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# Genetic Divergence Studies for Yield and Quality Traits in Okra (*Abelmoschus esculentus* (L.) Moench.)

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## ABSTRACT

The objective of the study was to evaluate genetic divergence among okra genotypes based on yield and yield contributing traits. The experiment comprised of 32 genotypes of okra, which were sown in Randomized Block Design with two replications at College of Horticulture, Sri Konda Laxman Telangana State Horticultural University, Rajendranagar, Hyderabad during the period *Kharif*, 2016. Analysis of variance indicated existence of large variability among the genotypes for all the traits. On the basis of  $D^2$  analysis, the 32 genotypes could be grouped into 6 clusters. Cluster I had the highest number of genotypes (15) followed cluster II (11) and cluster III and cluster V (2 genotypes in each group) and remaining clusters, *i.e.*, IV and VI were mono genotypic. Plant height had the highest contribution towards the total genetic divergence (42.94 %) followed by overall YVMV PDI percent (16.73). The highest intra-cluster distances were recorded in cluster II (73.17) followed by cluster V (66.30). The maximum inter-cluster distance was recorded between cluster III and cluster IV (775.06) followed by cluster IV and cluster VI (723.37). The genotypes which were in the cluster II, III and VI also exhibited significant performance for fruit yield per plant. Based on *per se* performance and genetic investigation methods superior genotypes RHBG-1, RHBG-7, VRO-6, IC-42490, IC-10265, IC-111515, Arka Abhay, Pusa A-4, IC-29119, RHBG-12, IC-90219. The identified genotypes are promising for hybrid breeding as parents for yield and YVMV resistance. IC-04328 and EC-755647 were identified for yield and yield attributing traits and YVMV resistance in okra. The identified genotypes are promising for hybrid breeding as parents for yield and YVMV resistance.

**Key words:** Randomized Block Design, Genetic Divergence,  $D^2$ , Okra genotypes.

## Introduction

Okra (*Abelmoschus esculentus* (L.) Moench) chromosome number ( $2n = 130$ ) is one of the important vegetable crop grown for its tender green fruits throughout the India. It is called lady's finger in England, Gumbo in U.S.A. and Bhindi in India. Okra is an allopolyploid belongs to the family Malvaceae and an often-cross pollinated crop due to protogyny. The green tender fruits of okra are good source of carbohydrate, protein, vitamins (A, B and C) and rich in calcium, potassium and other mineral

matters. It contains 1.9 g protein, 1.2 g fiber, 1.5 mg Fe and 88 IU Vit-A per 100 g of edible portion. Occurrence of out crossing to an extent of 4-19 percent with the maximum of 42.2 per cent is noticed with the insect assisted pollination (Yawalkar, 1965). In India, it is grown twice in a year for getting regular supply. In the country, a large number of okra varieties are grown, the variation occurs with regards to quantitative and qualitative traits. The plant height, number of branches plant<sup>-1</sup>, number of fruits plant<sup>-1</sup>, size of fruit *i.e.* length as well as weight of fruits are the yield contributing characters while, colour of

fruit and fiber content determine the quality of fruit. Knowledge and the nature and magnitude of variation existing in available breeding materials are requisite to choose characters for effective selection of desirable genotypes to undertake planned breeding programme. The success of breeding programme depends to a large measure on the degree of genetic divergence. Genetic diversity is a key factor for crop improvement. Genetic diversity is of paramount importance for heterosis. Hybridization between genetically divergent parents is expected to produce superior hybrids and desirable recombinants. The breeder also need to isolate the suitable genotypes on the basis of genetic divergence for the hybridization purpose, Mahalanobis  $D^2$ -statistic technique based on multivariate analysis of quantitative traits is a powerful tool as it measures the degree of divergence among groups. It also pin-points the suitable genotypes for their utilization in hybridization programme (Rao (1952) which resulted in the development and release of a good number of varieties in okra.

### Materials and Methods

Thirty-two genotypes collected from different parts of the country were evaluated using Completely Randomized Block Design with three replications at College of Horticulture, Sri Konda Laxman Telangana State Horticultural University, Rajendranagar, Hyderabad *Kharif*, 2016. Each genotype was accommodated in a single row of 3 m length. The row to row spacing of 60 cm and plant to plant spacing of 30 cm was adopted. The recommended packages of practices were followed for 13 traits were recorded on five randomly selected plants of each genotype and yield contributing traits like plant height (cm), days to initiation for first flowering, days to 50% flowering, number of branches plant<sup>-1</sup>, fruit length (cm), diameter of fruit (cm), weight of fruit (g), number of fruits plant<sup>-1</sup>, number of fruits plot<sup>-1</sup>, fruit yield plant<sup>-1</sup> (g), fruit yield (t ha<sup>-1</sup>), fiber content (%) and overall YVMV PDI (%). The analysis of variance was carried out for all the characters as per the procedure suggested by Panse and Sukhatme (1978). The multivariate analysis ( $D^2$  statistic) was carried out following to Mahalanobis. Grouping of genotypes into different clusters was carried out following Tocher's procedure and the relative contribution of different char-

acters towards total divergence was calculated as per Singh and Choudhary, 1985.

### Results and Discussion

The results of analysis of variance for 32 genotypes in okra are furnished in Table 1. High and significant differences among the genotypes were observed for all the characters indicating presence of sufficient amount of variability for all the characters studied. Based on  $D^2$  values, the 32 genotypes were grouped into six highly divergent clusters. Some of genotypes were so divergent in all the character; hence two single genotypes formed a separate cluster. Thus, two clusters cluster IV, cluster VI were solitary with one genotype. The two genotypes were also divergent in some character; hence they have formed two separate clusters viz., cluster III, cluster V. The remaining two clusters were having maximum number of genotypes. Cluster I was biggest with 15 genotypes followed by cluster II with 11 genotypes (Table 2), three-dimensional diagram (Fig. 2). The result on mean performance of 32 genotypes for 13 characters revealed that the genotype RHBG-7 was the superior genotype for yield and yield contributing characters *i.e.* weight of fruit, fruit yield plant<sup>-1</sup>, fruit yield (t ha<sup>-1</sup>) and fiber content when compared to other genotypes. The genotype EC-755647 was found early for the days to initiation for first flowering, days to 50% flowering and less incidence of YVMV. The Arka Abhay was superior variety in respect of fruit length. RHBG-11 genotype recorded maximum fruit diameter. The genotype RHBG-12 found superior in respect of plant height, number of fruits plant<sup>-1</sup> and number of fruits plot<sup>-1</sup>. The genotype IC-90219 reported with no incidence of YVMV (0) (Table 3). The cluster II had the maximum  $D^2$  value (73.17) followed by Cluster V (66.30). The inter cluster  $D^2$  values of the six clusters revealed that highest inter cluster generalized distance (775.06) was between cluster III and IV followed by cluster IV and VI (723.37) (Table 4 and Fig. 1). It was observed that plant height was contributed maximum (42.94%) towards divergence followed by overall YVMV PDI (%) (16.73%), numbers of branches plant<sup>-1</sup> (13.51%), fruit length (10.08 %), number of fruits plant<sup>-1</sup> (6.65%), fruit yield plant<sup>-1</sup> (3.83%), fiber content (2.22%), fruit weight (1.81%), diameter of fruit (1.21%) and days to initiation for first flowering (1.01). The remaining characters *viz.*,

**Table 1.** Analysis of variance for 13 characters in 32 okra genotypes

Source of Variation	Mean sum of squares							
	d.f	Plant height (cm)	Days to initiation for first flowering	Days to 50% flowering	Number of branches per plant	Fruit length (cm)	Diameter of fruit (cm)	Weight of the fruit (g)
Replications	1	0.155	0.006	4.111	0.090	0.000	0.000	0.052
Genotypes	31	1349.966 ***	23.521 ***	10.074 ***	2.007 ***	4.192 ***	0.044 ***	9.418 ***
Error	31	9.726	2.104	2.389	0.040	0.146	0.006	0.366
SEm ±	63	669.05	12.61	6.198	1.009	2.135	0.024	4.815
CV (%)		5.006	3.454	3.267	6.539	5.647	5.035	8.769
CD (P=0.05)		6.36	2.96	3.15	0.41	0.77	0.15	1.23

Continued..,

Source of Variation	d.f	Mean sum of squares					
		Number of fruits plant <sup>-1</sup>	Number of fruits plot <sup>-1</sup>	Fruit yield plant <sup>-1</sup> (g)	Fruit yield (t ha <sup>-1</sup> )	Fiber content (%)	YVMV (%)
Replications	1	1.35	542.89	19.52	0.063	0.480	87.89
Genotypes	31	17.29 ***	6918.58***	4126.85 ***	12.742 ***	12.77 ***	944.85***
Error	31	0.485	194.062	94.901	0.294	0.738	41.12
SEm ±	63	8.77	3508.49	2077.68	6.42	6.65	4.53
CV (%)		5.3366	5.3366	10.3866	10.4101	7.3041	17.50
CD (P=0.05)		1.4206	28.4116	19.8683	1.1055	1.7523	13.08

\*Significant at 5 per cent level; \*\* Significant at 1 per cent level; \*\*\* Significant at less than 1 per cent level;

**Table 2.** Cluster classification of 32 okra genotypes

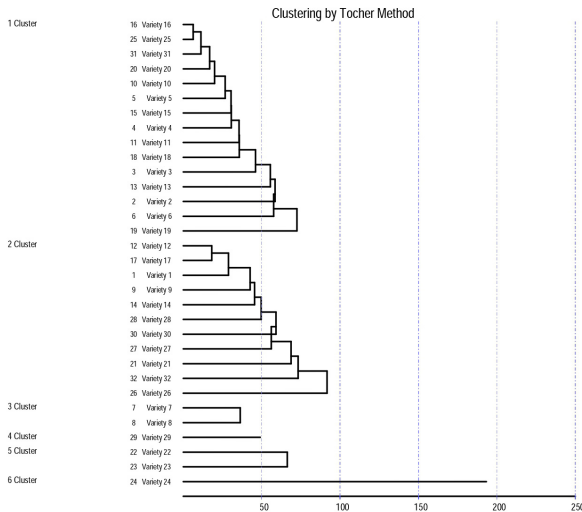
Cluster	No. of genotypes	Genotypes
I	15	IC-18960, Arka Anamika, IC-22237, IC-90004, IC-43743, RHBG-5, RHBG-8, RHBG-4, IC-45730, RHBG-9, RHBG-3, IC-10533, RHBG-2, RHBG-6, RHBG-13
II	11	IC-90219, IC-04328, RHBG-1, IC-42490, IC-10265, Pusa A-4, IC-29119, Arka Abhay, IC-111515, EC-755647, Pusa Sawani
III	2	RHBG-7, VRO-6
IV	1	EC-755648
V	2	RHBG-10, RHBG-11
VI	1	RHBG-12

**Table 3.** Mean values of clusters for 13 characters in 32 okra genotypes

Cluster	Plant height (cm)	Days to initiation for first flowering	Days to 50% flowering	Number of branches plant <sup>-1</sup>	Fruit length (cm)	Diameter of fruit (cm)	Weight of the fruit (g)	Number of fruits plant <sup>-1</sup>	Number of fruits plot <sup>-1</sup> yield	Fruit plant <sup>-1</sup> (g)	Fruit yield (t ha <sup>-1</sup> )	Fiber content (%)	Overall YVMV PDI (%)
I	41.04	43.97	47.40	2.91	6.66	1.44	5.42	10.38	207.57	56.32	3.13	13.74	51.33
II	86.39	38.76	46.26	2.55	7.72	1.51	9.13	14.92	298.42	136.58	7.59	9.11	17.73
III	100.23	38.70	46.38	3.41	5.70	1.41	10.30	17.08	341.50	175.79	9.76	8.50	12.50
IV	29.95	43.50	46.75	2.17	6.81	1.48	5.38	13.76	275.10	73.93	4.10	13.37	67.50
V	47.46	47.35	51.50	5.80	3.55	1.75	3.51	15.00	300.00	52.90	2.94	13.25	56.25
VI	102.45	42.20	51.45	5.50	6.03	1.77	6.16	19.95	399.00	122.79	6.82	13.22	2.50

**Table 4.** Average intra and inter-cluster D<sup>2</sup> values for 13 clusters in 32 okra genotypes

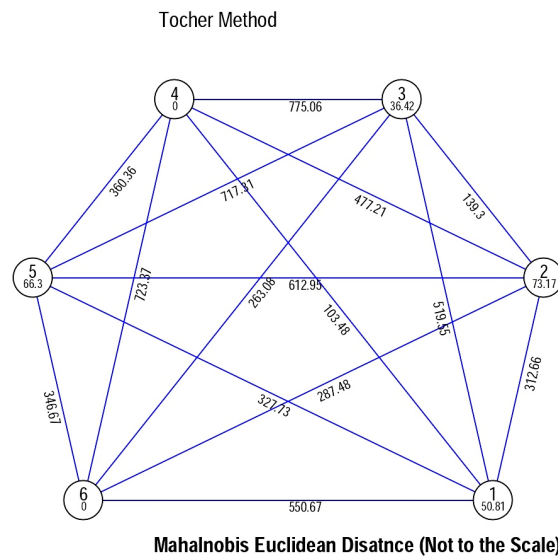
Clusters	I	II	III	IV	V	VI
I	50.81	312.66	519.55	103.48	327.73	550.67
II		73.17	139.30	477.21	612.95	287.48
III			36.42	775.06	717.31	263.08
IV				0.00	360.36	723.37
V					66.30	346.67
VI						0.00



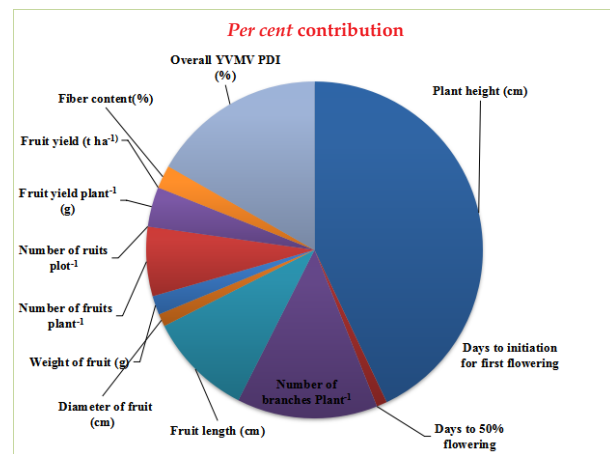
**Fig. 1.** Statistical distance among 32 genotypes in okra (Note: Variety 1:RHBG-1, Variety 2: RHBG-2, Variety 3: RHBG-3, Variety 4: RHBG-4, Variety 5: RHBG-5, Variety 6: RHBG-6, Variety 7: RHBG-7, Variety 8: VRO-6, Variety 9: IC-42490, Variety 10: IC-43743, Variety 11: IC-45730, Variety 12:IC-90219, Variety 13: IC-10533, Variety 14: IC-10265, Variety 15: RHBG-8, Variety 16: IC-18960, Variety 17: IC-04328, Variety 18: RHBG-9, Variety 19: RHBG-13, Variety 20: IC-90004, Variety 21: IC-111515, Variety 22: RHBG-10, Variety 23: RHBG-11, Variety 24: RHBG-12, Variety 25: Arka Anamika, Variety 26: Pusa Sawani, Variety 27: Arka Abhay, Variety 28: Pusa A-4, Variety 29: EC-755648, Variety 30: IC-29119, Variety 31: IC-22237, Variety 32: EC-755647)

days to 50% flowering, number of fruits plot<sup>-1</sup> and fruit yield (t ha<sup>-1</sup>) did not contribute to the total divergence (Fig. 3). 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.

Therefore, hybridization programme between the genotypes belonging to cluster II, III and VI may be undertaken for getting good segregants.



**Fig. 2.** Dendrogram showing clustering pattern (Tocher’s method) in 32 genotypes in okra



**Fig. 3.** Per cent contribution of different traits towards divergence

## Conclusion

Availability of desirable genetic diversity is utmost important to fulfill the present research objective *i.e.*, high yield as well as YVMV tolerant variety of okra. Based on extent of genetic divergence in respect to a particular character of interest and highest inter cluster distance, genotypes from cluster II, III and VI may be undertaken for getting good segregants. On the basis *per se* performance and genetic investigation methods, superior genotypes such as RHBG-1, RHBG-7, VRO-6, IC-42490, IC-10265, IC-111515, Arka Abhay, Pusa A-4, IC-29119, RHBG-12, IC-90219, IC-04328 and EC-755647 were found promising for using in the hybridization programme.

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