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Genetic divergence and its implication in breeding of desired plant type in okra (*Abelmoschus esculentus*)*

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Progress in breeding for economic characters often depends on the availability of a large germplasm representing a diverse genetic origin. In crops such as okra[*Abelmoschus esculentus* (L.) Moench], germplasm is available in the form of a multitude of homozygous lines which can be released as improved cultivars in specific ecological areas. 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. The limitations resulting from normal pollination concerning biparental heredity, makes a critical choice of parents in breeding programmes necessary, especially when polygenic characters are involved.

D^2 analysis following multivariate analysis plays an important role in screening germplasm lines for breeding purposes. Crosses between genetically diverse parents would manifest more heterosis than crosses of between closely related parents (Oriyo 1987). Hence, the present study was undertaken with the objectives: (i) to study the nature and magnitude of genetic divergence, (ii) to identify characters which contribute maximum to genetic diversity, and (iii) to identify suitable genotypes for use in breeding programme for broadening the genetic base in okra.

The 67 okra genotypes were grown in a completely randomized block design with three replications in summer season of 2010. The plot for each genotype consisted of five rows of 3 m spaced at 60 cm, while the plants were spaced at 30 cm. Recommended cultural practices were followed to raise a good crop. Field observation were recorded for plant height (cm), days to 50% flowering, first flowering node, stem diameter (cm^2), number of fruit/plant, fruit length (cm), fruit diameter (cm^2), 10 fruit weight and fruit yield/plant. Five competitive plants were randomly selected from the central row of each plot for observation on the quantative traits.

Mean data of each treatment over replications was used for statistical analysis. D^2 statistic was employed to determine the degree of differentiation among n (n-1)/2 pairs of 'n' population (Rao 1952). Grouping of genotypes was done according to Tochar's method (Rao 1952).

The analysis of plot means revealed significant differences among 67 genotypes for each of nine characters suggesting appreciable variability among the genotypes. The simultaneous testing of significance based on Wilk's (Lambda) criterion also showed significant differences among cultivars for aggregate of all the character (÷2 594 df = 2892.93**). The D^2 values estimated for 67 germplasm lines in n (n-1)/2 = 2211 combinations varied from 2.32 to 538.69 indicating the presence of substantial amount of genetic diversity in the population. The 67 genotypes were grouped in five clusters depending upon their morphological similarity. The cluster I was the largest having 33 genotypes, followed by clusters II having 27 genotypes. The cluster IV contains five genotypes. The minimum single genotype was noticed in cluster III and V. Clustering pattern (Table 1) indicated that majority of genotypes, i e 60 (89%) were genetically close to each other and grouped in two clusters, while apparent diversity was mainly noticed due to seven genotypes (11%) distributed over three clusters. The genotypes involved in clustering are group of Indian land races, improved varieties, exotic collections and selections obtained through different breeding programme maintained at Indian Institute of Vegetable Research, Varanasi for the last two decade. The clustering pattern was also confirmed by spatial distribution of genotypes under canonical analysis. The Distribution pattern of genotypes of diverse origin in a single cluster indicates that the geographical origin in okra was not related to genetic divergence (Oriyo 1987). The tendency of genotypes occurring in clusters cutting across the geographical

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*Short note

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Table 1 Composition of Different clusters in okra

Cluster	Number of genotypes	Genotypes
I	33	112-10-4-1, 2 156-10 -1, 2 139-10-3, GS 43, JKOH 3001, Larm 1, BO-2, VRO 6×29×Red Plant, SB 4, BO 13, P 7, 113-8-1×152-10, EC 324402, VRO 3, Sel 10, EMS 8-1, Sel 4, EC 329380, 67-10-2, VRO 4, OH 152×136-13, EC 65939, VRO 6×13-8-1×152-10, OH 152×136-3 Green, Pusa Sawani, P 4, Pusa Makhmali, EC-305616, HRB 108-2, HRB 55, SB 8, VRO 6, SPS 8
II	27	DOV 91-4, 463-9-1, VRO 5, OH 152×136-11, IIVR 10, 136thin×OH 152, 136thin, Bhindi Vaphy, OH 152×136-9, OH 152×136-3 Dark green, OH 152×136-10, EC 169359, 407-8-1, E 305662, 338-8-1, OH 152×136-3, 338×113-8-1×152-10, 329-8-1, 325-8-1, 329-8-1 Sath dhari, OH 152 × 136 thin red plant, EC 133336, 328-8-1, 113-8-1 × 152 RSGPPS, IIVR 11, D 1-87-5, EC 169366
III	1	SB 6
IV	5	SB 2, KS 410, OH 152, EC 169384, N 55
V	1	315

Table 2 Intra (bold) and Inter cluster distance (D^2) in okra

Cluster	I	II	III	IV	V
I	**7.04**	10.32	8.93	10.53	16.84
II		**7.70**	14.41	15.94	11.29
III			**0.00**	7.94	21.46
IV				**9.23**	23.38
V					**0.00**

boundaries demonstrate that geographical isolation need not necessary be related to genetic diversity and was at random (Bisht *et al*. 1995). This means that geographical diversity though important may not be factor in determining genetic divergence. The genotypes originating from one place as in present study were scattered in five clusters. Such parallelism between geographical distribution and genetic diversity might be due to some forces other than geographical distance like genetic architecture of population, heterogeneity, history of selection, proximity of development of traits etc. Genetic drift may be another cause for genetic diversity (Duzyaman and Vural 2002).

The intra-cluster value was variable between 0.0 and 9.23 (Table 2), the maximum being in cluster IV (9.23), followed by II (7.70) and I (7.04). The maximum intercluster distance was noticed between IV and V (23.38), followed by III and V (21.46), I and V (16.84). This indicates that the genotype of these clusters diverse much to each other. The magnitude of heterosis largely depends on degree of diversity in the parental lines, the higher distance between two clusters, the greater genetic diversity between genotypes. Crosses between genetically diverse parents would manifest more heterosis than the crosses between closely related parents (Dhankar *et al.* 2008). Hence genetic divergence seems to be more important tool to select perspective parents for crop improvement programme.

Considering the cluster means (Table 3) the maximum fruit yield/plant (258.73 g), stem diameter (1.22 cm^2), plant height (107.73 cm) and next to highest number of fruits/plant (15.73) and 10 fruit weight (162 g) was noticed in cluster IV. This cluster had moderate flowering (43 days) and medium fruit diameter (1.59 cm^2). Contrary to this the cluster V having single variety (No. 315) was separated by other clusters due to lowest mean values of plant height (25.83 cm), stem diameter (1.07 cm^2), number of fruits/plant (12.5), fruit length (12.20 cm) and highest fruit diameter (1.83 cm^2) and 10 fruit weight (190 g). The cluster I had lowest fruit yield/plant (214.58 g), fruit diameter (1.50 cm^2), and next to lowest fruit weight (159.09 g), number of fruits/plant (13.15), stem diameter (1.12 cm^2), and also had higher number of Ist flowering node (4.28). Contrary to this the cluster III having single variety (SB-6) was separated by other clusters due to minimum number of days to 50% flowering (40), maximum number of fruits/plant (17.67), fruit length (15.47 cm) and next to highest fruit yield/plant (251.23 g), fruit diameter (1.73 cm^2), plant height (101.67 cm), stem diameter (1.20 cm^2) and highest number of first flowering node (6.03). From cluster mean, it is evident that yield in okra is greatly influenced by different component traits mainly number of fruits/plant, fruit weight and fruit diameter (Dhankar *et al.* 2008).

Table 3 Cluster mean for different characters in okra

Cluster	Plant height (cm)	Days to 50% flowering	First flowering node	Stem diameter (cm^2)	Number of fruits/ plant	Fruit length (cm)	Fruit diameter (cm^2)	Ten fruit weight (g)	Fruit yield/ plant (g)
I	82.68	42.21	4.28	1.12	13.15	14.22	1.50	159.09	214.58
II	57.01	44.04	3.92	1.14	13.82	13.92	1.50	159.48	231.67
III	101.67	40.00	6.03	1.20	17.67	15.47	1.73	140.00	251.23
IV	107.73	43.00	4.20	1.22	15.73	13.57	1.59	162.00	258.73
V	25.83	41.00	4.17	1.07	12.50	12.50	1.83	190.00	241.13

Considering vector analysis plant height (0.969), number of first flowering node (0.138), and fruit yield/plant (0.127) in first vector, number of fruits/plant (0.915), days to 50% flowering (0.239), fruit yield/plant (0.077) and plant height (0.046) in second vector and days to 50% flowering (0.916), fruit length (0.170), stem diameter (0.120) and fruit weight (0.118) were noticed important contributor respectively to the total divergence. Out of total diversity, 84% was accounted by first three canonical roots and of these more than 74% was contributed by first two vectors (X + Y) suggesting that the differentiation for characters was nearly completed in three phases (Table 4). In present investigation plant height, first flowering node, fruit yield and days to 50% flowering exhibited maximum towards genetic divergence (Patel *et al.* 2006).

In genetic improvement (for high yield) the choice of parent is important and desirable component characters of yield should be taken into consideration for component breeding to obtain appropriate plant type (Bendale, *et al.* 2008). Overall cluster V, IV, and III showed greater potential as a breeding stock by virtue of high mean values of one or more component characters as well as high statistical distance. The crossing among genotypes of these clusters selected for specific component traits may be helpful in bringing new gene pool and expanding the range of adaptation. Continuous selection in advance generation may lead to develop lines with high yield combining desirable component traits.

Table 4 Canonical vectors showing best linear functions of variates in okra

Character	Vector 1	Vector 2	Vector 3
Plant height	096944	0.04608	0.08183
Days to 50% flowering	–0.04759	0.23850	0.91628
First flowering node	0.13756	0.02314	–0.11939
Stem diameter	–0.01857	0.6011	0.11974
Number of fruits/plant	–0.06145	0.91544	–015816
Fruit length	–0.06553	–0.26644	0.16995
Fruit diameter	–0.11734	0.02489	–0.08456
Ten fruit weight	0.02449	–0.14568	0.11863
Fruit yield/plant	0.12736	0.07734	0.22364
Canonical percentage	59.17639	14.82390	10.50293

SUMMARY

Sixty-seven germplasm lines of okra [*Abelmoschus esculentus* (L.) Moench] of diverse eco-geographical origin were undertaken in present investigation to determine the genetic divergence following multivariate and canonical analysis for fruit yield and its eight component traits. The 67 genotypes were grouped into five clusters depending upon the genetic architecture of genotypes and characters uniformity and confirmed by canonical analysis. Eighty-nine per cent of total genotypes (60/67) were grouped in two clusters (I, II), while apparent diversity was noticed for 11% genotypes (7/67) that diverged into three clusters (III, IV and V). The maximum intercluster distance was noticed between IV and V (23.38), followed by III and V (21.46), I and V (16.84). The cluster IV was very unique having genotypes of high mean values for most of the component traits. Considering high mean and inter cluster distance breeding plan has been discussed to select desirable plant types.

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