

Genetic diversity for morpho-physiological traits in parental lines of *Gossypium hirsutum* L.

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Accepted : May, 2009

SUMMARY

The important objective of biometrical measurements is to judge the possibilities of classifying individual genotypes into different groups which require sound knowledge about divergence between them. Intra and inter-cluster distances serves as an index for selection of genetically diverse parents. The 26 genotypes studied were grouped into ten clusters indicates the maximum genetic distance ($D = 137.51$) between the parental line RHC-056 and DS-28 while minimum ($D=10.24$) was observed between RHC-006 and RHBB-9923. Among 10 clusters, cluster I included maximum genotypes (8), cluster II (7), cluster IV (4) and remaining were monogenotypic/solitary. Cluster I showed characteristic feature of low CSI and low leafarea, while it showed highest harvest index and high lint yield per plant.

Key words : Genetic diversity, Morpho-physiological traits, *Gossypium hirsutum* L.

Cotton is the most important textile fibre crop and is the second most important oilseed crop in the world (Cherry and Leffler, 1984). Prerequisite of successful and efficient breeding programme is proper selection of parents. Ultimately the generation of genetic variability - depends on genetic diversity in the parental material being crossed to generate genetic variability. Time has come to maintain some level of genetic diversity at the parental level itself. Naturally, numbers of workers have studied the diversity for various agronomic, morphological and molecular traits in cotton (Kaur and Chahal, 2001 and Kumar *et al.*, 2003). However, very few attempts have been made to study genetic diversity jointly at physiological and morphological level. Important physiological attributes such as Chlorophyll Stability Index (CSI), stomata density need to be involved to get reliable improvement in yield both by selection and by exploitation of hybrid vigor. Hence the present investigation was undertaken to study genetic diversity among these parental lines.

MATERIALS AND METHODS

The material for present study consists of four restorer lines, nineteen female/male parental lines and three checks LRA-5166, JLH-168, PKV -Rajat (Table 1) were sown in Randomized Block Design with three replications on 14th May, 2007 at All India Coordinated Cotton Improvement Project, Mahatma Phule Krishi

Vidyapeeth, Rahuri. Each entry was sown in two rows of 4.8 m length spaced 90 cm apart and spaced at 60 cm within a row. Recommended cultural practices and fertilizers (@ 100 kg N: 50 kg P2O5: 50 kg K2O/ ha) were applied. The observations on nine morpho-physiological characters were recorded on ten random plants in each replication. The data on physiological parameters were recorded at 50 per cent flowering while those of yield and yield components were recorded after harvesting. The generalized distance between any two populations was worked out as per Mahalanobis (1936) and Tocher's method as described by Rao (1952) was followed for cluster formation.

RESULTS AND DISCUSSION

Twenty six parental lines were grouped into 10 clusters (Table 1) indicated that the genotypes studied possess ample variability for different characters under study. Parental line RHC-056 and DS-28 were genetically distanced because of maximum distance ($D = 137.51$) observed between them and naturally placed in different cluster. On the contrary the parental line RHC-006 and RHBB-9923 had the lowest genetic distance ($D = 10.24$) between them *i.e.* they are the most closely related and therefore placed in the same cluster. This indicated the relationship of genotypes expressed in individual distances from each other as a basis for clustering pattern.

The cluster I accommodated the largest number of (8) genotypes followed by cluster II and IV with 7 and 4 genotypes, respectively. Cluster III, V, VI, VII, VIII, IX and X were mono-genotypic. Among the clusters I, II and IV, cluster IV had least number of genotypes (4). Nevertheless it exhibited maximum intra-cluster

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Table 1: Distribution of 26 genotypes into ten clusters

Cluster No.	Number of genotypes included	Genotypes
I	8	RHC-003, RHC-006, RHC-2004, CNH-1009, RHBB-9712, RHBB-9923, RHRGP-9945 and LRA-5166
II	7	RHC-035, RHC-004, CPD-420, DS-28, LH-1556, RHC-98034 and AKH-8801
III	1	PKV-Rajat
IV	4	RHC-054, RHC-058, RHC-688 and JLH-168
V	1	RHC-056
VI	1	RHCb-001
VII	1	RHC-2022
VIII	1	AKH-8649
IX	1	RHBB-9714
X	1	VRS-7

of different species and male fertile/ sterile genotypes. Cluster VII and X exhibited maximum inter-cluster distance ($D = 128.92$) followed by cluster VI and VIII ($D = 121.80$), cluster VII and IX ($D = 117.42$), cluster VII and VIII ($D = 117.10$), cluster V and X ($D = 114.23$), cluster I and VI ($D = 114.00$) indicating that genetic makeup of genotypes included in this clusters may be entirely different from one another and hence substantial hybrid vigor can be expected by crossing the genotypes included in these clusters. However, cluster VI and VII recorded minimum distance ($D = 50.05$) followed by cluster V and IX ($D = 50.07$) suggesting that genotypes in these clusters were genetically close to each other and higher hybrid vigor will not be obtained by crossing them.

Sambamurthy *et al.* (1995) and Kowsalya and Ravendran (1996) reported that number of bolls per plant (31.4%) and days to 50% flowering (35.97%) had

Table 2: Average intra (diagonal) and inter (above diagonal) cluster distances in ten clusters

Clusters	C ₁	C ₂	C ₃	C ₄	C ₅	C ₆	C ₇	C ₈	C ₉	C ₁₀
C ₁	42.651	96.103	60.165	76.130	71.546	114.003	109.225	056.912	72.814	64.003
C ₂		49.808	85.512	77.163	111.954	85.155	70.160	78.151	101.121	79.230
C ₃			0.000	60.179	83.830	99.206	84.435	75.643	84.663	80.757
C ₄				52.627	63.771	64.400	71.824	82.995	67.389	98.364
C ₅					0.000	83.512	106.074	93.043	50.074	114.239
C ₆						0.000	50.054	121.808	100.059	128.928
C ₇							0.000	117.106	117.422	110.718
C ₈								0.000	66.776	50.819
C ₉									0.000	107.076
C ₁₀										0.000

divergence indicating that merely higher number of genotypes in the cluster does not necessarily involve wider diversity. Check PKV Rajat formed separate solitary cluster *i.e.* cluster III. Tatineni *et al.* (1996) also grouped 19 genotypes into 6 clusters because of wide diversity. Sambamurthy *et al.* (1995) grouped 50 genotypes into 9 clusters. However, none of them has detailed the distances between individual genotype.

The maximum intra-cluster distance (Table 2) was observed for the cluster IV ($D = 52.62$) followed by cluster II ($D = 49.80$). This implies that cluster IV and II accommodated the genotypes with varied genetic architecture. However, the genotypes included in the cluster I exhibited minimum intra-cluster distance ($D = 42.65$), implying that the genotypes included in the cluster I resembled more to each other. With only six clusters the range of intra-cluster distance reported by Kowsalya and Ravendran (1996) was too wide because of inclusion

maximum contribution to diversity. However, due to inclusion of physiological traits in this investigation it was observed that trichome density had maximum (24.62%)

Table 3 : Per cent contribution of various characters to divergence in *G. hirsutum*

Sr. No.	Characters	Per cent contribution
1.	Trichome density (No/ cm ²)	24.62 %
2.	Adaxial stomata density (No/ mm ²) (upper)	13.54 %
3.	Abaxial stomata density (No/mm ²) (lower)	2.77%
4.	Chlorophyll stability index (um)	29.10 %
5.	No. of leaves/ plant	14.15 %
6.	Leaf area (cm ² / 10 leaves/ plant)	2.20 %
7.	Seed cotton yield (g/ plant)	5.25 %
8.	Lint yield (g/ plant)	4.15 %
9.	Harvest index (%)	3.02 %
10.	Ginning percentage (%)	1.20 %

Table 4: Cluster means for 9 characters in *G. hirsutum*

Cluster No.	Trichome density (No./ cm ²)	Adaxial stomata density (No/ mm ²)	Abaxial stomata density (No/ mm ²)	CSI (nm)	No. of leaves/ plant	Leaf area (cm ² /10 leaves/ plant)	Seed cotton yield (g/ plant)	Lint yield (g/ plant)	Harvest index (%)	Ginning outturn (%)
Cluster-I	17031	133.88	162.31	0.650	114.64	587.25	98.47	36.09	31.54	36.67
Cluster-II	152.82	120.24	147.81	0.861	119.50	589.52	94.30	35.12	31.06	37.25
Cluster-III	241.03	155.43	189.84	0.715	162.40	502.00	112.20	43.66	20.54	38.87
Cluster-IV	218.75	103.80	136.98	0.752	140.07	647.25	95.16	35.02	29.61	36.79
Cluster- V	230.45	78.44	100.78	0.640	114.36	627.00	85.60	30.80	25.52	36.03
Cluster-VI	246.78	68.45	102.78	0.838	98.1 0	692.00	74.33	26.33	20.47	35.36
Cluster-VII	245.44	119.78	142.14	0.880	93.33	470.00	127.66	45.86	38.83	35.94
Cluster-VIII	126.20	127.68	158.73	0.698	139.63	642.00	87.56	34.00	32.40	38.82
Cluster-IX	153.38	83.89	105.75	0.660	159.90	683.00	109.20	35.80	41.04	32.77
Cluster- X	109.49	154.56	181. 72	0.735	89.76	630.00	74.60	27.66	24.66	37.09

Table 5: Source cluster for different characters

Sr. No.	Characters	Promising/source cluster (s) (in descending order of performance)
1.	Trichome density	VI, VII, III, IV
2.	Adaxial stomata density	VI, V, IX, IV
3.	Abaxial stomata density	V, VI, IX
4.	Chlorophyll stability index	V, I, IX
5.	No. of leaves/ plant	VI, VII, X, V
6.	Leaf area 10 leaves/ plant	VII, III, I
7.	Seed cotton yield/ plant	VII, IX, III
8.	Lint yield/plant	VII, IX, I
9.	Harvest index	VII, IX, I
10.	Ginning percentage	III, VIII, II, X

contribution to genetic diversity followed by CSI (Table 3). No such reports regarding the parental lines are

traceable in the past work. Contribution of adaxial and abaxial stomata density to divergence was substantially different *i.e.* 13.54 % and only 2.77 % due to higher variation in adaxial stomata density than abaxial stomata density.

Means for the clusters can indicate the desired parent for hybridization programme for the improvement in the character shown against them. In case of characters like abaxial stomata density, CSI, leaf area per 10 leaves per plant, seed cotton yield per plant, lint yield per plant and harvest index, the mean of the fourth cluster was substantially low than third cluster and, therefore, such clusters are not enlisted (Table 4). Therefore, to get reliable improvement in yield both by selection and exploitation of hybrid vigour, parents in the crossing programme or selection are to be utilize from the source cluster listed as in the Table 5.

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