International Journal of Agricultural Sciences
Volume **11** | Issue 1 | January, 2015 | 158-160 ■ e ISSN-0976-5670
☞ **DOI: 10.15740/HAS/IJAS/11.1/158-160**
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RESEARCH PAPER

Genetic divergence in okra [*Abelmoschus esculentus* L. (Moench)]

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Abstract : Twenty five genotypes of okra (*Abelmoschus esculentus* L.) were evaluated for genetic divergence for yield and its attributing characters. The genotypes were grouped in seven clusters on the basis of relative magnitude of D^2 values. The maximum genetic distance was observed between cluster II and VI followed by Cluster VI and VII. However, cluster III and IV showed lowest degree of divergence. The mean value of different clusters, genotypes having high yield along with plant height, internodal length, fruit weight, fruit length, 1000 seed weight were observed in cluster VI having genotypes like AE 13 and AE 21. Cluster II showed lowest mean values for maximum characters.

Key Words : Genetic divergence, D^2 analysis, Okra

View Point Article : Kandasamy, R. (2015). Genetic divergence in okra [*Abelmoschus esculentus* L. (Moench)]. *Internat. J. agric. Sci.*, **11** (1): 158-160.

Article History : Received : 12.11.2014**; Revised :** 30.11.2014**; Accepted :** 13.12.2014

INTRODUCTION

Okra [*Abelmoschus esculentus* (L.) Moench.] is an important warm season vegetable crop cultivated in tropical and subtropical parts of the world. Okra tender fruits are used as vegetable in culinary preparations and also for thickening soups and gravies, because of its high mucilage content. The fruit contain vitamin C (30 mg 100 g^{-1}), calcium (90 mg 100 g^{-1}), iron (1.5 mg 100 g^{-1}) and rich in iodine (97 mg 100 g^{-1}). India possesses a wide range of diversity in okra. Although a large number of high yielding cultivars, many landraces and wild forms have also been reported. The success of crop improvement programme is mainly based on genetic diversity available in the breeding material. Genetic diversity helps in selecting the suitable parents for hybridization and disease recombinants. Genetic diversity is a key factor for crop improvement. Genetic diversity is of paramount importance for heterosis. Mahalanobis D^2 statistics appears to be a fruitful approach which is 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 (Joshi and Dhawan, 1966); (Ghai *et al*., 2005; Kumari and Chaudhury, 2006; Singh *et al*., 2007; Bendale *et al.*, 2003). Keeping in view the above facts, the present study was carried out for the genetic divergence among 25 genotypes to select elite and divergent parents to use for desired improvement programmes.

MATERIAL AND METHODS

The present investigation was carried out at the Vegetable Unit, Department of Horticulture, Annamalai University during 2011-2012. The investigation material comprised of 25 genotypes of okra collected from various sources in India. All the genotypes were grown in Randomized Block Design with three replications. Observations were recorded on five randomly selected parents per replication for each genotype. All the package of practices was followed for growing a successful crop by giving necessary fertilizer with a spacing of 60×30 cm. The mean values of all the traits were subjected to statistical analysis. Multivariate analysis was done by utilizing Mahalanobis D^2 statistics (Mahalanobis, 1936) and the genotypes were grouped into different clusters through Tocher's method given by Rao (1952).

RESULTS AND DISCUSSION

In the present study, 25 genotypes were collected from different districts of Tamil Nadu. The cluster formation indicated the variability existed among the genotypes, since seven clusters were formed from 25 genotypes studied (Table 1). The genotypes used in this study whose origin from different districts grouped themselves into different clusters. Eight genotypes were grouped in cluster I from different places. Cluster VII consists of 6 genotypes; cluster V had three genotypes. All other cluster consists of two genotypes. A perusal of the Table 1 clearly showed the genotypes usually did not cluster according to geographical distribution. Similar observations were also reported by Susan *et al.* (1997); Hazra *et al.* (2002) and Bendale *et al.* (2003). One of the possible reason may be the fact that it is very difficult to establish the actual location of origin of a genotype. The free and frequent exchange of the genetic material among the farmers and breeders in the country makes it very difficult to maintain the real identity of the genotype. The absence of relationship between genetic diversity and geographical origin such as exchange of genetic stock, genetic drift, spontaneous variation, natural and artificial selection are responsible for genetic diversity may also be possible that causes of clustering pattern were much influenced by environment and genotype x environment interaction resulting in different expression. Another possibility may be that estimates of diversity based on the characters used in the present investigation might not have been sufficient to account for the variability caused by some other traits of physiological or biochemical nature which

Table 1 : Grouping of 25 okra genotypes using D^2 statistics

Sr. No.	Cluster	Number of genotypes	Genotypes
1.	I	8	AE 1,AE 2,AE 3,AE 4, AE 5,AE 6,AE 19, AE 22
2.	II	2	AE 16,AE 20
3.	III	2	AE 15,AE 25
4.	IV	2	AE 12,AE 24
5.	V	3	AE 7, AE 10,AE 23
6.	VI	2	AE 13,AE 21
7.	VII	6	AE 8,AE 9,AE 11,AE 14, AE 17,AE 18

Table 2 : Intra (bold) and inter cluster distance among clusters in okra

Cluster	I	II	III	IV	V	VI	VII
I	2131.72 (46.17)	3672.87 (60.60)	1551.35 (39.39)	1292.94 (35.96)	5289.74 (72.73)	7061.09 (84.03)	2315.94 (48.12)
II		92.81 (9.63)	1090.75 (33.03)	3456.82 (58.79)	12141.29 (110.19)	16563.75 (128.70)	1264.22 (35.56)
III			128.42 (11.33)	786.26 (28.04)	6639.32 (81.48)	9495.14 (97.44)	1073.43 (32.77)
IV				265.93 (16.31)	3671.03 (60.59)	5229.10 (72.31)	2367.02 (48.65)
V					4606.21 (67.87)	2328.23 (48.21)	8969.62 (94.71)
VI						425.68 (20.63)	12180.45 (110.36)
VII							1083.89 (32.92)

Table 3 : Cluster mean of 25 okra genotypes for twelve characters

Clusters / Traits	I	II	III	IV	V	VI	VII
Days to first flowering	45.11	42.93	40.93	45.27	41.16	41.63	46.28
Plant height (cm)	114.69	71.09	83.48	97.76	131.22	149.06	106.46
Number of branches per plant	2.74	2.90	3.10	3.33	2.91	3.13	2.76
Internodal length (cm)	6.30	5.94	5.69	5.11	7.46	8.90	6.35
Node at first fruit	3.86	2.93	4.10	3.37	3.62	4.37	4.31
Days to first harvest	56.12	52.80	51.17	55.23	51.78	50.63	57.96
Fruit length (cm)	15.56	14.40	12.27	13.32	14.55	19.44	15.25
Fruit girth (cm)	6.16	5.28	5.37	6.14	6.05	5.91	6.08
Fruit weight (g)	14.29	13.63	14.18	13.93	14.12	17.05	12.74
Number of fruits per plant	19.80	14.50	18.10	22.00	28.16	25.23	18.12
1000 seed weight (g)	52.59	44.64	48.48	53.09	56.14	58.75	48.02
Yield per plant (g)	285.96	195.36	257.67	307.19	392.58	438.57	225.67

might have been important in depicting the total genetic diversity in the population. Therefore, selection of genotypes for hybridization should be based on genetic diversity rather than geographic divergence.

The intra and inter cluster D^2 values among 25 genotypes presented in Table 2 revealed that cluster II showed minimum intra cluster D^2 values (9.63), whereas maximum intracluster value (67.83) was shown by cluster V indicated that genotype included in this cluster are very diverse and was due to both natural and artificial selection forces among the genotypes. The maximum distance at inter cluster level was between cluster II and cluster VI (128.70) followed by cluster VI and cluster VII (110.36), while minimum value was between III and IV (28.04) in D^2 analysis (Table 2). The genotypes from cluster II and cluster VI can be used as a parent in hybridization progamme to get high heterotic hybrids from the segregating populations. This is in agreement with results of Singh and Singh (2008); Santhakumar and Salimath (2011).

The cluster mean of 25 genotypes (Table 3) showed that the mean value of cluster varied in magnitude for all the twelve characters. Genotypes in cluster I showed maximum value for fruit girth (6.16 cm), while cluster IV showed maximum value for number of branches per plant (3.33). Cluster V showed maximum value for number of fruits per plant (28.16). Likewise cluster VI expressed highest mean values for plant height (149.06 cm), internodal length (8.90 cm), node at first fruit (4.37), fruit length (19.44 cm), fruit weight (17.05 g), 1000 seed weight (58.75 g) and yield per plant (438.57 g). Cluster VII showed maximum mean values for days to first flowering (46.28) and days to fruit harvest (57.96).

Cluster II showed lowest mean values for plant height (71.09 cm), node at first fruit (2.93), number of fruits per plant (14.50), fruit girth (5.28 cm), and 1000 seed weight (44.64 g) and yield per plant (195.56 g). Cluster III exhibited lowest mean value for days to first flowering (40.93) and fruit length (12.27 cm). While cluster I, IV, VI and VII showed the lowest mean values for number of branches per plant. Depending on the aim of breeding the potential lines to be selected from different clusters as parents in a hybridization programme should be based on genetic distance.In accordance with the findings of Edang *et al*. (1971) and Patro and Ravishankar (2004) expressed that the clustering pattern could be utilized in choosing parents for own combinations likely to generate the highest possible variability for various economic traits.

For breeding programme aimed at higher yield, the genotypes from cluster VI can be selected as parent showing highest mean for yield per plant along with plant height and fruit weight. To develop good varieties in small fruited type selection from cluster III will be highly useful and to breed long fruited types having some demand in specific region of our country, selection from cluster VI will be useful. The genotypes of highly divergent cluster may also be utilized in heterosis breeding programme for development of F_1 hybrids with superior yield and quality characters.

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