Journal of Agricultural Technology 2012 Vol. 8(2): 611-623
Available online http://www.ijat-aatsea.com
ISSN 1686-9141

Genetic divergence analysis of indigenous and exotic collections of okra (*Abelmoschus esculentus* (L.) Moench)

M. Thirupathi Reddy[1*], K. Haribabu[2], M. Ganesh[3], K. Chandrasekhar Reddy[4] and H. Begum[1]

[1]Vegetable Research Station, ARI, Rajendranagar, Hyderabad-500030, Andhra Pradesh, India, [2]Administrative Office, APHU, Venkataramannagudem, West Godavari (Dist.), Andhra Pradesh, India, [3]Administrative Office, ANGRAU, Rajendranagar, Hyderabad-500030, Andhra Pradesh, India, [4]College of Horticulture, Rajendranagar, Hyderabad-500030, Andhra Pradesh, India

M. Thirupathi Reddy, K. Haribabu, M. Ganesh, K. Chandrasekhar Reddy and H. Begum (2012) Genetic divergence analysis of indigenous and exotic collections of okra (*Abelmoschus esculentus* (L.) Moench). Journal of Agricultural Technology 8(2): 611-623.

Genetic divergence analysis following Mahalanobis D^2 statistics revealed considerable genetic diversity among 100 genotypes of okra (*Abelmoschus esculentus* (L.) Moench) for all the seventeen quantitative characters which pertaining to the growth, earliness and yield. Hundred genotypes were grouped into 11 distinct clusters depending upon the similarities of their D^2 values following Tocher's method. The clustering pattern of germplasm usually did not follow the geographical distribution. Appreciable diversity within and between 11 clusters was observed. The characters fruit length, internodal length and number of marketable fruits per plant were the potent factors in differentiating the germplasm of okra under study. The use of diverse genotypes from the clusters with high intercluster distance (cluster VI and X, VI and IX and VII and XI) in hybridization is expected to result in high heterosis and throw desirable transgressive segregants. The genotypes of six solitary clusters IV (IC043279-A) , IC033350(cluster VI), IC90210 (cluster VII), IC26375 (cluster IX), IC018530 (cluster X) and IC043751-B (cluster XI) being divergent from others may also serve as potential parents for breeding programmes.

Key words: clustering pattern, genetic diversity, Mahalanobis D^2 statistics, multivariate analysis, Tocher's method

Introduction

The cultivated okra (*Abelmoschus esculentus* (L.) Moench) also known as 'bhindi' or 'Lady's finger', belongs to the family Malvaceae. It is a native of Africa. It is widely distributed and cultivated in the tropics, sub-tropics and warmer portions of the temperate region of the world (Hammon and Van

* Corresponding author: Thirupathi Reddy, M.; e-mail: medagamtr@yahoo.co.in

Sloten, 1989). It is a multipurpose crop due to its various uses of the fresh leaves, buds, flowers, pods and stems, dry stems, pods and seeds (Martin, 1982; Kalra and Pruthi, 1984; Markose and Peter, 1990; Preston, 1998; Schippers, 2000). Okra has a prominent position among fruit vegetables due to its multiple virtues like high nutritive and medicinal value, ease of cultivation, wide adaptability, year round cultivation, good portability, export potential and bountiful returns. In spite of its multiple virtues, okra is being neglected because of the non-availability of high yielding, improved and locally adapted cultivars and reduction in yield due to frequent attack of shoot and fruit borer and yellow vein mosaic virus.

Evaluation of germplasm is pre-requisite to identify the desirable genotypes to feed the breeding programmes. The value of germplasm collection depends not only on the number of accessions it possesses, but also up on the genetic diversity present in those accessions for yield and yield components. India is one of the countries with largest collection of cultivated okra (*Abelmoschus esculentus* (L.) Moench) in the gene bank and as such its potential is not fully known. Further, being a potentially self pollinated crop, the cultivated okra has a narrow genetic base and concerted efforts, are therefore, required for exploring the full potential of available okra germplasm resources in the gene bank. Hence, the existing germplasm accessions need detailed evaluation for various horticultural traits to assess the nature and magnitude of genetic divergence among accessions, which is crucial for selecting genetically divergent parents for a productive breeding programme.

The success of breeding programme depends to a large measure on the degree of genetic divergence. Genetic diversity is a key factor for crop improvement. Genetic diversity is of paramount importance for heterosis. Hybridization between genetically divergent parents is expected to produce superior hybrids and desirable recombinants. 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). Multivariate analysis following Mahalanobis D^2 statistics revealed rich genetic diversity for various growth, earliness and yield associated traits in the germplasm offering a great scope for improvement of okra (Ghai *et al*., 2005; Kumari and Chaudhury, 2006; Singh *et al*., 2007; Bendale *et al*., 2003). The existing diversity has been exploited in various breeding programmes, which resulted in the development and release of a good number of varieties in okra. However, the released varieties cannot be continued longer due to genetic drift and susceptibility to various pests and diseases especially the fruit and shoot borer

and yellow vein mosaic virus. This demands replacement of current varieties by new varieties.

The present investigation was therefore, undertaken to assess the nature and magnitude of genetic diversity available in a large germplasm involving both indigenous and exotic collections of okra on the basis of various growth, earliness and yield attributes.

Materials and methods

The experimental material for the present study comprised of 100 genotypes of okra involving both indigenous and exotic collections augmented from National Bureau of Plant Genetic Resources Regional Station, Thrissur. The entire germplasm was evaluated in a randomized block design with two replications at Vegetable Research Station, Rajendranagar during *kharif* (rainy season), 2008. Each genotype was raised in a single-row plot of 3.00 m length x 0.60 m width. A row-to-row spacing of 60 cm and plant-to-plant spacing of 30 cm was adapted. A plant population of 10 plants per row, plot and genotype was maintained. Recommended agronomic practices were followed to raise the successful crop and necessary prophylactic plant protection measures were carried out to safeguard the crop from pests and diseases. Biometric data were recorded on five randomly selected plants in each genotype in each replication for plant height (cm), number of branches per plant, internodal length (cm), first flowering node, first fruiting node, fruit length (cm), fruit width (cm) and fruit weight (g) except days to 50 % flowering, total number of fruits per plant, number of marketable fruits per plant, total yield per plant (g), marketable yield per plant (g), fruit and shoot borer (FSB) infestation on fruits and shoots (%) and yellow vein mosaic virus (YVMV) infestation on fruits and plants (%) which were recorded on whole plot basis. The replicated mean values of fruit and shoot borer (FSB) infestation on fruits and shoots (%) and yellow vein mosaic virus (YVMV) infestation on fruits were subjected to square root transformation to restore the distribution to normality. The mean replicated data on various biometric traits were subjected to analysis of variance of randomized block design as per the standard statistical procedure (Panse and Sukhatme, 1985). The genetic divergence in the germplasm was assessed following Mahalanobis D^2 statistics (Mahalanobis, 1936). The genotypes were grouped on the basis of minimum generalized distance using Tocher's method as described by Rao (1952). The average intra and inter cluster distances were calculated by the formula given by Singh and Chaudhary (1979). The character contribution towards genetic divergence was computed using method given by Singh and Chaudhary (1979).

Results

The simultaneous significance of mean differences was tested by analysis of dispersion. The analysis of dispersion is presented in Table 1. The F-value is highly significant indicating large differences between the means of the populations based on pooled effect of all the seventeen characters and may be continued for further analysis for computing D^2 estimates.

Table 1. Analysis of variance for dispersion in okra germplasm

Source of variation	Degrees of freedom	Sum of squares	Mean sum of squares	F Ratio	Probability
Varieties	99	-1.1590E+09	-1.1708E+07	-8.3487E+13	0.0000**
Error	98	1.3743E-05	1.4023E-07		
Total	197	-1.1590E+09	-5.8835E+06		

** Significant at 1 % level.

Since all the seventeen variables were correlated, they were transformed into uncorrelated linear combination through pivotal condensation method. The quantitative assessment of genetic divergence among 100 genotypes of okra was made by adopting Mahalanobis D^2 statistics for seventeen characters following the procedure given by Rao (1952). The average D^2 values have been used for constellation of genotypes into clusters in such a way that the genotypes in the cluster had smaller average D^2 values than those belonging to different clusters.

The 100 genotypes of okra were grouped into eleven distinct clusters as evident from the clustering pattern (Table 2). The distribution of different genotypes into distinct clusters is shown in Table 1. Out of the eleven clusters formed, cluster II was the largest comprising of 33 genotypes, followed by cluster III with 25 genotypes, cluster V with 20 genotypes, cluster I with 10 genotypes, cluster VIII with 6 genotypes. Cluster VI, VI, VII, IX, X and XI were solitary with one genotype in each cluster.

Table 2. Clustering pattern of hundred genotypes of okra

Cluster	Number of genotypes	Genotypes included in cluster
I	10	IC033302, IC043748-B, IC013664, IC48948, IC90175, IC90205, IC90219, IC90233, IC103913, IC103998
II	33	IC032850, IC032855-A, IC033065-B, IC045791, IC113904, IC282238, IC282246, IC282276, IC128123, IC140898, IC218903, EC169447, EC169515, EC329356, IC008991, IC18542, IC33854-C, IC33953, IC39137-A, IC42485-B, IC42530, IC52298, IC89334, IC89712, IC89948, IC90077, IC90171 , IC90211, IC90213, IC90231, IC90234, IC99724, IC99757
III	25	IC282228, IC282245, IC282248, IC218900, IC003307, IC22237, IC27826-A, IC29119-B, IC29359-D, IC31398-A, IC31398-B, IC33854-B, IC45732, IC52298-B, IC58710, IC89819, IC89976, IC90107, IC90246, IC90249, IC99716, IC99780, IC111440, IC111443, IC413579
IV	1	IC043279-A
V	20	IC033301- Sel 86, IC033329, IC033345, IC043737, IC043745-B, IC069113-Sel 87, IC069261, IC282256, IC282294, EC169498, IC18537-A, IC28359, IC33854-A, IC52299, IC86008, IC90074, IC90082, IC90230, IC90251, IC90262
VI	1	IC033350
VII	1	IC90210
VIII	6	EC133408, EC329398, IC32398-A, 1C45747, IC90168, IC90209
IX	1	IC26375
X	1	IC018530
XI	1	IC043751-B

IC = Indigenous collection; EC = Exotic collection

Average intra and intercluster D^2 values are tabulated in Table 3, providing an interesting information on the nature of genetic divergence at intra and intercluster levels, respectively. In general, intracluster distances were much lesser than intercluster distances. The D^2 values computed for 1683 combinations among 100 genotypes ranged from 75.02 to 669.72. The group constellation showed that intracluster and intercluster D^2 values ranged from 0.00 (cluster IV, VI, VII, IX, X and XI) to 165.35 (cluster V) and 75.02 (between cluster IX and X) to 669.72 (between cluster VI and X), respectively.

Table 3. Inter (above diagonal) and intra (diagonal and bold) cluster distance (D^2 values) among genotypes of okra

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	43.57	96.24	129.56	96.20	116.06	281.19	194.14	243.29	193.41	147.55	205.84
II		68.91	167.53	93.15	134.20	199.99	130.41	148.09	274.48	272.32	347.29
III			112.20	230.20	196.21	463.23	257.33	340.42	174.79	140.80	313.93
IV				0.00	129.96	122.82	216.95	165.55	299.94	336.03	211.96
V					165.35	290.22	212.45	250.05	229.72	232.94	272.79
VI						0.00	294.73	140.29	614.82	669.72	537.19
VII							0.00	187.69	284.76	312.84	486.33
VIII								105.85	501.54	538.91	545.17
IX									0.00	75.02	176.56
X										0.00	246.49
XI											0.00

Among the eleven clusters, the intracluster distance was maximum in cluster V (165.35) followed by cluster III (112.20) and cluster VIII (105.85), while minimum in cluster I (43.57) followed by cluster II (68.91). The intracluster distance of solitary clusters IV, VI, VII, IX, X and XI was zero. The intercluster distance was maximum between cluster VI and X (669.72) followed by cluster VI and IX (614.82) and cluster VII and XI (545.17), while minimum between cluster IX and X (75.02) followed by cluster II and IV (93.15) and cluster I and IV (96.20).

The cluster means for different characters (Table 4) indicated considerable differences among the clusters. From the data, it can be seen that considerable differences exist for all the traits studied. The data indicated that cluster mean for plant height ranged from 79.90 cm (cluster XI) to 147.20 cm (cluster IX). Highest plant height was recorded in cluster IX (147.20 cm) followed by cluster X (147.00 cm) and cluster III (144.17 cm), while lowest plant height was recorded in cluster XI (79.90 cm) followed by cluster VI (81.00 cm) and cluster IV (90.20 cm). Number of branches per plant was highest in cluster I (3.63) followed by cluster IX (3.60) and cluster VIII (3.32), while the lowest in cluster IV and VII (2.20) followed by cluster III (2.23) and cluster II (2.64). Internodal length was maximum in cluster IX (10.00 cm) followed by cluster VII (9.20 cm) and cluster X (8.25 cm), while minimum in cluster VI (5.40 cm) followed by cluster IV (5.5 cm) and cluster I (6.00 cm).

Table 4. Cluster means of hundred germplasm lines for seventeen characters in okra

Character	I	II	III	IV	V	VI	VII	VII	IX	X	XI
1	106.36	118.25	144.17	90.20	115.93	81.00	109.20	113.90	147.20	147.00	79.90
2	3.63	2.64	2.23	2.20	3.09	3.30	2.20	3.32	3.60	3.10	3.30
3	6.00	6.60	7.07	5.50	6.90	5.40	9.20	6.55	10.00	8.25	6.20
4	46.40	46.20	42.96	51.00	49.43	51.00	45.00	49.17	48.50	45.50	53.00
5	5.12	5.00	4.84	5.70	5.60	8.10	5.10	5.87	5.30	5.70	4.70
6	5.20	5.04	4.88	5.80	5.64	8.10	5.10	5.93	5.30	5.70	4.70
7	13.55	11.57	13.57	12.60	12.93	10.00	10.00	9.37	14.90	15.50	16.30
8	1.82	1.80	1.92	1.85	1.87	1.85	1.65	2.15	1.95	1.75	2.15
9	15.42	13.24	15.38	15.05	14.23	13.50	16.67	13.42	17.76	17.95	20.50
10	12.50	13.05	15.89	10.59	11.51	6.90	6.77	11.68	9.42	12.16	8.19
11	10.24	10.32	13.14	7.11	8.93	4.74	5.64	9.19	7.08	10.45	5.77
12	192.17	172.59	242.61	159.61	161.27	93.37	112.86	156.26	166.86	217.75	167.41
13	156.98	136.66	200.00	107.05	124.84	64.17	94.08	123.12	125.31	187.08	118.00
14	2.76	2.90	2.86	2.97	2.94	3.00	2.66	2.86	3.00	2.85	3.01
15	2.31	2.46	2.34	2.55	2.50	2.52	2.12	2.39	2.57	2.42	2.66
16	3.20	3.56	3.03	4.91	3.67	4.71	3.10	3.61	3.98	2.44	4.54
17	38.00	45.91	42.60	60.00	47.75	55.00	30.00	47.50	55.00	30.00	60.00

1= Plant height (cm); 2= No. of branches per plant; 3= Internodal length (cm); 4= Days to 50% flowering; 5= First flowering node; 6= First fruiting node; 7= Fruit length (cm); 8= Fruit width (cm); 9= Fruit weight (g); 10= Total no. of fruits per plant; 11= No. of marketable fruits per plant; 12= Total yield per plant (g); 13= Marketable yield per plant (g); 14= FSB infestation on fruits (%); 15= FSB infestation on shoots (%); 16= YVMV infestation on fruits (%); 17= YVMV infestation on plants (%)

The genotypes of cluster III took minimum number of days to 50 % flowering (42.96 days) followed by cluster VII (45.00 days) and cluster X (45.5 days), while the genotypes of cluster XI took maximum number of days to 50 % flowering (53.00 days) followed by cluster IV and VI (51.00 days) and cluster V (49.43 days). The genotypes of cluster XI produced their first flower at the lowest node (4.70) followed by cluster III (4.84) and cluster II (5.00), while the genotypes of cluster VI produced their first flower at the highest node (8.10) followed by cluster VIII (5.87) and cluster IV and X (5.70). The genotypes of cluster XI produced their first fruit at the lowest node (4.70) followed by cluster III (4.88) and cluster II (5.04), while the genotypes of cluster VI produced their first fruit at highest node (8.10) followed by cluster VIII (5.93) and cluster IV (5.80).

The longest fruits were produced by the genotypes of cluster XI (16.30 cm) followed by cluster X (15.50 cm) and cluster IX (14.90 cm), whereas the shortest fruits were produced by the genotypes of cluster VIII (9.37 cm) followed by cluster VI and VII (10.00 cm) and cluster II (11.57 cm). The genotypes of cluster VIII and XI produced the widest fruits (2.15 cm), followed by cluster IX (1.95 cm) and cluster III (1.92 cm), while the genotypes of cluster VII produced the narrowest fruits (1.65 cm) followed by cluster X (1.75 cm) and cluster II (1.80 cm). The heaviest fruits were produced by the genotypes of

cluster XI (20.50 g) followed by cluster X (17.95 g) and cluster IX (17.76 g), while the lightest fruits were produced by the genotypes of cluster II (13.24 g) followed by cluster VIII (13.42 g) and cluster VI (13.50 g).

Total number of fruits per plant produced by the genotypes of cluster III was highest (15.89) followed by cluster II (13.05) and cluster I (12.50), while lowest by the genotypes of cluster VII (6.77) followed by cluster VI (6.90) and cluster XI (8.19). The genotypes of cluster III (13.14) produced maximum number of marketable fruits per plant followed by cluster X (10.45) and cluster II (10.32), while the genotypes of cluster VI (4.74) produced maximum total number of fruits per plant followed by cluster VII (5.64) and cluster XI (5.77).

The genotypes of cluster III (242.61 g) produced highest total yield per plant followed by cluster X (217.75 g) and cluster I (192.17 g), while the genotypes of cluster VI produced lowest total yield per plant (93.37 g), followed by cluster VII (112.86 g) and cluster VIII (156.26 g). The mean marketable yield of the genotypes of cluster III (200.00 g) was highest followed by cluster X (187.08 g) and cluster I (156.98 g), while lowest for the genotypes of cluster VI (64.17 g) followed by cluster VII (94.08 g) and cluster IV (107.05 g).

The per cent infestation of fruit and shoot borer on fruits was highest in the genotypes of cluster XI (3.01 %) followed by cluster VI and IX (3.00 %) and cluster IV (2.97 %), while lowest for the genotypes of cluster VII (2.66 %) followed by cluster I (2.76 %) and cluster X (2.85 %). The percent infestation of fruit and shoot borer on shoots was highest in the genotypes of cluster XI (2.66 %) followed by cluster IX (2.57 %) and cluster IV (2.55 %), while lowest for the genotypes of cluster VII (2.12 %) followed by cluster I (2.31 %) and cluster III (2.34 %).

The incidence of yellow vein mosaic virus on fruits was highest in the genotypes of cluster IV (4.91 %) followed by cluster VI (4.71 %) and cluster XI (4.54 %), while lowest for the genotypes of cluster X (2.44 %) followed by cluster III (3.03 %) and cluster VII (3.10 %). The incidence of yellow vein mosaic virus on plants was highest in the genotypes of cluster IV and XI (60.00 %) followed by cluster VI and IX (55.00 %) and cluster V (47.75 %), while lowest for the genotypes of cluster VII and X (30.00 %) followed by cluster I (38.00 %) and cluster III (42.60 %).

An assessment of relative contribution of seventeen characters towards total genetic divergence (Table 5) revealed that fruit length had contributed highest (40.02 %) by taking 1981 times first ranking followed by internodal length (16.89 %) by 836 times, number of marketable fruits per plant (10.81 %) by 535 times, fruit weight (8.04 %) by 398 times, first flowering node (4.95 %) by 245 times, fruit width (4.59 %) by 227 times, plant height (3.43 %) by 170 times, days to 50% flowering (3.39 %) by 168 times, YVMV infestation on

plants (2.81 %) by 139 times, total yield per plant (1.70 %) by 84 times, YVMV infestation on fruits (1.23 %) by 61 times, FSB infestation on fruits (1.09 %) by 54 times and number of branches per plant (1.01 %) by 50 times. In contrast, total number of fruits per plant and FSB infestation on shoots had contributed least (0.02 %) by taking 1 time. However, the traits first fruiting node and marketable yield per plant did not contribute materially towards total diversity.

Table 5. Percent contribution of different traits towards divergence of 100 genotypes of okra

Character	Number of times ranked first	Contribution towards divergence (%)
Plant height (cm)	170	3.43
No. of branches per plant	50	1.01
Internodal length (cm)	836	16.89
Days to 50% flowering	168	3.39
First flowering node	245	4.95
First fruiting node	0	0.00
Fruit length(cm)	1981	40.02
Fruit width(cm)	227	4.59
Fruit weight(g)	398	8.04
Total no. of fruits per plant	1	0.02
No. of marketable fruits per plant	535	10.81
Total yield per plant (g)	84	1.70
Marketable yield per plant (g)	0	0.00
FSB infestation on fruits (%)	54	1.09
FSB infestation on shoots (%)	1	0.02
YVMV infestation on fruits (%)	61	1.23
YVMV infestation on plants (%)	139	2.81

Discussion

The traditional approach to germplasm evaluation is based on morphological features. Evaluation of germplasm is done to provide information on genetic diversity within crop. Genetic diversity is an important factor for any heritable improvement. Divergence analysis generates valuable information on the nature and degree of genetic diversity, which is useful for selecting desirable lines from germplasm for successful breeding programme. Selection of lines based on individual attribute may not be as advantageous as the one based on a number of important traits collectively. Multivariate analysis provides valuable information on the extent of genetic diversity present in the germplasm. Mahalanobis D^2 statistics is a unique tool for quantifying degree of divergence between biological populations at genetic level. Mahalanobis D^2

statistics is based on multivariate analysis and serves to be a good index of genetic diversity. Very often phenotypic diversity has been taken as an index of the genetic diversity.

The results of Mahalanobis D^2 statistics revealed substantial and desirable genetic diversity among 100 germplasm lines included in the present study for all the seventeen characters under consideration collectively. Several authors also reported profound diversity in the germplasm of okra by assessing genetic divergence on the basis of quantitative traits following Mahalanobis D^2 statistics (Mishra and Chhonkar, 1979; Bindu *et al*., 1994; Sood and Jamwal, 1998; Bendale *et al*., 2003). Murthy and Arunachalam (1960) pointed that Mahalanobis D^2 statistics is an important breeding tool to evaluate the clustering pattern. Average inter and intracluster distances revealed that, in general, intercluster distances were much higher than those of intracluster distances, suggesting homogeneous and heterogeneous nature of the germplasm lines within and between the clusters, respectively. These results are in accordance with the findings of Partap *et al*. (1980), Mandal and Dana (1993); Vahab *et al*. (1994) in okra.

Mahalanobis D^2 statistic was found to be a useful tool to assess the relative contribution of different characters to the total divergence both inter and intracluster levels. In general, the characters responsible for discrimination between populations can narrow down the problem of selecting divergent parents for breeding programme.Amongst the yield contributing characters, the characters fruit length, internodal length and number of marketable fruits per were the major contributors towards divergence. Kumari and Chaudhury (2006) also observed such maximum contribution of fruit length (43.08%) to total divergence of okra germplasm during *kharif* season. De *et al*. (1988) opined that traits contributing maximum towards the D^2 values need to be given more emphasis for deciding the clusters to be taken for the purpose of choice of parents for hybridization. The characters that predominantly contributed to divergence in this study also happen to be the main components of yield. The results of the present study point out a positive contribution of genetic divergence and yield components; this can be of considerable help in selecting for yield and other economic traits. It can be concluded that there was more divergence for these characters offering greater scope while making selection of horticulturally superior genotypes of okra.

The germplasm utilized for the present study consisted of 94 indigenous and 6 exotic collections. Of the 94 indigenous collections, certain collections were grouped exclusively in eight distinct clusters (cluster I, III, VI, VII, IX, X and XI), while the remaining ones were grouped along with exotic collections in three clusters (cluster II, V and VIII). Of the 6 exotic collections (EC133408,

EC329398, EC169447, EC169498, EC169515 and EC329356), three genotypes, one genotype and two genotypes were grouped together along with indigenous collections in three different clusters *viz*., cluster II, V and VIII, respectively. The composition of clusters II, V and VIII revealed that these clusters comprised of heterogeneous geographic origin indicating that the genotypes were distributed amongst the different clusters randomly irrespective of their geographic origin. The grouping of genotypes from heterogeneous geographic origin in one cluster as observed in this cluster analysis could probably be due to the free exchange of breeding material from one place to another. This study thus brought out the fact that there is no parallelism between genetic diversity and geographical divergence in okra.

The germplasm utilized for the present study consisted of six solitary clusters (cluster IV, VI, VII, IX, X and XI). The genotypes in these solitary clusters being diverge from others may serve as potential parents for breeding programmes. They indicate their independent identity and importance due to various unique characters possessed by them.

In general, the genotypes grouped together in one cluster are less divergent than those which are placed in a different cluster. Further, higher intracluster distance indicates high degree of divergence within that cluster. In the present investigation, average intracluster distances revealed that the genotypes of cluster III (112.20) were highly divergent next to the cluster V (165.35), while the cluster means revealed that cluster III had not only third highest plant height, second highest number of branches per plant, second lowest first flowering and fruiting node with fruit size in acceptable limits of consumer preferences, but also had maximum number of total and marketable fruits and total and marketable yield per plant.

The choice of parents for hybridization depends on genetic diversity of parents. Precise information on the nature and degree of genetic divergence would help the plant breeder in choosing the selective parents for hybridization. The expression of heterosis is influenced by genetic diversity of parents. It is general belief that more diverse the parents within overall limits of fitness, the greater are the chances of obtaining higher amount of heterosis expression in the F_1s and a broad spectrum of variability in segregating generations (Arunachalam, 1981). Cress (1966) demonstrated that 'genetic diversity is necessary for significant heterosis but not sufficient to guarantee it'. Several reports are available to show that hybrids between genetically diverse parents manifest greater heterosis than those between more closely related parents (Ram and Panwar, 1970; Moll and Stuber, 1974; Singh and Sharma, 1989). In fact, such a conclusion is based upon a rather restricted range of genetic diversity and may not hold over the entire range of divergence encountered in a

species. In general, the level of heterosis increases with the increase in parental diversity up to some limit and decreases with further increase in parental diversity owing to cross-ability barriers. Thus maximum heterosis occurs at an optimal or intermediate level of parental diversity. Further, the occurrence of heterosis cannot be predicted on the basis of genetic divergence alone (Matzinger and Werusman, 1958). Apart from the high degree of divergence, the mean performance of genotypes and the characters with maximum contribution towards divergences should also be given due consideration. The best combination of parents for improvement in various economic characters can be recommended on the basis of *per se* performance of the genotypes and intercluster divergence.

Acknowledgements

The authors are highly grateful to the National Bureau of Plant Genetic Resources Regional Station, Thrissur for providing the germplasm for the present study.

References

Arunachalam, V. (1981). Genetic distance in plant breeding. Indian Journal of Genetics and Plant Breeding 41: 226-236.

Bendale, V.W., Bhare, S.G., Mehta, J.L., Pethe, U.B. and Kadam, S.R. (2003). Genetic variability and correlation studies in okra. Orissa Journal of Horticulture 31(2): 1-4.

Bindu, K.K., Manju, P. and Saraswathy, P. (1994). Genetic divergence in bhendi (Abelmoschus esculentus (L.) Moench). Journal of Tropical Agriculture 32: 115-117.

Cress, C.E. (1966). Heterosis of the hybrid related to gene frequency difference between two populations. Genetics 53: 269-274.

De, R.N., Seetharaman, R., Sinha, M.T. and Banerjee, S.P. (1988). Genetic divergence in rice. Indian Journal of Genetics and Plant Breeding 48: 189-194.

Ghai, T.R., Arora, D., Jindal, S.K. and Singh, P. (2005). Assessment of genetic divergence based on nutritional quality and agronomic traits in okra (Abelmoschus esculentus (L.) Moench). Journal of Genetics and Breeding 59(1): 1-6.

Hammon, S. and Van Sloten, D.H. (1989). Characterization and evaluation of okra. In: The use of plant genetic resources. pp. 173-174.

Joshi, A.B. and Dhawan, N.L. (1966). Genetic improvement of yield with special reference to self fertilizing crops. Indian Journal of Genetics and Plant Breeding 26: 101-113.

Kalra, C.L. and Pruthi, J.S. (1984). Chemistry and technology of okra (Hibiscus esculents L.), Central Food Technology Research Institute, Indian Food Packer, pp. 7-57.

Kumari, M. and Chaudhury, D.N. (2006). Genetic divergence in okra (Abelmoschus esculentus (L.) Moench). Vegetable Science 33(1): 71-72.

Mahalonobis, P.C. (1936). On the generalized distance in statistics. In: Proceedings of the National Academy of Sciences (India) 2: 49-55.

Mandal, M. and Dana, I. (1993). Heterosis and inbreeding depression in okra. Environment and Ecology 11(3): 649-652.

Markose, B.L. and Peter, K.V. (1990). Okra. In: Review of research on vegetable and Tuber crops. Technical Bulletin 16, Kerala Agricultural University Press, Mannuthy, Kerala, P. 109.

Martin, F.W. (1982). A second edible okra species and its hybrid with common okra. Annals of Botany 50: 277-283.

Matzinger, D.R. and Werusman, F.A. (1958). Four cycles of mass selection in a synthetic variety of an autogamous species, Nicotiana tobaccum L. Crop Science 8: 239-243.

Mishra, R.S. and Chhonkar, Y.S. (1979). Genetic divergence in okra. Indian Journal of Agricultural Sciences 49: 247-249.

Moll, R.H. and Stuber, C.W. (1974). Quantitative genetics empirical results relevant to plant Breeding. Advances in Agronomy 26: 277-313.

Murthy, B.R. and Arunachalam, V. (1960). The nature of divergence in relation to breeding system in some crop plants. Indian Journal of Genetics and Plant Breeding 26A: 188-198.

Panse, V.G. and Sukhatme, P.V. (1985). Statistical methods for agricultural workers, Indian Council of Agricultural Research, New Delhi.

Partap, P.S., Dhankar, B.S., Pandita, M.L. and Dudi, B.S. (1980). Genetic divergence in parents and their hybrids in okra. Genetica Agraria 34: 323-330.

Preston, S.R. (1998). Aibika/Bele-Abelmoschus manihot (L.) Medik. International Plant Genetic Resources Institute (IPGRI) Publication, P. 97.

Ram, J. and Panwar, D.V.S. (1970). Intra-specific divergence in rice. Indian Journal of Genetics and Plant Breeding 30: 1-10.

Rao CR (1952). Advanced statistical methods in biometrical research. John Wiley and Sons, New York.

Schippers, R.R. (2000). African indigenous vegetable an overview of the cultivated species. National Resources Institute (NRI), University of Greenwich, London, united Kingdom, P. 214.

Singh, A.K., Ahmed, N., Narayan, R. and Narayan, S. (2007). Genetic divergence studies in okra under temperate conditions. Haryana Journal of Horticultural Sciences 36(3/4): 348-351.

Singh, B., Pal, A.K. and Singh, S. (2006). Genetic variability and correlation analysis in okra (Abelmoschus esculentus (L.) Moench). Indian Journal of Horticulture 63(3): 63-66.

Singh, S.P. and Sharma, J.R. (1989). Genetic improvement of pyrethrum IV. Selective divergence and potential hybrid clones. Theoretical and Applied Genetics 78: 841-846.

Sood, S. and Jamwal, R.S. (1998). Studies on genetic divergence and interrelationship of yield components in the seed crop of okra (Abelmoschus esculentus (L.) Moench). South Indian Horticulture 46: 319-322.

Vahab, M.A., Devi, S.N., Mathew, S.K. and Prabhakaran, P.V. (1994). Genetic divergence in okra (Abelmoschus esculentus (L.) Moench). Horticultural Journal 7(2): 117-120.

(Published in March 2012)