Multivariate analysis in relation to breeding system in okra

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ABSTRACT

Fifty okra genotypes of different eco-geographical origin maintained at Indian Institute of Vegetable Research, Varanasi were evaluated to study the genetic divergence for fruit yield/plant and its 9 component traits following multivariate and canonical analyses. The genotypes were grouped in 15 clusters and confirmed by canonical analysis. Sixty eight per cent genotypes (34/50) were genetically close to each other and grouped in 5 clusters (I, II, III, IV, V), while apparent diversity was noticed for 32 per cent of the genotypes who diversed into rest 10 clusters (VI-XV). Inter-cluster distance ranged from 21.16 to 80.0. The maximum was between X and XV followed by X and XIII (79.69) and IX and X (77.09). The genotypes in cluster X, XIII, and XV had greater potential as breeding stock by virtue of high mean values of one or more component characters and high statistical distance among them. Based on findings of high cluster mean of component trait and inter-cluster distance among clusters, a breeding plan has been discussed.

Key words: Okra, multivariate, canonical analysis, cluster, eco-geographical, germplasm.

INTRODUCTION

Okra (*Abelmoshus esculentus* L.) is one of the important vegetable crops of India, which is cultivated as a pure culture as well as mixed crop during *Kharif* and *Zaid* seasons. The economic yield in majority of crops is a complex entity whose manifestation results from multiplicative interaction of several yield components. Therefore, for attaining higher yield levels, the breeder is required to simplify this complex situation through handling of the yield components. To breed desired plant type, the information about the nature and magnitude of genetic variability among base population and the degree of transmission of traits are prerequisite. For creating variability, crossing among parental lines is the most potent and assured method. However, selection of divergent parent is most important, as the greater genetic divergence among the parents for the characters; better are the chance of releasing the variability. Genetic study based on the multivariate analysis is a powerful tool for determining the degree of divergence between populations, the relative contribution of different components to the total divergence and the nature of forces operating at different levels. Therefore, expecting relative genetic potential differences, an attempt was made in present study to group 50 genotypes of okra on the basis of their degree of total genetic divergence measured by multivariate analysis.

MATERIALS AND METHODS

Fifty genotypes collected from different parts of India (Table 1), were grown in randomized block design with three replications during rainy season of 2007. Each plot consisted of single row of 3 m and spaced 30 cm apart. Five competitive plants were randomly selected for recording observation on plant height (cm), number of branches, number of internodes, internodal length (cm), days to 50% flowering, fruit length (cm), fruit diameter (cm²), 10-fruit weight (g), number of fruits per plant and yield per plant (g). The statistical analysis was done on the mean basis across the genotypes. The difference among population was tested by analysis of variance for individual traits and by Wilk's lambda criterion for pooled effect of all the 10 characters. D^2 analysis was done following Rao (7) to determine degree of differentiation among n(n-1)/2 pairs of 'n' population. Grouping of genotypes was done according to Tocher's method (Rao, 7).

RESULTS AND DISCUSSION

The analysis of plot means revealed significant differences among 50 genotypes for each of ten characters suggesting appreciable variability among the genotypes. The simultaneous testing of significance based on Wilk's (Lambda) criterion also showed significant differences among cultivars for aggregate of all the character (χ^2 294 df = 2892.93**). The D^2 values estimated for 50 germplasm lines in n (n-1)/2 = 1225 combinations varied from 0.98 to 186.0 indicating the presence of substantial amount of genetic diversity in the population.

Based on the relative magnitude of the D^2 values, genotypes were grouped into 15 clusters (Table 2). The maximum genotypes (8) were included in cluster I

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Table 1. List of germplasm lines and their source of collection.

Germplasm line (s)	Collected from	Germplasm line	Collected from
IC-69304, IC-282240, IC-113733, IC-218877, IC-43720, IC-128894, IC-43432, IC-43735, IC-21887, IC-45814, IC-2822296, IC-212269, IC-28224, IC-140880, IC-218444, IC-282229, IC-45815, IC-28228, IC-45805	NBPGR, Regional centre, Trichur	EC-329380, EC-20568, EC-169367, EC-329357, EC-324402, EC-169362, EC-329357, EC-329407	NBPGR, New Delhi
IIVR-389, IIVR-236, IIVR-1616, IIVR-1966, IIVR-435, IIVR-436, IIVR-1685, IIVR-1900	IIVR, Varanasi	SC-15, SC-108, SC-12, SC-35, SC-111	Saurashtra region
Pusa Sawani	IARI, New Delhi	JPMB-16-39,	JAU, Junagadh
200A, 211-A, 314-K, I-A, 365-A	BCKV, Kalyani	HRB-55, HRB-56	HAU, Hisar

followed by 7 in cluster II and III; 6 in cluster IV and V; 3 in cluster VI; 2 in cluster VII, VIII, IX and 1 in cluster X to XV. Clustering pattern (Table 2) indicated that majority of genotypes, *i.e.*, 34 (68%) were genetically close to each other and grouped in 5 clusters, while apparent diversity was mainly noticed due to 16 genotypes (32%) distributed over 10 clusters. The clustering pattern was also confirmed by spatial distribution of genotypes under canonical analysis. The distribution pattern of genotypes of diverse origin in a single cluster indicates that the geographical origin in okra was not related to genetic divergence. The tendency of genotypes occurring in clusters cutting across the geographical boundaries demonstrate that geographical isolation need not necessary be related to genetic diversity and was at random. This means that geographical diversity though important may not be factor in determining genetic divergence. The genotypes originating from one place as in present study were scattered in 11 clusters (Table 1). Such parallelism between geographical distribution and genetic diversity might be due to some forces other than geographical distance like genetic architecture of population, heterogeneity, history of selection, proximity of development of traits etc. Genetic drift may be another cause for genetic diversity (Duzyaman and Vural, 4). The findings are in close conformity with the report of Dhaduk *et al.* (2), Bendal *et al.* (1), Hazara *et al.* (5), and Mishra *et al.* (6) advocating lack of definite relationship between genetic and geographical diversity.

The value of intra-cluster distances were 0 (cluster X to XV) to 19.91 (cluster IX). Maximum inter-cluster distance (80) was found between cluster

Table 2. Clustering pattern of 50 okra germplasm lines on the basis of D^2 analysis for 10 characters.

Sl. No.	No. of germplasm	Genotype(s)
I	8	IC-69304, IC-282240, IC-113733, EC-329380, IC-218877, IIVR-389, IC-43720, IC-128894
II	7	IC-43432, IIVR-236, SC-15, EC-20568, IIVR-1616, IIVR-1966, 211-A
III	7	IC-43735, SC-108, IC-21887, IIVR-435, IIVR-436, SC-12, IC-45814
IV	6	EC-169367, 200A, 314-K, Pusa Sawani, IC-2822296, I-A
V	6	EC-169362, JPMB-16-39, EC-329357, EC-324402, IC-212269, 365-A
VI	3	EC-329357, HRB-55, IC-28224
VII	2	IC-140880, IC-218444
VIII	2	IC-282229, IIVR-1685
IX	2	IC-45815, IC-28228
X	1	HRB-55
XI	1	IC-45805
XII	1	SC-35
XIII	1	SC-111
XIV	1	IIVR-1900
XV	1	EC-329407

X and XV, followed by cluster X and XIII (79.69) and clusters X and IX (77.09), indicating wide diversity between these groups (Table 3). This indicates that the genotype of these clusters were much diverse to each other. The magnitude of heterosis largely depends on degree of diversity in the parental lines, the higher distance between two clusters, the greater genetic diversity between genotypes. Crosses between genetically diverse parents would manifest more heterosis than the crosses between closely related parents (Dhanbhan *et al.*, 3). Hence, genetic divergence seems to be more important tool to select perspective parents for crop improvement programme. Minimum distance between clusters I and V (21.16), I and VIII (21.44) and IV and XIII (21.51) indicated close relationship among these clusters.

The diversity present in the material was also supported by the appreciable amount of variation among cluster means for different characters (Table 4). Cluster X ranked first for yield per plant (158.39 g) and fruits/ plant (13.75%) and next to lowest days to 50% flowering. SC-111 which belonged to a separate cluster (XIII) showed shortest plant height (0.96 cm), internodal length (6.97 cm), early flowering (46.00) and maximum number of branches/plant. Cluster XV showed the maximum plant height, number of internodes, fruit length and 10-fruit weight per plant. It indicates that exploration and collection activities for better yielding genotypes should be concentrated in this area.

The contributions of different characters towards divergence, calculated by using Mahalanobis D^2 divergence, were 62.12% (fruits per plant), 20.00% (internodal length), 4.89 % (number of branches), 4.81% (10-fruit weight), 4.57% (days to 50% flowering), 1.55% (fruit yield/ plant), 1.00% (fruit length) and 0.89% (fruit diameter) (Table 5).

In genetic improvement (for high yield), the choice of parent is important and desirable component characters of yield should be taken into consideration for component breeding to obtain appropriate plant type (Bendale *et al*., 1; Singh and Kumar, 8). Genotype SC-111 with specific character (dwarfness) belonged to highly divergent cluster. The genotypes belonging to cluster X (HRB-55) showed maximum yield and fruits per plant, along with cluster XIII (SC-111), which showed that earliness, will help in broadening the genetic base of okra. Over all clusters X, XIII, and XV showed greater potential as a breeding stock by virtue of high mean values of one or more component characters as well as high statistical distance. The crossing among genotypes of these clusters selected for specific component traits may be helpful in bringing new gene pool and expanding the range of adaptation. Continuous selection in advance generation may lead to develop lines with high yield combining desirable component traits.

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Table 3. Intra-(bold) and inter-cluster distance (D^2) in okra.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV
I	**16.76**	38.76	22.57	29.98	21.16	37.14	62.33	21.44	28.11	65.23	23.46	26.15	29.81	45.90	47.01
II		**18.19**	33.59	21.92	29.25	26.14	33.16	52.85	52.06	31.89	48.86	40.38	29.62	24.57	38.24
III		-	**15.32**	25.40	24.14	26.06	52.71	31.89	32.64	58.49	23.56	30.48	26.84	43.69	33.17
IV			-	**15.35**	25.68	21.90	38.90	42.80	38.71	42.77	39.53	38.73	21.51	25.35	34.39
V				-	**17.31**	32.80	54.21	32.04	38.14	54.13	31.59	23.18	26.59	38.08	45.13
VI					-	**16.35**	34.08	49.09	43.59	42.70	39.49	45.83	23.77	34.83	21.38
VII						-	**15.05**	76.44	69.81	22.13	68.47	67.23	46.69	35.47	36.33
VIII							-	**16.05**	24.22	70.00	23.86	32.77	38.34	60.01	57.91
IX								-	**19.91**	77.09	28.82	45.41	33.79	55.67	51.13
X									-	**0.00**	75.30	65.79	79.64	32.98	80.00
XI										-	**0.00**	34.57	37.46	57.82	42.60
XII											-	**0.00**	40.90	50.47	56.60
XIII												-	**0.00**	36.11	38.60
XIV													-	**0.00**	47.50
XV														-	**0.00**

Table 4. Cluster means for different characters in okra.

Cluster No.	Plant height (cm)	No. of branches/ plant	No. of internode	Internode length (cm)	Days to 50% flowering	Fruit length (cm)	Fruit dia. (cm²)	Ten fruit weight (g)	Fruits per plant	Yield per plant (g)
Cluster-I	120	0.98*	13.78	8.67	51.79	10.91	1.66	106.24	3.83	40.46
Cluster-II	134	1.44	14.38	8.94	51.14	11.63	1.65	117.23	9.30	109.02
Cluster-III	119	1.42	15.30	7.76	51.57	11.96	1.64	120.22	4.51	54.29
Cluster-IV	117	1.33	14.87	7.92	53.83	10.73	1.62	100.37	7.37	74.22
Cluster-V	121	1.32	13.10*	9.27	49.11	10.96	1.62	112.62	5.70	64.33
Cluster-VI	156	2.29	18.42	8.57	50.00	11.57	1.70**	119.02	8.32	98.81
Cluster-VII	163	1.65	19.02	8.95	52.00	12.54	1.65	125.72	13.15	165.13
Cluster-VIII	109	1.33	13.20	8.27	52.00	10.53	1.69	101.35	1.44*	14.60*
Cluster-IX	116	1.91	15.82	7.38	58.00**	9.10	1.64	90.29	2.64	23.75
Cluster-X	133	1.65	14.86	9.00	47.00	12.33	1.65	115.17	13.75**	158.39**
Cluster-XI	170	1.25	17.70	9.62	49.00	11.60	1.53	116.82	2.84	33.18
Cluster-XII	109	1.25	11.15	9.85**	56.00	13.35**	1.68	131.44	4.15	54.56
Cluster-XIII	96*	3.00**	13.80	6.97*	46.00*	9.00	1.52*	89.33*	6.00	53.62
Cluster-XIV	126	1.07	14.70	9.26	58.00**	8.74*	1.63	89.82	10.70	96.16
Cluster-XV	186**	1.45	21.72**	8.56	48.00	13.35**	1.58	131.52**	8.20	107.85

*Lowest mean value; ** Highest mean value.

Table 5. Per cent contribution in cluster pattern for 50 germplasm okra lines.

Character	Percent contribution
Plant height (cm)	0.00
No. of branches	4.90
No. of internode	0.08
Internodal length	20.00
Days to 50% flowering	4.57
Fruit length (cm)	1.00
Fruit diameter (cm)	0.90
Ten fruit weight (g)	4.82
Fruits per plant	62.12
Yield per plant (g)	1.55

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