



Genetic Divergence in Introgressed Lines of Cotton

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ABSTRACT

In order to assess the divergence among sixty two introgressed lines developed through wild species of *Gossypium* at different Cotton Research Centres across the country and four local checks in American Cotton, Mahalanobis D^2 statistic was applied. The study revealed the existence of considerable amount of diversity. These genotypes were grouped into six clusters. Clusters I, V, III and II had 40, 11, 7 and 4 genotypes respectively. Cluster VI had three genotypes while cluster IV had one genotype only. The genotypes falling in cluster V had the maximum divergence followed by cluster VI and cluster II. Maximum inter cluster distance was observed between cluster II and cluster VI and genotypes included in these clusters had maximum divergence. The cluster VI exhibited high mean values for most of the traits. The character bundle strength contributed maximum (42.05%) to the divergence followed by 2.5% span length (17.90%) and seed cotton yield per plant (9.09%).

Key words : Cotton, Divergence, Introgressed lines.

Cotton is an important commercial crop of Andhra Pradesh. In recent times due to technological innovations in textile industry quality has assumed major importance along with yield. Besides above, various biotic and abiotic stresses tolerance, genetic variability was created by introgression of genes from wild relatives of *Gossypium* under Cotton Technology Mission Project across the Cotton Research Centres of the country. Hence the present study was carried out to measure the genetic diversity to identify suitable parents for hybridization for its seed cotton improvement.

MATERIAL AND METHODS

The experimental material consisted of sixty two introgressed lines developed through wild species of *Gossypium* along with four checks of introgression of genes from *Gossypium hirsutum* cotton collected from different Cotton Research Centres of the country under Cotton Technology Mission Project were grown in randomized complete block design with two replications at Regional Agricultural Research Station, Lam, Guntur, Andhra Pradesh for two consecutive years during *kharif* 2001-2002 and *kharif* 2002-2003. Each entry was sown in one row of 6m length and spaced 120 cm apart maintaining plant to plant distance of 60cm. All the recommended agronomic practices to the region were followed to

raise the good crop. Observations were recorded on five randomly selected plants from each entry, each replication for boll weight (g), number of bolls per plant, seed index (g), lint index (g), ginning outturn (%), 2.5% span length (mm), maturity coefficient, uniformity ratio, micronaire (10^{-6} g inch⁻¹), bundle strength (g tex⁻¹), fibre elongation (%), fibre quality index and seed cotton yield plant⁻¹ (g). Replication wise data was subjected for analysis of variance and covariances. Multivariate analysis was done utilizing Mahalanobis D^2 statistic and genotypes were grouped into different clusters following Tocher's method as described by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance for each trait in both the years as well as in pooled data showed highly significant differences among the genotypes for all the characters studied. Using Tocher's procedure, sixty two genotypes were grouped into six clusters (Table 1). Among these clusters, cluster I was the largest and consists of 40 genotypes followed by cluster V with 11 genotypes. Cluster III had 7 genotypes where as cluster II had 4 genotypes. Cluster VI accounted for 3 genotypes and cluster IV had only one genotype. The random distribution of genotypes was evident from cluster I having

Table 1. Distribution of 66 genotypes into different clusters by Tochers's method in cotton.

S.No	Cluster No.	No. of genotypes	Genotypes
1	I	40	IS 376/412/26, IS 376/411/7/64, IS 376/411/171/50, IS 376/412/8, IS 376/412/1, IS 376/411/1/82, IS 376/412/3/11, IS 376/411/39/11, IS 376/411/3/29, IS 376/411/23, IS 376/412/9, IS 376/41, Khandwa x Raimondii, IS 376/411/34, IS 376/412/30, IS 376/411/25, IS 376/412/31/24, IS376/411/41/7, IS 376/412/33, IS 376/411/29, IS 376/411/20/44, IS 376/412/28, IS 376/412/37-I, IS 376/411/31/27, Hirsutum x Raimondii, IS 376/412/1, IS 376/411/6, IS 376/411/13/12, Hirsutum x wild-V, IS 376/4/31/26, IS 376/411/2, AKH 2031
2	II	4	IS 376/411/33/21, IS 376/411/20/25, MSM, DSFH-1
3	III	7	IS 376/411/40, IS 376/411//43, IS 376/411/4, IS 376/411/20-I, IS 376/412/16, IS 376/412/87-I, L 603 X Palmeri
4	IV	1	Rai
5	V	11	TCH 1649, TCH 1651, TCH 1653, TCH 1652, TCH 1654, TCH 1650, IS 376/411/37/13, TCH 1648, MCU 5 X Palmeri, NA 1325, L 604
6	VI	3	L 603,MCU-5 , L 389

Table 2. Intra and inter cluster D² values in cotton.

S.No Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
1 Cluster I	4.61	7.90	6.79	5.87	7.24	11.22
2 Cluster II		5.02	12.06	6.47	9.10	12.43
3 Cluster III			4.57	9.29	8.86	12.29
4 Cluster IV				0.00	6.99	12.00
5 Cluster V					6.58	11.46
6 Cluster VI						5.44

Table 3. Per cent contribution of different characters to divergence in cotton.

S.No	Source	Times ranked first	Contribution (%)
1	Boll weight (g)	103	4.80
2	No. of bolls plant ⁻¹	121	5.64
3	Seed index (g)	25	1.17
4	Lint index (g)	61	2.84
5	Ginning outturn (%)	29	1.35
6	2.5% span length (mm)	384	17.90
7	Maturity coefficient	101	4.71
8	Uniformity ratio	94	4.38
9	Miconaire (10 ⁻⁶ g inch ⁻¹)	117	5.45
10	Bundle strength (g tex ⁻¹)	902	42.05
11	Fibre quality index	13	0.61
12	Seed cotton yield plant ⁻¹ (g)	195	9.09

Table 4. Cluster means for the twelve characters in cotton.

S.No	Source	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
1	Boll weight (g)	3.43	3.52	3.11	3.86	3.73	4.46
2	No. of bolls plant ⁻¹	34.11	29.00	49.49	15.65	35.10	38.40
3	Seed index (g)	8.26	8.66	7.92	7.35	9.11	10.18
4	Lint index (g)	3.66	4.29	3.54	4.20	4.47	5.11
5	Ginning outturn (%)	32.13	34.20	32.33	36.05	33.25	34.29
6	2.5% span length (mm)	23.72	24.67	22.53	25.12	28.91	29.20
7	Maturity coefficient	50.34	49.58	49.22	48.90	48.05	49.52
8	Uniformity ratio	3.44	3.25	3.48	3.18	3.02	3.98
9	Micronaire (10 ⁻⁶ g inch ⁻¹)	0.61	0.63	0.60	0.65	0.63	0.62
10	Bundle strength (g tex ⁻¹)	21.99	26.98	18.26	23.00	21.73	22.60
11	Fibre quality index	283.65	372.64	224.45	323.91	362.57	332.72
12	Seed cotton yield plant ⁻¹ (g)	103.50	92.65	137.53	55.55	107.33	233.93

maximum lines with wide distribution. The IS cultures, tri-species (*G.hirsutum*, *G. barbadense* and *G. arboreum*) derivatives developed at Agricultural Research Station, Nanded, Maharashtra were found distributed in different clusters. The inter racial derivatives of palmeri are also found distributed in different clusters. The grouping pattern did not show any relationship between genetic divergence and geographic diversity. Similar results were reported by Brown (1991), Rajarathinam *et al.* (1994), Sumathi and Nadarajan (1995), Murthy *et al.* (1995b) and Altaher and Singh (2003). Murthy and Arunachalam (1966) reported that genetic drift and selection in different environments could cause greater diversity than geographic distance.

Average intra and inter cluster D² values presented in table 2 revealed that cluster III showed minimum intra cluster distance (4.57) revealing that the cultivars within this cluster were similar. While cluster V showed maximum intra cluster D² value (6.58) followed by cluster VI (5.44) and cluster II (5.02) indicating thereby the existence of diverse cultivars in these clusters. The inter cluster D² values ranged from 5.87 to 12.43. Minimum inter cluster D² values was observed between cluster I and IV (5.87) indicating the close relationship among the genotypes included in these clusters. Maximum inter cluster value was observed between cluster II and VI (12.43) which revealed that the genotypes included in these clusters had maximum divergence. Hence inter mating between the cultivars included in these clusters may give high heterotic response and thereby better segregants.

The contribution of individual characters to the

total divergence has been worked out in terms of number of times it appeared first (table 3). The characters bundle strength (42.05%) followed by 2.5% span length (17.90%) and seed cotton yield (9.09%) contributed maximum towards genetic divergence. This is in conformity with Kumar *et al.* (2000). The remaining traits contributed low to this parameter.

The average cluster means (table 4) for characters indicates that cultivars included in cluster I showed maximum value for uniformity ratio (3.44). Cluster II had high bundle strength (26.98 g tex⁻¹) fibre quality index (372.64). Cluster III showed maximum number of bolls per plant (49.49), whereas cluster IV recoded maximum ginning outturn (36.05%). Cluster VI had the highest mean value for boll weight (4.46g), seed index (10.18g), lint index (5.11g), 2.5% span length (29.20 mm) and seed cotton yield per plant (233.93g) and was the best cluster. So hybridization between genotypes of cluster II and VI will lead to accumulation of favourable gene combinations in a single variety. In view of this it is suggested that for varietal improvement, the crosses between the genotypes of divergent clusters should be made rather than between the genotypes of those clusters which have the minimum divergence.

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