index (17.82 %). Among the eleven characters studied, the maximum contribution to the total divergence was by seed cotton yield followed by number of bolls per plant and lint index. The above results imply that in order to select genetically diverse hybrids, selection strategy should be based on the traits like seed cotton yield, number of bolls per plant and lint index. De *et al.* (1988) stated that traits contributing

maximum towards the D^2 values needed to be given more emphasis for deciding the clusters to be taken for the purpose of choice of parents for hybridization.

It is concluded as the inter-cluster distance was found to be highest between clusters III and IV, hence, it could be expected that the cross combinations involving hybrid in solitary cluster IV and best parents of cluster III could be used to develop triple cross hybrids for future breeding programs. Since hybrid CPD-462 × SB-YF-425 formed a solitary cluster (IV) apart from remaining 23 hybrids in cluster (I), it could indicate an opportunity for developing best double cross hybrids involving CPD-462 × SB-YF-425 with any good hybrid of cluster I. Similar result was reported by Antonio *et al.* (2016).

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