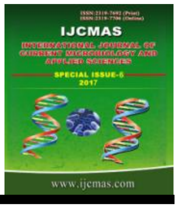
Int.J.Curr.Microbiol.App.Sci (2018) Special Issue-6: 2533-2537

International Journal of Current Microbiology and Applied Sciences
ISSN: 2319-7692 **Special Issue-6 pp. 2533-2537**
Journal homepage: http://www.ijcmas.com



Original Research Article

Studies on Genetic Divergence for Yield and Yield Components in Okra (*Abelmoschus esculentus* (L.) Moench.)

P. P. Gawande*, S. S. Nichal, S. P. Patil, S. S. Bhoyar, M. G. Dikkar and R. K. Patil

Chilli and Vegetable Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, Maharashtra, India
**Corresponding author*

ABSTRACT

Keywords

Clusters, diversity, genotypes, okra

A study of genetic diversity in 30 genotypes of okra for nine characters was conducted at Chilli and Vegetable Research Unit, Dr. PDKV, Akola (MS) in randomized block design with three replications. The results revealed that D^2 values obtained ranged from 8.78 to 106.88 and on the basis of relative magnitude of D^2 values, 30 genotypes were grouped into four clusters. The maximum inter-cluster distances were recorded between III and IV, II and IV, I and IV, while intra cluster divergence of solitary clusters II, III and IV was zero. Cluster I exhibited maximum mean values for number of nodes, fruit length, fruit girth and fruit yield per plant. Cluster II recorded highest mean values for plant height and average fruit weight whereas cluster IV showed maximum mean values for number of fruits per plant, fruit yield per plot and fruit yield quintal per hectare. However cluster III exhibited lowest mean values for six characters under study.

Introduction

Okra (*Abelmoschus esculentus* (L.) Moench.) is commonly known as “Bhindi” or “Lady’s Finger”, it is the sixth important vegetable crop cultivated throughout the country chiefly for its tender green fruits for consumption. Okra has a prominent position among the 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.

The high yielding varieties in okra has been developed by exploiting the genetic diversity available in the crop. But yield of the okra was reduced due to attack of shoot and fruit borer and yellow vein mosaic virus. The information on the nature and degree of genetic divergence is essential for the breeder to choose the right type of parents for purposeful hybridization in heterosis breeding and in order to benefit transgressive segregations, the knowledge of genetic distance between parents is necessary (Khodadabi, 2011).

Genetic diversity is a key factor for crop improvement. Success of the hybridization followed by selection depends largely on the selection of parents with high genetic diversity for traits of interest (Murthy and Arunachalam, 1966). The present investigation therefore undertaken to evaluate genetic diversity among the 30 okra genotypes.

Materials and Methods

The present experimental material comprised of 30 promising genotypes/varieties of okra enlisted in Table 1.

The genotypes were evaluated through a field experiment conducted at Chilli and Vegetable Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola (MS) in randomized block design with three replications during kharif 2012-13 The fertilizer doses were as per the recommendations for commercial cultivation and cultural practices were followed as when required. Five plants were selected randomly from each plot of each replication for recording the observations on plant height (cm), fruit length (cm), fruit girth, number of nodes, number of fruits per plant, average fruit weight (g) and fruit yield per plant (kg) while fruit yield per plot was recorded on plot basis and converted in qt./ha. multiplying by hectare factor. The mean values were used for statistical analysis. Following the analysis of variance, the data on 30 genotypes of okra were subjected to multivariate analysis (D^2 statistic) as suggested by Mahalanobis, (1936) and Grouping of genotypes into different clusters was carried out following Tocher's procedure (Rao, 1952) whereas relative contribution of different characters towards total divergence was calculated as per Singh and Choudhary (1985).

Results and Discussion

The analysis of variance showed that the genotypes under study differ significantly among themselves for all nine characters. The D^2 values obtained ranged from 8.78 to 106.88. On the basis of relative magnitude of D^2 values, 30 genotypes were grouped into four clusters (Table 2).

The cluster I had maximum number of genotypes i.e. twenty seven. The genotypes grouped into same clusters presumably diverge very little from one another. Crossing of genotypes belonging to the same cluster is not expected to yield desirable segregants. Consequently, a crossing programme should be conducted with putative parents belonging to different characters Yatung *et al.*, (2014).

Therefore crosses between the members of cluster separated by inter cluster distances are likely to be beneficial for future improvement. The cluster II, III and IV were solitary indicating wide diversity from one another and also from the rest for the characters under study. Earlier solitary cluster in okra was also reported by Akotkar *et al.*, (2010), Reddy *et al.*, (2012)

Intra and inter-cluster average D^2 values are presented in Table 3. Result indicated that highest inter cluster distance was observed between cluster III and IV (D^2= 106.88) followed by cluster II and IV (D^2= 93.08), I and IV (D^2= 64.07) I and III (D^2=56.00), I and II (D^2=47.76)' while lowest inter cluster distance was exhibited between cluster II and III (D^2=8.78) suggesting close relationship among these two clusters. However the maximum inter-cluster distances were recorded between III and IV, II and IV, I and IV.

Genotypes from these clusters if involve in hybridization may occurs a wide spectrum of segregating populations as genetic diversity is very distinct among these groups. The higher genetic distance between parents, the higher heterosis in progeny can be observed (Lahbib et. al 2012). The intra cluster divergence of solitary clusters II, III and IV was zero. Akotkar *et al.*, (2010) and Dutonde *et al.*, (2008) were also reported the same results in okra and chilli respectively.

Table.1 The list of okra genotypes under study

Sr. No.	Genotypes / Varieties	Sr. No	Genotypes / Varieties
1	AKOV- 117	16	AKOV-118
2	AKOV- 116	17	AKOV-122
3	Ajeet-331-F4-2-4-1-1-1	18	AKOV-110
4	DG- AKO-106-1-1-1	19	AKOV-114
5	AKOV-101-3	20	Akola Bahar
6	AKOV-121	21	Parbhani Kranti
7	DG- AKO-106-2-1	22	HRB-108-2
8	AKO-99-04-3	23	AKOV-119
9	DG- AKO-106-1-1-7	24	AKOV-102
10	AKO-107-4	25	AKOV-106
11	AKO-45	26	AKOV-107
12	AKOV-115	27	AKOV-111
13	AKOV-103	28	Pusa A-4
14	DG- AKO-106-3-1	29	Arka Anamika
15	AKOV-101-8-3	30	AKOV-98-04-1

Table.2 Clustering pattern of 30 okra varieties by Tocher's Method

Cluster Group	Genotypes	Number of genotypes
Cluster I	AKOV- 117, AKOV- 116, Ajeet-331-F4-2-4-1-1-1, DG- AKO-106-1-1-, AKOV-12, AKO-107-4 AKO-45, DG- AKO-106-2-, AKOV-103, AKOV-118, DG- AKO-106-1-1-7, AKOV-114, Akola Bahar, AKOV-115, Parbhani Kranti, HRB-108-2, AKOV-119, AKOV-102, AKOV-106, AKOV-107, AKOV-111, Pusa A-4, Arka Anamika, AKOV-98-04-1	27
Cluster II	DG- AKO-106-3-1	01
Cluster III	AKOV-101-3	01
Cluster IV	AKO-99-04-3	01

Table.3 Average intra and inter cluster distance (D^2) for 30 okra genotypes

Clusters	I	II	III	IV
I	27.25	47.76	56.00	64.07
II		**0.00**	8.78	93.68
III			**0.00**	106.88
IV				**0.00**

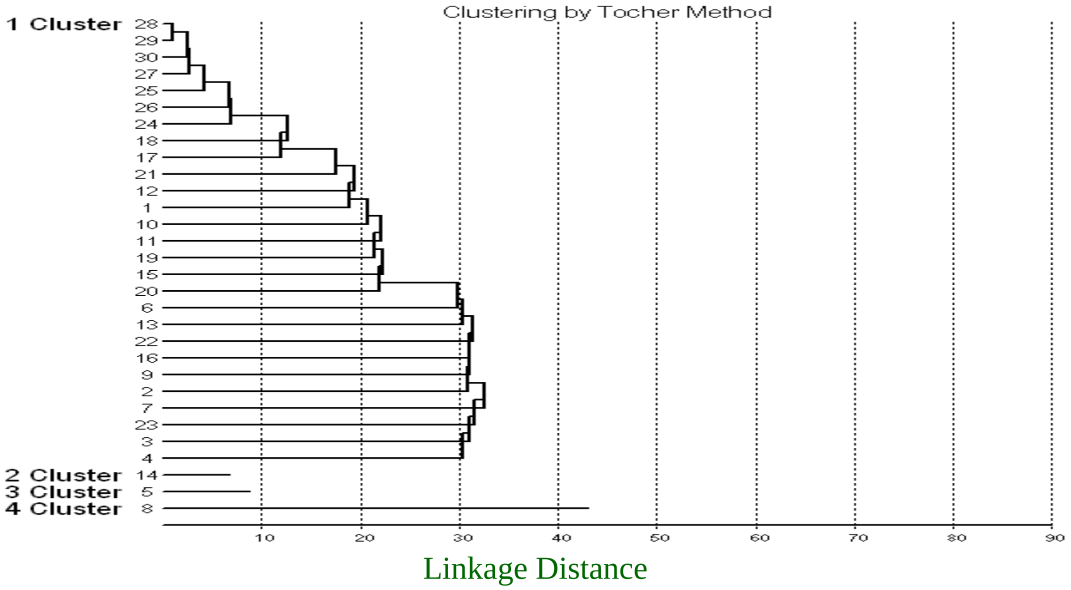
Table.4 Cluster means for 9 characters of 30 okra genotypes

Sr. No.	Components	Clusters			
		I	II	III	IV
1	Plant height (cm)	169.36	177.50	169.50	171.20
2	No. of nodes	21.85	21.30	18.90	21.70
3	Fruit length (cm)	11.42	9.35	10.51	11.20
4	Fruit girth	1.50	1.45	1.37	1.43
5	No. of fruits per plant	17.98	7.85	5.80	32.49
6	Avg. fruit weight (g)	12.53	12.77	11.51	11.18
7	Fruit yield per plant (kg)	0.33	0.10	0.07	0.28
8	Fruit yield per plot (kg)	7.23	3.14	2.11	9.04
9	Fruit yield qt. per hectare	83.68	36.32	24.43	104.58

Table.5 Percentage of ancillary characters towards total divergence

Sr. No.	Characters	Times ranked	Contribution (%)
1	Plant height (cm)	101	23.22
2	No. of nodes	18	4.14
3	Fruit length (cm)	31	7.13
4	Fruit girth	69	15.86
5	No. of fruits per plant	48	11.03
6	Avg. fruit weight (g)	03	0.69
7	Fruit yield per plant (kg)	160	36.78
8	Fruit yield per plot (kg)	05	1.15
9	Fruit yield qt. per hectare	00	00

Fig.1 Tree diagram of 30 genotypes of okra for 9 studied characters using hierarchical cluster analysis



The cluster mean values of 30 genotypes for nine characters under study was depicted in Table 4, showed that cluster I exhibited maximum mean values for number of nodes (21.85), fruit length (11.42 cm), fruit girth (1.50) and fruit yield per plant (0.33 kg), cluster II recorded highest mean values for plant height (177.50 cm) and average fruit weight (12.77 g) while cluster IV showed maximum mean values for number of fruits per plant (32.49), fruit yield per plot (9.04 kg) and fruit yield quintal per hectare (104.58 q). However cluster III exhibited lowest mean values for six characters under study viz. number of nodes, fruit girth, number of fruits per plant, fruit yield per plant, fruit yield per plot and fruit yield quintal per hectare.

As assessment of relative contribution of nine characters towards genetic divergence (Table 5) revealed that fruit yield per plant had contributed highest (36.78 %) by taking 160 time 1st ranking followed by plant height (23.22%) by 101 times, fruit girth (15.86%) by 69 times, number of fruits per plant (11.03%) by 48 times, fruit length (7.13%) by 31 times, number of nodes (4.14 %) by 18 times and fruit yield per plot (1.15%) by 5 times. Thus these characters will offer a good scope for improvement through selection. In contrast, average fruit weight had contributed least (0.69%) by taking 3 times. However the fruit yield quintal per hectare did not contribute materially towards total diversity.

References

Akotkar, P.K., De, D.K., and Pal, A.K. (2010). Genetic variability and Diversity in Okra (*Abelmoschus esculentus* (L.) Moench), Eelctronic journal of Plant Breeding 1(4): 393-398

Dutonde, S. N., Bhalekar, M.N., Patil, B.T., Khirsagar, D. B. and Dhumal, S. S. (2008) Genetic Diversity in Chilli (*Capsicum annuum* L.) Agric. Sci. Digest 28 (1): 45-47

Khodadabi, M., Fotokian MH, and Miransari, M. (2011) Genetic diversity of wheat genotypes based on cluster and principal component analyses for breeding strategies. Australian J. Crop Sci. 5(1):17-24

Lahbib, K., Bnejdi, F, Gazza EI (2010). Genetic diversity evaluation of pepper in Tunisia based on morphologic characters. Afr J Agric. Res. 7(23):3413-3417.

Mahalanobis PC (1936). On the generalized distance in statistics. Proc. Nat. Inst. Sci. India 49-55.

Murthy B.R. and Arunachalam, V (1966). The nature of genetic divergence in relation to breeding system in some crop plants, Indian Journal of Genetics and Plant Breeding 26: 188-198

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

Singh R.K., and Choudhary, B.D., (1985). In: Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi.

Yatung T., Dubey R. K, Singh, V. and Garima Upadhyay (2014) Genetic diversity of chilli (*Capsicum annuum* L.) genotypes of India based on morho-chemical traits. Australian J. Crop Science 8 (1): 97-102