Original Research Article

Assessment of genetic diversity in okra (*Abelmoschus esculentus* L.) genotypes with various quantitative traits

ABSTRACT

The study was conducted in 2019 at the Horticulture Research Centre, Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut, India. The analysis of variance data revealed substantial genetic differences for all morphological traits. According to Mahalanobis D^2 all the forty genotypes were found to have a significant amount of genetic diversity. The result indicated that the greatest mean value was found in cluster III for days to 50 per cent flowering, days to Ist flower initiation, days to Ist fruit set, days to Ist fruit picking, days to IInd fruit picking, number of primary branches, number of nodes / plant, duration of crop and also some characters was found highest mean value in cluster I like, plant height, fruit length, number of fruits / plant, length of internode, fruit yield / plant and fruit yield (q/ha.). Cluster II had the most genotypes recorded overall. (21 genotypes) followed by 11 genotypes in cluster I. The largest intra cluster distance was discovered in cluster III, whereas the largest inter cluster D^2 distance was measured between Cluster I and Cluster III. The genotypes of Cluster I and Cluster III are not closely related, according to the maximum inter-cluster D^2 distance, although the genotypes of Cluster I and Cluster II are, according to the minimum inter-cluster D^2 distance. Among all the characters that were contributed, the length of internode had the highest contribution %.

Keyword: Cluster, Genetic divergence, Okra, quantitative traits

INTRODUCTION

Okra (*Abelmoschus esculentus* L.), is an annual plant, belongs to Malvaceae family. It is tropical and subtropical areas of the world; it is one of the most significant and major vegetable crops. A limited number of vegetables are readily available in the market during the summer, which satisfies customer demand for highly sought-after vegetables in the early summer. Because it contains a lot of iodine, The fruits of okra are most helpful in

the treatment of goitre disease in human. In vegetable gardens, okra has the most exquisite blossoms that have great beauty value. According to **Bawa and Badrie ,** edible okra has a lot of nutrients, including protein, minerals, fat, fibre, calories, carbohydrate, maximum amount of water as well as good quantity of total phenolics, folate, and ascorbic acid.

Several experts have noted the medicinal and nutritional value of okra, including mineral components, protein, fibre, antioxidants, and vitamins. **Adetuyi *et al.* (2011).** Flavonoid and antioxidants such beta carotene, xanthein, and lutein are abundant in okra pods **(Dilruba *et al.* 2009).**

Okra is morphologically tall to medium in height plant and annual herbaceous nature. The leaves are alternate, broad, caudate, palmately with 3-7 lobed, hirsute, and serrate. The stem of okra is green or stained scarlet. Flowers are solitary, auxiliary, with a 2 cm long peduncle. The okra flower having 5 sepals and 5 petals. The petal colour of okra is yellow with a crimson spot. Okra flower has five to seven cm long staminal united column to the petal base with many stamens. Superior ovary with five to seven deep red stigmas.

Vegetables are mostly cultivated in India on an area of about 10.85 million hectares, total production about 200.4 million tonnes of produce year at a productivity of 18.55 tonnes per hectare (Anonymous, 2020-21). Okra is grown on 530 thousand hectares, and annual production of 6465.59 metric tonnes (Anonymous 2020-21). Gujarat is the top state for okra production, producing 1019.42 thousand Tonnes from an area of 85.15 thousand hectares. West Bengal comes in second with production of about 882.59 thousand tonnes from an area of 78.64 thousand hectare (Anonymous, 2020-21).

The D^2 statistic, which calculates two levels of genetic divergence, namely; inter cluster and intra cluster levels, aids in the choosing genetically diverse parents for use in hybridization programmes (Mahalanobis, 1936). Because hybrids between lines of different provenance typically demonstrate a stronger heterosis than those between closely related lines, genetic diversity exhibit plays a crucial role in breeding techniques (Murty and Arunachalam 1966).

MATERIALS AND METHODS

The research materials, which included a total of 40 genotypes of okra populations Hisar Naveen, Varsha Uphar, Punjab Kranti, Arka Anamika, Arka Abhay, Pusa Sawani, Pusa A-

4, Parbhani Kranti, Kashi Pragati, Mona, Kashi Kranti, U.S-8063, IC-090491, Y.V.S-9, IC-316/2,4,5, IIVR-II, VRO-3, VRO-4, VRO-5, VRO-6, 368-A, Hisar Unnat, IC-18530, EC-305642, EC-305643, EC-305644, EC-305645, EC-305639, IC-014026, EC-305638, EC-305637, EC-305635, EC-305768, IC-013356, IC-013664, EC-359637, IC-15027, EC-305640, IC-010265 and IC-14909 with 14 different characteristics, were gathered from a variety of locations in the okra-growing regions of HAU, Hisar, PAU, Ludhiana, IIHR, Bengaluru, Dr. PDKV, Akola, IARI, New Delhi, MPKV, Rahuri, IIVR, and Varanasi. Using a Randomized Block Design (RBD) with three replications, the experiment was carried out in the summer season of 2019 at the Horticulture Research Centre of the Sardar Vallabhbhai Patel University of Agriculture & Technology in Meerut. To determine the reliability of each variety's performance, the genotypes were analysed statistically for all of the morphological findings of a 60x30 cm row-to-row and plant-to-plant sowing. The experimental location is situated in SVP University of Agriculture & Technology, Meerut, which is about 70 km from the National Capital of Delhi on National Highway No. 58 (Delhi - Haridwar Highway). Geographically, the trial location in the North Western Plain Zone of Uttar Pradesh at an elevation of about 297 metres above MSL and at 29° 01 N latitude and 77° 45 E longitude.

Data were gathered on agronomic and morphological traits, namely days to Ist flower initiation, days to 50% flowering, plant height, number of primary branches, number of nodes / Plant, length of internode, fruit length, days to Ist fruit set, number of fruits / plants, days to Ist fruit picking, days to IInd fruit picking, duration of crop, fruit yield / plant and fruit yield. Following the analysis of variance, multivariate analysis (using the D^2 statistic) was performed on the data of 40 genotypes of okra (Mahalanobis, 1936). By using crucial condensation, standardized uncorrelated variables were created from the original measurements. (Rao, 1952). Tocher's method (Rao,1952) was used to divide genotypes into several clusters, and Singh and Choudhury's (1985) formula were used to discovered the parallel contribution of various traits to total divergence.

RESULT AND DISCUSSION

The analysis of variance on the basis of data in Table-1 there is a highly significant variation for each character. The findings suggested that the genotypes under study exhibit

adequate diversity. Okra has also seen this type of crop variability, according to **Kumar *et al.* (2020).** According to D^2 analysis, there were three clusters formed. From the pattern of clustering, it might be extrapolated that sufficient divergence was present to enable the establishment of individual character. According to the clustering pattern, geographic diversity is not a reliable indicator of genetic diversity. As a result, Mahalanobis D^2 analysis of quantitative traits is an effective tool for assessing genetic divergence among materials chosen even from the same geographic region.

Table-2 shows the cluster mean value for the fourteen traits that were the focus of the inquiry. The results showed that Cluster III had the greatest mean value for days to 50% flowering (54.89) and Cluster II had the lowest mean value for days to 50% flowering (45.48). Days to I^{st} flower initiation showed that clusters III and II, respectively, had the greatest mean value (51.94) and the lowest mean value (42.47). The highest mean value for the character like days to I^{st} fruit set was in cluster III, while the lowest mean values were in clusters II (53.67) and (44.39), respectively. Cluster III had the greatest mean value for days till the first fruit picking, while cluster II had the lowest (58.30 and 49.32, respectively). Days second fruit picking showed that cluster III had the highest mean value and cluster II had the lowest mean value (63.04). (54.17). Plant height was showed highest mean value (93.64) and lowest mean value (71.17) found in cluster I and III. Fruit length was observed, and clusters I and III had the highest mean value (9.71) and the lowest mean value (8.83). For the number of fruits / plants, clusters I and III had the greatest mean values (11.84) and (9.60). Number of primary branches was showed highest mean value (2.92) and lowest mean value (2.03) found in cluster III and cluster II respectively. Number of nodes / Plant showed highest mean value (22.95) and lowest mean value (18.79) was found in cluster III and cluster II. Length of internode was recorded highest mean value in cluster I (4.88) and lowest cluster mean in cluster III (3.40) respectively. Fruit yield and its traits that influence fruit production, such as fruit yield / plant, had a mean value that was highest in cluster I (119.30) and lowest in cluster III. (98.47). Fruit yield highest mean value in cluster I (76.78) and lowest cluster III (65.45). In other character like duration of crop highest mean value in cluster III (101.55) and lowest in cluster II (109.88) **Kumar *et al.* (2020), Nanthakumar *et al.* (2021) and**

Yadav *et al.* (2022). Breeding programmes may be using genotypes that performed good, meaning they have these traits in different clusters, to create high yielding okra cultivars.

The 40 genotypes in total were divided by Tocher's methods, which are shown in Table 3 & Figure 1, into three distinct genetic clusters based on genetic affinity or diversity. Cluster I comprised of 11 genotypes *viz,* Varsa Uphar, Punjab Kranti, Arka Anamika, Arka Abhay, Parbhani Kranti, Kashi Pragati, VRO-3, VRO-5, 368-A, EC-305635, IC-14909. Cluster II comprised of 21 genotypes *viz,* Hisar Naveen, Pusa Sawani, Pusa A-4, Mona, Kashi Kranti, Y.V.S-9, IIVR-II, VRO-4, VRO-6, Hisar Unnat, IC-18530, EC-305644, EC-305645, EC-305639, IC-014026, EC-305638, EC-305637, IC-013356, IC-013664, IC-15027, IC-010265. Cluster III comprised of 8 genotypes *viz,* U.S-8063, IC-090491, IC-316/2,4,5, EC-305642, EC-305643, EC-305768, EC-359637, EC-305640. The parallels between genetic and geographic variety were evident. The viewpoint, which indicates a large deal of variability among the clusters, has been hold up by the study of **Kumar *et al.* (2020), Nanthakumar *et al.* (2021), and Yadav *et al.* (2022).** This shows how drastically different the genetic architecture of the lines in one cluster is from the genetic architecture of the lines in the other cluster. Based on the minimal cluster distance found between clusters I and III, in order to create the desired recombinants, a hybridization application may use the genotypes in this cluster as parents. The varieties that will act as parents in a hybridization are chosen using the inter cluster distance criterion in a D^2 analysis.

The average D^2 values between and within clusters are shown in Table-4. Cluster I and Cluster III had the largest inter cluster D^2 distance (6.14), whereas Cluster I and Cluster II had the smallest inter cluster D^2 distance (3.59). Cluster III (3.32) had the greatest intra-cluster distance, followed by cluster I. (2.59). Cluster II recorded the shortest distance within a cluster (2.17). The genotypes of Cluster I and Cluster III are not closely related, based on the maximum inter-cluster D^2 distance, although the genotypes of Cluster I and Cluster II are, as determined by the minimum inter-cluster D^2 distance. As can be seen from the modest variance of D^2 values, the genotypes of the cluster do not significantly differ in terms of their relative genetic distance. In the past, reported similar outcomes **Kumar *et al.* (2020), Nanthakumar *et al.* (2021) and Yadav *et al*. (2022).**

Crosses suggesting parent belonging to most divergence clusters would be expected to manifest highest heterosis and also wide heterogeneity of genomic architecture. In order to create high heterotic populations, segregates, and/or to be used for the production of hybrid in okra, crossings between the genetically varied genotypes of clusters I and III may be based on supremacy for any characteristic or genetic diversity.

Contributions of several characters towards overall genetic divergence are reported in Table-5 & Figure-2. The genetic divergence was influenced by measuring the D^2 value for each character individually and summing the rank for each trait across all entries and alterable. Among all the characters that were supplied, the length of the internode had the highest contribution rate (8.72%), followed by fruit yield (8.15 %), days to IInd fruit picking (8.14 %), fruit yield / plant (8.01 %), days to 50 per cent flowering (7.69 %), number of fruits / plant (7.69 %), days to Ist fruits set (7.25 %), number of primary branches (7.24 %), number of nodes / plant (7.20 %), days to Ist fruit picking (7.09 %), fruit length (6.45 %), duration of crop (6.25 %), days to Ist flower initiation (5.83 %) and lowest contribution of plant height (4.29 %). The maximum divergence was directly brought on by **Kumar *et al.* (2020), Nanthakumar *et al.* (2021).** Thus, choosing variable parents based on these characteristics that indicated to producing high-quality hybrids as well as segregants in okra, according to **Yadav *et al.* (2022).**

In combined over conditions, the analysis of variance revealed significant amount of variations between the genotypes in fourteen morphological characteristics. According to a diversity analysis, Different clusters were formed by genotypes from the same location, and vice versa. This is implied that choosing parents for crop improvement should be focused more on genetic variety than on the geographic areas' clustering patterns, which demonstrated that surroundings have a significant impact on D^2 statistics. Clusters I and III had the greatest inter cluster distance and the highest cluster means, indicating that these clusters could be most effectively used in breeding for high producing okra.

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Table-1: ANOVA for 14 characters in Okra [*Abelmoschus esculentus* (L.) Moench]

Source of variation	DF	DFI	DF	PH (cm)	NPB	NN/P	LI (cm)	FL (cm)	DFS	NF/P
Replication	2	1.25	3.48	0.08	0.03	0.67	0.04	0.24	0.49	0.29
Treatment	39	54.73**	52.77**	428.93**	1.73**	33.75**	1.81**	2.25**	52.96**	6.29**
Error	78	3.77	3.80	4.28	0.06	1.10	0.12	0.66	3.86	0.17

*, ** significant at 5% and 1% level, respectively. DFI (Days to Ist flower initiation, DF (days to 50 % flowering), PH (plant height), NPB (number of primary branches), NN/P (number of nodes/P), LI (length of internode), FL (fruit length), DFS (days to Ist fruit set), NF/P (number of fruits/plant), DFP (days to Ist fruit picking), DSFP (days to IInd fruit picking), DC (duration of crop), FY/P (fruit yield/plant) and FY/h (fruit yield/ha).

Table-2: Cluster means

Characters		DFI	DF	PH (cm)	NPB	NN/P	LI (cm)	FL (cm)	DFS	NF/P	DFP
Cluster I	**Mean**	43.05	46.19	93.64	2.71	20.03	4.88	9.71	45.09	11.84	50.10
	± SE	2.18	2.08	8.24	0.43	0.99	0.50	0.76	2.18	1.65	2.31
Cluster II	**Mean**	42.47	45.48	75.06	2.03	18.79	4.08	8.87	44.39	9.64	49.32
	± SE	1.87	1.77	8.24	0.31	2.27	0.45	0.81	1.93	0.77	1.78
Cluster III	**Mean**	51.94	54.89	71.17	2.92	22.95	3.40	8.83	53.67	9.60	58.30
	± SE	2.46	2.35	7.27	1.35	5.67	0.97	0.80	2.40	0.73	2.42

Table-3: Clustering pattern of 40 genotypes of okra on the basis of genetic divergence

Clusters	Number of genotypes	Genotypes Name
Cluster I	**11**	Varsa Uphar, Punjab Kranti, Arka Anamika, Arka Abhay, Parbhani K VRO-5, 368-A, EC-305635, IC-14909.
Cluster II	**21**	Hisar Naveen, Pusa sawani, Pusa A-4, Mona, Kashi Kranti, Y.V.S-9 Unnat, IC-18530, EC-305644, EC-305645, EC-305639, IC-014026, 013356, IC-013664, IC-15027, IC-010265.
Cluster III	**8**	U.S-8063, IC-090491, IC-316/2,4,5, EC-305642, EC-305643, EC-3

Table-4: Inter and intra cluster distances

Clusters	Cluster I	Cluster II	Cluster II
Cluster I	**2.59**		
Cluster II	3.59	**2.17**	
Cluster III	6.14	5.52	**3.32**

Table-5: Contribution of various characters towards total genetic divergence

S. No	Characters	Contribution %
•	DFI	5.83
•	DF	7.69
•	PH (cm)	4.29
•	NPB	7.24
•	NN/P	7.20

•	LI (cm)	8.72
•	FL (cm)	6.45
•	DFS	7.25
•	NF/P	7.69
•	DFP	7.09
•	DSFP	8.14
•	DC	6.25
•	FY/P (gm)	8.01
•	FY (q/ha)	8.15