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## GENETIC DIVERGENCE ANALYSIS IN OKRA (*ABELMOSCHUS ESCULENTUS* L. MOENCH)

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## ABSTRACT

The  $D^2$  statistics was applied to assess the diversity among 17 genotypes of okra using Mahalanobis  $D^2$  analysis. The analysis of variance revealed significant differences among the genotypes for all the characters under study. The genotypes were grouped into three clusters, first which comprised of 15 genotypes, while rests of the clusters are solitary clusters with one genotype each. Inter-cluster difference was maximum between the clusters I and III which indicated that genotypes included in this cluster may give heterotic response and thus better segregants and hence may be used for further hybridization programme. Average fruit weight (g) contributed the most to the genetic divergence of the genotypes followed by OLCV incidence, days to first picking, plant height and number of nodes / plant.

## INTRODUCTION

Okra (*Abelmoschus esculentus* L. Moench) is an important vegetable crop grown in World as well as India. Hybrid vigor was already successfully exploited in okra with commercial hybrid development; therefore genetic divergence among the parents is important factor while selecting the parents for hybridization. Rao (1960) and Ramanujam *et al.* (1974) also observed that a cross involving genetically diverse parents is more likely to produce high heterotic effects as compared with lines which are more closely related with each other. Moll *et al.* (1974) indicated that the level of heterosis exhibited by a hybrid is a function of the genetic divergence between the parents. Cress (1966) demonstrated that 'genetic diversity is necessary for significant heterosis but not sufficient to guarantee it,' The importance of genetic diversity for selecting the parents in recombination breeding of different autogamous crops to obtain transgressive segregants has been very well emphasized by Khanna and Mishra (1977), Singh and Ramanujan (1981), Cox and Murphy (1990). Also, while performing selection more importance should be given to the characters which contribute more towards diversity.

Evaluation of germplasm is pre-requisite to identify the desirable genotypes to feed the breeding programmes. The value of germplasm collection depends not only on the number of accessions it possesses, but also up on the genetic diversity present in those accessions for yield and yield components. India is one of the countries with largest collection of cultivated okra (*Abelmoschus esculentus* (L.) Moench) in the gene bank and as such its potential is not fully known. Further, being a potentially self pollinated crop, the cultivated okra has a narrow genetic base and concerted efforts, are therefore, required for exploring the full potential of available okra germplasm resources in the gene bank. Hence, the existing germplasm accessions need detailed evaluation for various horticultural traits to assess the nature and magnitude of genetic divergence among accessions, which is crucial for selecting genetically divergent parents for a productive breeding programme.

The existing diversity has been exploited in various breeding programmes, which resulted in the development and release of a good number of varieties in okra. However, the released varieties cannot be continued longer due to genetic drift and susceptibility to various pests and diseases especially the fruit and shoot borer and yellow vein mosaic virus. This demands replacement of current varieties by new varieties.

The present investigation was therefore, undertaken to assess the nature and magnitude of genetic diversity available in a large germplasm involving both indigenous and exotic collections of okra on the basis of various growth, earliness and yield attributes.

## MATERIALS AND METHODS

The present field experiment entitled "Genetic Divergence analysis in Okra (*Abelmoschus esculentus* L. Moench)" was conducted on experimental farm, Department of Agricultural Botany, College of Agriculture, Latur, MKV, Parbhani,

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during *kharif* 2011-12. The experiment was laid out in Randomized Block Design with three replication. The standard agronomic practices were followed throughout period of crop growth. The observation were recorded on five randomly selected plants from each entry per replication for days to 50 % flowering, plant height, number of nodes / plant, days to first picking, number of fruits / plant, average fruit length, average fruit weight, yield / plant (g), yield / plot (kg), yield / ha (q), YVMV incidence and OLCV incidence.

Genetic divergence was analyzed using Mahalonobis  $D^2$  statistics (1936) and genotypes were grouped into clusters by following the Tocher's method described by Rao (1952).

## RESULTS AND DISCUSSION

Analysis of variance revealed that significant differences among genotypes for all the characters under study. Based on  $D^2$  statistics and Tocher's method, 17 genotypes were grouped into three clusters with variable number of entries revealing the presence of considerable amount of genetic diversity in the material (Table 1). The cluster I comprised of maximum number of 15 genotypes, while the rest of the clusters are solitary clusters with one genotype each. The pattern of distribution of genotypes into different clusters was based on  $D^2$  values, which ranged from 3.74 to 4.27 (Table 2). Highest inter cluster  $D^2$  values observed between cluster I and III (4.27) followed by II and III (3.86), whereas lowest observed in between I and II (3.74). Highest intra-cluster distance was shown by cluster I (2.19), while rests of the clusters were having zero intra-cluster distance. Genotypes for hybridization should be selected from the more distant clusters as chances are more to obtain heterotic combinations as compared to combinations involving genotypes from same cluster. Similar results were found by Ahamad *et al.* (2014), C. Vidhya and N. Kumar (2014), Shinde *et al.* (2013), Reddy *et al.* (2012), Moll *et al.* (1974), Pradip *et al.* (2010), Shaikh *et al.* (2013), Reddy *et al.* (2012), Martin *et al.* (1981) Mandal and Dana, (1993) and Abdul *et al.* (1994).

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Cluster means indicate the variation for the quantitative trait among the cluster (Table 3). Considering major yield contributing characters along with earliness to flowering and maturity cluster I and III shown high cluster means for yield and yield components, therefore genotypes from these diverse clusters should be used for further hybridization and isolating transgressive segregants in later generations. Similar results were found by Ahamad *et al.* (2014), C. Vidhya and N. Kumar (2014), Shinde *et al.* (2013), Moll *et al.* (1974), Pradip *et al.* (2010), Shaikh *et al.* (2013), Reddy *et al.* (2012), Martin *et al.* (1981) Mandal and Dana, (1993) and Abdul *et al.* (1994).

Analysis of contribution of the characters to genetic divergence (Table 4) revealed that average fruit weight contributed highest upto 30.15 %, followed by OLCV incidence (17.65%), days to first picking (16.18%), plant height (9.56%) and number of nodes / plant (8.09%), however character days to 50 % flowering (0.00%) not contributed in genetic divergence. De *et al.* (1988) proposed that traits contributing maximum towards the  $D^2$  values need to be given more emphasis for deciding clusters to be taken for further selection and choice of parents for hybridization programme. Similar results were found by Ahamad *et al.* (2014), C. Vidhya and N. Kumar (2014), Shinde *et al.* (2013), Reddy *et al.* (2012), Moll *et al.* (1974), Pradip *et al.* (2010), Shaikh *et al.* (2013), Martin *et al.* (1981) Mandal and Dana, (1993) and Abdul *et al.* (1994).

The data on inter-cluster differences were used to select genetically diverse and agronomically superior genotypes. The genotypes exceptionally good within one or more characters were seemed to be desirable. Inter-crossing of divergent groups would lead to greater opportunity for crossing over, which releases hidden potential variability by disrupting the undesirable linkages.

**Table 1: Distribution of Okra genotypes in three different clusters**

Cluster	Genotypes	Number of genotypes
I	JOH – 05-09 x VNR (Super Green), Arka anamika x VNR (Super Green), JOH – 05-09 x Shagun, Parbhani Kranti, JOH – 05-09, VNR (Super Green), P. Kranti x A. anamika, A. anamika x Shagun, P. Kranti x Shagun, A. anamika, M-10, JOH – 05 – 09 x A. anamika, Sonal, P. Kranti x JOH-05-09, Shagun	15
II	Shagun x VNR (Super Green)	1
III	P. Kranti x VNR (Super Green)	1

**Table 2: Average intra (diagonal) and inter cluster distances ( $D^2$ ) for three clusters of okra**

Cluster	I	II	III
I	2.19	3.74	4.27
II		0.00	3.82
III			0.00

**Table 3: Cluster Means for Twelve Characters in Okra**

Cluster No.	Days to 50 % Flowering	Plant Height	No of Nodes/ Plant	No of Nodes/ Plant	No. of Fruits / Plant	Fruit Length	Fruit Wt. (g)	Yield / Plant (g)	Yield / Plot (Kg)	Yield / Hectare (q)	YVMV	OLCV
I	50.33	187.15	25.62	52.51	27.47	11.10	12.34	22.04	338.14	139.48	3.88	4.06
II	50.00	179.00	28.33	52.33	34.73	10.33	11.88	23.12	413.50	146.37	15.79	18.01
III	50.00	205.67	23.13	52.67	27.92	11.80	11.57	21.29	323.03	134.77	0.00	26.59

**Table 4: Percentage contribution of different characters towards Genetic Divergence in Okra**

Sr. No.	Characters	Percentage Contribution (%)
1	Days to 50 % Flowering	0.00
2	Plant Height	9.56
3	No of Nodes / Plant	8.09
4	No of Nodes / Plant	16.18
5	No. of Fruits / Plant	2.94
6	Fruit Length	6.62
7	Fruit Wt. (g)	30.15
8	Yield / Plant (g)	1.47
9	Yield / Plot (Kg)	2.21
10	Yield / Hectare (q)	2.21
11	YVMV incidence	2.94
12	OLCV incidence	17.65

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