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Genetic divergence in okra among genotypes [*Abelmoschus esculentus* (L.) *Moench*]

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Abstract
An investigation was conducted during the year 2016-2017 with 20 germplasm accessions of Okra (*Abelmoschus esculentus* (L.) Moench) were evaluated in a randomized block design with two replications at Vegetable Research Farm, The field experiment was carried out at Horticulture Research Scheme (Vegetable) and Department of Horticulture, College of Agriculture, VNMKV, Parbhani, during the *Kharif* season,2016-17 to identify the diverse genetic stocks for the use in hybridization programme through genetic diversity based on Mahalanobis D2 statistics. The data was recorded on eighteen yield contributing characters on accessions raised in Randomized Block Design in two replications. The germplasm accessions were grouped into five different clusters. The maximum inter-cluster distance was found between clusters IV and V (D=281.31) followed by clusters I and V (D=253.84), clusters I and III (D=228.56), cluster III and IV (D=228.16) and clusters II and IV (D=180.62) indicated that these groups of genotypes were highly divergent from each other. Among the five clusters, the Cluster I recorded high mean performance for five characters viz., Plant height, Number of branches per plant, Fruit weight, Iron content, Fruit yield per plant,. Regarding the grouping of clusters, cluster I has maximum number of entries i.e., 10 genotypes followed by Cluster II with 6 genotypes, Cluster IV with 2 genotypes and Cluster III and Cluster V with one each respectively. The D^2 analysis for eighteen characters partitioned the twenty genotypes into five clusters. The maximum genetic divergence was observed between cluster III and V followed by between clusters I and V. The maximum intra cluster distance was shown by cluster II. The characters number of branches per plant, number of fruits per plant, total number of pickings, fruit weight, fruit length and fruit yield per plant contributed greatly towards diversity. The clusters showing high genetic divergence could be effectively utilized in heterosis breeding programme. If a breeding programme is used at improving growth attributes like plant height, then cluster III showing maximum plant height can be utilized in breeding programme. Therefore, a plant breeder may keep in mind the above aspects to obtain superior hybrids and good recombinants.

Keywords: Okra, divergence, cluster

Introduction

Okra (Abelmoschus esculentus (L.) Moench) India is the largest okra growing country contributing about 72.9 per cent of the world okra production. In India, okra occupies an area of 5.0 million hectares with an annual production of 5.8 million tones accounting to an average productivity of 11.90 metric tons per hectare, contributing 3.9 percent of the total vegetable production. The major okra producing states are Andhra Pradesh, West Bengal, Bihar, Orissa, Gujarat, Jharkhand, Karnataka and Tamil Nadu (Indian Horticulture Database, 2015).

Multivariate analysis is a potent tool in divulging the divergence among the genotypes based on multiple characters. Generalized distance estimated by D² statistic (Mahalanobis, 1936) [8] has been generally used as an efficient tool in the quantitative estimation of genetic diversity for a rational choice of potential parent in a breeding programme. The estimate of direct selection parameters like coefficient of variation, heritability, genetic advance and genetic divergence are useful in formulating suitable selection strategy for higher yield in okra. For creating desirable variability, parents should be selected carefully and some biometrical tools can be used. For assessing the genetic diversity in the germplasm collections, D2 statistics is used which measures the forces of differentiation at intra and inter cluster levels. Above all, the greatest potential of soybean lies in increasing the available food supply for the rapidly increasing population. Precise information on the nature and degree of genetic divergence helps the plant breeder in choosing the diverse parents for hybridization program. The development of new varieties is mainly governed by the magnitude of genetic variability present in the base material. Therefore, in the present investigation, an effort was made to

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understand the quantum and nature of genetic variability present in a set of twenty elite okra accessions using Mahalanobis D2 statistics.

Material and Methods

The experiment was conducted using 20 germplasm accessions of okra in a randomized block design with two replications during *Kharif* 2016-17 at Vegetable Research Farm The field experiment was carried out at Horticulture Research Scheme (Vegetable) and Department of Horticulture, College of Agriculture, VNMKV, Parbhani, during the *Kharif* season, 2016-17. The D2 analysis was carried out for all the eighteen characters to access genetic divergence using Mahalanobis D2 statistics (1936) [8]. The traits included under study were plant height, number of branches per plant, Inter nodal length, days to first flowering, days to 50% flowering, days to first harvest, days to last harvest, fruit length, fruit girth, fruit weight, number of fruit per plant, number of seeds per fruit, fruit yield per plant, 100 seed weight, Total number of picking, Crude fiber content, Iodine content, Iron content.

The genotypes were grouped on the basis of minimum generalized distance using the Tocher's method (Singh and Choudhary 1997) [13]. In this method, the population was arranged in order of their relative distance (D² values) from each other and a table was formed. In the table, the values were arranged in the descending order of magnitude. In the present study, 20 genotypes were grouped into five clusters with the assumption that the genotypes within the cluster have smaller D2 values among themselves than those from groups belonging to different clusters.

After establishing the clusters, the intra cluster distances were worked out by taking average of the component genotypes in that cluster. The average inter cluster distance was arrived at by taking into consideration all the component D² values possible among the members of the two clusters considered.

The square root of the average D² values gave the genetic distance D between clusters. Based on the D values (inter cluster distances), the following scale for rating the distance was adopted (Rao, 1952) [11]. The average intra and inter cluster distances were calculated by the formula given by Singh and Chaudhary (1985) [14].

Ranking was done as per the method outlined by Singh and Choudhary (1997) [13]. Each character is ranked based on the transformed correlated 'Y' values. The relative contribution towards genetic divergence was worked out by using computer software. The character contribution towards genetic divergence was computed using method given by Singh and Chaudhary (1985) [14].

Results and Discussion

Based on D2 statistics and Tocher's method, the 20 germplasm accessions were grouped into five clusters with variable number of entries revealing the presence of variable amount of diversity in the material (Table 1). The cluster I has maximum number of genotypes i.e.,10 followed by cluster II with 6, cluster IV with 2 and clusters III and V with one each respectively (Table 1). The maximum inter cluster distance was found between cluster IV and V (D=281.31) followed by I and V (D=253.84), and clusters I and III (D=228.56), cluster III and IV (D=228.16) and clusters II and IV (D=180.62).The minimum inter cluster distance was observed for clusters IV and V (D=82.90) and cluster II and V (D=135.09). The genotypes belonging to the clusters separated by high

statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates (Table 2). The cluster I consists of the highest number of 10 genotypes. Similar results were recorded by Bendal *et al*. (2003) [2], Dhaduk *et al*. (2004) [3] Kumari and Choudhary (2006) [7], Patel *et al*. (2006) [10], Dhankar *et al*. (2008) [4], and Akothar *et al*. (2010) [1], Shaikh *et al*. (2013) [12]. The cluster III had the highest mean value for plant height, number of branches per plant, fruit weight, fruit yield per plant and iron content and the lowest mean value for crude fiber content and iodine content. Similar results recorded by Bendale *et al*. (2003) [2], Effing *et al*. (2009).

Cluster IV had the highest mean value for inter nodal length, Days to first flowering, Days to 50% flowering, Days to first harvest, Days to last harvest, Fruit length crude fiber content and Number of seeds per fruit Similar results were recorded in okra by Dhaduk *et al*. (2004) [3], Sharma *et al*. (2008) [15], Shaikh *et al*. (2013) [12].

Cluster V had the highest mean value for Number of fruits per plant and lowest mean value in cluster II and Cluster V had the lowest mean value for days to first flowering, Days to 50% flowering(Table No 4).

Hence, apart from selecting genotypes from the clusters which have high inter cluster distance for hybridization, one can also think of selecting parents based on extent of genetic divergence in respect to a particular character of interest. This is to mean that, if breeder's intention is to improve fruit yield, he can select parents which are highly divergent with respect to these characters.
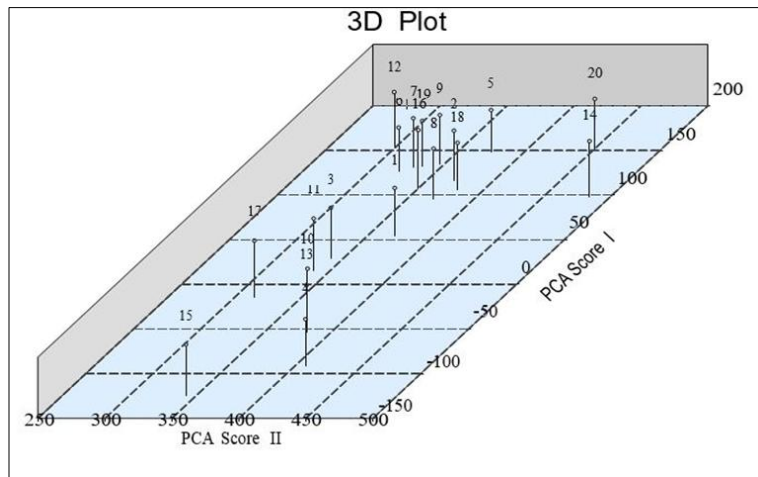
Table 1: Distribution of Okra genotypes in five clusters

Clusters	No. of Genotypes	Name of genotypes
I	10	IC-45804, PBNOK-6, IC-42490, IC-18960, Arka Anamika, PBNOK-1, PBNOK-3, PBNOK-5, IC-10533, IC-10265
II	6	Arka Abhay, Parbhani Kranthi, Pusa Sawani, PBNOK-4, IC-22237, EC-755647
III	1	IC-43743
IV	2	EC-755648, PBNOK-7
V	1	PBNOK-2

Table 2: Average intra (bold) and inter-cluster D2 values for five clusters in twenty genotypes of okra

Clusters	I	II	III	IV	V
I	59.37	141.01	228.56	132.56	253.84
II		75.57	118.52	180.62	135.09
III			0.00	228.16	82.90
IV				67.52	281.31
V					0.00
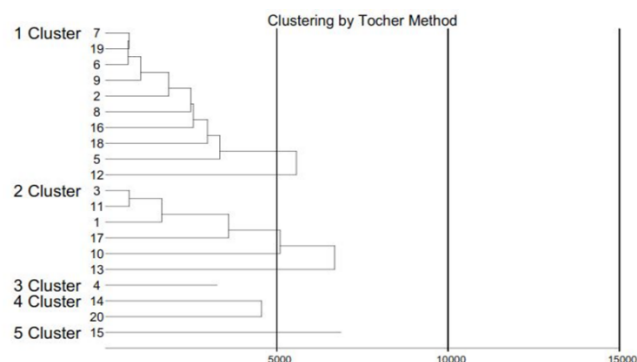
Fig 2: 3 Dimensional Plot showing clustering pattern of okra germplasm

Table 3: Percent contribution of different characters towards diversity in okra genotypes

SI. No.	Characters	Times Ranked 1st	Percent Contribution
1	Plant height	0	0.00 %
2	Number of branches	0	0.00 %
3	Inter nodal length	0	0.00 %
4	Days to first flowering	0	0.00 %
5	Days to 50 % flowering	0	0.00 %
6	Days to first harvest	0	0.00 %
7	Days to last harvest	0	0.00 %
8	Fruit length	0	0.00 %
9	Fruit girth	0	0.00 %
10	Fruit weight	0	0.00 %
11	Number of fruits per plant	0	0.00 %
12	Number of seeds per fruit	1	0.53 %
13	Fruit yield per plant	8	4.21 %
14	100 seed weight	1	0.53 %
15	Number of picking	0	0.00 %
16	Crude fiber content	6	3.16 %
17	Iodine content(mg/100g)	116	61.05 %
18	Iron content(mg/100g)	58	30.53 %

Table 4: Mean contd values of clusters for eighteen characters in twenty okra genotypes of okra

Clusters	Plant height	No. of branches per plant	Inter nodal length	days to first flowering	days to 50% flowering	days to first harvest	days to last harvest	Fruit length (cm)	fruit girth (cm)
I	92.05	3.32	5.81	37.61	42.84	49.77	90.89	15.96	5.61
II	92.49	3.66	5.94	37.96	43.24	48.87	91.86	15.64	5.73
III	108.56	4.60	5.59	37.90	41.20	49.20	91.90	16.25	5.62
IV	103.60	3.90	6.21	47.55	55.45	60.40	103.03	16.60	5.80
V	73.97	3.10	5.40	35.35	40.30	44.70	92.70	14.29	6.28

Table 4: Contd Mean values of clusters for eighteen characters in twenty okra genotypes of okra

Clusters	fruit weight (g)	number of fruit per plant	number of seeds per fruit	fruit yield per plant	100 seed weight	Total number of picking	Crude fiber content (mg/100g)	Iodine content (mg/100g)	Iron content (mg/100g)
I	33.98	8.06	72.98	67.38	5.17	8.25	7.79	73.86	23.77
II	30.38	7.90	76.37	198.44	5.48	8.61	8.28	77.41	23.42
III	42.01	9.40	78.40	300.92	5.35	8.54	5.44	58.63	35.26
IV	21.96	8.73	81.50	79.65	5.13	7.35	10.40	75.84	28.87
V	30.63	10.10	79.50	294.37	5.45	9.60	12.20	69.09	28.43

Relative contribution of the characters to genetic divergence

It was observed that Iodine content contributed maximum (61.05%) towards divergence followed by Iron content (30.53%), fruit yield per plant (4.21%), crude fiber content (3.16%), number of seeds per fruit (0.53%), 100 seed weight (0.53).

The remaining characters *viz.,* plant height, number of branches per plant, inter nodal length, days to first flowering, days to 50% flowering, days to first harvest, days to last harvest, fruit length, fruit girth, fruit weight, number of fruits per plant and number of pickings did not contribute to the total divergence.

In recent times, the D² statistic has found favor as a tool for estimating the genetic divergence for use in plant breeding. In the present study, the D² analysis was utilized to assess the distance between the genotypes, to study the contribution of different characters to diversity, to identify promising genotypes and to initiate a crossing programme in a collection of twenty genotypes for eighteen characters in okra.

The high variability existing among the genotypes was confirmed by the D² analysis, where in the twenty genotypes formed as many as five clusters. Large number of clusters formed indicated that okra is marked by considerable genetic diversity. The clustering of genotypes from same geographical regions in one cluster showed the presence of similar genetic architecture of the genotypes from the same region.

The use of D² statistic is to estimate the relative contribution of various characters to the total genetic divergence. Murthy and Arunachalam (1966) [9] suggested that in Mahalanobis' generalized distance (D²), the relative importance of different characters in relation to their contribution to the total genetic divergence was given by their respective rank totals. This criterion was tested by Jawahar and Panwar (1970) [6] and Vairavan et al. (1973) [16].

In this study, fruit yield per plant, plant height, number of fruits per plant, inter nodal length, days to first flowering, days to 50% flowering, days to first harvest, days to last harvest, fruit length, fruit girth, fruit weight, number of fruits per plant, number of pickings and iodine content contributed for genetic divergence. The variability present for these characters could be exploited for improvement in okra.

Conclusions
Genetic diversity was assessed by using Mahalanobis's D² statistics for eighteen characters. Grouping of genotypes into clusters using Tocher's method resulted in formation of five clusters. The maximum intra-cluster distance was shown by cluster II. The maximum inter cluster distance was observed between cluster IV and V. Therefore, the genotypes belonging to cluster II, III and clusters V may be undertaken in a hybridization programme for getting good sergeants.

Plant height, number of branches per plant, inter nodal length, average fruit weight, fruit girth, fruit length, number of fruits per plant, fruit yield per plant, number of pickings, iron content and iodine content were major contributors to the genetic divergence in the germplasm. The clusters showing high genetic divergence could be effectively utilized in heterosis breeding programme. Therefore, a plant breeder may keep in mind to obtain superior hybrids and good recombinants.

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