



STUDIES ON CHOICE OF PARENTS AND TRAITS FOR FRUIT YIELD IMPROVEMENT THROUGH BREEDING IN OKRA (*ABELMOSCHUS ESCULENTUS* (L.) MOENCH)

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Abstract

An experiment was conducted with fifty eight genotypes to assess the genetic divergence for ten quantitative characters. Analysis of variance indicated the existence of large differences among the genotypes for all the traits of interest. Fifty eight genotypes were grouped into as many as nine distinct clusters based on the D^2 value. Cluster I had maximum number of genotypes (25), followed by, cluster IV and VI (09 genotypes), cluster VII (05 genotypes), cluster III (03 genotypes), cluster II, V and VIII each possessed two genotypes. The intra-cluster distance was maximum with cluster VII. The genotypes grouped in this cluster may also be different genetically. On other hand, the genotypes grouped in the cluster X may be similar for the traits of interest, as it evinced minimum D^2 value. The inter-cluster distance was maximum between the clusters IX and cluster V. The genotypes gathered in these clusters might be different genetically. They may be inter-crossed to evolve high yielding hybrids and/or segregants. Fruit yield per plant registered maximum (49.00) contribution towards the total genetic divergence.

Keywords: Okra, fruit yield, genetic divergence, D^2 .

Introduction

Okra (*Ablemoschus esculentus* (L.) Moench) ($2n=130$) is one of the most important vegetable crop grown for its tender green fruits throughout India. It is native of Tropical Africa. It is commonly known as Bhendi or lady's finger and okra in India. Okra is amphidiploid in nature (Joshi and Hardas, 1956). It belongs to the family Malvaceae and is an often-cross pollinated crop, due to protogyny. Occurrence of out crossing up to an extent of 50-20 percent has been recorded with the insect assisted pollination (Ramgiry and Singh, 2017).

Importance of genetic diversity for selecting parents in breeding programme of different crop to recover high yielding hybrids and/or transgressive segregants has been emphasized by Singh and Ramanujam (1981), Cox and Murphy (1990). Mahalanobis' D^2 statistic appears to be a fruitful approach to quantify genetic distance, which is

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based on multivariate analysis and serves to be a good index of genetic diversity. This technique, therefore, deserves to be tested on a wide range of crops.

Multivariate analysis following Mahalanobis' D^2 statistic revealed rich genetic diversity for various growth, earliness and yield associated traits in the germplasm offering a great scope for improvement of okra (Ghai *et al.*, 2005, Mamta and Choudhury, 2006, Singh *et al.*, 2007). The existing diversity has been exploited in various breeding programme, which resulted in the development and release of a good number of varieties in okra. The present inquiry as was made to certain the genetic diversity among 58 genotypes, obtained from NPBGR, New Delhi.

Materials and Methods

Fifty eight genotypes of diverse were grown in on Randomized Block Design with three replications, with a spacing of 45× 30 cm in two row plots of 4.5 m length.

The experiment was conducted Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, during 2018. The genotypes were collected from National Bureau of Plant Genetic Resources (NBPGR) New Delhi. Observations were recorded on five randomly selected plants per entry, per replication on 10 agronomic *viz.*, days to first flowering, plant height at maturity (cm), number of nodes to first fruiting, days to first fruit harvest, number of branches per plant, number of fruits per plant, average fruit weight (g), fruit length (cm), fruit girth (cm) and fruit yield per plant (g). Recommended agronomic practices and need based plant protection measures were judiciously followed. Multivariate analysis (D^2) was carried out by adopting Mahalanobis' D^2 statistic. Grouping of genotypes into different cluster was carried out following Tocher's method (Rao, 1952). The relative contribution of different traits towards total genetic divergence was calculated as per Singh and Choudary (1985). The statistical analysis have done with Indo Statistical Package, licensed at NRRI, Cuttack, Orissa, India.

Results and Discussion

The analysis of variance indicated significant variation among the fifty eight okra genotypes for all the traits of interest. This suggested that large variability existed among the genotype and further analysis is appropriate.

On the basis of D^2 analysis, fifty eight genotypes were grouped into as many as nine clusters (Table 1). A maximum number of 25 genotypes were grouped in cluster I (TCR 149-IC45813, TCR 157-IC45821, TCR 159-IC45823, TCR 160-IC45824, TCR 164-IC4528, TCR 167-1-IC45831-1, TCR 114-IC45838, TCR 208-IC45881, TCR 232-IC69113, TCR 291-IC69172, TCR 330-IC6924,

TCR 338B-IC45802B, TCR 351-IC69232, TCR 360-IC69242, TCR 367-IC248, TCR 373-IC69254, TCR 376-IC69257, TCR 377-IC69258, TCR 380-IC69261, TCR 382-IC69263, TCR 429-IC69290, TCR 422-IC69303, TCR 423-IC69304, TCR 605-IC72082, TCR 960-IC28222 where as clusters IV and VI each included nine genotype (TCR 767-IC282226, TCR 769-IC282227, TCR 771-IC282209, TCR 772-IC282230, TCR 780-IC282232, TCR 834-218886, TCR 837-IC282243, TCR 906-IC21800, TCR 998-IC282263) and (TCR 931-IC282275, TCR 964-IC282284, TCR 999-IC282264, TCR 1002-IC282266, TCR 1248-IC140897, TCR 1452-218903, TCR 1485-IC218904, TCR 2145-IC117202, TCR 2306-IC205147). The cluster VII had five genotypes (Akra Anamika (Selection 10), Ankur 40*, Hisar Unnat (HRB 55), Varsha Uphar (HRB 9-2), Pusa A₄). Cluster III had (TCR 616-IC72093, TCR 908-IC111466, TCR 970-IC282286) three genotypes. The cluster II, V and VII, each had two genotypes (TCR 937-IC282278, TCR 845-IC282248), (TCR 1000-IC282265, TCR 1250-IC140898) and (Parbhani Kranti, P 7*) cluster IX was monogenotypic. (Punjab Padmini Ludhiana selection-1).

The estimates of intra-cluster and inter-cluster D^2 and D value are presented in table 2. The intra-cluster distance was maximum with the cluster VII (44.25). The genotypes grouped in this cluster may also be different genetically. On other hand, the genotypes grouped in the cluster IX may be similar for the traits of interest, as it registered minimum D^2 value. The inter-cluster distance was maximum between the clusters IX and cluster V. The genotypes gathered in these clusters might be different genetically. They may be inter-crossed to evolve high yielding heterotic hybrids and/or superior recombinants (segregants).

Table 1: Composition of clusters.

Clusters	Number of genotypes	Name of genotype
I	25	TCR 149-IC-45813, TCR 157-IC-45821, TCR 159-IC45823, TCR 160-IC45824, TCR 164-IC4528, TCR 167-1-IC45831-1, TCR 114-IC45838, TCR 208-IC45881, TCR 232-IC69113, TCR 291-IC69172, TCR 330-IC6924, TCR 338B-IC45802B, TCR 351-IC69232, TCR 360-IC69242, TCR 367-IC248, TCR 373-IC69254, TCR 376-IC69257, TCR 377-IC69258, TCR 380-IC69261, TCR 382-IC69263, TCR 429-IC69290, TCR 422-IC69303, TCR 423-IC69304, TCR 605-IC72082, TCR 960-IC282283.
II	2	TCR 937-IC282278, TCR 845-IC282248
III	3	TCR 616-IC72093, TCR 908-IC111466, TCR 970-IC282286
IV	9	TCR 767-IC282226, TCR 769-IC282227, TCR 771-IC282209, TCR 772-IC282230, TCR 780-IC282232, TCR 834-218886, TCR 837-IC282243, TCR 906-IC21800, TCR 998-IC282263
V	2	TCR 1000-IC282265, TCR 1250-IC140898
VI	9	TCR 931-IC282275, TCR 964-IC282284, TCR 999-IC282264, TCR 1002-IC282266, TCR 1248-IC140897, TCR 1452-218903, TCR 1485-IC218904, TCR 2145-IC117202, TCR 2306-IC205147
VII	5	Akra Anamika (Selection 10), Ankur 40*, Hisar Unnat (HRB 55), Varsha Uphar (HRB 9-2), Pusa A ₄
VIII	2	Parbhani Kranti, P 7*
IX	1	Punjab Padmini (Ludhiana selection – 1)

Table 2: Intra-cluster and Inter-cluster distances (D^2 values) of bhendi genotypes.

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	(1030.09) (32.10)	(1776.26) (42.15)	(1411.59) (37.57)	(1061.15) (32.58)	(1034.26) (32.16)	(1154.54) (33.98)	(3675.68) (60.63)	(2690.44) (51.87)	(4948.10) (70.34)
II		(73.78) (8.59)	(3271.12) (57.19)	(897.710) (29.96)	(575.10) (23.98)	(2620.24) (51.19)	(1510.49) (38.87)	(2546.70) (50.47)	(1222.48) (34.96)
III			(1489.21) (38.59)	(1886.19) (43.430)	(1887.99) (43.45)	(1147.87) (33.88)	(6003.43) (77.48)	(3650.90) (60.42)	(7582.95) (87.08)
IV				(816.19) (28.57)	(557.21) (23.61)	(1504.28) (38.79)	(2766.83) (52.60)	(2700.84) (51.97)	(3461.70) (58.84)
V					(214.05) (14.63)	(1560.35) (39.50)	(2888.79) (53.75)	(3272.86) (57.21)	(3229.86) (56.83)
VI						(1185.22) (34.43)	(4741.65) (36.25)	(2936.64) (54.19)	(2936.64) (79.70)
VII							(1313.69) (36.25)	(2630.65) (51.29)	(1320.09) (36.33)
VIII								(1957.87) (44.25)	(3631.31) (60.26)
IX									(0.000) (0.000)

Cluster mean indicated the variation for the quantitative traits among the clusters (Table 4). Cluster VIII recorded the minimum number of days to first flowering (38.97) followed by cluster IX (41.05) and cluster III (41.57). Cluster VII (115.99) recorded the minimum Plant height at maturity followed by cluster VI (116.02) and cluster VIII (120.22). Cluster V (3.11) recorded minimum number of nodes to first fruiting followed by cluster II (3.21) and cluster IX (3.27). Cluster IX (50.47) recorded minimum days to first fruit harvest, followed by cluster V (51.15) and cluster VII (51.59). Cluster IX (3.77) registered maximum number of branches per plant followed by cluster II (3.22) and cluster VIII (3.10). Cluster IX (22.80) recorded maximum number of fruits per plant followed by cluster VI (21.82) and cluster VII (21.57). Cluster I (19.13) recorded maximum average fruit weight which was followed by

cluster V (19.14) and cluster IX (18.63). Cluster IX (19.04) had maximum fruit length followed by cluster II (16.77) and cluster V (15.23). Cluster V (3.33) recorded the minimum fruit girth followed by cluster III (3.38) and cluster VI (3.68). Cluster IX (425.04) recorded the maximum fruit yield per plant followed by cluster I (420.07) and cluster V (386.99). Similar results were earlier reported in Prakash *et al.*, (2017).

Fruit yield per plant contributed maximum towards total genetic divergence followed by fruit girth. These two traits may be suggested as choice of traits for yield improvement through breeding in okra (Table 4).

The genotype grouped in cluster VII, VIII and X viz., Akra Anamika (Selection 10), Ankur 40*, Hisar Unnat (HRB 55), Varsha Uphar (HRB 9-2), Pusa A₄, Parbhani Kranti, P 7*, Punjab Padmini (Ludhiana

Table 3: Cluster mean performance of bhendi genotypes for various characters.

Traits Clusters	Days to first flowering	Plant height at maturity (cm)	Number of nodes to first fruiting	Days to first fruit harvest	Number of branches per plant	Number of fruits per plant	Average fruit weight (g)	Fruit length (cm)	Fruit girth (cm)	Fruit yield per plant (g)
I	45.23	131.32	4.02	56.17	2.68	20.40	19.13	13.93	3.78	420.07
II	42.28	135.02	3.21	53.72	3.22	20.21	16.48	16.77	4.43	335.73
III	44.75	128.82	5.99	55.25	3.06	20.21	17.63	14.82	3.38	371.59
IV	46.77	123.58	4.08	56.27	3.02	20.02	18.54	15.22	3.94	372.04
V	41.57	128.55	3.11	51.15	2.59	20.22	19.14	15.23	3.33	386.99
VI	44.67	116.02	4.68	52.78	2.72	21.82	17.11	13.90	3.69	374.69
VII	42.65	115.99	3.84	53.46	2.51	21.57	13.57	12.56	5.32	300.78
VIII	38.97	120.22	4.75	51.59	3.10	19.41	14.33	12.95	5.32	350.44
IX	41.05	159.97	3.27	50.47	3.77	22.80	18.63	19.04	6.17	425.04

Table 4: Percentage contribution of each character towards genetic divergence of bhendi genotypes.

S. No.	Characters	Times ranked	Contribution (%)
1.	Days to first flowering	0	0.01
2.	Plant height at maturity	1	0.06
3.	Number of nodes to first fruiting	161	9.73
3.	Days to first fruit harvest	0	0.01
4.	Number of branches per plant	81	4.90
5.	Number of fruits per plant	47	2.84
6.	Average fruit weight	24	1.45
7.	Fruit length	188	11.37
8.	Fruit girth	341	20.63
10.	Fruit yield per plant	810	49.00
	Total	1653	100

selection-1) may be declared as choice of parents for hybrid breeding as well as recombination breeding, as they were genetically divergent as well as high yielders.

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