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ANALYSIS OF GENETIC DIVERGENCE IN OKRA [*ABELMOSCHUS ESCULENTUS* (L.) MOENCH]

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ABSTRACT

The present investigation was carried out at College of Agriculture, UAHS, Shivamogga during kharif 2014. In this study 49 genotypes were grouped into eight clusters based on D^2 values. The minimum diversity was within the clusters and maximum diversity is between the clusters were noticed. Cluster I was the biggest with 35 genotypes followed by the cluster IV, VI and remaining clusters are solitary. The distance among the genotypes values ranges from 108.00 to 1360.74. The intra cluster D^2 values exhibited a range of 120.00 to 253.95 and inter cluster D^2 values ranged from 108.00 to 1360.74. The highest contribution to diversity was recorded by fruit diameter followed by number of flowering nodes on main stem, number of branches per plant and fruit yield per plant.

INTRODUCTION

Okra [*Abelmoschus esculentus* (L.) Moench, $2n = 8X = 56-200$] is commonly known as Lady's finger in English, Bhendi in Hindi, Gombuo in French and Bamiah in Arabic. Even within India different names have been given in different regional languages. It is one of the economically important fruit vegetable crop mainly grown in tropical, subtropical and warm sections of temperate regions of world (Charrier, 1984). It is native to tropical and subtropical Africa (Chevalier, 1940) and also to India (Yawalker, 1969).

The world okra production was 83.59 lakh tonnes and India ranks first with 60.00 lakh tonnes (72 per cent) of production from over 5.00 lakh ha (Anon., 2012). Multivariate analysis is a potential tool for measuring divergence among a set of populations based on multiple characters. D^2 statistic proposed by Mahalanobis (1936) 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.

Keeping in view the above facts present investigation was undertaken to its precision and versatility with an objective to study of genetic diversity in 49 genotypes of okra based on thirteen important traits, to help the breeders in selecting promising and genetically diverse parents for desired improvement.

MATERIALS AND METHODS

The present investigation was carried out at Department of Genetics and Plant Breeding, College of Agriculture, UAHS, Shivamogga during kharif 2014. The experimental material composed of 49 Okra genotypes collected from IIHR (Bangalore) and NBPGR Regional Research Station Akola and locally available landraces. The experiment was laid out in simple lattice design with two replication. Every genotype in each replication was grown in two rows of each was 4 m with a spacing of 60 cm between rows and 30 cm between plants. The seeds were hand-dibbled at given spacing in the respective blocks and recommended agronomic practices were followed to raise the crop. Observations were recorded on 13 quantitative traits. Mean across two replications were calculated for each traits and the analysis of variation was carried out. Multivariate analysis was done utilizing Mahalanobis D^2 statistic (Mahalanobis, 1936) and genotypes were grouped into different clusters following Tocher's method.

RESULTS AND DISCUSSION

Based on D^2 values the genotypes were grouped into eight clusters (Table 1 and Fig. 1) using Tocher's method given by Rao (1952). The cluster divergence was proved by the high inter-cluster and low intracluster D^2 values.

There were 35 genotypes in cluster I, 5 genotypes in cluster IV, 4 genotypes in cluster VI and remaining clusters II, III, V, VII and VIII are solitary. The solitary clusters may be due to total isolation preventing the formation of gene flow or natural or human selection for diverse adaptive complexes. In general, the genotypes

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Table 1: Clustering pattern of 49 genotypes in Okra based on D² analysis.

Sl. No.	Clusters	No. of genotype	Name of genotype
1	I	35	IC43732, VRO-103, Kashi Kiranthi, IC 45818, IC 45980, IC 43587, Arka Anamika, IC42530, IC 90243, Kashi Sathadhari, IC18536, EC 693227, SB-2, IC 90247, HRB-55, Punjab Padmini, IC 42518, 307-10-1, IC 90246, Kashi Leela, BCO-1, Kashi Birathi, IC90284, IC 90285, S-11, IC 90245, IC 96230, Parbhani Kranthi, ZARS, Varsha Uphar, VRO-106, Phule Utkashi, IC 90242, Pusa Makhmali, IC 13664
2	II	1	Kashi Mangala
3	III	1	IC 90270
4	IV	5	IC 90235, IC 90234, IC 90244, EC 693222, EC 693226
5	V	1	VRO- 109
6	VI	4	No. 135, VROB- 178, EC 693224, IC 43720
7	VII	1	Navin
8	VIII	1	IC 43735

Table 2: Average intra and inter cluster D² values of clusters in Okra

	I	II	III	IV	V	VI	VII	VIII
I	120.40	190.58	257.50	257.25	190.03	350.64	331.32	718.32
II		0.00	223.92	256.15	108.00	470.96	296.63	536.91
III			0.00	112.30	283.30	352.27	528.00	387.62
IV				155.15	348.97	502.46	653.58	351.59
V					0.00	365.05	149.89	830.68
VI						253.95	395.69	1144.82
VII							0.00	1360.74
VIII								0.00

*Diagonal values indicate intra cluster distances; *above diagonal values indicate inter cluster distances

grouped together in one cluster are less divergent than those which are placed in a different cluster.

Inter cluster distance

The inter cluster D² values are given in Table 2 and Fig. 2. The inter cluster D² value was maximum (1360.74) between cluster VII and VIII followed by between cluster VI and VIII with high D² value of 1144.82. The minimum inter cluster distance observed was 108.00 between cluster II and V which indicate close relationship among the genotypes involved. Cluster VIII was the most diverse as many clusters showed a maximum inter cluster distances with it followed by cluster VII.

Cluster IV was most diverse as many genotypes showed maximum intra cluster distance with it indicated that there is good scope for selection within the cluster for hybridization. In general, it can be stated that the clusters separated by largest genetic distances, which reflect maximum divergence includes cluster VII and VIII. Hence, it is preferable to select genotypes from these clusters as potent parents in crossing programme to obtain desirable segregants. Average inter and intra cluster distances revealed that, in general, inter cluster distances were much higher than those of intra cluster distances, suggesting heterogeneous and homogeneous nature of the germplasm lines between and within the clusters respectively.

Intra cluster distance

The intra cluster D² values are given in Table 2 and Fig. 2. The intra cluster distance was observed only in cluster I, IV and VI as remaining five clusters II, III, V, VII and VIII contained only one genotype each. Intra cluster distance was highest in cluster VI (253.95) followed by cluster IV (155.15) and cluster I (120.40). Further, higher intra cluster distance indicates high degree of divergence within that cluster. This indicates the

presence of divergent genotypes within these clusters. However, in solitary clusters intra cluster distance was nil as they are composed of single genotype each. The genotypes in these solitary clusters being diverge from others may serve as potential parents for breeding programmes. They indicate their independent identity and importance due to various unique characters possessed by them. While, other clusters showed low to moderate in intra cluster indicating their independent identity and importance due to unique characters possessed by them. Several authors also reported profound diversity in the germplasm of tomato by assessing genetic divergence on the basis of quantitative traits following Mahalanobis D² statistics (Daduk *et al.*, 2004, Hazra *et al.*, 2002 and Prakash *et al.*, 2011).

Cluster mean analysis

Cluster mean is presented in Table 3. The mean comparison of the different characters indicated considerable differences among the clusters for all the characters. Maximum mean for days to 50 per cent flowering (45.00) was observed in cluster III while, minimum cluster mean of 42.50 observed in cluster II and VIII. The highest mean for plant height was recorded in cluster II (141.36 cm) while, lowest mean of 46.95 cm was shown by cluster VI.

The highest mean for inter-nodal length was recorded in cluster VIII (15.13 cm) while, lowest mean of 5.09 cm was shown by cluster VII. First flowering node recorded a maximum mean in cluster V of 4.90 and minimum mean of 3.20 was observed in cluster II. The number of branches had a highest mean of 2.50 in cluster III and lowest for genotypes under cluster VII (1.10).

The cluster mean observed in number flowering node on main stem was highest for cluster V (16.80) and it was lowest in

Table 3: Cluster mean analysis of different genotypes for 13 quantitative characters in Okra

Clusters No. of geno types	Days to 50 % flowering	Plant height (cm)	Inter-nodal length (cm)	First flowering node	No. of flowering branches per plant	No. of flowering nodes on main stem	Stem diameter (cm)	Days to 80 per cent maturity	Fruit length (cm)	Fruit diameter (cm)	No. of fruits per plant	Average weight of fruit (g)	Fruit yield per plant (g)	Cluster score	Cluster rank
I	42.70(6)	86.55(4)	9.46(5)	4.11(2)	1.91(6)	10.00(5)	1.45(5)	58.61(6)	12.86(5)	1.66(7)	15.52(4)	20.60(3)	313.15(5)	63	V
II	42.50(7)	141.36(1)	10.33(3)	3.20(8)	2.40(3)	14.55(3)	1.75(1)	57.50(8)	13.60(2)	1.89(3)	21.00(3)	18.77(6)	393.93(1)	49	II
III	45.00(1)	53.30(7)	7.04(6)	4.00(4)	2.50(1)	9.10(6)	1.38(7)	61.00(2)	9.00(7)	1.80(4)	13.70(8)	19.19(5)	262.90(8)	66	VI
IV	44.00(4)	71.24(6)	9.78(4)	3.84(6)	2.46(2)	8.00(7)	1.51(3)	59.80(4)	10.91(6)	1.97(2)	15.32(5)	20.42(4)	291.22(6)	59	III
V	43.00(5)	120.88(2)	11.07(2)	4.90(1)	2.27(4)	16.80(1)	1.46(4)	59.00(5)	14.24(1)	1.77(6)	22.70(1)	16.99(7)	385.70(2)	41	I
VI	44.88(2)	46.95(8)	5.27(7)	3.70(7)	1.91(6)	10.89(4)	1.42(6)	62.13(1)	12.87(4)	1.79(5)	14.50(7)	25.42(1)	359.79(3)	61	IV
VII	44.50(3)	79.05(5)	5.09(8)	4.10(3)	1.10(7)	15.10(2)	1.36(8)	60.50(3)	13.27(3)	1.44(8)	21.40(2)	13.06(8)	279.50(7)	67	VII
VIII	42.50(7)	109.45(3)	15.13(1)	3.90(5)	2.00(5)	7.90(8)	1.72(2)	58.50(7)	6.92(8)	2.52(1)	14.60(6)	22.27(2)	325.00(4)	59	III

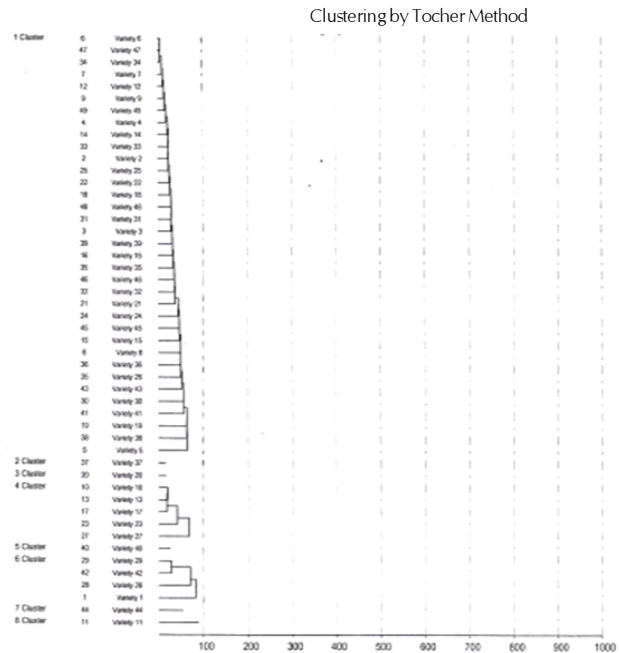


Figure 1: Clustering pattern of 49 Okra genotypes drawn according to Tocher method

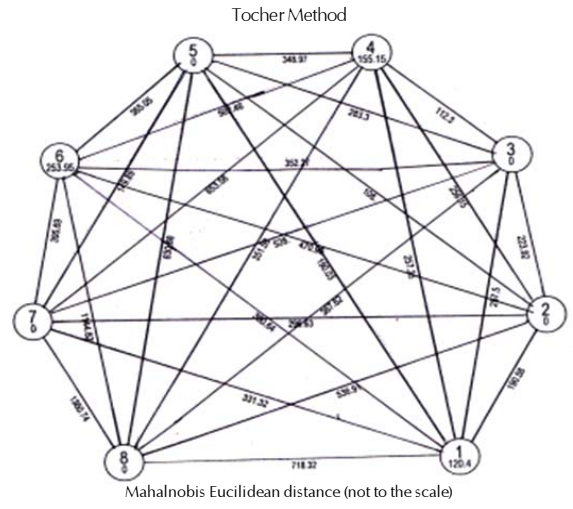


Figure 2: Intra and inter cluster distances among eight clusters of Okra genotypes

cluster VIII (7.90). The cluster mean of stem diameter was recorded highest for cluster II (1.75 cm) and it was lowest for genotypes under cluster VII (1.36 cm). Cluster VI had a maximum mean of 62.13 for days to 80 per cent maturity and cluster II recorded minimum mean of 57.60.

Fruit length recorded maximum mean in cluster V (14.24 cm) and minimum mean of 6.92 cm in cluster VIII. The cluster mean for fruit diameter was highest for cluster VIII (2.52 cm) followed by cluster IV (1.96 cm) and it was lowest for genotypes under cluster VII (1.44 cm).

Cluster V with one genotype recorded maximum cluster mean of 22.70 for the trait number of fruits per plant followed by cluster VII (21.40) and minimum cluster mean was recorded

Table 4: per cent contribution of yield and yield related characters towards divergence in Okra

Sl. No.	Character	Contribution (in per cent)
1	Fruit diameter (cm)	25.00
2	No. of flowering nodes on main stem	13.78
3	No. of branches per plant	10.20
4	Fruit yield per plant (g)	9.44
5	Inter-nodal length (cm)	9.27
6	Days to 80 per cent maturity	7.57
7	Fruit length (cm)	6.04
8	Plant height (cm)	5.87
9	No. of fruits per plant	5.70
10	First flowering node	3.49
11	Average weight of fruit (g)	3.49
12	Stem diameter (cm)	0.17
13	Days to 50 per cent flowering	0.00

for cluster III (13.70). The highest mean for average weight of fruit was recorded in cluster VI (25.42 g) followed by cluster VIII (22.27 g), while lowest mean of 13.06 g was shown by cluster VII. The cluster mean observed for fruit yield per plant was highest for cluster II (393.93 g) followed by cluster V (385.70 g) and it was lowest for genotypes under cluster III (262.90 g).

Cluster V with one genotype secured first rank with overall score of 41 across 13 characters and cluster VII obtained 7th rank with overall score of 67.

Out of 13 characters studied, fruit diameter contributed maximum to divergence (25.00 %) (Table 4). Number of flowering nodes on main stem contributed maximum to the diversity (13.78 %) followed by number of branches per plant (10.20 %), fruit yield per plant (9.44 %), inter-nodal length (9.27 %), days to 80 per cent maturity (7.57 %), length of fruit (6.04 %), plant height (5.87 %), number of fruits per plant

(5.70 %), first flowering node (3.49 %), average weight of fruit (3.49 %), stem diameter (0.17 %). Days to 50 per cent flowering contributed negligible amount to divergence.

This confirms the existence of ample amount of divergence in the genotypes with respect to above traits and hence selection of best genotypes for such traits will be helpful in utilizing maximum heterosis in the breeding programme.

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