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Shafiqurrahman Mohammad
Department of Genetics and
Plant Breeding, SHUATS, Naini,
Utter Pradesh, India

Shailesh Marker
Department of Genetics and
Plant Breeding, SHUATS, Naini,
Utter Pradesh, India

Multivariate analysis for selection of elite parents in breeding programme in Okra (*Abelmoschus esculentus* L. Moench)

Shafiqurrahman Mohammad and Shailesh Marker

Abstract

Genetic divergence was studied among 23 okra genotypes using Mahalanobis D^2 analysis. Analysis of variances indicated significant differences among the genotypes and they were grouped into five clusters. The cluster I consist of seven genotypes, whereas cluster II contain two genotypes, cluster III contain nine genotypes, cluster IV consist of four genotypes and cluster V consist of single genotype respectively. Highest inter cluster distance observed between clusters II and cluster V, while cluster II shown maximum intra cluster distance. Character YVMV infestation on plants (38.74%) towards genetic divergence followed by number of seeds per fruit (22.13%). The mean value of different clusters, genotypes having high yield and attributing traits were observed in cluster V having a genotype namely 2012/OKYVRES-5. Cluster I shown lowest mean values for maximum characters.

Keywords: Okra, genetic divergence, yield components, D^2 analysis

Introduction

Okra (*Abelmoschus esculentus* L. Moench) also known as 'bhindi' or 'Lady's finger', belongs to family Malvaceae. Chromosome number $2n=130$. It is native of Africa. It is widely distributed and cultivated in the tropics, sub-tropics and warmer portions of temperate region of world on a varying scale ^[1]. It is a multipurpose crop due to its various uses. The selected material with novel traits can be used as parents in breeding programme. India possesses a wide range of diversity in okra. The success of crop improvement programme is mainly based on genetic diversity available in the breeding material. Importance of genetic diversity for selecting parents in combination-breeding programme of different autogamous crop to recover transgressive segregates has been emphasized by ^[2, 3]. 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 ^[4]. Keeping in view the above facts, the present study was carried out for the genetic divergence among 23 genotypes to select elite and divergent parents to use for desired improvement programmes.

Material and Methods

The present investigation conducted in Randomized Block Design with three replications at Experimental Research Field, Department of Genetics and Plant breeding, SHUATS, U.P during the Kharif season. The experimental material for this study comprised twenty three genotypes including four standard checks varieties collected from Indian Institute Vegetable Research, Varanasi, U.P. Data were recorded on five randomly selected plants in each genotype in each replication for days to 50% flowering, first flowering node, first fruiting node, fruit length (cm), fruit width (cm), fruit girth (cm), fruit weight (g), fruits per plant, marketable fruits per plant, total yield per plant (g), marketable yield per plant (g), plant height (cm), branches per plant, leaves per plant, internodal distance (cm), seeds per fruit, 100 seed weight (cm), days to first appearance of YVMV infestation in plot, YVMV infestation on plants (%), YVMV infestation on fruits (%), severity of YVMV infestation (%), co-efficient of YVMV infection (%), fruit and shoot borer infestation on shoots (%), fruit and shoot borer infestation on fruits (%). The mean values of all the traits were subjected to statistical analysis. Multivariate analysis was done by utilizing Mahalanobis D^2 statistics ^[5] and the genotypes were grouped into different clusters through Tocher's method given by ^[6].

Correspondence
Shafiqurrahman Mohammad
Department of Genetics and
Plant Breeding, SHUATS, Naini,
Utter Pradesh, India

Results and Discussion

Analysis of variances revealed significant differences among the 23 genotypes for all the 24 characters studied. Wilk's criteria used to test the aggregate effects of all the traits. It indicated the significant differences among the genotypes. Twenty-three genotypes were grouped into five clusters (Table 1), Maximum of nine genotypes were grouped in to cluster III followed by cluster I with seven genotypes, cluster IV with four genotypes, cluster II with two genotypes and cluster V with single genotype [7] also reported similar type of distribution of genotypes. The distribution of the genotypes into different clusters was based on D values, which ranged from 56.33 to 198.14 (Table 2). Highest inter cluster D values observed between cluster II and V (198.14) followed by cluster I and V (165.65) and III and V (160.64), whereas

lowest observed in between I and III (72.76).

Highest intra cluster distance was shown by cluster II (64.04), while cluster V having zero intra cluster distance. 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 means indicate the variation for the quantitative trait among the cluster (Table 3). Considering major yield attributing traits highest mean in cluster V and lowest in cluster I. Therefore, genotypes from these diverse clusters should be used for further breeding programme. Analysis of contribution of the characters to genetic diversity (Table 3) revealed that character YVMV infestation on plants (38.74%) contributed highest towards genetic divergence followed by number of seeds per fruit (22.13%).

Table 1: Composition of clusters

Clusters	No. of Genotypes	Distance	Name of Genotypes
I	7	3173.16	2011/okyvres-4,10/okyvres-9, 10/okyvres-5, arka anamika, 2011/okyvres-5, 10/okyvres-1 Arka abhay
II	2	4101.89	10/okyvres-2, 10/okyvres-6
III	9	4063.63	10/okyvres-3, vro-6, 2011/okyvres-2, 10/okyvres-7, 2012/okyvres-4, 10/okyvres-8, pusa sawani, 2012/okyvres-6, 2012/okyvres-3
IV	4	3795.68	2011/okyvres-6, 10/okyvres-4, 2012/okyvres-1, 2012/okyvres-2
V	1	0.00	2012/okyvres-5

Table 2: Average Inter and Intra cluster D2 and D values in Okra.

Clusters	I	II	III	IV	V
I	3173.16 (56.33)	6762.81 (82.23)	5294.31 (72.76)	10600.32 (102.95)	27441.72 (165.65)
II		4101.89 (64.04)	7377.94 (85.89)	23860.01 (154.4)	39262.13 (198.14)
III			4063.63 (63.74)	14712.75 (121.29)	25808.32 (160.64)
IV				3795.68 (61.6)	21637.92 147.09
V					0.00 (0.00)

Table 3: Mean performances of different cluster

Character	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Contribution %	Times Ranked
Days to 50% Flowering	39.47	37.50	39.37	38.91	42.33	0.01	0
First Flowering Node	6.38	6.52	6.60	6.12	6.37	0.01	0
First Fruiting Node	6.82	7.00	7.01	6.48	6.43	0.01	0
Fruit Length	11.10	10.90	11.02	11.59	10.50	0.01	0
Fruit Width	1.80	1.72	1.77	1.76	2.22	0.01	0
Fruit Girth	5.62	5.56	5.47	5.39	5.77	0.01	0
Fruit Weight	10.80	14.47	11.89	11.16	16.17	0.01	0
Fruits/ Plant	11.42	11.58	12.05	13.18	18.63	0.01	0
Marketable Fruits/ Plant	9.65	9.89	8.35	11.92	17.50	0.01	0
Total Yield/ Plant	122.69	168.98	147.12	148.39	301.44	0.01	0
Marketable Yield/ Plant	104.31	144.34	103.16	133.69	283.01	0.01	0
Plant Height	57.73	59.40	63.00	58.97	38.00	0.79	2
Branches/ Plant	2.46	2.26	2.77	2.44	3.85	0.01	0
Leaves/ Plant	21.85	16.56	21.99	19.63	41.67	0.01	0
Internodal Distance	3.62	3.87	3.64	3.48	2.77	0.01	0
Seeds/ Fruit	42.79	36.68	48.05	53.74	82.50	22.13	56
100 Seed Weight	5.21	4.54	4.64	4.87	4.17	4.35	11
Days to First Appearance of YVMV Infestation in Plot	49.10	67.33	47.04	0.00	70.33	6.32	16
YVMV Infestation on Plants	21.49	44.15	55.94	0.00	14.87	38.74	98
YVMV Infestation on Fruits	11.90	0.00	42.17	0.00	0.00	5.14	13
Severity of YVMV Infestation	27.43	44.36	54.21	0.00	32.50	0.40	1
Co-efficient of YVMV Infection	7.58	19.32	31.87	0.00	4.84	0.40	1
Fruit and Shoot Borer Infestation on Shoots	49.94	58.43	37.22	33.17	45.93	19.37	49
Fruit and Shoot Borer Infestation on Fruits	15.65	15.90	20.83	8.79	5.74	0.79	2

However, characters days to 50% flowering , first flowering node, first fruiting node, fruit length (cm), fruit width (cm), fruit girth (cm), fruit weight (g), fruits per plant, marketable fruits per plant, total yield per plant (g), marketable yield per plant (g), branches per plant, leaves per plant and internodal

distance (cm) contributed lowest (0.01 %). [8] proposed that traits contributing maximum towards the D² values need to be given more emphasis for deciding the clusters to be taken for further selection and choice of parents for hybridization. [9, 10, 11] also observed similar level of contribution for seeds per

fruit, 100 seed weight. Based on inter cluster distance, clusters II and V were identified as more divergent clusters and genotype namely 2012/OKYVRES-5 (cluster V) and 10/OKYVRES-2, 10/OKYVRES-6 (cluster II) of these diverse clusters should be used for further improvement in heterosis in yield targeted traits with creation of wider variability.

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