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Genetic divergence study in Cotton (*Gossypium hirsutum* L.)

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Abstract

Genetic divergence was studied among twenty germplasm lines of cotton (*Gossypium hirsutum* L.) by using Mahalanobis D^2 analysis. Analysis of variances for dispersion showed significant differences among the genotypes and these genotypes were grouped into two clusters. The cluster I consisted of nineteen genotypes, whereas cluster II has single genotype. Highest inter cluster distance observed among both clusters, while cluster I shown maximum intra cluster distance. Characters ginning outturn (26.84 %) contributed maximum towards genetic divergence followed by days to 50 percent flowering (23.68 %), average boll weight (g) (14.74 %), number of bolls per plant (13.68 %). Cluster I and II shown high cluster means for yield and yield components, therefore genotypes *viz.* GBHV170, SCS793, DHY286, AKH081, AKH081, PKV RAJAT, LRA5166 and ADB 542 of these diverse clusters may be used for further hybridization.

Keywords: cotton, genetic divergence, yield components

1. Introduction

Cotton is an important cash crop grown all over world as well as in India. Hybrid vigor was successfully exploited in cotton with development of commercial hybrids. India is pioneer country for cultivation of commercial hybrids of cotton. The genetic divergence among the parents is very important factor in selection of parents for hybridization. It has also been observed that greater the genetic variability among population greater will be the chance of obtaining the desirable gene combination. In crop improvement program genetics divergence is of considerable practical interest. Ramanujam *et al.* (1974) [9] and Rao (1960) [11] also observed that the cross involving genetically diverse parents is more likely to produce high heterotic effects as compared with lines which are more closely related with each other. Cress (1966) [4] demonstrated that 'genetic diversity is necessary for significant heterosis but not sufficient to guarantee it'. Ashok and Nanda (2006) [1] found that the inter-cluster distances were be greater than intra-cluster distances, revealing considerable amount of genetic diversity among genotype studied. The importance of genetic diversity for selecting parents in breeding program of different autogamous crops to develop transgressive segregants has been very well emphasized by Khanna and Mishra (1977) [6], Singh and Ramanujan (1981) [12], Cox and Murphy (1990) [3]. Therefore the present study was carried out to understand the genetic diversity among the 20 germplasm lines of cotton and to identify the lines for further hybridization.

2. Material and methods

Twenty genotypes of cotton (*Gossypium hirsutum* L.) were collected from VNMKV, Parbhani, Dr. PDKV, Akola and CICR, Nagpur and grown in randomized block design with three replication and spacing of 90 x 60 cm at the Department of Botany, Government Imstitute of Science, Auranagabad, Maharashtra in *kharif* 2013. The observations were recorded on randomly selected five plants from each genotype for eight quantitative characters *viz.* days to 50 per cent flowering, plant height (cm), number of bolls per plant, Average boll weight (g), Seed cotton yield, ginning outturn, seed index and lint index. Genetic divergence was analyzed using the Mahalanobis D^2 statistics method (1936) and genotypes were grouped into clusters by following the Tocher's method described by Rao (1952).

3. Results and discussion

Analysis of variances exhibited significant differences among the twenty genotypes for all studied eight characters. According to Wilk's criteria aggregate effects of all the eight traits tested. It showed significant differences among the genotypes. Similar results were observed by Moll *et al.* (1974) [8], Ashok and Nanda (2006) [1] and Dhivya *et al.* (2014) [5]. Twenty genotypes were grouped into two clusters (Table 1), nineteen genotypes were grouped in to cluster I and cluster II was solitary cluster with single genotype. Chaudhary *et al.* (2010) also reported similar type of distribution of genotypes. Distribution of the genotypes into different clusters was based on D^2 values, which ranged from 4.65 to 8.92 (Table 2). Inter cluster distance between cluster I and II was (8.92). Highest intra cluster distance was shown by cluster I (4.65), while rest of the cluster having zero intra cluster distance. Genotypes for the hybridization should be selected from the more distant clusters as chances are more to obtain heterotic combinations. Cluster means indicates the variation for the quantitative traits among the cluster (Table 3). Both clusters i.e. cluster me and II showed considerable cluster means for considering major yield contributing characters along with earliness to flowering and maturity, genotypes from these diverse clusters should be used for further hybridization and isolating transgressive segregants in later generations. The analysis of contribution of the characters for genetic diversity (Table 3) reveled that characters ginning outturn (26.84 %) contributed maximum towards genetic divergence followed by days to 50 percent flowering (23.68 %), average boll weight (g) (14.74 %), number of bolls per plant (13.68 %), Seed index (8.42 %), lint index (6.84 %) and plant height (5.79 %), however the character seed cotton yield contributed zero percent. De *et al.* (1988) proposed that traits contributing maximum towards the D^2 values need to be given more emphasis for deciding the clusters to be taken for further selection and choice of parents for hybridization. Moll *et al.* (1974) [8], Sunder *et al.* (2014) and Ashok and Nanda (2006) [1] observed similar level of contribution phenotypic yield and yield contributing traits. On the basis of inter cluster distance, clusters I and II were identified as divergent clusters, and genotypes *viz.* GBHV170, SCS793, DHY286, AKH081, AKH081, PKV RAJAT and LRA5166 (cluster I) and ADB 542 (cluster II) of these diverse clusters should be used for further improvement in heterosis in yield targeted traits with creation of wider variability.

Table 1: Grouping of twenty genotypes into different clusters

Cluster	Number of genotypes	Genotypes
I	19	RAH1065, PH1075, P2151, GBHV170, SCS793, DHY286, AKH8828, G. Cot.10, F414, H777, AKH081, PKV RAJAT, LRA5166, PH348, L 147, B 1007, SCS1062, NH615 and Sharada.
II	1	ADB542

Table 2: Average intra (diagonal) and inter cluster distance (D2) in cotton**.**

Cluster	I	II
I	4.65	8.92
II		0.00

Table 3: Cluster means and per cent contribution of different characters in Cotton

Cluster	Days to 50 % Flowering	Average boll weight (g)	No. of bolls / plant	Plant height	Seed cotton yield	Ginning %	Seed index	Lint index
I	63.04	2.91	32.14	98.78	1.17	34.36	6.66	3.35
II	58.00	3.87	69.56	91.21	1.19	35.70	5.33	2.99
Contribution of individual characters towards total genetic divergence (%)	23.68	14.74	13.68	5.79	0.00	26.84	8.42	6.84

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