RESEARCH PAPER International Journal of Agricultural Sciences, Vol. 7 Issue 2 (June, 2011) : 440-443

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

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ABSTRACT

Fourty four okra genotypes were assessed for genetic divergence using Mahanalobis D^2 statistics. The population was grouped in to twelve clusters. The cluster III was the largest with eight genotypes followed by cluster I and VIII with seven, cluster II with five, cluster XII with three while, clusters IV, V, VI, IX, X and XI included only two genotype in each. The clustering pattern indicated that there was no association between geographical distribution of genotypes and genetic divergence. The intra-cluster distance was maximum in cluster XII (28.14), while inter-cluster distance was maximum between cluster VI and VIII (35.57) followed by I and IX (35.31), thus being a good source for attempting hybridization. The characters namely days to 50% flowering (35.62%), 100 seed weight (28.44%), number of seeds per fruit (17.23%) and average fruit weight (8.14%) were directly contributed towards maximum divergence and, therefore, selection of divergent parents based on these characters is recommended for getting good hybrids or segregants in okra.

Prakash, K., Pitchaimuthu, M., Venugopalan, R., Hongal, Shivanand and Jainga, K. (2011). Genetic diversity studies in okra [*Abelmoschus esculentus* (L.) Moench]. *Internat. J. agric. Sci.*, **7**(2): 440-443.

Key words : Okra, Genetic divergence, D^2 statistics

INTRODUCTION

Okra [*Abelmoschus esculentus* (L.) Moench] is an economically important vegetable of tropical and sub-tropical part of India. It is mainly grown for its tender fruits, which are cooked and consumed as vegetable. For any crop improvement program it is essential that sufficient variability or diversity exist for economically important traits in the germplasm. The importance of genetic diversity in selecting the parents for recombination breeding in crops has been repeatedly emphasized by many workers (Murthy and Anand, 1996; Pillai, 2002). Hence, estimation of genetic divergence of economically important characters based on sound statistical procedures like Mahanalobis D^2 statistics is required to identify diverse genotypes for crossing. Therefore, the present study was carried out to examine the nature and magnitude of genetic divergence in 44 genotypes of okra collected from different geographical areas.

MATERIALS AND METHODS

The experimental material consisted of 44 diverse genotypes of okra. The experiment was laid out in Randomized Block Design with three replications during *Kharif* season 2009 at Vegetable Breeding Block, Indian Institute of Horticultural Research (IIHR), Bangalore, Karnataka. Each entry was sown at 30 x 15 cm spacing, accommodating 30 plants in each row per replication. All the recommended package of practices was followed for raising a healthy crop. The observations were recorded from five competitive plants from each replication on twelve parameters *viz.*, plant height (cm), inter-nodal length (cm), days to 50 % flowering, days to 80 % maturity, stem girth (mm), fruit length (cm), fruit width (mm), number of fruits per plant, average fruit weight (g), number of seeds per fruit, hundred seed weight (g) and total fruit yield per plant (g). Genetic diversity between groups was estimated by using D^2 statistics given by Mahalanobis (1936) following the procedure given by Rao (1952). The mean values were computed to calculate D^2 values between all possible pairs of genotypes. The grouping of genotypes was done using Tocher's method as described by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance revealed that the genotypes varied significantly for all the characters under study. After compiling D^2 values for all the possible pairs, the 44 genotypes were grouped in to twelve clusters (Table 1). Number of genotypes per cluster ranged from two to eight. The cluster III was the largest with eight genotypes

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Table 1: Clustering patterns of 44 okra genotypes based on D^2 analysis

Cluster number	No. of accessions in each cluster	Accessions names
I	7	IIHR-15, IIHR-18, IIHR-20, IIHR-31, IIHR-55, IIHR-134, IIHR-181
II	5	IIHR-72, IIHR-81, IIHR-91, IIHR-10 (Arka Anamika), IIHR-04 (Arka Abhay)
III	8	IIHR-101, IIHR-108, IIHR-116, IIHR-133, IIHR-182, IIHR-213, IIHR-219, IIHR-239
IV	2	IIHR-237, IIHR-251A
V	2	IIHR-238, IIHR-241
VI	2	IIHR-247, IIHR-249
VII	2	IIHR-242, IIHR-252
VIII	7	IIHR-224, IIHR-225, IIHR-226, IIHR-227, IIHR-229, IIH-230, IIHR-231
IX	2	IIHR-243, IIHR-246
X	2	IIHR-232, IIHR-244
XI	2	IIHR-233, IIHR-240
XII	3	IIHR-245, IIHR-248, IIHR-250A

Maximum D^2 value= 2841.827 Minimum D^2 value= 32.275 Current critical D^2 value= 936.51

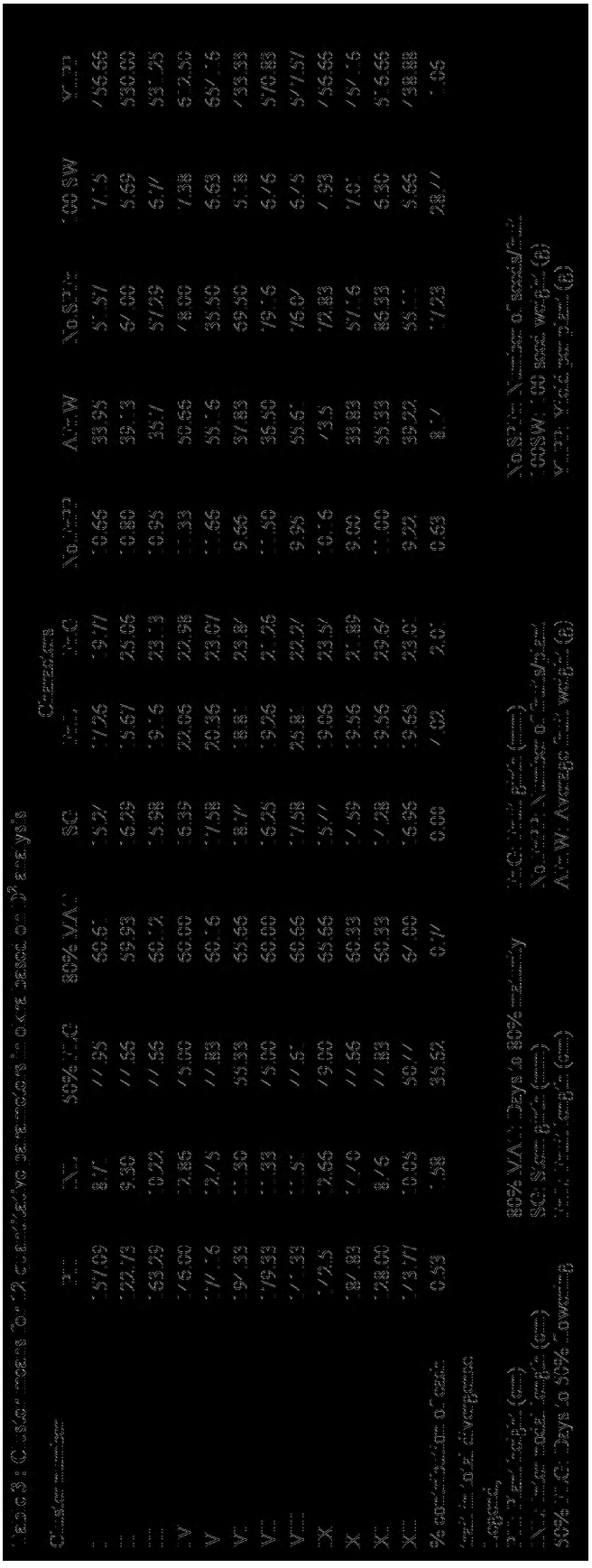
followed by cluster I and VIII with seven, cluster II with five, cluster XII with three genotypes while, clusters IV, V, VI, IX, X and XI were included two genotypes each. The genotypes distributed randomly among the different clusters irrespective of their geographical origin. Genotypes from different geographical regions were grouped in the same cluster indicating no relationship between geographic distribution and genetic divergence. Present results supported the findings of Martin *et al.* (1981) and Mandal and Dana, (1993).

The intra and inter-cluster distance D represent the index of genetic diversity among clusters as given in Table 2. The cluster XII (28.14) recorded the maximum intra cluster distance followed by cluster VIII (24.71). Maximum inter-cluster distance was observed between cluster VI and VIII (35.57) followed by that between cluster I and IX (35.31) suggesting thereby that the genotypes belonging to cluster I, VIII and IV, III were more divergent than the rest of the clusters, can be undertaken in a hybridization programme for evolving good hybrids or segregants. The inter-cluster distance was least between cluster IV and V indicating close relationship among the genotypes included in these clusters. The selection of parents on large phenotypic differences may be useful but there are several instances where a single gene can provide large scale differences in height, maturity and yield. Therefore, measures based on genetic criteria qualifying diversity have become important in classifying the material for use by breeders.

Among them, assessment of divergence for a set of characters utilizing multivariate analysis like distance analysis, canonical analysis, factor analysis and cluster analysis has been attempted and effectively utilized in a number of crop plants including vegetable crops with

Table 2 : Inter and intra-cluster (bold) distance (D) values in 44 genotypes of okra

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	21.28	28.19	19.44	21.83	27.88	34.51	21.04	33.77	35.31	17.76	33.28	30.91
II		18.99	22.54	27.54	24.68	28.04	20.32	28.71	20.79	26.29	24.76	25.56
III			17.28	19.63	23.73	30.51	15.74	29.51	29.46	16.56	28.08	27.38
IV				7.7	14.22	33.05	20.66	24.26	32.01	19.33	24.63	29.18
V					8.72	30.81	24.90	23.75	26.62	26.11	23.39	27.17
VI						9.3	29.16	35.57	19.74	31.97	32.72	21.21
VII							10.03	26.39	26.48	17.00	23.52	27.80
VIII								24.71	28.69	30.92	22.15	33.09
IX									14.21	32.77	24.96	22.76
X										17.97	30.66	29.00
XI											20.70	31.45
XII												28.14



diverse breeding systems (Murthy, 1979). Kalloo *et al.* (1980) also suggested that the crosses between selected genotypes from widely separated clusters were most likely to give desirable recombinants.

Comparison of cluster means for different characters indicated considerable differences between clusters for all the characters (Table 3). Cluster VI had genotypes (IIHR-247, IIHR-249) with maximum plant height, days to 50% flowering, days to 80% maturity, stem girth and fruit girth observed. Cluster V had genotypes (IIHR-238, IIHR-241) with maximum number of fruits per plant and total yield per plant (g) recorded. Genotypes (IIHR-224, IIHR-225, IIHR-226, IIHR-227, IIHR-229, IIHR-230 and IIHR-231) in cluster III recorded maximum mean values for fruit length and average fruit weight. Cluster X had genotype (IIHR-232, IIHR-244) with maximum mean value for inter-nodal length; cluster XI had genotypes (IIHR-233, IIHR-240) with maximum number of seeds per fruit and cluster IV had genotypes (IIHR-237, IIHR-251A) showing maximum mean value for hundred seed weight.

Per cent character contribution towards genetic divergence among the okra genotypes was maximum from, days to 50% flowering (35.62%), 100 seed weight (28.44%), number of seeds per fruit (17.23%) and average fruit weight (8.14%), showing the possibility for selection of these characters (Table 3). Hence, selection for divergent parents based on these characters will be useful for heterosis breeding in okra.

Apart from the above findings it can be concluded that, selection and hybridization of genotypes from high divergent clusters and few genotypes from other less divergent clusters are expected to yield potential F1s and transgressive seggregants for further exploitation and hence, these findings are in conformity with earlier reports of Martin *et al*. (1981); Abdul *et al*. (1994); Hazara *et al*. (2002) and Bendale *et al*. (2003).

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Received : December, 2010; Accepted : May, 2011