J. Cotton Res. Dev. **29** (1) 16-18 (January, 2015)

Genetic diversity in upland cotton (*Gossypium hirsutum* L.)

SANTOSHKUMAR PUJER*, S.S. SIWACH, R.S. SANGWAN, O. SANGWAN AND JAGDISH DESHMUKH

Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar- 125004
**e-mail- pujer_851@rediffmail.com*

ABSTRACT : The study of genetic diversity and identification of genotype with broad genetic base quicken the crop improvement programme. It enables the plant breeders to choose the parental sources that will generate diverse population. Genetic divergence was studied among 68 genotypes of American cotton (*Gossypium hirsutum* L.) using D^2 technique which indicated the presence of substantial genetic diversity among the material. The 68 genotypes were grouped into 8 clusters, based on the inter cluster distances C I and C VI were found to be most divergent followed by C V and C VI, C I and C VIII and C II and C VI. The use of diverse genotypes included in these clusters is advocated in crossing programme to evolve high heterotic hybrids and for taping the good transgressive segregants in segregating generations.

Key words: Clusters, Genetic divergence, D^2 statistic, *Gossypium hirsutum*

Cotton (*Gossypium* spp.) is the most extensively used natural fibre in textile manufacturing and is one of the most abundantly grown fibre crop, with a yearly average range from $27 –29 billion world wide from lint fibre production (Campbell *et al.,* 2010). Cotton is also an important food source for livestock. China, India, USA and Pakistan are the top four cotton growing nations, accounting for approximately 2/3 of the world's cotton acreage. In India, inspite of severe competition from synthetic fibres in recent years, it is occupying the premiere position with 70 per cent share in the textile industry.

Knowledge of the nature and magnitude of genetic variance present in the breeding material is the most important pre requisite for successful breeding programme. The genetic diversity of different fibre quality parameters has been studied only to a limited extent. In order to development of hybrids in 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. In order to develop better genotypes/ hybrids, the choice of diverse parents is of greater concern. Hence, genetic divergence was estimated using Mahalonobis D^2 statistics in 68 genotypes of American cotton in order to initiate a systematic hybrids/recombinants development programme.

Sixty eight diverse genotypes of American cotton were grown at Research Area of Cotton Section, Department of Genetics and Plant Breeding, CCS HAU, Hisar during *kharif*, 2011-2012 in randomized block design with 3 replications having row length 4.2 m with row to row 67.5 cm and plant to plant 30 cm. The observations were recorded on 5 competitive plants for 13 characters, *viz.,* days to first flowering, plant height (cm), monopods and bolls/ plant, boll weight (g), seed index (g), lint index (g), ginning outturn (%),2.5 per cent span length (mm), fibre fineness (micronaire value), bundle strength (g/tex), uniformity ratio (%) and seed cotton yield/plant (g). The lint quality parameters were studied at Central Institute for Research on Cotton Technology (CIRCOT), Regional Research Station, Sirsa. The genetic divergence was worked out by using Mahalanobis D^2 statistic and genotypes were grouped into different clusters by employing Euclidean's method.

Based upon the D^2 analysis, all the 68 cotton genotypes were grouped into 8 clusters (C). The composition of different clusters is given in Table 1. The cluster VII (C VII) possessed the largest number of genotypes (20) followed by C II

(14), C III (9), C IV (7), C I (6), C VIII (5), C V (4) and C VI possessed only 3 genotypes. The present findings are in agreement with those obtained by Gopinath *et al.*, (2009) and Kulkarni *et. al.*, (2011). The intra and inter cluster D^2 values are presented in Table 2 which indicated that maximum intra-cluster D^2 values of 4.918 was observed for C V followed by 4.890 for C VI, 4.764 for C I and 4.001 for C VIII.

The geographical distribution of genotypes is not only factor that causes genetic diversity. This may be due to exchange of breeding material over the location and further selection at different location which could result in genetic drift stated that force of genetic drift and natural selection under diverse environmental conditions causes the considerable diversity then geographical isolation. So, selection of parents for hybridization programme should be based on genetic rather then geographical diversity. The maximum inter cluster distance was observed between C I and C VI (7.868) followed by C V and C VI (7.394), C I and C VIII (7.132) and C II and C VI (6.442). Since these clusters had higher inter cluster distances among them, crossing between members of these clusters would result in increased heterosis and isolation of desirable recombinants/transgressive segregants in the segregating generations. The inter cluster distance was found to be minimum (4.378) between C III and C VII suggesting a close relationship between members of them and a low degree of diversity among the genotypes. Since the magnitude of heterosis largely depends on the degree of genetic diversity among parents

Table 1. Clustering pattern of 68 genotypes of upland cotton

Cluster number	Genotypes	Number of genotypes
C I	TCH 1728, BS 37, Bro3 007, CCH 820, L 770, BS 39	6
C II	LH 2170, P 2150, CSH 3114, GJHV 500, BGDS 801, F 2276, H 1454, ARBH 1001, PRT/09-3, SCS 793, LH 2152, FYT/09-17, Bro4 017, Bro3 001	14
C III	H 1422, FYT/09-19, KH 1001, CPD 1001, Bro4 014, MR68, FYT/09-14, FYT/09-12, H 1439	9
C IV	TCH 1717, GSHV 159, GJHV 503, TSH 0250, F 2337, SCS 792, CNH 1094	7
C V	CPD 1002, CNH 1106, H 1435 NP 48, PRT/09-6	4
C VI	SR 1, H 1300, GSHV 160	3
C VII	F 1861, RS 2013, H 1451, CSH 2810, H 1462 NP 47, CA 107, GTHV 07/1, RAH 803, Bro2 342, RS 2596, HS 288, H 1316, H 1428, H 1442, PRT/09-4, RS 2620, Bro2 301, Bro2 306, ADB 532, CCH 10-1	20
C VIII	H 1462, PRT/09-8, RHC 0717, ADB 531, H 1117	5

and hence, selection of parents from these clusters should be avoided for combination breeding.

Cluster mean values of 13 characters are furnished in Table 3. High range of mean values among the clusters was noted for all the characters. The genetic differences between the clusters were reflected by cluster mean differences also. The maximum mean values for characters *viz.,* plant height and bundle strength were recorded in C V. Whereas, C VI was found superior for monopods/plant and uniformity ratio. Maximum number of bolls and seed cotton yield was observed in C II, while C III was observed to be superior for boll weight and lint index. Seed index and 2.5 per cent span length were found maximum in C I whereas, ginning outturn and fibre fineness in C VIII. Based upon the mean performance of different clusters, it would be appropriate to use the genotypes of C II and C III in crossing programme to get desirable recombinants for seed cotton yield and bolls/plant and boll weight for getting genetic variability. To get desirable seed index , 2.5 per cent span length, ginning outturn and fibre fineness the C I and C VIII can be utilized.

Table 2. Intra (diagnol) and inter cluster D^2values among 68 genotypes of upland cotton

Clusters	C I	C II	C III	C IV	C V	C VI	C VII	CVIII
I	4.764	5.476	5.710	5.472	5.769	7.868	6.450	7.132
II		3.860	4.547	4.766	5.540	6.442	5.107	5.255
III			3.647	4.640	5.628	5.953	4.378	5.475
IV				3.588	5.100	5.244	4.633	4.964
V					4.918	7.394	5.705	6.177
VI						4.890	5.926	5.711
VII							3.780	4.632
VIII								4.001

Table 3. Mean performance of different clusters for 13 characters in upland cotton

Characters	I	II	III	IV	V	VI	VII	VIII
Days to first flowering	54.44	53.31	49.40	59.76	52.66	72.22	50.26	54.73
Plant height(cm)	146.94	159.80	149.75	151.82	162.66	144.44	141.30	152.44
Monopods/plant	2.78	3.03	2.62	3.78	2.55	4.01	2.23	2.93
Bolls/plant	24.85	26.65	22.17	21.63	22.77	23.22	21.71	25.95
Boll weight (g)	15.59	16.19	16.40	14.58	14.60	14.14	15.04	13.80
Seed index (g)	7.96	7.35	7.47	7.41	7.09	7.24	7.28	7.17
Lint index (g)	4.33	4.25	4.72	4.25	4.37	4.59	4.20	3.91
Ginning outturn (%)	36.08	36.21	36.89	36.05	36.10	37.90	36.37	37.02
2.5 per cent span length (mm)	29.45	27.16	26.83	27.24	29.15	24.97	26.07	25.26
Fibre fineness (micronaire value)	4.21	4.33	4.43	4.54	4.73	4.56	4.66	5.07
Bundle strength (g/tex)	22.56	20.88	20.25	21.11	23.52	19.71	20.38	20.04
Uniformity ratio (%)	45.05	48.07	48.07	47.57	47.66	49.44	49.25	48.80
Seed cotton yield/plant (g)	76.95	86.15	71.77	63.55	67.33	61.22	64.63	71.68

REFERENCE

Campbell, B., Saha, S., Percy, R., Frelichowski, J. and Jenkens, J. 2010. Status of the global cotton Germplasm Resources

Gopinath, M., Rajmani, S., Krishna Naik, R. and Mallikarjuna, Rao. 2009. Genetic divergence for lint characters for upland cotton (*Gossypium hirsutum* L.). *J. Cotton Res. Dev.* **23** : 46-48

Kulkarni, A., Nanda, H.C. and Patil, S.G., 2011. Studies on genetic divergence in upland cotton (*Gossypium hirsutum* L.). *J. Cotton Res. Dev.* **25** : 9-13.

Recieved for publication : March 30, 2013
Accepted for publication : September 2, 2013