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Diversity studies in okra (*Abelmoschus esculentus* L. Moench.)

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Abstract

Genetic divergence was studied among 35 okra germplasm lines using Mahalanobis D² analysis. Analysis of variances for dispersion indicated significant differences among the genotypes and they were grouped into nine clusters. The cluster A consisted of 25 genotypes followed by cluster E contain 3 genotypes, whereas cluster B, C, D, F, G, H and I and were solitary clusters. The highest inter cluster distance observed between clusters E and cluster G while cluster E shown maximum intra cluster distance. The characters diameter of fruit (43.53%) contributed maximum genetic divergence followed by length of fruit (23.53%), plant height (10.92%). Cluster I and F shown high cluster means for yield and yield component, therefore genotypes viz. G-15, G-16, G-24 from cluster E and G-2 from cluster G of these diverse clusters may be used for further hybridization.

Keywords: Divergence, Clusters, genotypes, Okra, inter, intra cluster distance

Introduction

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)^[9] 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)^[7] indicated that the level of heterosis exhibited by a hybrid is a function of the genetic divergence between parents. Cress (1966)^[4] 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).^[5, 12, 3] 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 35 germplasm lines and to identify the lines for further hybridization.

Materials and Methods

Thirty five genotypes of okra collected from Indian Institute of Vegetable Research, Varanashi (U.P.) were grown in randomized block design with two replications and planted at spacing of 30x 15 at All India coordinated Research Project on Vegetable crops, Department of Horticulture, Mahatma Phule Krishi Vidyapeeth, Rahuri (Maharashtra state) India, 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 15 quantitative characters viz, plant height (cm), days to 50 flowering, number of nodes/plant, number of lobes/leaf, number of branches/plant, number of ridges/fruit, node at which first flower appear, intermodal length (cm), length of fruit (cm), diameter of fruit (cm), average weight of fruit, number of fruits/plant, fruit yield/plant (g), yield/plot and per hectare. Genetic divergence was analyzed using the Mahalanobis D² statistics (1936)^[6] and genotypes were grouped into clusters by following the Tocher's Method described by Rao (1952)^[10].

Results and Discussions

Analysis of variances revealed significant differences among the 35 genotypes for all the fifteen characters studied (Table 1). Wilk's criteria used to test the aggregate effects of all the thirteen traits. It indicated that significant differences among the genotypes. Similar results were found by Moll *et al.* (1974) Pradip *et al.* (2010) and Shaikh *et al.* (2013)^[7, 8, 11].

Thirty five genotypes were grouped into nine clusters (Table 2). Maximum of 25 genotypes were grouped into cluster A, followed by cluster E contain 3 genotypes and cluster B,C,D,F,G, H and I were solitary clusters with single genotype. Pradip *et al.* (2010) [8] also reported similar type of distribution of genotypes. The distribution of genotypes into different clusters was based on D² values, which ranged from 385.25 to 4153.54 (Table 4). The highest inter cluster D² observed between cluster E and cluster G (4153.54) followed by cluster E and I (3525.03), cluster B and E (3007.86) and cluster B and I (2908.66), whereas lowest observed in between cluster H and I (385.25). The highest intra cluster distance was shown by cluster E(729.64) followed by cluster A (365.03), while rest of clusters were having zero intra cluster distance because they were monogenotypic. Similar finding was reported by Choukhande (2010), Bairagi (2010) and Prakash *et al.* (2011) Shaikh *et al.* (2013) [2, 1, 11]. Genotypes for the hybridization should be selected from the more distant clusters as chances are more to obtain heterotic combinations as compared to combinations involving genotypes from same clusters.

Cluster mean indicate that the variation for the quantitative trait among the clusters (Table.5). Considering major yield

contributing characters along with earliness to flowering and maturity cluster I and F 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 3) revealed that characters diameter of fruit contributed highest upto 43.53 followed by length of fruit (23.53%), plant height (10.92%) however, character intermodal length contributed the lowest (0.50%). De *et al.* (1988) proposed that trait contributing maximum towards D² values need to be given more emphasis for deciding the clusters to be taken for further selection and choice of parents for hybridization. Moll *et al.* (1974), John *et al.* (1992), Pradip *et al.* (2010) Choukhande (2010) and sheikh *et al.* (2013) [7, 8, 2, 11] also observed similar level of contribution for various growth and yield contributing characters.

On the basis of inter cluster distance, cluster E and cluster G were identified as more divergent clusters and genotypes viz. G-15, G-16, G-24 from cluster A and G-2 from cluster G of these diverse cluster should be used for further improvement in heterosis in yield targeted traits with creation of wider variability.

Table 1: Analysis of variance (M.S.S.) for 15 characters in okra

Sr. No.	Characters	Mean sum of square		
		Replication (1)	Treatment (34)	Error (34)
1	Plant height (cm)	37.74	1272.16*	21.69
2	Days to 50% flowering	10.41	11.94*	1.82
3	Number of nodes/plant	0.91	18.54*	0.53
4	Number of lobes on leaves	0.01	0.32*	0.11
5	Number of branches/plant	0.12	1.49**	0.12
6	Number of ridges/++fruit	0.01	3.89*	0.00
7	Internodal length (cm)	0.05	2.69*	0.21
8	Node at which 1 st flower appear	0.01	0.22*	0.10
9	Length of the fruit (cm)	0.04	9.16*	0.06
10	Diameter of fruits (cm)	0.03	0.10*	0.01
11	Average weight of fruit (g)	5.71	19.68**	0.44
12	Number of fruits /plant	1.10	17.72**	0.66
13	Fruit yield / plant (g)	994.14	4659.65**	117.44
14	Fruit yield / plot in (kg)	7.50	33.39**	2.20
15	Fruit yield (q/ha)	2454.31	11421.84**	753.36

Table 2: Distribution of 35 genotypes of okra in clusters

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

Table 3: Contribution of various characters to divergence

Sr. No.	Characters	Contribution %
1	Plant height (cm)	10.92%
2	Days to 50 % flowering	1.00%
3	Number of nodes / plant	2.35%
4	Number of lobes / leaf	0.84%
5	Number of branches / plant	0.84%
6	Internodal length (cm)	0.50%
7	Length of fruit (cm)	23.53%

8	Diameter of fruits (cm)	43.53%
9	Average weight of fruit (g)	2.69%
10	Number of fruits / plant	1.01%
11	Fruit yield / plant (g)	3.70%

Table 4: Average inter and intra cluster D and D² values

	A	B	C	D	E	F	G	H	I
A	365.03 (19.10)	900.78 (30.01)	870.66 (29.50)	1055.99 (32.49)	2594.17 (50.93)	1112.62 (33.35)	839.02 (28.96)	946.48 (30.76)	1333.71 (36.52)
B		00 (0)	1798.69 (42.41)	425.06 (20.61)	3007.86 (54.84)	2040.05 (45.16)	1889.98 (43.47)	2432.46 (49.32)	2908.66 (53.93)
C			00 (0)	1498.84 (38.70)	922.82 (30.37)	314.95 (17.74)	1795.47 (42.37)	645.46 (25.40)	1188.59 (34.47)
D				00 (0)	2611.51 (51.10)	1820.64 (42.66)	2762.65 (52.56)	1835.00 (42.83)	2037.25 (45.13)
E					729.64 (27.01)	1449.09 (38.06)	4153.54 (64.44)	2470.88 (49.70)	3525.03 (59.37)
F						00 (0)	2065.97 (45.45)	812.53 (28.50)	1136.90 (33.71)
G							00 (0)	1859.59 (43.12)	2425.16 (49.24)
H								00 (0)	385.25 (19.62)
I									00 (0)

Table 5: Cluster mean performances for various characters of okra

Sr. no	Character	A	B	C	D	E	F	G	H	I
1	Plant height (cm)	92.12	130.60	71.55	162.10	98.06	75.70	28.95	94.35	103.45
2	Days to 50% flowering	57.40	58.00	56.50	59.00	56.00	59.50	60.50	58.00	54.00
3	Number of nodes/plant	15.48	21.50	16.50	23.50	15.33	20.50	12.00	16.00	20.00
4	Number of lobes/leaf	4.84	5.00	5.00	5.00	5.00	5.00	5.00	5.00	5.00
5	Number of branches/plant	2.24	4.00	3.00	3.50	2.00	4.00	2.50	3.00	3.50
6	Internodal length (cm)	5.89	5.75	4.30	6.65	6.47	3.65	2.35	5.80	5.10
7	Length of fruit (cm)	9.55	6.45	8.35	8.95	5.00	8.10	8.50	13.70	14.45
8	Diameter of fruit (cm)	1.54	1.31	1.93	1.43	2.13	1.86	1.47	1.83	1.78
9	Average weight of fruit (g)	9.37	5.25	11.30	6.65	11.32	14.65	6.40	20.10	16.10
10	Number of fruits/plant	11.38	17.10	12.00	19.10	10.83	15.90	7.60	11.50	16.95
11	Fruit yield/plant (g)	103.21	86.75	130.05	123.05	108.68	227.40	44.80	221.10	255.20

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