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Genetic Divergence Analysis in Upland Cotton (*Gossypium arboreum* L. Genotypes

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Abstract Mahalanobis D^2 statistics was applied to assess the genetic divergence among 169 cotton (*Gossypium arboreum* L.) germplasm lines and grouped into 15 clusters. Cluster XV was the largest with maximum number of genotypes (87) followed by 56 genotypes in the cluster I. Boll weight contributed 53.03% to the total divergence followed by GOT (38.11%) and seed cotton yield (4.63). The inter-cluster distances varied from 27.99 (between cluster 1 and XII) to 31.08 (between clusters 1 and VII). The intra cluster distance varied from 1.64 in cluster-II to maximum distance of 23-38 in cluster-XV. Cluster I possessed the genotypes with high boll weight (4.13) which in turn contributed for high seed cotton yield, hybridization among the genotypes of above said clusters would produce transgressive segregants for more than one economic traits or also be used as a improved variety.

Keywords Cotton, Divergence , D^2 statistics, *Gossyplum arboretum,* Genotypes.

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Introduction

Cotton (*Gossypium* spp.) is the most extensively used natural fiber in textile manufacturing and is one of the most abundantly grown fiber crop and also second most important oilseed crop in the world. It is the principal raw material for a flourishing textile industry and provides livelihood to about 60 million people and is an important agricultural commodity providing remunerative income to millions of farmers both in developed and developing countries. *Gossypium arboreum* is a native of India and cultivated from Punjab in the North to Kanyakumari in the South and Assam in the East to Kutch (Gujarat) in the West. *G. arboreum* genotypes matures between 150 to 180 days and is usually having coarse and short fiberd and has high degree of resistance to disease and insect pests and is very valuable germplasm resources and have great export value [1]. In India, in spite of several competitions from synthetic fibers in recent years, it is occupying the premier position with 70% share in the textile industry. Existence of genetic diversity is an essential requirement for successful hybridization program. Development of superior and heterotic hybrids is possible only by involving diverse parents in the hybridization program. In order to take the program of development of hybrid cotton successfully, choice of suitable parent through careful and critical evaluation is of paramount importance. This is because *per se* performance of a parent is not always true indicator of its potential in hybrid combination. There are several critical methods by which a breeder can choose suitable parents for successful

Table 1. Relative contribution of seven quantitative traits towards total genetic divergence in cotton genotypes.

Sl. No.	Characters	% Contribution
1	Plant height (cm)	0.30
2	No. of monopodial branches	0.20
3	No. of sympodial branches	0.30
4	No. of bolls/plant	3.39
5	Boll weight (g)	53.03
6	Seed cotton yield (kg/ha)	4.63
7	GOT (%)	38.11
	Total	100

hybridization, of which an important one is the estimates of genetic diversity among parents. 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 programs. In this context, the present study has been taken up to study the genetic diversity in 169 cotton (*Gossypium arboreum* L.)

Materials and Methods

The experiment was conducted during *rabi* of 2012-13 at Main Agricultural Research Station, Raichur, Karnataka. About 169 diverse cotton genotypes including released varieties were evaluated in simple lattice design with two replication for assessing diversity based on yield and its attributing characters. Five plants were selected at random from each germplasm line to record the observations on yield and its attributing characters. Mahalanobis D^2 [2] was used for assessing the genetic divergence among the population. All the n (n - 1)/2 D^2 values were clustered using Tocher's method as described by Rao [3]. The intra, inter-cluster distance and the character contribution towards diversity were calculated by the formula given bt Singh and Chaudhary [4].

Results and Discussion

Among seven characters studied, boll weight (53.03%) followed by GOT (38.11%) has contributed largely to the total genetic divergence in the studied cotton genotypes. Seed cotton yield and number of bolls per plant have contributed about 4.63% and 3.39% respectively to genetic divergence (Table 1). Higher contribution of seed cotton yield and boll weight to total divergence was also reported by Pushpam et al. [5] in upland cotton. The above results imply that in order to select genetically diverse genotypes, the material should be screened for the important traits like seed cotton yield and boll weight. Traits like plant height, number of branches per plant and number of sympodial branches have contributes less to genetic divergence.

The data were subjected to D^2 statistic analysis and 169 genotypes were grouped into 15 clusters. The list of all the 15 clusters along with the genotypes included is presented in the Table 2. Among the different clusters, the cluster size varied from 2 to 87 genotypes. The maximum number of genotypes were included in cluster XV having 87 genotypes followed by 56 genotypes in the cluster I and remaining all the clusters were having two genotypes each. 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 different populations. The present pattern of grouping of genotypes indicated that the genetic diversity was not fully related to the geographical diversity. These results are in agreement with the findings of earlier reporters [1, 6, 7].

The intra and inter cluster distances revealed that inter cluster distances were greater than intra cluster distances which suggest considerable amount of genetic diversity among genotypes. The farthest and nearest cluster of each cluster is presented in the Table 3. The genotypes included in clusters 1 and VII were found to be very diverse in nature as they shown maximum inter-cluster distance D^2 value of 31.08 followed by cluster 1 and XII (27.99) and cluster VII and XV (27.12) suggesting the existense of more diversity among the genotypes in respect of the characters studied. Hence crossing between genotypes belonging to these clusters may results in high heterosis which could be exploited in crop improvement. Thus the genotypes in cluster 1 and VII should be involved in the hybridization program. The minimum D^2 value is between the cluster II and VI (2.49) indicating the close relationship and similarity for most of the characters studied for genotypes of these clusters. Maximum genetic divergence between the cluster points

Table 2. Clustering pattern of 169 cotton genotypes.

Clusters	No. of genotypes	Genotypes
I	56	RCR-125, IPS-102, RCR-112, RH-341, RAH-3011, HLS-1, 432536, RCR-51, RAH-385, HLS-2, 432502, IPS-1014, RAC-6565, C-11, RAH-283, AH-292, IPS-22, 432512, RAH-338, IPS-1007, SCS-4011, 432532, RAH-276, RAH-363, RAH-236, SC11-8-90, SC-11, RCR-101, RCR-11-28, AH-278-18, IPS-40, RCR-125, RAMPBS-155, CCH-1831, C-11-1, RAS-299-1, 432507, RAH-236, RAH-352, 43050502A, RAH-241, IPS-201, 432514, CPB-758, RAH-258, IPS-1008, RAH-347, RAH-348, RAH-349, IPS-1009, IPS-1010, IPS-1011, RCR-335, RCR336, IPS-35
II	2	GISV-103-2, IPS-15
III	2	F-2609F, AKH-138
IV	2	SC-68, RCR-103
V	2	CCH-56612, RCR-116
VI	2	HBF-21, GTHV-13
VII	2	RCR-9577, RAC-95118
VIII	2	RCR-11-LS-11, SC-31NS
IX	2	CCH-1386, GISV-163
X	2	RAMP-296, RAC-95139
XI	2	RAC-9681, RCR-117
XII	2	RCR4-75, RAH-100-5
XIII	2	RAH-100 77, IPS-13
XIV	2	F-9827, RCR-8-85
XV	87	RAH-361, CH-11, DS-28, SC-7-58, CH-9, RACH-115, 432504, 4305038, 7341, RAH-101, RAH-221, 43050506, HBF-FEMALE, L-755, HAG-786, RCR-122, R777, SC-65, RAH-272, LAKSHMI-77, ARB-816, 432516, RAH-336, GIHV-110113, RAH-273, IPS-85, RCR-39-69, LPD-814, RCR-102, RCR-103, RCR-113, RCR-124, RCR-1131(M), RCR-123, B101NS, ACP-71, CH-12, RAH-274, RAH-101-99, RAH-144, RAH-296, RAH-126A, SC-71, RAH-226, RAH-249, ERB-75, 432525, IPS-9, RAS-299-1, 432533, RAH-314, SC18-105, GISV-97/107, 432534, ARB-7-118, NARASHIMHA, HAG 811-410, SANDIPS-37, RAC9555, SC-81-4C, R5AC9532, RAC1011, RAC1010, G-COT-16, RAH-217A, SC-38-52, SC-1-15, SP-46, RAC-99152, NAWB-19, RCR-125-88, 92PL-24, RCR-122, RCR-115, RCR-111, RAMP-153B, IPS-35, IPS-150, RCR-299-1, RCR-299-3, RCR-299-5, IPS-55, RCR-249-1, RCR-249-5, IPS-2012-1, IPS-2012-3, IPS-2012-15

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. [7] and Sakhti et al. [8].

Cluster mean for seven traits (Table 4) revealed that considerable differences were noticed between the cluster means for different characters. Cluster XI (104.5) and III (104.00) included plants which are taller whereas cluster XII (78.50) included dwarf plants. Cluster IV and VII included genotypes having less number of monopodial branches whereas cluster V and I included genotypes having more number of monopodial branches . Cluster XIII (21.50) and II (20.00) composed of genotypes producing more number of sympodial branches per plant whereas cluster VII (11.00) included genotypes producing less number of sympodial branches. Genotypes of cluster XI (26.25) and XII (25.00) exhibited more number of bolls per plant and of cluster XIV (15.00) and XIII (17.50) showed less number of bolls per plant. Cluster I (4.13) and cluster VII (2.97) recorded highest and lowest values of boll weight respectively. Genotypes of cluster III (2402.08) and 1 (2133.55) exhibited high seed cotton yield whereas genotypes of cluster XIV (1136.27) and XIII (1262.26) shown low seed cotton yield. GOT parameters observed high in genotypes of cluster VII (38.7) and minimum in cluster XI (31.22), When we consider cluster mean value for 7 traits, it was maximum in cluster 1 followed by cluster III. Genotypes of cluster 1 possessed high boll weight (4.13) which in turn contributed for high seed cotton yield. It was observed that genotype or genotypes grouped under cluster III ranked first by having four charac-

Table 3. Average inter and intra cluster D^2 values.

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV
I	21.08	16.71	23.67	15.30	16.93	16.81	31.08	15.38	18.29	18.82	19.95	27.99	25.24	23.40	22.81
II		1.64	12.25	5.32	4.28	2.49	20.04	4.23	5.04	4.36	7.50	16.59	12.86	10.87	16.61
III			1.70	16.21	11.48	11.46	11.22	15.28	9.06	9.32	7.36	7.94	10.63	12.18	20.89
IV				1.78	6.10	5.60	24.73	3.73	8.15	9.13	10.50	21.06	17.50	15.59	16.83
V					1.8	2.74	20.00	5.83	3.44	5.45	5.94	16.23	13.76	12.50	16.82
VI						1.86	19.75	4.89	3.46	4.33	6.20	16.12	12.87	11.34	16.62
VII							1.87	23.46	17.60	16.07	16.01	4.372	10.21	12.89	27.12
VIII								1.89	7.87	7.86	10.63	20.04	16.57	14.18	16.67
IX									2.05	4.20	3.39	13.78	11.42	10.89	17.29
X										2.20	5.81	12.66	9.22	7.66	17.49
XI											2.25	12.11	10.70	11.29	18.28
XII												2.28	8.03	10.83	24.37
XIII													2.35	4.65	22.21
XIV														2.37	20.99
XV															23.28

ters (1-3 scores) at desirable direction followed by genotypes under cluster I with three characters (1-3 scores). Genotypes grouped under cluster VII and XII (last rank) recorded characters in negative direc-

Table 4. Cluster mean values for seven quantitative parameters in cotton genotypes.

Clusters	Plant height (cm)	Monopodial branches	Sympodial branches	Bolls per plant	Boll weight (g)	Seed cotton yield (kg/ha)	GOT%	Total score	Rank
I	97.50 (6)	1.26 (2)	16.68 (9)	23.76 (6)	4.13 (1)	2133.55 (2)	34.58 (4)	35	II
II	94.50 (10)	1.25 (3)	20.00 (2)	22.75 (10)	3.81 (5)	1909.69 (10)	35.37 (5)	45	VII
III	104.00 (2)	1.00 (4)	18.25 (5)	32.50 (1)	3.35 (11)	2402.08 (1)	38.11 (2)	26	I
IV	83.75 (12)	1.00 (4)	19.00 (4)	22.25 (11)	3.98 (2)	1949.86 (9)	32.49 (12)	54	IX
V	95.50 (9)	1.75 (1)	14.25 (11)	24.50 (5)	3.76 (7)	2028.92 (5)	32.43 (13)	51	VIII
VI	103.75 (3)	1.25 (3)	18.25 (5)	23.50 (9)	3.77 (5)	1952.44 (8)	33.56 (10)	44	VI
VII	78.50 (13)	1.00 (4)	11.00 (13)	25.00 (3)	2..97 (14)	1638.03 (13)	38.70 (1)	61	XII
VIII	94.00 (11)	1.00 (4)	16.50 (10)	23.75 (7)	3.97 (3)	2077.81 (3)	36.41 (3)	41	III
IX	104.50 (1)	1.25 (3)	17.50 (7)	24.75 (4)	3.64 (8)	1983.63 (6)	32.09 (14)	43	V
X	96.25 (8)	1.25 (2)	17.25 (8)	22.25 (11)	3.64 (8)	1784.88 (11)	35.20 (7)	56	X
XI	99.25 (5)	1.25 (3)	19.50 (3)	26.25 (2)	3.53 (9)	2039.44 (4)	31.22 (15)	41	III
XII	78.50 (13)	1.00 (4)	11.50 (12)	25.00 (3)	3.10 (13)	1705.15 (12)	35.93 (4)	61	XII
XIII	101.25 (4)	1.00 (4)	21.50 (1)	17.50 (12)	3.28 (12)	1262.26 (14)	33,37 (11)	58	XI
XIV	97.50 (6)	1,25 (3)	18.25 (5)	15.00 (13)	3.44 (10)	1136.27 (15)	35.31 (6)	58	XI
XV	96.48 (7)	1.26 (2)	17.98 (6)	23.55 (8)	3.88 (4)	1970.16 (7)	34.72 (8)	42	IV

tion. Therefore use of genotypes in chster III, I, VIII and XI would desirable to generate the variability in the desired direction. It is suggested that hybridization among the genotypes of above said clusters would produce segregants for more than one economic character which can serve as parents of hybrids. These findings coincides with results of earlier studies of earlier reporters [1, 7, 9–11]. Diversity has been used as a powerful tool in the classification of cultivars and also to study taxonomic status. Knowledge of gentic variation and relationships among genotypes will assist breeders to develop appropriate breeding strategies to solve production constraints by providing an index of parental lines to be used in breeding programs.

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