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Research Article

D^2 analysis for assessing genetic diversity in okra (*Abelmoschus esculentus* (L) Moench)

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Abstract
Genetic divergence analysis following Mahalanobis D^2 statistics revealed considerable genetic diversity among 46 genotypes of Okra (*Abelmoschus esculentus* (L) Moench) for all the fourteen quantitative characters pertaining to growth, earliness and yield. Forty six genotypes were grouped into five distinct clusters depending up on the similarities of their D^2 values following Tocher's method. The germplasm collected from same place scatted in to different clusters indicating genetic diversity not parallel with geographical diversity. Appreciable diversity within and between five clusters was observed. The traits *viz.,* yield per plot (36.45%), plant height (26.27%), number of seeds per plant (16.83%), number of fruits per plant (6.47%) and yield per plant (4. 53%) were the potent factors in differentiating the germplasm of okra under study. The use of diverse genotypes from the clusters with high inter cluster distance (clusters IV and V, III and IV, I and IV and II and IV) in hybridization is expected to result in high heterosis and throw desirable transgressive segregants.

Key words: Okra, Mahalanobis D^2 analysis, Cluster, Diversity

INTRODUCTION

Okra (*Abelmoschus esculentus* (L) Moench) is also known as bhendi and lady's finger. Okra is an economically important traditional vegetable crop, grown in tropical and subtropical part of the world. Though okra is native of tropical Africa, India is the leading producer in the world. The potential and worth of germplasm depend on the number of collections and their variability (Ren *et al.,* 1995). Information on the genetic divergence among the genotypes is important for pedigree as well as heterosis breeding programmes. Mahalanobis D^2 statistics technique, which is based on the multivariate analysis of quantitative traits, is a powerful tool for measuring genetic divergence. The difference within and between the species are the foundation for any crop improvement programme. In a population, if all the individuals are similar, then no chance for improvement in plant performance for various traits. Since the successful plant breeding start with variability between the crops have been extensively identified and used in the improvement of crop species. The degree of genetic diversity is worked out in a population based on the characters taken into account for the study. Genetically divergent population falls into different groups on clustering, thus enabling selection of parent for hybridization and pedigree breeding programme for development of superior okra variety with diverse climatic adaptation.

MATERIALS AND METHODS

The present investigation was conducted at Adiparasakthi Agricultural College Farm, Kalavai, Vellore district of north eastern Tamil Nadu located at 12º 77' north latitude, 79º42'east longitudes and at an altitude of 147 m above mean sea level (MSL). The experimental material comprised of 46 okra diverse genotypes representing different geographical origins and pure seeds of these genotypes were procured from different breeding

institutes across the world and evaluated in Randomized Block Design (RBD) with two replications (**Table 1**). The data for different characters were recorded for each replication selecting five random plants and mean values of each genotype for fourteen different characters were used for statistical analysis. Grouping of the genotypes into different clusters was done by using Tocher's method (Rao, 1952). The criterion used in clustering is the genotypes belonging to a single cluster have smaller D^2 values and belonging to different cluster have larger D^2 values. Average intra cluster distance was calculated by using formula and inter cluster distance was calculated by estimating distance between clusters 1 and II, I and III, I and IV likewise for all the clusters.

RESULTS AND DISCUSSION

The analysis of variance showed significant difference for most of the characters indicating the presence of a wide range of variability among the genotypes. Based on this knowledge one can go for further diversity study. Mahalonobis's D^2 was calculated for all possible pairs of forty six okra genotypes and genetic diversity was assessed. Forty six genotypes were placed into five different clusters (**Table 2**). Clusters V was the largest cluster comprised for 31 genotypes followed by cluster I (7 genotypes), cluster IV (4 genotypes) and clusters II and III were consisted of two genotypes each.

The average intra cluster distance ranged from 39.31 to 823.87 (**Table 3**). Maximum intra cluster distance was observed in cluster IV (823.87) followed by cluster I (729.58), cluster V (616.61) and cluster III (42.23). The minimum intra cluster distance was found in cluster II (39.31). Cluster IV followed by cluster I had the maximum intra-cluster distance indicating that genotypes in these clusters were more divergent than any other cluster. Inter cluster distance was maximum between IV and V (2282.81) followed by III and IV (2082.69), I and IV (1970.01) and II and IV (1735.21), while minimum distance was exhibited by cluster II and III (88.25). The highest inter cluster distance is observed between IV and V cluster followed by I and IV. Hence, the genotypes belonging to these clusters were also highly divergent and the parent could be selected from these clusters for crossing programme to obtain superior F_1 hybrids and segregants (Bandabe *et al.,* 2003; Dhanduk *et al*,

Table 1. List of genotypes used in the study

Genotypes	Source
EC- 755647, EC- 755648, EC- 755649, EC- 755650, EC- 755651, EC- 755653, EC- 755654	AVRDC, Taiwan
IC- 90221, IC- 9049, IC- 90004, IC- 99646, IC-52303, IC- 99709, IC- 11321, IC- 33332, IC- 755652, IC- 90210, IC- 1128065, IC- 128036, IC- 128037, IC- 11319 (S), IC- 90212, IC- 52305, IC- 90170, IC- 90169, IC- 128071, IC- 117095, IC- 43023 (S), IC- 111515, IC- 111551, IC- 117116, IC- 111520	NBPGR, New Delhi
Akola bhar	Dr. PDKV, Akola, Maharashtra.
Arka Anamika, Arka Abhay	IIHR, Hessargatta, Bangalore.
Pusa Sawani, Pusa A4	IARI, New Delhi.
Parbhani Kranti	MKV, Parbhani, Maharashtra.
Varsha Uphar	HAU, Hisar.
Prerana, Kamini	Collected from Kerala (local)
VRO-6, VRO-22	IIVR, Varanasi
LOCAL-1, 2, 3	Dharmapuri (local)

Table 2. Clustering pattern of 46 genotypes of okra

Clusters	Number of genotypes	Genotypes
I	7	EC- 755647, EC- 755648, EC- 755649, EC- 755650, EC- 755651, IC- 11319 (S), IC- 117095
II	2	IC- 128071, PUSA A4
III	2	IC- 99709, Varsha Uphar
IV	4	EC- 755653, EC- 755654, IC- 111515, VRO-22
V	31	IC- 90221, IC- 9049, IC- 90004, IC- 99646, IC- 52303, IC- 11321, IC- 33332, IC- 755652, IC- 90210, IC- 1128065, IC- 128036, IC- 128037, IC- 90212, IC- 52305, IC- 90170, IC- 90169, IC- 43023 (S), IC- 111551, IC- 117116, IC- 111520, Akola Bhar, Arka Anamika, Arka Abhey, Pusa Sawamni, Parbhani Kranti, Prerana, km Kamini, VRO-6, LOCAL-1, LOCAL-2, LOCAL-3

Table 3. Intra and inter cluster D^2 values and distance (D) values in the bracket

Cluster	I	II	III	IV	V
I	27.01 (729.58)	23.85 (539.85)	24.26 (588.69)	44.39 (1970.01)	29.22 (853.56)
II		6.27 (39.31)	9.39 (88.25)	41.66 (1735.21)	18.62 (346.62)
III			6.49 (42.13)	45.64 (2082.69)	18.35 (336.82)
IV				28.70 (823.87)	47.78 (2282.81)
V					24.83 (616.61)

Table 4. Cluster mean for 14 characters in okra

S.No.	Traits	I	II	III	IV	V
1	Days to first flowering	41.86	44.75**	42.75	38.38*	42.63
2	Node at which first flowering	4.24	4.03	4.56**	3.24*	4.26
3	Days to 50 % flowering	61.14	61.25	61.25	56.75*	61.89**
4	Plant height (cm)	66.77	60.46	56.58	88.43**	55.60*
5	Intermodal length (cm)	7.61	7.11	7.00	9.46**	6.70*
6	Number of branches per plant	2.99	2.81	1.88*	6.64**	2.32
7	Fruit length (cm)	13.32*	14.41	14.16	15.85**	13.41
8	Fruit girth (cm)	5.59	5.37*	5.72	6.19**	5.76
9	Number of ridges per fruit	5.80**	5.40	5.10*	5.50	5.44
10	Number of fruits per plant	13.90*	15.45	14.90	18.45**	15.26
11	Number of seeds per fruit	69.59**	48.80	53.05	49.43*	52.19
12	Individual fruit weight(g)	12.80	11.57*	16.33	17.76**	13.94
13	Yield per plant (g)	182.43	178.57*	243.27	328.14**	214.85
14	Yield per plot (kg)	2.37	2.32*	3.16	4.27**	2.79

2004; Hazara *et al*., 2005). The inter cluster distance was found to be high between cluster IV and V. Hence, it could be expected that the cross combinations involving the parents from each of these clusters would produce maximum heterosis and also the chances for isolating superior or transgressive segregants in an advanced generation. The inter cluster distance was greater than intra clusters distance revealing a considerable amount of genetic diversity among the genotypes studied. This is in accordance with the findings of Patel *et al.* (2006). Selection of genotypes based on large intra cluster and inter cluster distance for hybridization can offer to get a useful combination of trait for improvement of okra varieties.

The character wise analysis was conducted for five clusters (**Table 4**). The mean of clusters for all the characters were found significant. It is obvious that different clusters exhibited distinct mean values for almost all the fourteen characters. Cluster 1 exhibited the lowest mean values for fruit length (13.32 cm) and number of fruits per plant (13.90) and maximum value for number of ridges per fruit (5.80) and number of seeds per fruit (69.59). Cluster II possessed the highest mean values for days to first flowering (44.75) and lowest mean value for fruit girth (5.37 cm), individual fruit weight (11.57 g), yield per plant (178.57 g) and yield per plot (2.32 kg). Cluster III showed the lowest mean for number of branches per plant (1.88), number of ridges per fruit (5.10) and it had the highest mean value for node at which first flowering (4.56). Cluster IV showed the highest mean value for plant height (88.43), inter nodal length (9.46), number of branches per plant (6.64), fruit length (15.85 cm), fruit girth (6.19 cm), number of fruits per plant (18.45), individual fruit weight (17.76 g), yield per plant (328.14 g) and yield per plot (4.27 kg). Whereas, it showed the lowest mean value for days to first flowering (38.38), node at which first flowering (3.24), days to 50% flowering (56.75) and number of seeds per fruit (49.43).

Table 5. Relative contribution of different characters to genetic diversity in okra

S.No.	Traits	Number of first rank	Per cent contribution
1	Days to first flowering	0	0.00
2	Node at which first flowering	0	0.00
3	Days to 50 % flowering	0	0.00
4	Plant height	284	26.27
5	Intermodal length	14	1.31
6	Number of branches per plant	1	0.08
7	Fruit length	27	2.50
8	Fruit girth	0	0.00
9	Number of ridges per fruit	20	1.85
10	Number of fruits per plant	70	6.48
11	Number of seeds per fruit	182	16.84
12	Individual fruit weight	40	3.70
13	Yield per plant	49	4.53
14	Yield per plot	394	36.44
	Total	**1081**	**100**

Cluster V exhibited the maximum mean value for days to 50% flowering (61.89) and the lowest mean value for plant height (55.60 cm) and intermodal length (6.70 cm). Based on the *per se* performance and D^2 value, the parents could be selected. The line EC-755648 was selected based on *per se* performance of the number of seeds per fruit and the lines EC755653, EC 755654, IC-755652 and IC111515 were selected based on the genetic D^2 divergence which can be used as the female parent. A broad genetic base with notified varieties should be selected as male parents for crossing programme.

The relative contribution of each character towards genetic divergence was estimated (**Table 5**). The character, the plant height contributed the maximum percentage of 26.27 per cent towards genetic divergence followed by number of seeds per fruit (16.84 %), number of fruits per plant (6.48 %), yield per plant (4.53%), individual fruit weight (3.70 %), fruit length (2.50%), number of ridges per fruit (1.85 %) and inter nodal length (1.31.%) per cent. Similar results were also made by Kumari and Chaudhury (2006), Patel *et al*. (2006), Pradip *et al*. (2010) and Reddy *et al*. (2012). The trait, number of branches per plant had contributed very minimum divergence of 0.09%. The traits days to first flowering, days to 50% flowering, node at which first flowering and fruit girth were not contributed towards genetic divergence in the present study.

Genotypes collected from the same location were grouped into different clusters and the cultivar collected from different place grouped into single cluster. Hence, geographical diversity, though appears as an important factor, it seems that it is not only the factor determining the genetic divergence but also be indicates that factors other than geographical diversity may also responsible for such grouping. A similar result of non-association of geographic origin with genetic diversity was also reported by Balai *et al.* (2015). Therefore the selection of parents for breeding should be based on genetic divergence rather than geographical diversity.

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