



Determination of Genetic Divergence in Okra Genotypes [*Abelmoschus esculentus* (L.) Moench]

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The investigation was executed at Main Experimental Station, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya during *Kharif*, 2019 in Randomized Block Design with three replications comprising thirty-six genotypes of okra collected from various sources to study the existence of genetic divergence among the germplasm by Mahalanobis D2 statistics. The germplasm was grouped into six clusters. Out of six clusters, cluster 1 contained maximum number of genotypes (22) followed by cluster VI (5), cluster II (3) and cluster III (2) Cluster IV (2) cluster V (2). The minimum intra cluster diversity was found for cluster III (8.39) and maximum intra-cluster distance was exhibited for cluster I (16.95). The highest inter-cluster distance was recorded between cluster I and III (30.83) preceded by cluster III and VI (30.15) and cluster 1 and V (24.89), it suggested that the genotypes of these two (cluster I and III) clusters are genetically very dissimilar to each other. The minimum inter-cluster distance was found between cluster IV and V (13.08) followed by cluster III and IV (14.24) and cluster II and IV (14.62). Highest per cent contribution in favour of total genetic diversity was showed by total fruit yields per plant (75.08%) followed by average fruit weight (12.38). Each clusters have higher mean values for

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different traits and the genotypes of cluster I followed by II and VI have more mean value for traits studies and deserve to be mentioned as important clusters of genotypes which could be use for further yield improvement plan of okra.

Keywords: Genetic divergence; D^2 analysis; okra (*Abelmoschus esculentus*).

1. INTRODUCTION

Okra or Lady's finger [*Abelmoschus esculentus* L. (Moench)] is an economically very important vegetable crop cultivated in mainly tropical and sub-tropical region of the world. It is suitable for grown as a kitchen garden as well as on large commercial farms. Okra is a popular crop of India because of easy cultivation, higher yield and suitable to various moisture conditions. Despite being used as a vegetable, okra is grown for its green, soft, and nutritious fruits, which are used for freezing and canning. The D^2 statistic is a very important tool to evaluate huge number of genotypes for their genetic distance and helps to identify genetically diverse genotypes for utilization in hybridization plan, as hybridization between genotypes of diverse origin show a greater level of heterosis than those which are closely related. Roy and Panwar [1] advocated that the range of resulting heterosis was largely depends on the degree of genetic distance in the genotypes. Multivariate analysis with Mahalanobis D^2 statistics is a most powerful tool to know the similarity and dissimilarity pattern to find the relationship between genetical and geographical diversity [2] and to quantify the role of different polygenic characters towards the diversity [3].

2. MATERIALS AND METHODS

The experiment took place in the Kharif of 2019 at the Main Experimental Station of the Department of Vegetable Science at Acharya Narendra Deva University of Agriculture and Technology in Narendra Nagar (Kumarganj), Ayodhya (U.P.), India. Geographically, the experimental site (Kumarganj, Ayodhya) is situated at an altitude of 113 metres above mean sea level and has a humid subtropical climate. It is situated at 26.47° N latitude and 82.12° E longitude. To evaluate the performance of 36 genotypes, the experiment used a Randomized Complete Block Design with three replications. Observations were noted on thirteen polygenic characters viz. days to 50% flowering, plant height (cm), node to first flower appearance, crop duration, days to first fruit harvesting, number of branches per plant, fruit length (cm), fruit

circumference (cm), average fruit weight, total number of fruits per plant, marketable fruit yield per plant (g), unmarketable fruit yield per plant (g). The genetic distance among 36 okra germplasm was judged by Mahalanobis D^2 statistics [4]. The average intra cluster distances were estimated by following the formulae as given by Singh and Chaudhary [5]. The grouping of genotypes was done using Tocher's method, as described by Rao (1952).

3. RESULTS AND DISCUSSION

Perusal of Table 1 revealed that thirty-six genotypes were grouped into 6 non over lapping clusters. Cluster 1 has maximum number of genotypes (22) followed by cluster VI (5), cluster II (3) and cluster III (2) Cluster IV (2) cluster V (2). Similar finding was also reported by Shyam et al. [6], Ranpise et al. [7] and Maurya and Yadav [8]. The estimation of intra and inter-cluster diversity represented by D^2 values are given in Table 2. The minimum intra cluster distance was observed for cluster III (8.39) and maximum was recorded for cluster I (16.95). The maximum inter-cluster distance was found between cluster I and III (30.83) followed by cluster III and VI (30.15) and cluster 1 and V (24.89), which revealed that genotypes of these two (cluster I and III) clusters are genetically very diverse to each other. Similar result were also found by Priyanka et al. [9] and Maurya and Yadav [8]. The minimum inter-cluster distance was observed between cluster IV and V (13.08) followed by cluster III and IV (14.24) and cluster II and IV (14.62). The low inter-cluster values between the clusters advocated that the genotypes of the clusters were not genetically diverse from each other. The intra-cluster mean for 13 characters in okra are given in Table 3. Perusal of Table 3 revealed that clusters mean for different traits reflected considerable differences between the clusters. For total fruit yield per plant, cluster I had the highest cluster mean, followed by cluster VI and cluster II. Similar result was found by Karthika et al. [10]. Cluster V showed minimum cluster mean (2.67) for number of branches per plant. Highest per cent contribution towards total genetic diversity (Table 4) was exhibited by total fruit yields per

Table 1. Clustering pattern of thirty-six genotypes of okra on the basis of Mahalanobis D² statistics

Clusters	No. of genotypes	Genotypes
I	22	NDO-21, NDO-22, NDO-23, NDO-24, NDO-25, NDO-26, NDO-27, NDO-28, NDO-29, NDO-30, NDO-31, NDO-32, NDO-33, NDO-34, NDO-35, NDO-36, NDO-37, NDO-38, NDO-39, NDO-40, NDO-41, NDO-42
II	3	NDO-43, NDO-44, NDO-45
III	2	NDO-50, NDO-51
IV	2	NDO-49, Arka Abhay ©
V	2	NDO-52, NDO-53
VI	5	NDO-46, NDO-47, NDO-48, Arka Anamika (C), VRO-6 (C)

Table 2. Estimates of average inter and intra cluster distance for 13 characters in okra

Clusters	I	II	III	IV	V	VI
I	16.95	20.97	30.83	24.73	24.89	16.45
II		16.37	18.42	14.62	18.32	20.49
III			8.39	14.24	18.86	30.15
IV				8.40	13.08	22.91
V					9.14	21.80
VI						16.04

**Bold diagonal values indicate intra cluster distance, rest of the values show the inter cluster distances*

Table 3. Cluster mean for 13 characters in okra

Clusters/ Characters	Node to first flower appearance	Days to 50 % flowering	Days to first fruit harvest	Fruit length (cm)	Fruit circumfer ence (cm)	Plant height (cm)	Number of branches per plant	Crop duration (days)	Petiole length (cm)	Average fruit weight (g)	Node per plant	Number of fruit per plant	Total fruit yield per plant (g)
I	7.26	44.61	54.99	14.20	6.04	114.09	3.32	101.49	13.71	20.39	22.61	12.05	193.64
II	7.38	43.45	53.33	14.48	6.09	117.20	3.06	103.78	12.65	20.56	22.76	12.33	173.99
III	6.88	43.67	54.83	12.80	6.45	105.36	3.25	99.50	12.73	21.88	23.50	12.50	153.24
IV	6.69	43.00	54.00	15.56	5.51	121.21	3.68	98.17	13.16	19.11	23.88	12.50	164.77
V	7.83	44.83	56.00	13.99	5.48	113.07	2.67	102.50	14.76	19.01	23.80	13.00	165.45
VI	6.85	45.53	56.60	14.46	6.12	116.79	3.00	102.67	13.97	19.33	24.15	12.33	191.16

Table 4. Per cent contribution of genetic advance for 13 characters in okra

S. no	Character	Percent contribution
1	Node to first flower appearance	0.63
2	Days to 50 % flowering	0.63
3	Days to first fruit harvest	0.00
4	Fruit length (cm)	0.00
5	Fruit circumference (cm)	2.06
6	Plant height (cm)	0.00
7	Number of branches per plant	2.38
8	Crop duration (days)	0.00
9	Petiole length (cm)	5.24
10	Average fruit weight (g)	12.38
11	Node per plant	0.16
12	Number of fruits per plant	1.43
13	Total fruit yield per plant (g)	75.08
	Total	100.00

plant (75.08%) followed by average fruit weight (12.38). Similar results were also reported by Samiksha et al. [11] and Kumar et al. [12]. While petiole length (5.24) contributed lowest towards total genetic diversity. Rest of the characters showed average contribution towards total genetic divergence.

4. CONCLUSION

Clustering pattern among the available genotypes indicated that there exists ample diversity among the germplasm of okra. Clusters I and III showed maximum inter cluster distance and high cluster mean value for yield per plant. This indicated that these genotypes can be best utilized in breeding for high yielding hybrid of okra in future. Contribution of different traits towards divergence indicated that yield per plant, plant height, fruit length and first fruiting node per plant contributed most towards genetic divergence among the available germplasm of okra.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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