Studies on Genetic Divergence in Upland Cotton (*Gossypium hirsutum* L.)

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Genetic divergence in twenty nine upland cotton (*Gossypium hirsutum* L.) genotypes were studied for nineteen yield attributes and quality characters. The pattern of grouping of genotypes reveled that the genetic diversity is not fully related to the geographical diversity. The inter-cluster distances were found to be greater than intra-cluster distances, revealing considerable amount of genetic diversity among genotype studied. Intra-cluster distances, inter-cluster distances, cluster mean for all the characters studied and cluster-wise performance of all the genotypes suggest that the genotypes selected for improvement of yield and quality components are JK-54, Khandwa-2, CNH-120MB, LRA-5166, CAT-834, C-1084, C-YG-2859 and JBWR-13-1. The hybridization programme with the selected genotypes by considering inter-cluster distances may produce high magnitude of heterosis or desirable segregants, which would be meaningful for improvement in yield and quality attributes of cotton.

Key words: Cluster, Genetic Divergence, Upland cotton, Intra-cluster distance, Inter-cluster distance

Cotton is the most important fibre crop and backbone of textile industry of India. It alone accounts 70 per cent of total fibre consumption in textile sector with approximately 38 per cent of the country's export. India ranks first in area under cotton cultivation as compared to the other major cotton growing countries of the world with unique distinction for growing all the four linted cotton species.

Among four linted cotton species, upland cotton (*Gossypium hirsutum* L.) is a predominant species of cotton in world as well as in India. It alone contributes about 90 per cent to the global production. By virtue of its wider adaptability, higher yield and good fibre quality, it gradually replaced Asiatic diploid cottons and grown under irrigated as well as rainfed conditions. Varieties and hybrids of *Gossypium hirsutum* L. occupies about 75 per cent area and 85 per cent cotton production of country (Singh, 2004), and have played a significant role in achieving self-sufficiency in cotton production of India. However, Indian cotton productivity is quite low (403 kg lint/ha) as against the worlds productivity (600 kg lint/ha) (Singh and Ramasundaram, 2005). It is experiencing a plateau which needs to be rectified urgently.

Genetic diversity plays a key role in analyzing the general distance among the genotypes selected as parent. Within a certain limit, hybridization of more diverged parents is expected to enhance the level of heterosis in hybrids and generate wide range of variability in segregating generations (Joshi and Dhawan, 1966). Therefore, the present investigation was undertaken to study the nature and magnitude of genetic divergence in twenty nine upland cotton (*G. hirsutum* L.) genotypes evaluated in Chhattisgarh state under rainfed conditions.

Materials and Methods

The study was conducted in the Instructional Farm, College of Agriculture, Indira Gandhi Agricultural University, Raipur (Chhattisgarh), India. Twenty nine upland cotton genotypes obtained from Central Institute for Cotton Research (CICR), Nagpur (Maharashtra), India, were planted in Randomized Complete Block Design with three replications. Uniform spacing of 90 x 45 cm and all standard manorial and cultural treatments were adopted. In each replication, five plants were randomly selected and observations were recorded for nineteen characters *viz.*, seed cotton yield/plant, days to 50 per cent flowering days to 50 per cent boll opening, plant height, number of sympodial branches as well as monopodial branches plant/ha, lint weight and seed weight boll/ha, number of seeds boll/ha, boll weight, lint and seed index, lint per cent, boll length and girth, 2.5 per cent span length elongation per cent, fibre fineness and fibre strength. The lint quality parameters were studied in Ginning Training Center (GTC), Central Institute for Research on Cotton Technology (CIRCOT), Nagpur (Maharashtra). The genetic divergence was worked out by using Mahalanobnis D^2 statistic as described by Rao (1952). On the basis of D^2 values, investigated genotypes were grouped into different clusters by employing Tochers's method as outlined by Rao (1952).

Results and Discussion

The analysis of variance indicated significant differences among all the genotypes for all the characters studied and specified existence of considerable genetic diversity among genotypes. Hence, further analysis was carried out for relative magnitude of D^2 values for all the characters and all the genotypes and groped them into five clusters (Table 1).

The maximum number of germplasm accessions (7) were included each in clusters I and III followed by cluster V (5), cluster IV (4) and the lowest in cluster II (4). Generally, geographical diversity has been considered as a measure of genetic diversity. However, this is an inferential criterion and it may not be so effective in quantifying or differentiating different populations. The present pattern of grouping of genotypes in study indicates that the genetic diversity is not fully related to the geographical diversity. This was in accordance with the results of Singh and Bains (1968), Singh *et al.* (1971), Singh and Gill (1994), Sumathi and Nadarajan (1994) and Pushpam *et al.* (2004). Hence, it indicated that the geographic diversity though important might not be the only factor in determining genetic divergence. It may be the outcome of several other factors such as genetic drift, natural selection forces and diverse environmental conditions within the country. Therefore, choice of the parents for hybridization should be decided on the basis of genetic diversity rather than geographical diversity.

Table 1. Group constellation

Cluster no.	Number of genotypes	Genotypes
I	7	SB-166. JBWR-25. BW-28. BBR-310, CAT-834, C-1084 and LRA-5166
II	4	JBWR-36, JBWR-14. JK-54 and C-YG-2859
III	7	Mahalaxmi Narmada. C-YG-1830. C-2076. C-2889, C-2625 and EC 11 0788
IV	5	CAT-2923 C-1857,C-3718. C-1489and JBWR-13-1
V	6	Bikaneri Narma, Khandwa-2. JBWR-13-2. EG-2932 Buri0394. and CNH 120mb

Table 2. Inter- and intra-cluster distances

Cluster number	1	2	3	4	5
I	(3.825)				
II	4.574	(3.176)			
III	3.455	5.121	(3.164)		
IV	4.066	3.891	4.124	(2.934)	
V	3.603	5.236	3.469	5.457	(3.410)

Note: Values in parenthesis are of intra-cluster distance

In the present study intercluster distances were found to be greater than intracluster distances, revealing considerable amount of genetic diversity among genotypes studied (Table 2). The highest intracluster distance was observed in cluster V (3.410) followed by cluster II (3.176), cluster III (3.164) and cluster IV (2.934). Whereas, the highest intercluster distance was observed in between the clusters V and IV (5.457) followed by clusters V and II (5.236), clusters III and II (5.121), clusters 11 and I (4.574), clusters IV and 111 (4.124), clusters IV and I (4.066), clusters IV and II (3.89), clusters V and III (3.469), clusters I and III (3.455) and the lowest in between clusters V and I (3.603). 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 too. Use of genetically distant genotypes as parents to get the most promising breeding material had also been suggested by Singh and Singh (1984), Sambamurthy *et al.* (1995a), Sambamurthy *et al.* (1995b) and Pushpam *et al.* (2004). However Arunachalam and Bandopadhyay (1984) and Altaher and Singh (2003) experimentally proved that more number of heterotic combinations with higher level of heterosis were from the parents grouped into moderate divergent groups like cluster II and I in this study. The results obtained from clustering pattern are in agreement with hypothesis of moderate divergence for the best heterotic combinations.

Divergence reflecting in the material was also evidenced by an appreciable amount of desirable variation among cluster means for different characters as shown in Table 3. The component of cluster means for seed cotton yield plant^{-1} was the highest for cluster II (126.15 g) and the lowest for cluster III (81.3 g). Minimum days to 50 per cent flowering and days to 50 per cent boll opening were observed for cluster II (77.42 and 107.58 days, respectively) and maximum for cluster III (81.90 and 113.86 days, respectively). For plant height, the highest cluster mean was recorded in cluster IV (129 cm) followed by cluster III (126.88 cm), cluster II (123.97 cm) and cluster I (116.77 cm), while it was the lowest in cluster V (109.43 cm).

For number of sympodia and monopodia plant^{-1} cluster II (22.45 and 2.38, respectively) exhibited the highest cluster mean, while cluster I (16.51 and 0.93, respectively) had minimum cluster mean. The cluster IV had the highest cluster mean (1.93 g) for lint weight

Table 3. Components of intracluster D^2 of cotton

Cluster no.	Number of geno-types	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
I	7	78.33	108.9	116.77	16.51	0.93	1.68	2.36	26.96	5.44	5.23	7.56	39.87	5.73	10.23	28.16	4.96	4.29	23.02	68.37
II	4	77.42	107.58	123.97	22.45	2.38	1.57	2.79	30.58	5.83	5.37	9.02	39.64	5.65	10.07	29.97	4.43	4.43	22.89	126.15
III	7	81.9	113.86	126.88	18.18	1.36	1.59	2.23	28.28	4.94	5.61	8.76	38.66	5.6	10.21	24.79	5	3.54	20.91	81.3
IV	5	79.67	108.53	129	19.19	1.42	1.93	2.87	30.24	5.9	6.9	9.42	40.29	5.81	10.47	27.12	4.84	4.36	21.72	102.52
V	6	78.72	111.83	109.43	17.27	1	1.39	2.18	31.22	4.18	5.12	8.9	40.29	5.41	9.36	26.6	4.75	4.1	21.92	61.43

Note: 1: Days to 50% flowering; 2: days to 50% boll opening; 3: plant height; 4: no. of sympodia plant^{-1}; 5: no. of sympodia plant^{-1}; 6: lint weight boll^{-1}; 7: seed weight boll^{-1}; 8: Number of seeds boll^{-1}; 9: Boll weight (g); 10: Lint index (g); 11: Seed index (g); 12: Lint per cent; 13: Boll length (cm); 14: Boll girth (cm); 15: 2.5 per cent span length (mm); 16: Elongation (%); 17: Fibre fineness; 18: Fibre strength (g tex^{-1}); 19: Seed cotton yield plant^{-1} (g)

boll^{-1}and the lowest value was recorded for cluster V (1.39 g). For character seed weight/boll cluster IV showed the highest mean value (2.87 g) and it was the lowest in cluster V (2.18g).

The highest cluster mean for number of seeds/boll was exhibited by cluster V (31.22) followed by cluster II (30.58), cluster TV (30.24), and cluster III (28.28), while it was the lowest in cluster I (26.96). The cluster IV had the highest cluster mean for boll weight (5.9 g) followed by cluster II (5.83 g), cluster 1 (5.44 g), cluster III (4.94 g) and the lowest in cluster V (4.18 g). For characters namely lint index, seed index, boll length and boll girth cluster IV possessed the highest cluster mean (6.9 g, 9.42 g, 5.81 cm and 10.47 cm, respectively) and the lowest cluster mean was observed for cluster V (5.12 g, 8.9 g, 5.41 cm and 9.36 cm, respectively).

For character lint per cent, cluster IV and V exhibited the highest cluster mean (40.29 % each) and was lowest in cluster III (38.66 %). However, for the character 2.5 per cent span length cluster II possessed the highest cluster mean (29.97 mm) followed by cluster I (28.16 mm), cluster IV (27.12 mm), cluster V (26.6 mm) and cluster III (24.79 mm). For character elongation per cent cluster III had the highest cluster mean (5.00 %), whereas it was lowest in cluster II (4.43 %). For character fibre fineness cluster II possessed the highest cluster mean (4.43 micronaire) and was lowest in cluster III (3.54 micronaire). For fibre strength the highest cluster mean was exhibited by cluster I (23.02 g per tex) followed by cluster II (22.89 g per tex), cluster V (21.92 g per tex), cluster IV (21.72 g per tex) and it was lowest in cluster III (20.91 g per tex).

The better genotypes selected for all the characters under consideration are presented in table 4. Among them JK-54 included in cluster II possessed the highest seed cotton yield/plant (157.33 g). Similarly, genotype LRA-5166 of cluster I and CAT-2923 of cluster IV showed minimum days to 50 per cent flowering (76.67) and days to 50 per cent boll opening (103), respectively. Similarly for the traits namely plant height, number of sympodia as well as monopodia per plant and seed weight per boll the genotype JK-54 included in cluster II was recorded the highest mean value (148.73 cm, 26.73, 3.33 and 3.25 g, respectively) for these traits. The genotype CAT-834 of cluster I exhibited the highest mean value for lint weight per boll (2.25 g), lint per cent (44.92 %), boll weight (6.64 g) and fibre fineness (5.40 micronaire). The highest mean performance for number of seeds per boll

Table 4. Desirable genotypes for the important traits of cotton

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Days to 50 per cent flowering	LRA-5166	JBWR-36	Narmada	C-1489	CNH-120MB
Days to 50 per cent boll opening	BW-28	JBWR-14	C-2625	CAT-2923	JBWR-13-2
Plant height (cm)	LRA-5166	JBWR-36	C-YG-1830	C-1489	Buri0394
Number of sympodia plant^{-1}	BW-28	JK-54	C-2625	JBWR-13-1	EG-2932
Number of monopodia plant^{-1}	BBR-310	JK-54	C-YG-1830	C-1857	CNH-120MB
Lint weight boll^{-1} (g)	CAT-834	JK-54	Narmada	C-1857	Bikaneri Narma
Seed weight boll^{-1} (g)	BBR-310	JK-54	C-YG-1830	JBWR-13-1	JBWR-13-2
Number of seeds boll^{-1}	SB-166	JBWR-36	EC-110788	JBWR-13-1	Khandwa-2
Boll weight (g)	CAT-834	JBWR-36	Narmada	JBWR-13-1	Khandwa-2
Lint index (g)	BBR-310	JK-54	EC-11 0788	JBWR-13-1	Bikaneri Narma
Seed index (g)	JBWR-25	JK-54	C-2625	JBWR-13-1	CNH-120MB
Lint per cent	CAT-834	JBWR-14	Narmada	C-3718	CNH-120MB
Boll length (cm)	C-1084	JBWR-14	C-YG-1830	C-1489	Bikaneri Narma
Boll girth (cm)	C-1084	JBWR-14	EC-11 0788	C-1489	EG-2932
2.5 per cent span length (mm)	JBWR-25	C-YG-2859	C-2889	JBWR-13-1	JBWR-13-2
Elongation (%)	LRA-5166	C-YG-2859	Mahalaxmi	JBWR-13-1	EG-2932
Fibre fineness (micronaire)	CAT-834	JBWR-36	C-2076	CAT-2923	CNH-120MB
Fibre strength (g tex^{-1})	LRA-5166	C-YG-2859	C-2076	JBWR-13-1	Khandwa-2
Seed cotton yield plant^{-1} (g)	BW-28	JK-54	C-2625	JBWR-13-1	Khandwa-2

(38.25) was exhibited by the genotype Khandwa-2 included in cluster V. Likewise the genotype CNH-120MB grouped in cluster V showed the highest seed index (11.28 g). For character lint index, the highest mean value was exhibited by the genotype JBWR-13-1 (7.60 g) of cluster IV. The highest mean for boll length and girth was recorded in genotype C-1084 of cluster I. However, the genotypes C-YG-2859 of cluster II found superior for 2.5 per cent span length (33.40 mm) and genotype LRA-5166 of cluster I for elongation (5.70 %) and fibre strength (26.20 g per tex).

Based on the present findings of genetic divergence and its component analysis it can be concluded that intercrossing among the genotypes of genetically diverse clusters showing superior mean performance may be helpful for obtaining desirable segregants with higher yield and better lint quality. In view of this, genotypes namely Khandwa-2, CNH-120 MB of cluster V; JBWR-13-1 of cluster IV; JK-54 and C-YG-2859 of cluster II and LRA-5166, CAT-834 of cluster I possessing superiority for more than two characters may be utilized as parents in hybridization programme for obtaining desirable combinations. It is also evident that cross combinations between the genotypes falling in cluster V and IV; V and II and II and I may be most compatible considering the high inter cluster distances among them.

Intracluster distances, intercluster distances, cluster mean for all the characters studied and cluster-wise performance of all the genotypes suggested the selected genotypes improvement of yield and quality components-JK-54, Khandwa-2, CNH-120MB, LRA-5166, CAT-834, C-1084, C-YG-2859 and JBWR-13-1. The hybridization programme with the selected genotypes by considering intercluster distances may produce high magnitude of heterosis or desirable segregants, which would be meaningful for improvement in yield and quality attributes of cotton.

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