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GENETIC VARIABILITY AND DIVERGENCE ANALYSIS IN OKRA [*Abelmoschus esculentus*(L.) Moench]

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ABSTRACT : An investigation was undertaken to assess genetic diversity of 50 genotypes based on 11 traits using Mahalanobis D^2 statistics. Significant variation was noticed for all the traits. High heritability estimates were observed for all the traits except thickness of the fruit. In general phenotypic coefficients of variability were greater than their corresponding genotypic coefficients of variability denoting environmental factors influencing their expressions to some degree or other. High estimates of heritability coupled with high genetic advance and moderate to high GCV were observed for plant height up to 1st fruiting node (cm), no. of first fruiting nodes / plant, no. of branches/ plant and number of fruits per plant. Mahanalobis D^2 statistics cluster analysis distributed the 50 genotypes into eight broad clusters. The inter-cluster distance was maximum between cluster II and VII (6.956) followed by cluster I and VII (6.69), cluster IV and cluster VII (6.64) and cluster V and cluster VII (6.588), whereas minimum inter cluster distance was between I and IV (2.239). The characters viz. plant height (cm), plant height up to first fruiting node, no. of branches/ plant and weight per fruit (g) contributed maximum towards genetic divergence and, therefore, selection of divergent parents based on these characters is recommended for getting good hybrids or segregates in okra. The cluster VII genotypes were Parbhani Kranti, ParbhaniTripti and Bio Aparajita were diverse from other clusters and also having highest mean values for plant height (cm), plant height up to first fruiting node and weight per fruit (g). The cluster II genotypes viz.; BO-22 , BH-9, IC-8899, IC-12930, IC-10256 and White Snow had highest mean values for no. of branches/ plant.

Keywords : *Genetic diversity, multivariate analysis, okra germplasm, lines, pod yield, yield components.*

India is the largest producer of okra in the world, grown in an area of 0.53 m hectares with annual production of 6.35 million tones and a productivity of 12 MT/ha (Indian Hort. Data Base, 9). It is considered as an important fruit vegetable crop of the tropical and sub-tropical regions of the world. It is cultivated on a wider scale in warmer parts of temperate Asia, southern Europe, northern Africa, the United States of America, and almost all parts of the tropics. Successful development of new cultivars depends largely on the availability of source germplasm with desirable traits such as biotic and abiotic tolerance and other improved characteristics. The important objective of plant-breeding programme is the diversification of the genetic base of cultivars, which is achieved by intercrossing the genetic sources of diverse origin. Heterosis has already been successfully exploited in okra for the development of hybrids; therefore genetic divergence among the parents is important factor while selecting the parents for hybridization. Rao (17) and Ramanujam *et al.* (18) 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. D^2 statistic developed by Mahalanobis (13) is a powerful tool to measure genetic divergence among genotypes in any crop. Hence the present study was undertaken to understand the genetic diversity among the 50 genotypes of okra to identify the lines for hybridization programme and to identify the characters relatively contributing more in differentiating the genotypes as these characters are important as far as selection is concerned.

MATERIALS AND METHODS

A set of 50 lines was grown at the Research Farm of C.S.S.S. (P. G.) College, Machhra, Meerut during summer and rainy seasons of 2007 and 2008 with two sowing dates *viz*., early and late. Each genotype was raised in a plot of 1.5 meter square (2 rows x 3m length x 0.25m inter row distance) with a planting distance of 30 x 25 cm having 20 plants per plot with three replications. All the recommended agronomic practices were followed to raise a good crop. Observations were recorded on eleven characters. Observations on plant height up to first fruiting node (cm), number of first fruiting nodes per plant, number of fruiting nodes per plant, final plant height (cm), number of branches per

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plant, length of the fruit (cm), thickness/girth of the fruit (cm), weight per fruit (g), number of fruit per plant and fruit yield per plant (g) were recorded on randomly selected five plants in each replication, whereas observation on number of days to first flower was recorded on plot basis in each replication. The mean performance over eight environments was pooled and used for statistical analysis.

Analysis of Variance (ANOVA) was computed by using CropStat7.2 and the mean values of traits were used for further analysis. The heritability was computed based on the methods of Falconer (6). The genetic advance and genetic advance as percentage ofmean were estimated (Johnson *et al.*, 11; Hanson *et al.,*8).The phenotypic and genotypic coefficients of variation were estimated according to the method suggested by Burton and De Vabe (3) as follows :

Environmental variance $(\sigma^2 e) = MS_e$

Genotypic variance $(\sigma^2 g) = \left[- \frac{MS_g - MS_e}{r} \right]$

Phenotypic variance $(\sigma^2 p) = \sigma^2 g + \sigma^2 e$

Phenotypic coefficient of variation (PCV)

$= \frac{\sigma p}{x} \times 100$

Genotypic coefficient of variation (GCV)

$= \frac{\sigma g}{x} \times 100$

Where, x = grand mean of a character

Broad sense heritability (h^2) expressed as the percentage of the ratio of the genotypic variance to the phenotypic variance (ó^{2}p) and was estimated on genotype mean basis as described by Allard (2) as:

$$h^2 = \frac{\sigma^2 g}{\sigma^2 p} \times 100 \; (\sigma^2 g)$$

Genetic advance in absolute unit (GA) and per cent of the mean (GAM), assuming selection of superior 5 % of the genotypes was estimated in accordance with the methods illustrated by Johnson *et al.* (11) as:

$GA = K\sigma ph^2$

$GAM = (GA/x) \times 100$

Where, k = the standardized selection differential at 5 % selection intensity (K = 2.063) and x is the mean of base population.

Mahalanobis D^2 statistics was used for assessing the genotypic divergence between populations (Mahalanobis, 13). The square generalized distance (D^2) between any two populations can be calculated with the help of following formula :

$D^2 = \Sigma\Sigma\lambda ij \; \sigma_{ai} \; \sigma_{aj}$

where,

D^2 = Square of generalized distance

λ_{ij} = Reciprocal of the common dispersal matrix

$\sigma_{ai} = (\mu_{i1} - \mu_{i2})$

$\sigma_{aj} = (\mu_{i1} - \mu_{i2})$

μ = General mean

Since, the formula for computation requires inversion of higher order determinant, transformation of the original correlated unstandardized character mean (Xs) to standardized uncorrelated variable (Ys) was done to simplify the computational procedure. The D^2 values were obtained as the sum of squares of the differences between pairs of corresponding uncorrelated values of any two uncorrelated genotype of D^2 value (Rao, 17). All n (n - 1)/2 D^2 values were clustered using Tourcher's method described by Rao (17).The intra - cluster distances were calculated by the following formula given by Singh and Choudhary (19).

Square of the intra cluster distance $= \frac{\Sigma D^2 i}{n}$

where,

$\Sigma D^2 i$ is the sum of distance between all possible combinations of the entries included in a cluster.

n = Number of all possible combinations.

The inter cluster distances were calculated by the formula described by Singh and Choudhary (19).

Square of the intra cluster distance $= \frac{\Sigma D^2 i}{n_i \; n_j}$

Where,

$\Sigma D^2 i$ is the sum of distance between all possible combinations ($n_i n_j$) of the entries included in the clusters under study.

n_i = Number of entries in cluster i

n_j = Number of entries in cluster j

RESULTS AND DISCUSSION

The univariate mean squares (ANOVA) showed significant ($p<0.01$) variation among the okra genotypes for all the eleven traits under study. Similar results were found by Moll *et al.* (15) and Pradip *et al.* (16). The significance signifies the possibility of using all traits for further analysis. The mean performance of the 50 genotypes along with range and CD for all the characters is presented in Table 1. The genetic constants for the characters revealed that the magnitude of phenotypic co-efficient of variation (PCV) was higher than the corresponding genotypic co-efficient of variation (GCV) denoting environmental factors influencing their expressions to some degree or other. Narrow difference between PCV and GCV suggested their relative resistance to environmental alteration. In the present study, the PCV and GCV were higher for number of branches per plant, number of first fruiting nodes per plant and fruit yield per plant (Table 1). High amount of GCV and PCV suggested ample scope for selection of superior genotypes for these traits. The estimation of heritability along with the coefficient of variability would mean the amount of advance expected. Burton (4) also suggested that GCV and heritability estimate would give better information about the efficiency of the selection. The utility of heritability is increased when it is used to estimate genetic advance (Johnson *et. al.,* 11). Cultivar development is, however, firstly based on the exploitation of genetic variability of the genotypes with the traits of interest (Makanda *et al.,* 14).The genetic advance has an added edge over heritability as a guiding factor to breeders in selection programme. High heritability coupled with high genetic advance as percentage

Table1: Estimates of mean, range, phenotypic & genotypic coefficient of variation, heritability (h^2) and genetic advance as per cent of mean for eleven characters in okra.

Characters	Mean	Mean square	Range	H^2(broad sense)	GA	GA as % mean	GCV	PCV
Number of days to first flower	52.50	266.93**	45.68-65.45	95.20	9.20	17.52	8.72	8.93
Plant height up to Ist fruiting node (cm)	22.87	192.56**	12.35-31.15	92.60	7.81	34.15	17.23	17.91
No. of first fruiting nodes / plant	8.29	33.99**	4.99-12.22	92.10	3.26	39.32	19.89	20.72
Final plant height (cm)	86.89	1303.79**	70.89-119.83	97.30	20.93	24.09	11.85	12.02
No of branches/ plant	5.61	15.04**	3.27-8.26	82.80	2.04	36.36	19.43	21.35
No of fruiting nodes /plant	19.07	116.42**	14.38-26.83	95.20	6.20	32.52	16.17	16.58
Length of the fruit (cm)	12.32	26.59**	9.69-15.45	85.90	2.81	22.80	11.96	12.90
Thickness of the fruit (cm)	2.09	0.91**	1.63-2.86	52.90	0.37	17.71	11.88	16.34
Weight per fruit (g)	12.65	40.56**	8.48-17.79	93.10	3.62	28.62	14.41	14.94
Number of fruits per plant	16.29	31.90**	12.31-19.36	84.80	3.02	18.53	9.79	10.63
Fruit yield per plant (g)	184.61	14592.3**	134.29-314.71	91.50	67.75	36.70	18.62	19.46

Table 2: Number of genotypes in each cluster for 11 characters of okra genotypes.

Cluster	No of genotypes	Genotypes
I	5	KS-1713 (G_{20}), VRO-5 (G_{25}), Barkha (G_{36}), Sel-1 (G_{37}),SSH-325 (G_{42})
II	6	BO-22 (G_{31}), BH-9 (G_{44}), IC-8899 (G_{45}), IC-12930 (G_{46}), IC-10256 (G_{49}), White Snow (G_{50})
III	7	KS-404 (G_2), KS-312 (G_4), P.L.Green (G_{13}), Arka Anamika (G_{17}), Pusa Sawani (G_{18}), Varsha Uphar (G_{34}), Pusa Arkit (G_{40})
IV	15	IC-43750 (G_{14}), IC-43720 (G_{15}), IC-33332 (G_{16}), KS-423 (G_{19}), KS-7219 (G_{21}), KS-314 (G_{22}), KS-7109 (G_{23}), AB-2 (G_{24}), KS-455 (G_{26}), KS-450 (G_{27}), KS-454 (G_{28}), KS-442 (G_{29}), KS-440 (G_{30}), Komal (G_{35}), EC-32598 (G_{47})
V	3	Dwarf Green (G_9), L.G.Smooth (G_{10}), P-77 (G_{32})
VI	6	KS-208 (G_1), KS-305 (G_3), P-7 (G_5), BO-2 (G_6), Pusa Makhamali (G_{11}), White Velvet (G_{12})
VII	3	Parbhani Kranti (G_7), Parbhani Tripti (G_8), Bio Aparajita (G_{39})
VIII	5	Hissar Unnat (G_{33}), Sel. Vibha (G_{38}), Meeruti Local-1 (G_{41}), Local-2 (G_{43}), L.G.Velvet (G_{48})

of mean was found for the number of first fruiting nodes / plant suggesting presence of additive gene action making these characters to respond better to selection. The higher estimates of heritability and lower estimates of genetic advance as percentage of mean may be attributed to the non-additive gene effects. Medium heritability and low genetic advance as percentage of mean suggests that these traits are under the control of epistatic interactions.

Fifty genotypes were grouped into eight clusters (Table 2), Maximum of 15 genotypes were grouped into cluster IV (Table 2). The intra–cluster (within cluster) distance was ranging from 1.797 to 2.351 and inter–cluster (between cluster) distance was ranging from 2.239 to 6.956 (Table 3). The inter-cluster distance was higher than intra-cluster distance, which indicated wide genetic diversity among the accessions of different groups than those of same cluster. This suggested that genotypes occupying the same cluster have little diversity and selection of parents from within the cluster may not be considered promising for the development of good segregants through hybridization programme (Goel *et al.*, 7). The inter cluster distances were greater than the intra cluster distances, further indicating the considerable amount of diversity among the genotypes studied. Inter-cluster distance is the main criterion for selection of genotypes on the basis of D^2 analysis. Genotypes for the 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 clusters.

The diversity among the present set of material was also supported by the appreciable amount of variation among cluster means for different characters (Table 4).The cluster VII registered the highest mean value for fruit yield per plant 207.54 (g/per plant), number of fruits per plant (18.42), weight per fruit (g) (15.90), length of the fruit (14.99 cm.), no of fruiting nodes /plant (25.45), final plant height (cm) (103.15), no of first fruiting nodes / plant (11.84) and plant height up to first fruiting node (19.37cm.). The second lowest mean value for number of days to first flower (48.12), which is desirable, is also attached to this cluster after lowest mean value of cluster III (46.76).

Analysis of contribution of the characters to genetic diversity (Table 4) revealed that plant height (cm) and plant height up to first fruiting node contributed 18% and 16.2% respectively followed by no of branches/ plant (11.41%) and weight per fruit (g) (9.76%), however, fruit yield per plant (g) contributed lowest (2.09%). Hence, selection for divergent parents based on highly contributing characters will be useful for heterosis breeding in okra. De *et al.* (5) proposed that traits contributing maximum towards the D^2 values need to be given more emphasis for deciding the clusters to be taken for further selection and choice of parents for hybridization. Moll *et al.* (15), John *et. al.,* (10), Abdul *et al.* (1) and Pradip *et al.* (16) also observed similar level of contribution of plant height (cm), fruit length (cm) and weight of fruits per plant (g).The characters contributing maximum to D^2 values are to be given greater emphasis for deciding the clusters for the purpose of further selection and hybridization. The maximum per cent contributing towards genetic divergence was showed by the final plant height, plant height up to first fruiting node and no. of branches/ plant followed by weight per fruit, no of fruiting nodes /plant and no. of fruit per plant. These six characters contribute 73.77% towards total divergence. Here it is obvious that cluster VII is a divergent cluster and having favourable means for almost all the characters under study. The selection of diverse genotypes with desirable traits and in turn utilizing them for multiple crossing programmes

Table 3: Intra and inter cluster distance (D) values in 50 genotypes of okra.

Cluster	I	II	III	IV	V	VI	VII	VIII
I	**1.947**							
II	3.300	**1.797**						
III	3.782	3.736	**2.351**					
IV	2.239	3.178	3.820	**2.063**				
V	3.429	2.993	3.551	3.820	**2.045**			
VI	3.272	4.033	2.821	2.885	3.558	**2.126**		
VII	6.690	6.956	3.969	6.640	6.588	5.417	**2.210**	
VIII	3.807	4.442	3.863	3.386	5.378	4.216	4.889	**2.045**

Table 4: Cluster means and per cent contribution of different characters.

Character / Cluster	Number of days to first flower	Plant Heightup to first fruiting node (cm)	No of first fruiting nodes / plant	Final plant height (cm)	No of branches/ plant	No of fruiting nodes /plant	Length of the fruit (cm)	Thickness (girth) of the fruit (cm)	Weight per fruit (g)	Number of fruit per plant	Fruit yield per plant (g)
I	51.28	23.60	5.78	85.26	5.88	19.85	11.47	2.27	13.37	14.79	167.56
II	50.27	20.90	8.00	80.10	7.06	17.34	10.55	1.91	10.54	17.14	157.82
III	46.76	22.50	9.19	98.71	5.13	20.84	12.86	2.00	12.38	18.04	200.38
IV	55.85	25.29	8.27	81.95	5.44	16.73	12.03	2.17	12.60	14.77	165.73
V	48.02	15.86	6.03	84.92	5.29	18.28	12.99	1.86	10.38	16.40	160.33
VI	54.52	19.91	8.58	89.82	4.41	19.31	13.13	2.46	12.12	17.22	184.76
VII	48.12	19.37	11.84	103.15	5.26	25.45	14.99	1.83	15.90	18.42	270.54
VIII	57.34	27.68	8.93	82.91	6.70	21.29	12.57	1.92	15.08	16.52	231.22
Contribution of individual characters towards total genetic divergence (%)	8.69	16.2	3.87	18	11.41	9.43	5.65	8.02	9.76	8.97	2,09

amongst themselves is expected to be effective in accumulation of favourable genes for bringing together different desirable traits in to the common genetic background. On the other hand genotype included in the same cluster with a high order of divergence will be expected to provide the best breeding material for achieving the maximum genetic gain for yield. It is encouraging that the divergence revealed in the present genotypes based on the studied characters will offer a good scope as far as improvement in okra is concerned.

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