Research Article

Multivariate analysis for assessing genetic diversity in different genotypes of okra (*Abelmoschus esculentus* L. Moench) for varietal improvement

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Abstract

Accurate assessment of genetic diversity facilitates the strategic identification of superior genotypes, enabling the development of high-yielding, climate-resilient cultivars and promoting effective crop improvement strategies. The present study was carried out with 48 different genotypes of Okra (*Abelmoschus esculentus* (L.) Moench) during (Jan-April 2022) to investigate their genetic diversity. The analysis of genetic divergence using D^2 statistics revealed substantial variation among genotypes for the twelve traits studied. The 48 genotypes were grouped into nine clusters, with cluster IV having the highest representation of 24 genotypes, followed by cluster II with 12 genotypes, cluster I with 4 genotypes, cluster III with 3 genotypes, and the remaining clusters with one genotype each. The intra and inter-cluster D^2 values ranged from 0 to 95.29 and 103.00 to 588.71, respectively. The highest intra-cluster distance was observed in Cluster III (95.29), and highest inter-cluster distance was observed between cluster V and IX (588.71). This range clearly demonstrated that the inter-cluster distance was greater than the intra-cluster distance indicating wide diversity across the groups. Cluster VII showed a high mean for traits plant height (112.53), peduncle length (3.14), fruit length (20.03), and number of locules (7.87). Cluster V showed the highest mean for the number of fruits (39.33) and yield per plant (1.18). The analysis of all characters' relative contributions showed that the number of fruits per plant and the number of locules per fruit contributed most to genetic divergence. High heterotic effects and desired transgressive segregants are anticipated when different genotypes from clusters with the greatest inter-cluster distance are used for hybridization.

Keywords: Clusters, Genetic Diversity, Intra and Inter-cluster distance, Multivariate analysis

INTRODUCTION

Okra or Bhendi (*Abelmoschus esculentus* (L.) Moench), often referred to as "Lady's finger", is a significant vegetable crop that is widely cultivated in both tropical and subtropical regions (Patel *et al.,* 2019). Although the chromosome numbers of cultivated okra vary significantly, the most frequently detected chromosome number is 2n = 130 (Kumar *et al.,* 2017). It is a member of the Malvaceae family. Although the origin of okra is still obscure, West Africa, India, and Southern Asia are where their genetic diversity is centred (Koli *et al.,* 2020). Due to the numerous uses for its leaves, fruits, seeds, and even dried stems, it is a crop with many benefits. Because of its strong dietary and medicinal value, it occupies a significant position among fruits and vegetables (Reddy *et al.,* 2012). In the context of genetic diversity in okra, the successful development of commercial hybrids has emphasized the importance of genetic divergence as a crucial factor in selecting suita-

ble genotypes for hybridization programs. This consideration ensures the exploration and utilization of diverse genetic resources, leading to enhanced hybrid vigor and improved traits in the resulting progeny (Nanthakumar *et al.,* 2021). The advancement of breeding, when considering the improvement of economic traits, frequently depends upon the accessibility of genetically diverse and vast germplasm. Genetically distinct parents should result in better hybrids and more desirable recombinants than closely related ones. The D^2 statistics method developed by P.C. Mahalanobis, based on multivariate analysis of quantitative variables by genotype discrimination, is an effective technique for determining genetic divergence (Sood *et al.,* 2017). The population's level of diversity is determined based on the study's characteristics. Upon clustering, a genetically diverse population separates into various groups. Any program for crop development is structured on the differences identified both within and between species. The present research aimed to investigate the nature and magnitude of genetic diversity across 48 okra genotypes, including indigenous, exotic collections, and many landraces, to discover diverse genotypes for use in breeding programs.

MATERIALS AND METHODS

The study was conducted in an Agriculture farm, Sivapuri village, Cuddalore district of Tamil Nadu from Jan 2022-May 2022. The experimental material comprised 48 okra genotypes, including exotic, indigenous collections and landraces (Table 1). Each genotype was planted in three replications in Randomized Block Design (RBD) spaced at 60 x 30 cm. All the requisite practices for raising the crop were followed. The observations were taken from five plants of each genotype selected randomly in each replication for twelve characters, *viz.,* number of primary branches per plant, plant height, days to first harvest, days to 50% flowering, fruit thickness, fruit weight, fruit length, peduncle length, number of locules per plant, no of fruits per plant, harvest period and fruit yield per plant. The genetic diversity within the 48 genotypes was evaluated using Mahalanobis' D^2 statistics (Mahalanobis, 1936). All of the genotypes utilized were classified into separate clusters using Tocher's approach (Rao, 1952). The average inter-cluster and intra-cluster distances were computed using Singh and Choudhury's (1985) formula. The statistical tool used for the assessment of genetic diversity

Table 1. Showing genotypes and their source

S. No	Name of the Genotype	Source	S. No		Source
1	IC 45732	NBPGR, New Delhi	25	Ruchi	Sun Gold Agri Sciences, Hyd.
2	IC 45780	NBPGR, New Delhi	26	Arka Anamika	IIHR, Bengaluru
3	IC 45815	NBPGR, New Delhi	27	Super Champion	Bharat Crop Sciences, Jodhpur
4	IC 45799	NBPGR, New Delhi	28	Nol 1307 (Silky)	Novel Seeds, Jalgaon
5	IC 45805	NBPGR, New Delhi	29	Hari Pari	Hari Bhumi Seeds, Hisar
6	IC 45821	NBPGR, New Delhi	30	Kashi Mangli (VRO-4)	IIVR, Varanasi
7	IC 45818	NBPGR, New Delhi	31	Rani 792	Ramzin Affan Seeds, Ludhiana
8	IC 44896	NBPGR, New Delhi	32	Lush Green	East-West Seeds, Aurangabad
9	IC 45791	NBPGR, New Delhi	33	Maharani	Mahashakti seeds, Hisar
10	IC 45727	NBPGR, New Delhi	34	Super Lady	Nath Bio Genes, Aurangabad
11	IC 45802	NBPGR, New Delhi	35	Takath TS-102	Taiyo Gold Agri Biotech, Hyd.
12	EC 329362	NBPGR, New Delhi	36	Palam Komal	CSKHPAU, Himachal Pradesh
13	EC 329364	NBPGR, New Delhi	37	Red Round	PDR Gardens, Chennai
14	EC 329366	NBPGR, New Delhi	38	1 Foot	PDR Gardens, Chennai
15	EC 329368	NBPGR, New Delhi	39	Bommidi	PDR Gardens, Chennai
16	EC 329370	NBPGR, New Delhi	40	Sunai	PDR Gardens, Chennai
17	EC 329382	NBPGR, New Delhi	41	Tree	PDR Gardens, Chennai
18	EC 329384	NBPGR, New Delhi	42	Colorful	PDR Gardens, Chennai
19	Kashi Pragati	IIVR, Varanasi	43	Dark Green	PDR Gardens, Chennai
20	GFS Gold V4	Gujarat Farm Seeds, Anand	44	IC 45811	NBPGR, New Delhi
21	Harika	Golden Valley Seeds, Hyd.	45	EC329375	NBPGR, New Delhi
22	Dhanvi 66	Dhanvi Seeds, Hyderabad	46	EC 329372	NBPGR, New Delhi
23	Ajeet 121	Ajeet Seeds, Aurangabad	47	EC 329378	NBPGR, New Delhi
24	Gold 207	Green Gold Seeds, U. P	48	Suguna A51	Ananya Seeds, Hisar

is TNAUSTAT (Tamil Nadu Agricultural University Statistical package).

RESULT AND DISCUSSION

According to their D^2 values, the 48 genotypes were categorized into nine diverse clusters. The clustering pattern of these genotypes is mentioned in Table 3. The Cluster Dendrogram is represented in Fig. 1, which shows the separation of genotypes into different clusters. Among them, Cluster IV was the largest with 24 genotypes, followed by Cluster II with 12 genotypes, Cluster I with 4 genotypes, Cluster III with 4 genotypes, and Cluster V, VI, VII, VIII, and IX were solitary clusters with single genotypes each. The genotypes were segregated into discrete clusters according to the diversity, indicating that the materials could be a credible source for selecting parents from a variety of genetic origins for a hybridization program. Asha *et al.* (2015) observed 8 clusters among 49 genotypes within which 5 clusters are solitary, Ranpise *et al.* (2018) observed similar 9 clusters within 35 genotypes among which 7 clusters were solitary, Priyanka *et al.* (2017) observed 5 distinct clusters for 29 genotypes of Okra (*A. esculentus* (L.) Moench). These findings suggest that by incorporating genotypes from diverse genetic origins represented in different clusters, breeders can access a wider pool of genetic variation, increasing the chances of developing hybrid progeny with improved traits and adaptability.

The average inter-cluster and intra-cluster values are mentioned in Table 4. The intra-cluster D^2 values ranged from 0.00 to 95.29. Cluster III has the greatest intra-cluster distance (95.29), followed by Cluster II (90.72). Clusters V, VI, VII, VIII, and IX have no intra-cluster distance since they are mono-genotypic as observed in the clustering pattern in Table 3. The highest intra-cluster distance indicates that the genotypes within that cluster are having a greater degree of heterogeneity. The intra-cluster values are significantly lower than the inter-cluster values, revealing that genotypes inside the cluster are homogeneous while genotypes between the clusters are heterogeneous. The inter-

Table 2. Showing cluster means for 12 characters in Okra (*Abelmoschus esculentus* (L.) Moench)

S. No.	Characters	I	II	III	IV	V	VI	VII	VIII	IX
1	Days to 50% flowering	42.25	43.72	43.00	43.69	39.00	41.67	48.67	47.00	52.33
2	Plant height (cm)	81.29	90.78	77.47	88.74	77.67	72.43	112.53	83.47	65.63
3	Number of primary branches per plant	2.99	3.79	3.34	3.57	5.06	3.20	4.10	4.40	2.13
4	Days to first harvest	49.25	49.58	49.22	48.67	46.67	49.00	53.67	44.67	56.00
5	Fruit length (cm)	13.84	14.56	16.23	13.97	15.46	13.62	20.03	9.33	9.73
6	Fruit thickness (mm)	17.39	20.42	21.33	17.76	23.63	21.14	30.30	38.58	35.80
7	Fruit weight (gm)	19.82	19.20	31.94	16.09	29.67	37.43	34.47	49.33	33.87
8	Peduncle length (mm)	1.76	2.19	2.35	2.36	2.37	2.12	3.14	1.75	1.83
9	Number of locules per fruit	6.40	6.90	5.22	5.23	6.93	6.13	7.87	7.33	6.59
10	Number of fruits per plant	32.75	22.24	28.02	26.37	39.33	38.93	16.13	19.80	13.00
11	Harvest period	62.00	58.33	61.11	58.81	64.00	51.67	68.33	64.67	68.33
12	Fruit yield per plant (kg)	0.63	0.42	0.93	0.42	1.18	0.97	0.55	0.97	0.43

Table 3. Showing clustering pattern of 48 genotypes of Okra (*Abelmoschus esculentus* (L.) Moench)

Clusters	Number of genotypes	Genotypes
I	4	IC 45732, IC 44896, EC 329366, KASHI PRAGATI
II	12	IC 45780, EC 329364, EC 329378, IC 45818, EC 329382, EC 329362, EC 329384, EC 329372, BOMMIDI, IC 45802, IC 45791, SUGUNA A51
III	3	IC 45815, SUNAI, RUCHI
IV	24	IC 45799, EC 329375, SUPER LADY, ARKA ANAMIKA, HARI PARI, GFS GOLD V4, HARIKA, AJEET 121, RANI-792, VRO-4, MAHARANI, RED ROUND, LUSH GREEN, IC 45811, NOL 1307 SILKY, GOLD 207, TAKATH-102, DARK GREEN, SUPER CHAMPION, IC 45821, IC 45727, EC 329370, DHANVI-66, PALAM KOMAL
V	1	IC 45805
VI	1	EC 329368
VII	1	1 FOOT OKRA
VIII	1	TREE OKRA
IX	1	COLOURFUL OKRA

cluster distances varied from 103.00 to 588.71. Cluster V and Cluster IX had the greatest inter-cluster distance (588.71), followed by Cluster VI and VII (560.80), and Cluster I and IV had the smallest inter-cluster distance (103.00). Crossing between the different genotypes of clusters separated by large inter-cluster distances would be desirable in increasing the chances of isolating excellent heterotic combinations in segregating generations. When selecting parents for hybridization program, rioritizing the most significant character for genetic divergence is crucial. This ensures that the chosen parents possess contrasting characteristics, maximizing the potential of producing offspring with enhanced trait expression. Nanthakumar *et al*. (2021) cited reports on 46 genotypes of Okra (*A. esculentus* (L.) Moench), noting that maximum inter-cluster distance was observed between cluster IV and V (2282.81), and the inter-cluster distances ranged from 39.31 to 2282.81 which are in contrary with the current study. Saleem *et al.* (2023) reported that maximum inter-cluster distance was observed between cluster I and II (1213.97) in 24 genotypes of Okra (*A. esculentus* (L.) Moench).

Fig. 2 shows the percentage contribution of each trait to genetic divergence. The attribute number of fruits per plant (29.07%) was the most significant contributor to divergence. It was then followed by the number of locules per fruit (27.30%) and weight (11.43%). These three traits collectively contribute 67.8% to total divergence. Asha *et al.* (2015) reported that fruit diameter (25%) in Okra (*A. esculentus* (L.) Moench) contributed

most to divergence, which is in contrast with the current study. The variables that ranked the most times were the number of fruits per plant and the number of locules per fruit, which were 328 and 308 times, respectively, as mentioned in Fig. 1. This indicates that these variables have higher significance or influence on overall genetic diversity. While selecting parents for hybridization, these attributes should be highlighted. According to Jagadev *et al.* (1991), the character adding the most to the divergence should be given considerable importance in determining the type of cluster to be chosen for further selection and the choice of parents for hybridization. Priyanka *et al.* (2017) observed that the variable yellow vein mosaic virus infestation ranked most (224) followed by fruit length (58).

Based on the cluster mean given in Table 2, it could be concluded that for yield improvement program genotypes in cluster VII, characterized by maximum mean values for plant height (112.53), fruit length (20.03), peduncle length (3.14), number of locules per fruit (7.87), harvest period (68.33), and cluster V having the highest mean values for the number of primary branches per plant (5.06), number of fruits per plant (39.33), and fruit yield per plant (1.18), could be exploited, and using the genotypes of these clusters in the hybridization program is predicted to increase the chances of obtaining better primary recombinant genes. The least mean value for days to 50% flowering was observed in cluster V, indicating that genotypes of this cluster were early flowering and can be utilized for stress breeding programmes. Similarly, Kumari *et al.,* (2019) observed
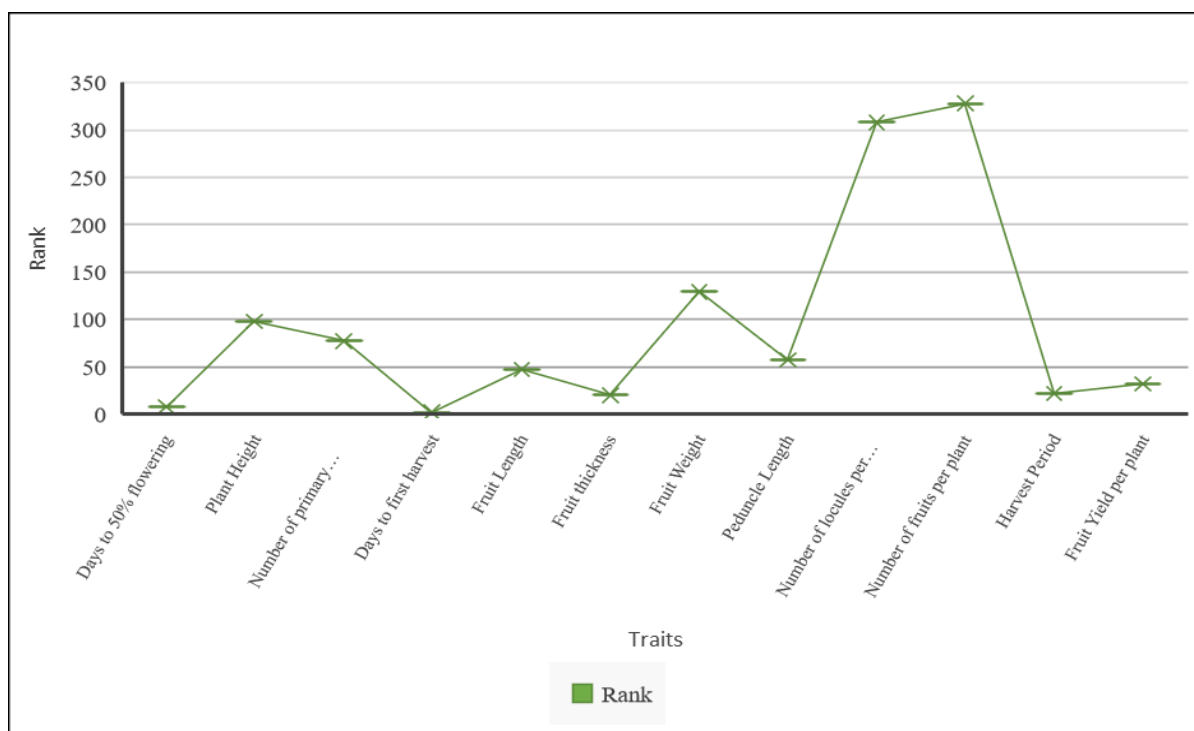

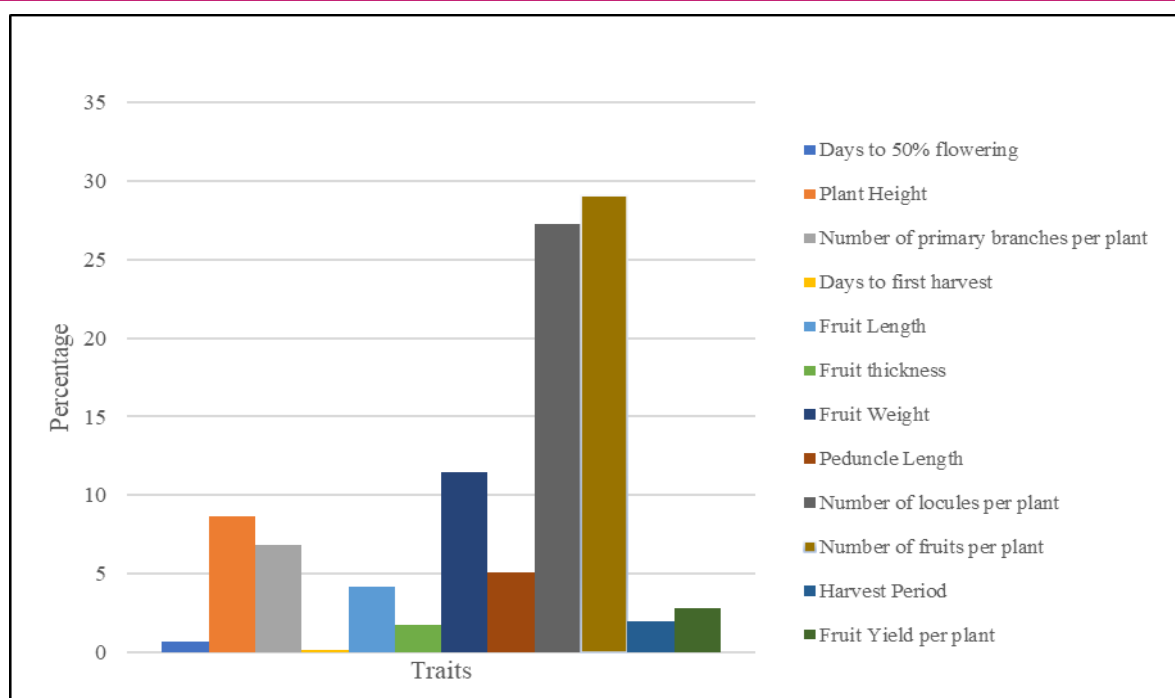**Fig 1.** *Contribution of traits of Okra (Abelmoschus esculentus (L). Moench.) to diversity by rank*

Fig 2. *Percentage contribution of traits of Okra (Abelmoschus esculentus (L). Moench.) to diversity*

Table 4. Showing Intra and Inter-cluster D^2 Values

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	68.01	139.69	132.65	103.00	152.72	122.49	427.12	478.56	417.66
II		90.72	172.46	133.90	212.29	254.38	220.27	355.97	320.05
III			95.29	118.28	164.31	184.59	367.11	410.70	365.80
IV				50.78	230.81	184.30	403.87	524.55	419.80
V					0.00	233.71	428.82	458.56	588.71
VI						0.00	560.80	460.25	450.70
VII							0.00	270.11	287.18
VIII								0.00	128.30
IX									0.00

least mean value for days to 50% flowering in cluster I among 20 genotypes of Okra (*A. esculentus* (L.) Moench).

Conclusion

In the present study, a significant level (0.05 or 5%) of genetic divergence was witnessed across 48 distinct okra (*A. esculentus* (L.) Moench) genotypes. The factors that contributed the most to genetic diversity were the number of total fruits per plant, the number of locules per fruit, and fruit weight. These characters should be most preferred while selecting parents for further breeding. High levels of hybrid vigor and good recombination can result from parents' choice for hybridization between clusters V and IX, which exhibited the highest inter-cluster distances. Early flowering genotypes were observed in cluster V, which can be utilized for devel-

oping early maturing cultivars to avoid stress conditions. The inclusion of marker-assisted breeding is advised to facilitate the selection of genotypes and aid trait improvement in Okra (*A. esculentus* (L.) Moench.

Conflict of Interest

The authors declare that they have no conflict of interest.

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