

Short Communication

Estimation of genetic divergence in okra [*Abelmoschus esculentus* (L.) Moench]

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Okra [*Abelmoschus esculentus* (L.) Moench $2n = 2x=130$] is one of the important members of the family Malvaceae and is well-known by many regional names as Bhindi in India, lady's finger in England, Gumbo in USA, Dherosh in Bangladesh, Huang GiuKui in China and Quingombo in Spanish. It is a summer and rainy season crop and is widely cultivated from tropics to sub tropics (Kochar 1986). In India, it is cultivated round the year in one or other regions due to wide range of climatic condition in different parts of the country. In India, the major okra producing states are West Bengal, Bihar, Orissa, Andhra Pradesh, Gujarat, Jharkhand, Chhattisgarh and Maharashtra. The largest area and production are in India followed by Nigeria in the world. India ranks first in the world with 72% of the total world production of okra. In India, the total area covered under okra is 0.509 million ha which has produced 6.094 million tones green fruits with the productivity of 12.0 t/ha in the year 2017-18 (Anonymous 2018). In view the productivity and future requirements of okra fruits there is urgent need to develop varieties/ hybrids with high yield and biotic and abiotic resistance. Keeping in view the above facts the present experiment was undertaken to estimate the genetic diversity using Mahalanobis D^2 analysis for obtaining desirable hybrids or segregates of okra after hybridization between divers' groups of genotypes in future.

The present investigation was carried out at the Main Experimental Station, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology Narendra Nagar, Kumarganj, Ayodhya, UP during the *Kharif*, 2016. The experiment was conducted in a Randomized Complete Block Design (RBD) with three replications to assess the performance of 30

genotypes of okra including 3 check *viz.*, Arka Anamika, Arka Abhay, Kashi Kranti. Each entry was sown in three rows with 2.7 m, net row length spaced 60 cm with plant to plant spacing of 30 cm in each replication. The observations were recorded on five randomly selected plants in each replication. Observation were recorded for each genotype on 13 characters *viz.*, days to 50% flowering, node to first flower appearance, plant height, crop duration, number of branches per plant, days to first fruit harvest, fruit length, fruit circumference, average fruit weight, number of fruits per plant, marketable fruit yield per plant, unmarketable fruit yield per plant and total fruit yield per plant. The data were analyzed as per Mahalanobis D^2 analysis (Mahalanobis, 1928) to measure the genetic divergence among 30 genotypes.

In present investigation thirty genotypes of okra were grouped into 6 distinct non- overlapping clusters (Table 1). This indicated presence of considerable diversity in the genotypes. The major clusters in the above-mentioned genetic divergence analysis contained frequently the genotypes of heterogeneous origin. Although the genotypes of same origin or geographic region were also found to be grouped together in the same cluster. The instances of grouping of genotypes of different origin or geographic region in same cluster were frequently observed. This suggested that there is no parallelism between genetic and geographic diversity. Cluster II had maximum number of genotype (7) followed by clusters I, III, IV (5) and cluster V, VI each with 4 genotypes.

The intra-cluster D^2 values (Table 2) ranged from 14.213 (cluster V) to 26.906 (cluster IV). The maximum intra-cluster distance was observed in cluster IV followed by cluster II and cluster III. The maximum inter cluster distance was observed between cluster II and cluster IV (235.57) which suggested that members of these two clusters were genetically very diverse to each other. The inter clusters distance between cluster II and cluster V (165.393), cluster II to VI (159.022), cluster II to III

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Table 1: Clustering pattern of thirty genotypes of okra on the basis of Mahalanobis D² statistics

Cluster number	No. of genotype	Genotypes
I	5	NDO-15, NDO-19, NDO-20, NDO-22, NDO-23
II	7	NDO-11, NDO-12, NDO-13, NDO-16, NDO-18, Arka Anamika (C), Arka Abhay (C)
III	5	NDO-25, NDO-28, NDO-29, NDO-34, NDO-36
IV	5	NDO-26, NDO-27, NDO-30, NDO-32, NDO-37
V	4	NDO-24, NDO-31, NDO-33, NDO-35
VI	4	NDO-14, NDO-17, NDO-21, Kashi Kranti (C)

Table 2: Intra and inter cluster D² values for six cluster in okra

Cluster number	I	II	III	IV	V	VI
I	18.508	47.216	59.395	119.913	74.957	72.579
II		25.263	121.132	235.57	165.393	159.022
III			22.605	92.531	94.255	73.332
IV				26.906	45.213	39.886
V					14.213	27.974
VI						15.635

Table 3: Cluster means for thirteen characters in okra

Characters	Days to 50% flowering	Node to first flower appearance	Plant height	Crop duration	No. of branches per plant	Days to first fruit harvest	Fruit length	Fruit circumference	Average fruit weight	Number of fruits per plant	Marketable fruit yield per plant	Unmarketable fruit yield per plant	Total fruit yield per plant
I	41.06	7.22	109.59	105.20	4.05	46.33	11.61	5.61	20.20	8.33	94.61	48.76	143.34
II	40.42	7.09	106.74	105.23	3.69	45.90	11.01	5.10	20.72	8.64	85.18	31.81	118.18
III	39.00	7.33	127.27	109.50	3.82	44.33	10.96	5.33	19.81	12.01	137.88	48.97	185.05
IV	46.16	7.01	134.62	114.41	4.04	51.25	12.82	5.38	20.14	12.62	120.37	78.05	197.61
V	46.66	7.75	108.85	105.91	4.19	52.50	13.15	5.12	20.92	10.38	114.23	62.16	173.35
VI	47.00	7.07	120.27	112.22	4.04	52.77	12.65	6.18	20.50	10.94	128.58	56.75	185.02

(121.132) and cluster I to IV (119.913) were very high. The minimum inter cluster D² value was recorded in case of cluster V and cluster VI (27.974) followed by cluster IV to cluster VI (39.886). The higher inter cluster distance indicated greater genetic divergence between the genotypes of these clusters, while lower inter cluster values between the clusters suggested that the genotypes of the clusters were not much genetically diverse from each other. These findings are in conformity with as reported by earlier workers (Balai et al. 2015). Perusal of Table 3 revealed that cluster IV showed maximum mean values for the total fruit yield per plant, unmarketable fruit yield per plant, number of fruit per plant, plant height and crop duration followed cluster V showed maximum mean values for the fruit length, number of branches per plant and node to first flower appearance, average fruit weight and cluster VI showed maximum mean values for the days to 50% flowering, days to first fruit harvest, fruit circumference and marketable fruit yield per plant. Similar results have been also reported by Sharma et al. (2008), Akotkar et al. (2010) and Shaikh et al. (2013).

The maximum contribution in manifestation of total genetic divergence (Table 4) was made by unmarketable fruit yield per plant (59.08) followed by days to 50% flowering (13.79). The minimum contribution was

Table 4: Per cent contribution of thirteen characters toward total genetic divergence in okra

S. No.	Sources	Time Ranked 1 st	% contribution
1	Days to 50% flowering	60	13.79
2	Node to first flower appearance	18	4.14
3	Plant height (cm)	24	5.52
4	Crop duration	1	0.23
5	Number of branches per plant	11	2.53
6	Days to first fruit harvest	0	0.00
7	Fruit length (cm)	9	2.07
8	Fruit circumference (cm)	9	2.07
9	Average fruit weight (g)	2	0.46
10	Number of fruit per plant	8	1.84
11	Marketable fruit yield per plant (g)	34	7.82
12	Unmarketable fruit yield per plant (g)	257	59.08
13	Total fruit yield per plant (g)	2	0.46

notices in case of days to first fruit harvest (0.00) toward genetic divergence. Prakash et al. (2010) and Shaikh et al. (2013) had also reported maximum contribution by days to 50% flowering. Thus, the genotypes of clusters with high fruit yield per plant should be given due consideration during selection for improvement of this crop. Likewise, crossing between genotypes of cluster IV and cluster II may give rise desirable F₁/segregates in future breeding programme.

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