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Short Communication

Genetic divergence in okra (*Abelmoschus esculentus* L. Moench.)

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Okra (*Abelmoschus esculentus* L. Moench) is an important vegetable crop grown in world as well as India. Hybrid vigour was already successfully exploited in okra with commercial hybrid development; therefore, genetic divergence among the parents is important factor while selecting the parents for hybridization. Ramanujam *et al.* (1974) 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. Moll *et al.* (1974) indicated that the level of heterosis exhibited by a hybrid is a function of the genetic divergence between parents. Cress (1966) demonstrated that 'genetic diversity is necessary for significant heterosis but not sufficient to guarantee it '. The importance of genetic diversity for selecting parents in recombination breeding of different autogamous crops to obtain transgressive segregants has been very well emphasized by Khanna and Mishra (1977), Singh and Ramanujan (1981), Cox and Murphy (1990). Also, while performing selections more importance should be given to the characters which contribute more towards diversity. Hence, the present study was undertaken to understand the genetic diversity among the 40 germplasm lines and to identify the lines for further hybridization.

Forty genotypes of okra collected from Indian Institute of Vegetable Research, Varanasi were grown in Randomized Block Design with three replications and planted at spacing of 30 Í 15cm at All India coordinated Research Project on Vegetable crops, Department of Horticulture, Mahatma Phule Krishi Vidyapeeth, Rahuri in summer, 2015. Recommended agronomic package of practices were followed as and when required during entire growth period of crop. The observations were recorded on 5 randomly selected plants from each genotype for 13 quantitative characters *viz*, plant height (cm), days to 50 flowering, number of nodes/plant, number of lobes/leaf, number of branches/plant, intermodal length (cm), length of fruit (cm), diameter of fruit (cm), average weight of fruit (g), number of fruits/plant, fruit yield/plant (g), incidence of YVMV (%) and fruit borer. Genetic divergence was analyzed using the mahalanobis D^2 statistics (1936) and genotypes were grouped into clusters by following the Tocher's Method described by Rao (1952).

Wilk's criteria used to test the aggregate effects of all the traits. Analysis of variances revealed significant differences among the 40 genotypes for all the fourteen characters studied. Similar results were found by Moll *et al.* (1974), Pradip *et al*. (2010) and Shaikh *et al*. (2013). Forty genotypes were grouped into nine clusters (Table 1). Maximum of genotypes were grouped into cluster A followed by cluster H containing 31 and 2 genotypes, respectively. The clusters B, C, D, E, F, G and I were solitary clusters with single genotype. Pradip *et al.* (2010) also reported similar type of distribution of genotypes. The distribution of genotypes into different clusters was based on D^2 values, which ranged from 33.18 to 409.66 (Table 2). The highest inter cluster D^2

Table 1. Distribution of 40 genotypes of okra in different clusters

Sr. No.	Cluster	Genotype number	No. of Genotypes
1	A	G-17, G-27, G-19, G-4, G-10, G-8, G-25, G-36, G-23, G-38, G-7, G-40, G-16, G-18, G-37, G-9, G-35, G-33, G-28, G-12, G-14, G-5, G-34, G-22, G-20, G-6, G-21, G-11, G-30, G-3, G-1	31
2	B	G-31	1
3	C	G-2	1
4	D	G-32	1
5	E	G-13	1
6	F	G-29	1
7	G	G-24	1
8	H	G-26, G-39	2
9	I	G-15	1
Total			40

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Table 2. Average inter and intra cluster D and D^2 values

	A	B	C	D	E	F	G	H	I
A	33.18	91.39	88.74	163.33	79.21	137.12	78.32	220.52	157.50
	(5.76)	(9.56)	(9.42)	(12.78)	(8.90)	(11.71)	(8.85)	(14.85)	(12.55)
B		0.00	33.41	40.70	135.96	48.86	138.77	198.53	225.60
		(0.00)	(5.78)	(6.38)	(11.66)	(6.99)	(11.78)	(14.09)	(15.02)
C			0.00	117.94	141.13	48.86	116.64	175.83	162.56
			(0.00)	(10.86)	(11.88)	(6.66)	(10.80)	(13.26)	(12.75)
D				0.00	256.64	100.60	257.60	359.86	409.66
				(0.00)	(16.02)	(10.03)	(16.05)	(18.97)	(20.24)
E					0.00	216.38	75.17	140.90	77.44
					(0.00)	(14.71)	(8.67)	(11.87)	(8.80)
F						0.00	151.29	213.45	237.78
						(0.00)	(12.30)	(14.61)	(15.42)
G							0.00	206.21	98.01
							(0.00)	(14.36)	(9.90)
H								64.96	148.84
								(8.06)	(12.20)
I									0.00
									(0.00)

Table 3. Cluster mean performances for various characters of okra

Sr. No	Character	A	B	C	D	E	F	G	H	I
1	Plant height (cm)	72.33	39.40	46.60	46.80	37.70	52.80	69.90	47.05	56.30
2	Days to 50 % flowering	51.81	52.50	55.50	53.00	56.00	54.00	55.00	61.00	55.00
3	Number of nodes/plant	17.07	12.40	18.50	12.10	14.70	21.10	13.90	16.15	24.30
4	Number of lobes/ leaf	3.48	3.30	4.10	3.30	3.00	3.10	3.10	3.50	3.10
5	Number of branches/plant	1.77	2.60	3.90	1.80	1.70	2.50	1.80	3.50	3.40
6	Number of ridges/fruit	5.31	6.10	6.60	5.60	5.30	6.80	7.20	5.55	6.00
7	Internodal length (cm)	4.27	3.18	2.52	3.87	2.57	2.52	5.03	3.10	2.33
8	Length of fruit (cm)	9.86	8.35	7.13	9.65	8.50	6.85	9.75	6.90	7.55
9	Diameter of fruit (cm)	1.80	1.83	1.83	1.80	1.82	1.85	1.83	1.93	1.84
10	Average weight of fruit (g)	8.84	8.80	7.60	8.90	10.20	8.00	12.00	9.50	10.40
11	Number of fruits/ plant	13.89	10.00	15.00	9.00	11.50	19.00	11.00	12.25	22.00
12	Fruit yield/plot (kg)	14.57	10.62	13.80	9.48	13.86	18.00	15.90	13.68	27.36
13	Incidence of YVMV (%)	7.17	13.78	10.64	21.25	3.34	14.68	4.17	3.61	1.42
14	Fruit borer incidence (%)	13.84	14.50	13.50	13.00	15.00	12.50	15.50	12.00	13.00

Table 4. Contribution of various characters to divergence

S. No.	Characters	Contribution %
1	Plant height (cm)	6.67
2	Days to 50 % flowering	1.15
3	Number of nodes / plant	1.03
4	Number of ridges/fruit	7.05
5	Number of branches / plant	2.56
6	Internodal length (cm)	0.13
7	Node at which 1st flower appear	1.67
8	Length of fruit (cm)	7.18
9	Diameter of fruit (cm)	9.62
10	Average weight of fruit (g)	4.10
11	Number of fruits / plant	3.08
12	Fruit yield / plant (g)	4.62
13	Incidence of YVMV (%)	49.23
14	Fruit borer incidence (%)	1.92

observed between cluster D and cluster I (409.66) followed by cluster D and H (359.86) and cluster D and G (257.60), whereas lowest observed in between cluster B and C (33.41). The highest intra cluster distance was shown by cluster H (64.96) followed by cluster A (33.18), while rest of clusters wee having zero intra cluster distance because they were monogenotypic. Similar finding was reported by Choukhande (2010), Bairagi (2010) Prakash et al. (2011) and Shaikh et al. (2013).

Cluster mean indicated variation for the quantitative trait among the clusters (Table.3). Considering major yield contributing characters along with earliness to flowering and maturity cluster A, F, G and I shown high cluster means for yield and yield component, therefore genotypes from these diverse cluster should be used for further hybridization and isolating transgressive segregants in the later generations. Analysis of contribution of the characters to genetic diversity (Table 4) revealed that characters incidence of YVMV contributed highest upto 49.23% followed by diameter of fruit (9.62%), length of fruit (7.18%) and number of ridges per fruit (7.05) whereas, the characters internodal length (0.13%), days to 50% flowering (1.15%) and number of nodes/plant (1.03%) contributed the lowest. Moll *et al.* (1974), John *et al.* (1992), Pradip *et al.* (2010), Choukande (2010) and sheikh *et al.* (2013) also observed similar level of contribution for various growth and yield contributing characters.

On the basis of inter cluster distance, cluster I and cluster A were identified as more divergent clusters and genotypes viz. G-36, G-37, G-25 from cluster A and G-15 from cluster I of these diverse cluster should be used for further improvement in heterosis in yield targeted traits with creation of wider variability.

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