



Genetic variability and divergence in okra (*Abelmoschus esculentus*)

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Okra [*Abelmoschus esculentus* (L.) Moench.], a member of the family Malvaceae, is an important vegetable crops grown extensively in tropical to subtropical climates. Genetic improvement mainly depends on the amount of genetic variability present in the population. In any crop, the germplasm serves as a valuable source of base population and offer major source of variability (Ramya and Senthil Kumar 2009). The total variability can be partitioned into heritable and non-heritable components with the help of genetic parameters like phenotypic and genotypic coefficients of variation, heritability and genetic advance. Heritability denotes the proportion of phenotypic variation repeatable and is due to genes and thus helps the breeders to select the elite variety for a character. However, heritability indicates only the effectiveness with which selection of a genotype can be based on phenotypic performance but it fails to indicate the expected genetic progress in one cycle of selection. Heritable variation can be effectively used with greater degree of accuracy when heritability is studied in conjunction with genetic advance (Johnson *et al.* 1955). The wide genetic diversity that exists in the available germplasm provides an ample scope for further improvement. Progress in breeding for economic characters often depends on the availability of large germplasm representing a diverse genetic origin. However, for a long term improvement programme, a large and diverse germplasm collection is an invaluable source of supply of parental strains for hybridization and subsequent development of improved varieties (Sanwal *et al.* 2012). The clustering of okra genotypes on the basis of genetic divergence (D^2) may provide the basis for selection of suitable parents for hybridization programme.

The present study with forty genotypes of okra in randomized block design (RBD) with three replications was carried at the research farm of the Department of Vegetable

Science, CCS Haryana Agricultural University, Hisar, during spring summer season 2010-11. Phenotypic and genotypic co-efficients of variability, broad sense heritability (h^2) and expected genetic advance were estimated as suggested by Burton (1952), Hanson *et al.* (1956) and Johnson *et al.* (1955) respectively. The genetic divergence among genotypes was estimated by using D^2 statistics (Mahalanobis 1936). All the genotypes used were clustered into different groups by following Tocher's method (Rao 1952). The average intra and inter cluster distances were calculated by the formulae given by Singh and Chaudhary (1985).

The genetic parameters for different characters are presented in Table 1. In general, the values of phenotypic co-efficient of variations were higher magnitude than that the corresponding genotypic co-efficient of variations for all the characters showing that the environment had an important role in influencing the expression of these characters, but in present study almost similar trend and similar magnitude of PCV and GCV showed that environment did not much influence the estimates of genetic performance. Majority of the characters except first fruiting node, branches/plant and seeds/fruit recorded smaller differences between PCV and GCV values as they were less influenced by the environment indicating reliability of selection based on these traits. The estimates of PCV and GCV were moderate for plant height, internodal length, branches/plant, fruits/plant, seeds/fruit, test weight and fruit yield/plant indicating phenotypes reflected the genetic worth of the genotypes. Moderate PCV and low GCV values were observed for first fruiting node. Low PCV and GCV values were observed for stem diameter, days to first flowering, days to 50% flowering, days to first harvest, fruit length, fruit diameter and fruit weight indicating limited scope for improvement for these traits using these genotypes. The results were supported by Yadav *et al.* (2010).

High heritability estimates were found for the characters, viz. plant height, stem diameter, internodal length, days to first flowering, days to 50% flowering, fruits/plant, days to first harvest, fruit length, fruit diameter, fruit weight, test

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Table 1 The genetic parameters for various characters in okra

Characters	Mean	Range		PCV (%)	GCV (%)	h ² (%)	GA	GAM
		Min	Max					
Plant height (cm)	122.2	90.3	164.8	15.31	12.98	71.80	27.68	22.65
Stem diameter (cm)	1.11	0.97	1.29	7.28	6.47	79.16	0.13	11.86
Internodal length (cm)	4.84	3.13	6.07	16.3	14.35	77.48	1.26	26.01
Branches/plant	2.57	1.67	3.2	17.87	13.47	56.79	0.54	20.91
Days to first flowering	42.4	38.9	49.6	6.33	5.62	78.90	4.36	10.3
Days to 50% flowering	45.3	40	52	6.45	5.5	72.58	4.37	9.65
First fruiting node	4.19	3.47	5.2	11.63	6.16	28.04	0.28	6.72
Fruits/plant	14.7	10.6	20.6	17.79	16.28	83.80	4.52	30.7
Days to first harvest	51.3	46	58	5.7	4.85	72.58	4.37	8.52
Fruit length (cm)	8.91	8.08	10.2	6.76	5.34	62.30	0.77	8.67
Fruit diameter (cm)	1.39	1.28	1.55	4.94	4.42	79.86	0.11	8.13
Fruit weight (g)	7.67	6.62	9.12	8.72	7.74	78.77	1.09	14.14
Seeds/fruit	55.9	38.4	69.7	16.14	12.27	57.79	10.74	19.22
Test weight (g)	63.8	50.4	75.2	11.49	10.8	88.29	13.34	20.9
Fruit yield/plant (g)	112.9	80.6	170.2	19.44	17.9	84.76	38.32	33.95

weight and fruit yield/plant advocating that the selection based on phenotypic performance of these characters would be more operative and these were witnessed by Singh *et al.* (2006), Yadav *et al.* (2010) and Kumar *et al.* (2011). High genetic advance as percent of mean (GAM) was observed for plant height, internodal length, branches/plant, fruits/plant, test weight and fruit yield/plant and moderate for stem diameter, days to first flowering, fruit weight and seeds/fruit. Characters like days to 50% flowering, first fruiting node, days to first harvest, fruit length and fruit diameter displayed low GAM values.

High heritability coupled with high genetic advance as percent of mean was observed for the characters like plant height, internodal length, fruits/plant, test weight and fruit yield/plant, which indicated that these traits were under the strong influence of additive gene action and hence simple selection based on phenotypic performance of these traits would be more effective. Similar results were obtained by Singh *et al.* (2006). High heritability and moderate GAM values were observed for the characters stem diameter, days to first flowering and fruit weight. High heritability and low GAM values were observed for days to 50% flowering, days to first harvest, fruit length and fruit diameter. This indicated the influence of non-additive gene action and considerable influence of environment on the expression of these traits. It showed that the material is to be evaluated over locations and years to get the representative estimates for use in breeding.

Genetic variability studies indicated that there was considerable variability among all the genotypes as long as individual characters were considered, but grouping of genotypes in divergence study indicated that the genotypes in a group were almost similar for the characters under study.

Moreover, genetic variability, heritability and genetic advance could be used to formulate effective selection criteria, but these would not be reliable for selection of parents for hybridization programme, which could be fulfilled by divergence study as genetically divergent parents within the compatible region would give more heterotic hybrids.

Based on D² values, the genotypes were grouped into nine highly divergent clusters (Table 2). The magnitude of D² values confirmed that there was considerable amount of diversity in the experimental material evaluated. Cluster-5 contained highest number of genotypes (8), while cluster-6 had lowest number of genotypes (2).

The mean intra and inter cluster D² values (Table 3) revealed that the least intra cluster distance, while the maximum intra cluster distance was recorded in cluster-9, which may be due to limited gene exchange or selection practices among the genotypes for diverse characters. The highest inter cluster generalized distance was between cluster-6 and 9 followed by clusters-4 and 7 indicating wider genetic diversity among the genotypes included in these groups. Among these four clusters, cluster-6 and 4 had higher cluster mean values (Table 2) for important yield components, whereas cluster 7 and 9 had poor cluster mean values for various important traits. Therefore, the other clusters, which fulfill the criteria of having high cluster mean values for most of the yield attributing characters, were cluster-5 and 8. Out of six possible combinations from these clusters (6, 4, 5 and 8) most divergent cluster combinations 6-8 (6.166), 4-8 (6.101) and 4-6 (5.753) were isolated. The involvement of genotypes belonging to cluster-6 and 8, 4 and 8, and 4 and 6 in hybridization would help in achieving novel recombinants. Similar observations were reported in okra by Dhankhar *et al.* (2008).

Table 2 Mean values of clusters for fifteen characters in forty okra genotypes

Cluster Number	No. of genotypes	Plant height (cm)	Stem diameter (cm)	Inter nodal length (cm)	Branches/plant	Days to first flowering	Days to 50% flowering	First fruiting node	Fruits/plant	Days to first harvest	Fruit length (cm)	Fruit diameter (cm)	Fruit weight (g)	Seeds/fruit	Test weight (g)	Fruit yield/plant (g)
1	3	126.4	1.08	5.32	1.93	42.0	45.1	4.00	14.0	51.1	9.47	1.33	7.35	56.9	6.03	102.73
2	5	127.6	1.12	5.43	2.69	41.1	44.1	3.97	12.6	50.1	8.50	1.37	8.05	59.2	6.34	101.57
3	4	105.3	1.05	3.79	2.85	42.0	44.8	4.27	12.6	50.8	8.91	1.36	7.66	56.7	6.20	96.70
4	4	106.6	1.12	5.13	2.50	39.4	41.3	3.90	14.5	47.3	9.62	1.40	8.23	62.7	6.84	119.20
5	8	136.2	1.08	4.85	2.61	40.8	44.0	4.23	17.9	50.0	8.86	1.38	7.68	55.7	6.74	137.77
6	2	139.1	1.28	4.82	2.17	41.2	44.0	4.43	18.4	50.0	9.04	1.29	7.86	58.6	6.22	142.92
7	5	125.0	1.10	4.75	2.67	46.3	48.9	4.76	12.9	54.9	8.87	1.39	7.96	50.8	5.91	102.54
8	6	114.2	1.15	4.21	2.51	43.5	46.8	4.19	15.3	52.8	8.67	1.49	7.31	52.9	5.89	112.01
9	3	115.1	1.16	5.78	2.82	45.8	48.4	3.84	12.9	54.4	8.62	1.42	6.77	52.2	7.35	87.52

Table 3 Average intra (bold) and inter-cluster D² values for nine clusters among forty genotypes of okra

Cluster number	1	2	3	4	5	6	7	8	9
1	3.863	4.579	5.125	4.960	5.003	5.932	5.722	5.342	6.098
2		3.845	4.763	4.716	4.829	5.682	5.755	5.322	5.852
3			4.248	5.333	5.398	6.559	5.446	5.058	6.369
4				3.487	4.986	5.753	7.229	6.101	7.208
5					3.913	4.845	6.195	5.358	6.748
6						4.439	6.758	6.166	7.653
7							4.428	5.179	6.041
8								4.204	5.773
9									5.350

SUMMARY

Forty genotypes of okra were evaluated for estimating the genetic variability and divergence. Moderate PCV and GCV values for plant height, internodal length, branches/plant, fruits/plant, seeds/fruit, test weight and fruit yield/plant indicated sufficient genetic variability present among the genotypes for these characters. High heritability coupled with high genetic advance as percent of mean was observed for the characters like plant height, internodal length, fruits/plant, test weight and fruit yield/plant. The forty lines were grouped into nine clusters based on D² values. The cluster-4 displayed the least intra cluster distance, while the maximum intra cluster distance was recorded for cluster-9. The highest inter cluster generalized distance was found between cluster-6 and cluster-9 followed by clusters-4 and 7. The involvement of genotypes belonging to cluster-6 and 8, 4 and 8, and 4 and 6 in hybridization would help in achieving novel recombinants.

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