

# Indentification of genetic divergence in okra genotypes [*Abelmoschus esculentus* (L.) Moench]

■ K.V. VIJAYA KUMAR, K.T. VENKATESHA, M. ASIF, E. GANGAPPA AND M. PITCHAIMUTHU

## SUMMARY

Using Mahalonobis D<sup>2</sup> statistic and Tocher method, 166 germplasm lines were grouped into 18 divergent clusters. Clustering pattern was not associated with geographical region of genotypes. Hence, Geographical separation may not be referred as index of genetic diversity. Yield per plant, Mean inter-node s length and nodes per plant contributed largely for total divergence, revealing ample scope for improvement of these traits. Maximum number of genotypes were congregated in cluster XVIII followed by cluster I. the highest inter cluster distance between cluster I and cluster XVIII emphasized the possibilities of getting high heterotic F<sub>1</sub> hybrids as well as transgressive segregants in advanced generations for different traits , when hybridization is carried out involving genotypes between these two divergent clusters.

**Key Words :** Intra and inter clusters distances, Intra and inter clusters divergence and per cent contribution

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Okra [*Abelmoschus esculentus* (L) Moench.] an annual, often cross pollinated crop belongs to the family Malvaceae; it is an important vegetable crop of the tropics and subtropics of the world. It has found its place in India since time immemorial. Okra is also referred as gumbo, lady's finger and bhendi.

The D<sup>2</sup> statistic is a tool to evaluate large number of germplasm lines for their genetic diversity and helps to identify genetically divergent parents for utilization in hybridization programmes, as hybridization between lines of diverse origin display a greater magnitude of heterosis than those between closely related strains. Roy and Panwar (1993) suggested that

the magnitude of resulting heterosis was largely depended on the degree of genetic diversity in parental lines. Multivariate analysis with Mahalonobis D<sup>2</sup> statistics is a powerful tool to know the clustering pattern to establish the relationship between genetic and geographic divergence Dhaduk *et al.* (2004) and to determine the role of different quantitative characters towards the maximum divergence (Murthy and Arunachalam, 1966).

## MATERIALS AND METHODS

The material for the study comprised of 166 collections of okra genotypes. The details of the genotypes used in the present study are given in Table A. Field evaluation of the genotypes was carried out at vegetables section in Department of Horticulture, UAS, GKVK, Bengaluru, during *Kharif* 2008. The observations for the present study were recorded on 11 characters, *viz.*, Yield and its attributing characters such as days to 50 per cent flowering, Plant height (cm), Primary branches per plant, nodes per plant, inter-node length (cm), green pods per plant, Fruit length (cm), Fruit diameter (cm), Number of ridges per fruit, Average fruit weight (g) and green fruit yield per plant (g). Observations were made on five randomly selected competitive plants per treatment in each

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**Table A: List of okra collections used in the present study**

Sr. No.	Name of variety	Source	Sr. No.	Name of variety	Source
1.	IC 43720	NBPGR	43.	1084	Vibha
2.	IC 39137-A	NBPGR	44.	1018	Vibha
3.	IC 43736	NBPGR	45.	1081	Vibha
4.	IC 43750	NBPGR	46.	1114	Vibha
5.	EC 305619	NBPGR	47.	1108	Vibha
6.	IC 265147	NBPGR	48.	1003	Vibha
7.	IC 069286-Sel-87-1	NBPGR	49.	1089	Vibha
8.	SEL 7	Mahyco	50...	2	Vibha
9.	SEL 13	Mahyco	51.	Parbani Kranti	Parbhani
10.	Mahyco 12- F	Mahyco	52.	Arka Abhay	IIHR
11.	SEL 6	Mahyco	53..	1080	Vibha
12.	SEL 10	Mahyco	54.	Pusa Sawani	IARI
13.	Nunhems -M	Nunhems	55.	Arka Anamika	IIHR
14.	SEL 2	Mahyco	56..	IC 43733	IIHR
15.	SEL 11	Mahyco	57.	IC 69242	IIHR
16.	SEL 8	Mahyco	58.	IC 140915	IIHR
17.	SEL 9	Mahyco	59.	IC 33344	IIHR
18.	Punkaj	Mahyco	60.	PUSA A4	IARI
19.	PB 7	ACRP (VC)	61.	IC 282279	IIHR
20.	Mahyco 112-M	Mahyco	62.	IC 282294	IIHR
21.	SEL 1	Mahyco	63.	EC 329406	IIHR
22.	SEL 4	Mahyco	64.	IC 45800	IIHR
23.	Shagun	Mahyco	65.	IC 28226	IIHR
24.	SEL 16	Mahyco	66.	IC 43746	IIHR
25.	SEL 12	Mahyco	67.	IC 43732	IIHR
26.	SEL 3	Mahyco	68.	IC 69257	IIHR
27.	1111	Vibha	69.	IC 43750	IIHR
28.	1080	Vibha	70.	EC 169362	IIHR
29.	1113	Vibha	71.	IC 69290	IIHR
30.	1119	Vibha	72.	IC 282296	IIHR
31.	1007	Vibha	73.	IC 140906	IIHR
32.	1096	Vibha	74.	IC 282292	IIHR
33.	1002	Vibha	75.	IC 282284	IIHR
34.	1085	Vibha	76.	IC 140910	IIHR
35.	1004	Vibha	77.	IC 218894	IIHR
36.	3	Vibha	78.	IC 282286	IIHR
37.	1117	Vibha	79.	IC 45806	IIHR
38.	1012-1	Vibha	80.	IC 282282	IIHR
39.	1097	Vibha	81.	Hissar Unnath	Hissar
40.	1006	Vibha	82.	IC 140877	IIHR
41.	1114-1	Vibha	83.	IC 140927	IIHR
42.	1008	Vibha	84.	IC 282266	IIHR

Table 1: Contd.....

Table A: Contd.....

85.	IC 128885	IIHR	127.	111	Hyderabad
86.	EC 329357	IIHR	128.	114	Hyderabad
87.	IC 282232	IIHR	129.	KA 032	Raichur
88.	IC 128893	IIHR	130.	IC159	IIHR
89.	IC 282277	IIHR	131.	Barka	ACRP (VC)
90.	EC 169337	IIHR	132.	DOV 2	ACRP (VC)
91.	IC 282241	IIHR	133.	PB 266	ACRP (VC)
92.	IC 45814	IIHR	134.	102	Hyderabad
93.	IC 282233	IIHR	135.	Punjab Padmini	PAU
94.	IC 85595	IIHR	137.	KA 079	Raichur
95.	IC 128894	IIHR	138.	INDOL 03	ACRP (VC)
96.	IC 45831	IIHR	139.	HRB55 × HRB-9-2	GKVK
97.	IC 43752	IIHR	140.	KA006 × Punjab Padmini	GKVK
98.	EC 329380	IIHR	141.	Mughal Konda Collection	Raichur
99.	IC 69237-SEL 86	IIHR	142.	DVS 125	ACRP (VC)
100.	IC 282293	IIHR	143.	DSN 1	ACRP (VC)
101.	EC 169378	IIHR	144.	KA006	Raichur
102.	IC 282269	IIHR	145.	Punjab Phalgani	PAU
103.	IC 4792	IIHR	146.	KA 016	Raichur
104.	IC 128873	IIHR	147.	Ujwal Seeds	Raichur
105.	EC 329360	IIHR	148.	PB266 × Arka Abhay	GKVK
106.	IC 218873	IIHR	149.	DOV 1	ACRP (VC)
107.	IC 282289	IIHR	150.	29	Hyderabad
108.	IC 140929	IIHR	151.	DSN 28	ACRP (VC)
109.	IC 128889	IIHR	152.	PB266 × 101	GKVK
110.	IC 218877	IIHR	153.	GS 33	ACRP (VC)
111.	IC 140912	IIHR	154.	HRB 9-2	Hissar
112.	IC 282230	IIHR	155.	HRB 55	Hissar
113.	IC 282229	IIHR	156.	Pusa Sawani × HRB-9-2	GKVK
114.	IC 282231	IIHR	157.	Larma1 × Punjab Padmini	GKVK
115.	KA 035	Raichur	158.	KA 026	Raichur
116.	Arya Dhanalaxmi	ACRP (VC)	159.	KA006 × HRB55	GKVK
117.	Karishma -33152	ACRP (VC)	160.	114 × Larma1	GKVK
118.	DSV 1	ACRP (VC)	161.	Kamini	ACRP (VC)
119.	Larma -1	Raichur	162.	KA 013	Raichur
120.	KA 052	Raichur	163.	P-7	ACRP (VC)
121.	KA 075	Raichur	164.	KA006 × 101	GKVK
122.	Punjab Padmini × Arka Abhay	GKVK	165.	Hosalli Local	Koratagere
123.	AOL- 03-1	ACRP (VC)	166.	Holavanahalli Local	Koratagere
124.	KA 010	Raichur			
125.	106	Hyderabad			
126.	Local Collection	Raichur			

replication for above characters and the mean of these five plants was considered for statistical analysis.

Mahalanobis's (1936)  $D^2$ - statistic analysis was employed for assessing the genetic divergence among the test entries. All the  $n(n-1)/2$   $D^2$  values were clustered using Tocher's method as described by Rao (1952). The average intra cluster distances were calculated by following the formulae as given by Singh and Chaudhary (1977).

## RESULTS AND DISCUSSION

The experimental findings obtained from the present study have been discussed in following heads:

### Clustering pattern of genotypes :

On the basis of magnitude of  $D^2$  values, all the genotypes evaluated were grouped into 18 clusters so that genotypes

within a cluster had smaller  $D^2$  values among themselves than those belonging to different clusters. Cluster 18 consisted of the maximum number of genotypes (95) followed by cluster 1 with 39 genotypes. The remaining 16 clusters had two genotypes each (Table 1). This indicated the existence of high divergence among genotypes of okra. All the remaining clusters were having two genotypes each. Ariyo (1987) grouped 30 genotypes for five clusters; Bindhu *et al.* (1994) grouped 70 genotypes in six clusters and Dash (1997) grouped 27 genotypes in six clusters.

### Intra and inter cluster divergence in okra varieties :

The average intra and inter cluster  $D^2$  values are presented in Table 2 and average inter and intra cluster distances ( $D = \sqrt{D^2}$ ) are presented in Table 3.

Cluster XVIII had the maximum intra cluster distance ( $D=7.273$ ) followed by cluster I ( $D=5.985$ ); while the lowest

**Table 1: Composition of different clusters for diversity in okra genotypes**

Clusters	Number of varieties	Genotypes
Cluster 1	39	IC43720, IC39137-A, IC43736, IC43750, EC305619, IC265147, IC069286-Sel-87-1, Sel7, Sel13, Mahyco12 Female, Sel6, Sel10, Nunhems Male, Sel2, Sel11, Sel8, Sel9, Pankaj, PB7, Mahyco12 Male, Sel1, Sel4, Shagun, Sel16, Sel12, Sel3, 1111, 1080, 1113, 1119, 1007, 1096, 1002, 1085, 1004, 3, 1117, 1012-1, IC43732
Cluster 2	2	KA016, 29
Cluster 3	2	1114-1, Pusa Sawani
Cluster 4	2	1081, HRB55
Cluster 5	2	DOV1, KA026
Cluster 6	2	Karishma33152, DVS125
Cluster 7	2	IC282296, IC282284
Cluster 8	2	IC69290, Local Collection
Cluster 9	2	KA035, DOV2
Cluster 10	2	IC128893, Pusa Sawani $\times$ HRB-9-2
Cluster 11	2	DSN28, P7
Cluster 12	2	IC282266, Indol03
Cluster 13	2	Barka, PB236
Cluster 14	2	HRB55 $\times$ HRB-9-2, KA006 $\times$ Punjab Padmini
Cluster 15	2	PB266, PB266 $\times$ Arka Abhay
Cluster 16	2	IC282294, IC43746
Cluster 17	2	1089, HRB-9-2
Cluster 18	95	1097, 1006, 1084, 1018, 1081, 1114, 1108, 1003, 1089, 2, Parbani Kranthi, Arka Abhay, PB-7, Pusa Sawani, Arka Anamika, IC43733, IC69242, IC140915, IC33344, Pusa A4, IC282279, EC329406, IC45800, IC28226, IC69257, IC43750, EC169362, IC140906, IC282292, IC140910, IC218894, IC282286, IC45806, IC282282, Hissar Unnath, IC140877, IC140927, IC128885, EC329357, IC282232, IC282277, EC169337, IC282241, IC45814, IC282233, IC85595, IC128894, IC45831, IC43752, EC329380, IC69237 SEL86, IC282293, EC169378, IC282269, IC4792, IC128873, EC329360, IC218873, IC282289, IC140929, IC128889, IC218877, IC140912, IC282230, IC282229, IC282231, Arya Dhanalakshmi, Larma1, KA052, KA075, 1114 $\times$ Lorma1, KA010, 106, AOL03-1, 111, KA032, 114, IC159, 102, KA079, Panjab Padmini, Lorma1 $\times$ Punjab Padmini, Holavana halli, Mugalkhod Collection, DSN1, Hosa halli, KA006, Punjab Phalguni, Ujwal Seeds, PB266 $\times$ 101, KA013, KA006 $\times$ 101, GS33, Punjab Padmini $\times$ Arka Abhay, Kamini, HRB55

intra cluster distance was noticed in cluster II (D=1.34). The other clusters viz., cluster III (1.359), cluster IV (1.391), cluster V (1.434), cluster VI (1.544), cluster VII (1.549), cluster VIII (1.58), cluster IX (1.587), cluster X (1.608), cluster XI (1.61),

cluster XII (1.689), cluster XIII (1.728), cluster XIV (1.744), cluster XV (1.833), cluster XVI (1.92) and cluster XVII (1.94) showed medium intra cluster distance. Indicating their independent identity and importance due to the unique

**Table 2: Average inter and intra cluster divergence (D<sup>2</sup>) in okra genotypes**

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII
I	35.82																	
II	27.59	1.79																
III	20.79	8.68	1.85															
IV	25.53	4.83	4.75	1.94														
V	28.2	3.72	8.21	3.68	2.06													
VI	25.8	9.57	8.8	6.04	5.88	2.39												
VII	25.7	19	14.2	18.9	16.4	12.6	2.4											
VIII	22.15	16.39	7.09	10.01	14.08	7.73	10.7	2.5										
IX	30.68	11.39	7.69	7.62	10.53	15.04	21.81	17.34	2.52									
X	26.49	17.7	11.69	14.53	19.51	15.22	22.36	8.14	23.06	2.59								
XI	24.69	12.93	7.15	8.31	14.66	13.97	20.76	7.66	15.09	3.88	2.59							
XII	21.54	10.94	7.49	7.78	8.91	6.03	5.87	5.01	12.41	11.63	9.16	2.85						
XIII	22.1	10.62	7.03	11.16	13.34	11.77	11.91	8.05	12.89	6.97	6.76	7.02	2.99					
XIV	29.73	8.13	6.29	5.04	10.71	13.22	27.7	14.96	7.75	18.92	11.82	15.46	14.23	3.04				
XV	22.13	8.99	5.41	8.6	9.53	10.06	6.55	9.09	8.22	15.32	10.76	4.61	5.43	12.22	3.36			
XVI	26.65	8.45	6.86	11.44	10.18	15.67	13.71	16.04	12.1	24.09	18.45	13.32	11.93	11.6	6.65	3.69		
XVII	26.61	24.81	16.93	24.82	22.03	16.21	4.37	12.9	30.91	25.73	26.34	10.71	17.24	33.06	12.51	16.62	3.76	
XVIII	45.14	32.31	28.96	32.18	32.97	33.33	34.23	32.72	34.43	36.49	33.94	30.17	29.04	35.96	28.62	32.19	37.92	52.9

Diagonal values = intra cluster D<sup>2</sup> values

**Table 3: Average inter and intra cluster distances (D) in okra genotypes**

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII
I	5.99																	
II	5.25	1.34																
III	4.56	2.95	1.36															
IV	5.05	2.2	2.18	1.39														
V	5.31	1.93	2.87	1.92	1.43													
VI	5.08	3.09	2.97	2.46	2.43	1.54												
VII	5.07	4.36	3.77	4.34	4.05	3.55	1.55											
VIII	4.71	4.05	2.66	3.16	3.75	2.78	3.27	1.58										
IX	5.54	3.38	2.77	2.76	3.25	3.88	4.67	4.17	1.59									
X	5.15	4.21	3.42	3.81	4.42	3.9	4.73	2.85	4.8	1.61								
XI	4.97	3.6	2.67	2.88	3.83	3.74	4.56	2.77	3.88	1.97	1.61							
XII	4.64	3.31	2.74	2.79	2.99	2.46	2.42	2.24	3.52	3.41	3.03	1.69						
XIII	4.7	3.26	2.65	3.34	3.65	3.43	3.45	2.84	3.59	2.64	2.6	2.65	1.73					
XIV	5.45	2.85	2.51	2.24	3.27	3.64	5.26	3.87	2.78	4.35	3.44	3.93	3.77	1.74				
XV	4.71	3	2.33	2.93	3.09	3.17	2.56	3.02	2.87	3.91	3.28	2.15	2.33	3.5	1.83			
XVI	5.16	2.91	2.62	3.38	3.19	3.96	3.7	4.01	3.48	4.91	4.3	3.65	3.45	3.41	2.58	1.92		
XVII	5.16	4.98	4.12	4.98	4.69	4.03	2.09	3.59	5.56	5.07	5.13	3.27	4.15	5.75	3.54	4.08	1.94	
XVIII	6.72	5.68	5.38	5.67	5.74	5.77	5.85	5.72	5.87	6.04	5.83	5.49	5.39	6	5.35	5.67	6.16	7.27

Diagonal values = intra cluster D values

**Table 4: The nearest and farthest clusters from each cluster based on D<sup>2</sup> values in okra genotypes**

Cluster	Nearest cluster	Farthest cluster
I	III (20.79)	XVIII (45.14)
II	V (3.72)	XVIII (32.31)
III	IV (4.75)	XVIII (28.96)
IV	V (3.68)	XVIII (32.18)
V	IV (3.68)	XVIII (32.94)
VI	V (5.88)	XVIII (33.33)
VII	XVII (4.37)	XVIII (34.23)
VIII	XII (5.01)	XVIII (32.72)
IX	IV (7.62)	XVIII (34.43)
X	XI (3.88)	XVIII (36.49)
XI	X (3.88)	XVIII (36.94)
XII	XV (4.61)	XVIII (30.17)
XIII	XV (5.27)	XVIII (29.04)
XIV	IV (5.04)	XVIII (35.96)
XV	XII (4.61)	XVIII (28.62)
XVI	III (6.86)	XVIII (32.19)
XVII	VII (4.37)	XVIII (37.92)
XVIII	XV (28.62)	I (45.14)

**Table 5: The mean values of clusters for quantitative parameters in okra varieties**

Clusters	DFP	PH	NPB	NPP	MIL	FL	FG	NOR	AFW	NFP	YPP
I	40.68	105.43	2.21	16.46	6.8	13.53	6.54	6.22	14.82	17.67	266.49
II	38	139	1.96	16.27	8.6	13.53	7.01	6.25	16.08	16.25	260.57
III	39.75	133.13	1.83	17.71	7.94	13.83	6.59	6.19	15.94	20.27	324.55
IV	36.75	120.44	1.75	15.25	8	13.11	6.76	6.01	16.04	18.81	300.61
V	37.75	124.5	1.67	14.25	8.92	13.25	6.94	5.93	14.24	17.33	244.85
VI	37	90.63	1.77	11.13	8.11	13.95	6.42	5.84	13.73	16.44	225.93
VII	43.25	75.06	2.1	11.21	6.79	14	6.68	5.62	13.04	15.06	194.3
VIII	39.5	67.92	1.67	9.75	6.91	12.18	6.2	6.01	13.19	16.33	215.07
IX	38.5	160	2.67	18.5	8.87	13.63	7.05	6.11	16.02	22.46	358.72
X	37.75	72.69	1.58	10.04	7.26	12.91	6.67	6.85	15.19	16.75	255.18
XI	37.75	88.13	1.58	12.58	6.95	12.9	6.85	6.57	16.98	18.42	312.59
XII	39.5	78.75	2.17	12.01	6.62	13.19	6.73	5.9	13.6	16.76	227.61
XIII	40.25	106.17	2.25	12.46	8.44	13.59	6.87	6.62	16.87	16.67	280.7
XIV	37	155.65	2	18.52	8.25	13.42	6.52	6.19	16.61	20.13	339.26
XV	41.25	117.81	2.25	15.19	7.66	14.17	6.91	6.02	16.01	18.13	290.3
XVI	42.75	159.69	1.86	18.99	8.71	13.79	6.71	6.03	15.3	18.05	271.56
XVII	44.25	77.92	2.03	13.73	6.11	14.09	6.28	5.63	10.8	14.82	159.13
XVIII	40.5	121	2.26	15.58	8.15	13.66	6.79	6.27	15.56	17.69	277.08
GM	39.57	110.77	1.98	14.42	7.73	13.48	6.69	6.12	15	17.67	266.92

DFP= Days to 50 % flowering, PH= Plant height (cm), NPB= Number of primary branches per plant, NPP= Number of nodes per plant, MIL= Mean inter-node length (cm) FL= Fruit length (cm), FG= Fruit girth (cm), NOR= Number of ridges per fruit, AFW= Average fruit weight (g) NFP= Number of fruits per plant, YPP= Fruit yield per plant (g) GM= Grand mean

characters processed by the strains in these clusters. These genotypes serve as potential parents for breeding programme.

Among the 18 clusters, the most distant clusters were cluster I and cluster XVIII ( $D^2=45.14$ ) cluster XVII and cluster XVIII ( $D^2=37.92$ ) depicted in Table 4 which had equal divergence followed by cluster XI and XVIII (36.94), cluster X and XVIII (36.49) and cluster XIV and XVIII (35.96). The cluster XVIII maintained greater distance with majority of clusters. Hence, it is advisable to select genotypes from these clusters as potent parents in crossing programme (Table 2 and 3).

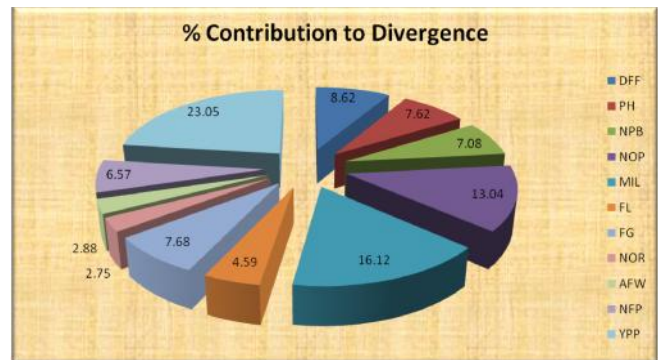
**Cluster means for yield and yield attributes :**

Cluster IV included genotypes which are early flowering (36.75) whereas cluster XVII (44.25) comprised of late flowering genotypes, cluster IX (22.46) having less number of fruits per plant and cluster XVII (14.82) has high number of fruits per plant. For number of ridges, cluster VII (5.62) lowest number of ridges and cluster X (6.85) highest number of ridges, the cluster VIII (6.20) comprised of lowest fruit girth genotypes and cluster IX shows largest fruit girth. With respect to fruit length cluster VIII (12.18) included shorter fruit length compared to cluster XV (14.17), in case of fruit weight cluster XVII (10.80) included genotypes with lighter weight compared to the cluster XI (16.98),

Cluster IX (2.67) comprised of genotypes with high number of primary branches compared to cluster X (1.58), with respect to nodes per plant cluster VIII (9.75) comprised genotypes with maximum nodes compared to cluster XVI (18.99), cluster IX included taller genotypes (160.00) compared to the cluster VIII which included dwarf (67.92) genotypes. In case of mean inter-node length genotypes include in cluster V (8.92) comprised more inter-node length compared to cluster XVII (6.11), the fruit yield per plant was more in genotypes included in the cluster IX (358.72) while cluster XVII (159.13) comprised of genotypes with less fruit yield per plant. This suggests the selection of parents from different clusters for improvement of specific characters.

**Contribution of various characters towards genetic divergence :**

The contribution of individual character is given in Table 6 and depicted in Fig. 1. It is evident from the table that, the most important characters contributing to divergence was yield per plant (23.05) followed by mean inter-node length (16.12), number of nodes per plant (13.04), days to 50 per cent flowering (8.62), fruit girth (7.68), plant height (7.62) and number of primary branches (7.08). The remaining characters viz., number of fruits per plant, fruit length, average fruit weight and number of ridges had lesser contribution towards the genetic divergence.



**Fig. 1: Per cent contribution of each character to divergence in okra genotypes**

DFF = Days to 50% flowering, FG = Fruit girth (cm), PH=Plant height (cm), NOR = Number of ridges per fruit, NPB = Number of primary branches per plant, AFW = Average fruit weight (g), NOP = Number of nodes per plant NFP = Number of fruits per plant, MIL = Mean inter-node length (cm) YPP = Fruit yield per plant (g), FL = Fruit length (cm) GM = Grand mean, SE = Standard error

The important characters contributing towards divergence were fruit yield per plant followed by mean inter-node length, number of nodes per plant, days to 50 per cent

**Table 6: Contribution of each character to divergence in okra genotypes**

Character	% Contribution	Rank
Days to 50% flowering	8.62	4
Plant height (cm)	7.62	6
Number of primary branches per plant	7.08	7
Number of nodes per plant	13.04	3
Mean inter-node length (cm)	16.12	2
Fruit length (cm)	4.59	9
Fruit girth (cm)	7.68	5
Number of ridges per fruit	2.75	11
Average fruit weight (g)	2.88	10
Number of fruits per plant	6.57	8
Fruit yield per plant (g)	23.05	1
Total	100	

flowering, fruit girth, plant height, number of primary branches per plant and number of fruits per plant. These characters together contribution was to maximum to the total diversity. Patil *et al.* (1996) found that mean inter-node length followed by number of pods per plant, weight of pod and plant height contributed most towards divergence. These results implied that in order to select genetically diverse parents to obtain heterotic hybrids /transgressive segregants, it is better to classify the materials on the basis of traits such as yield per plant, number of fruits per plant, number of branches per plant, fruits diameter, number of inter-node s and intermodal length.

## REFERENCES

- Ariyo, O.J. (1987). Multivariate analysis and choice of parents for hybridization in okra [*Abelmoschus esculentus* (L.) Moench]. *Theor. Appl. Genet.*, **74**: 361-363.
- Bindhu, K. K., Manju, P. and Saraswathy, P.(1994). Genetic divergence in Bhendi [*Abelmoschus esculentus* (L.) Moench]. *J. Tropical Agric.*, **32**: 115-117.
- Dash, G.B. (1997). Multivariate analysis in okra [*Abelmoschus esculentus* (L.) Moench]. *Environ. Ecol.*, **15**: 332-334.
- Dhaduk, L.K., Mehta, D.R. and Patel, K.D. (2004). Genetic diversity in okra. *Orissa J. Hort.*, **32**(1): 70-72.
- Mahalonobis, P.C. (1936). On the generalized distance in Statistics. *Proc. Nat. Inst. Sci., India* **2**: 49-55.
- Murthy, B.R. and Arunachalam, V. (1966). The nature of divergence in relation to breeding system in some crop plants. *Indian J. Genet.*, **26** : 188-98.
- Patil, Y.B., Madalageri, B.B., Biradar, B.D. and Hosamani, R. M. (1996). Variability studies in okra [*Abelmoschus esculentus* (L.) Moench]. *Karnataka J. Agric. Sci.*, **9**(2): 289-293.
- Rao, C.R. (1952). Advance statistical methods in biometric research. *John Wiley and Sons Inc.*, NEW YORK, U.S.A.
- Roy and Panwar, D.V.S. (1993). Genetic divergence in some rice (*Oryza sativa* L.) genotypes. *Ann. Agric. Res.*, **14**: 276-281.
- Singh, R.K. and Chaudhary, B.D. (1977). Biometrical methods in quantitative genetic analysis, *Kalyani Publishers.*, NEW DELHI, INDIA.

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