Evaluation of genetic divergence among different okra genotypes

ABSTRACT

Genetic divergence of thirty okra genotypes was studied using Mahalanobis D^2 statistics which revealed that there was considerable genetic diversity observed in both qualitative and quantitative characters.The clustering, inter and intra-cluster distances, and trait contributions provided insights into the genetic variability and diversity within the studied okra population. Thirty diverse genotypes were grouped into five clusters with the highest of eighteen genotypes in the cluster I, five in the cluster III & V and one each genotype in the cluster II and IV. Inter and intra cluster D^2 values ranged from 8.00 to 16.7 and 0.0 to 7.4 respectively. It showed that inter cluster distance was higher than the intra cluster distance indicating wide genetic diversity among the genotypes of different groups. The cluster means of 11 characters among five clusters indicated that high genetic variability range present for yield per plant (222.1-253.1), number of fruits per plant (31.8-38.9), plant height (59.0-100.7) and days to fifty percent flowering (42.8-54.0). The per cent contribution of yield and its attributing characters in genetic divergence were reported maximum for number of fruits per vine (46.4%) followed by first fruit node (16.3%), fruit diameter (10.8%), plant height (10.3%), fruit length (3.9%), yield per plant (3.04%), days taken to 50% flowering (2.3%), internodal length (2.3%), fruit weight (2.0%), petiole length (1.65).

Keywords: Genetic Divergence, Mahalanobis D^2, Genetic diversity, Variability, Inter-cluster, Intra-cluster

1. INTRODUCTION

Okra (*Abelmoschus esculentus* L. Moench), locally known as Bhindi, belongs to the Malvaceae family and originated from West Africa and Southeast Asia [1]. It is an allotetraploid resulting from the natural hybridization of a wild progenitor, A. tuberculatus (2n = 58), and another unidentified species with chromosome number (2n=78).Okra is widely consumed in tropical and subtropical regionsof the world [2]. It is mostly cultivated for its fresh and succulent pods [3]. It is an autogamous species, predominantly self-pollinating, but varying levels of cross-pollination can occur due to insect pollinators and growing conditions [4].The edible parts of okra, including the fruits and seeds, are rich in dietary fibre, carbohydrates and vitamins [5]. 100 g of edible okra comprises plentiful components including protein (2.1 g), minerals (175.2 mg), fat (0.2 g), fibre (1.7 g), calories (36), carbohydrate (8 g), maximum quantity (88 ml) of water, and also contains good quantities of total phenolic, folate and vitamin C [6]. The seed oil content ranges from 20–40%, with major fatty acids including linoleic acid (49.54%), palmitic acid (28.60%) and oleic acid [7]. Despite being relatively drought-tolerant, okra may experience reduced yields, especially during the flowering and pod development stages, leading to marketable pod yield losses. For example, 37 to 83% yield losses attributed to drought stress occurred during the reproductive stage [8,1]. India holds the highest global production, but there are differences in yield potential attributed to the unavailability of high-yielding varieties, quality seeds, and limited adoption of improved production practices [9]. To enhance the quality and yield of okra, the primary step in the improvement process involves a thorough appraisal of the germplasm.

The focus of the germplasm appraisal is on identifying diversity, particularly in traits related to quality and yield. With a clear understanding of the diversity in the breeding material, the next step involves the selection of the best-performing genotypes. By utilizing the best-performing genotypes, breeding programs can focus on selecting and propagating individuals that carry the desired traits. This selective breeding process helps improve the overall performance of the crop [10]. Principal component analysis and cluster analysis are tools employed in various crops to understand genetic variability and associations among economically important parameters for genetic improvement [11].Knowledge of genetic diversity is crucial for breeding programs aimed at improving agronomic traits and enhancing resistance to environmental stresses [12].Characterizing plant material allows for the exploitation of genetic resources in breeding programmes, facilitating the selection of promising genotypes for further improvement [13]. The genetic variability or crop improvement, researchers are proposing to use the scores of the first principal component as input variables for clustering. This means that the information captured by PC_1, which represents the most significant source of variability in the data, is considered as input for clustering analysis [14, 15]. Cluster analysis has been extensively utilized for classifying a pool of genotypes based on the similarity and dissimilarity present among them. This involves grouping together genotypes that share common characteristics or genetic traits. The clusters formed help in identifying distinct groups within the germplasm. Similarly, both cluster as well as principal component analysis is used to the classification of different accessions [16,17]. It is essential to clearly understand the degree of genetic diversity in okra germplasm to plan a selection program aimed at improvement in quality and yield.

2. MATERIALS AND METHODS

The research was conducted at the Department of Vegetable Science Research Farm, CCS HAU, Hisar (Haryana) during the rainy season of 2021. The farm is locatedin the subtropics at 290 10' North latitude and 750 46' East longitude. Hisar has a semi-arid climate with hot and dry summers, extremely cold winters, little rainfall and temperature extremes. The experimental material comprised of thirty genotypes of okra. The details of the genotypes studied are given in Table 1. The experiment material was laid out in Randomized Block Design (RBD) with three replications with plot size 3.6 m × 1.2 m, maintaining crop geometry of 60 cm x30 cm. Five plants from each plot were chosen at random and tagged. The observations were recorded during the course of study, on the basis of DUS (Distinctness, Uniformity and Stability) traits.The observations recorded include plant height (cm), branches per plant, days to 50% flowering, intermodal length (cm), first fruit node, petiole length (cm), fruit length(cm), fruit diameter (mm), fruit weight (g), number of fruits per plant, fruit yield per plant (g), number of seeds per fruit, test weight(g).Mahalanobis method was used to cluster all of the genotypes into different groups [18]. Mahalanobis [18] device began with two closely related populations and found a third population with the smallest average of D^2 from the first two. Similarly, the fourth was selected to have the lowest average D^2 value of the first three, and so on. If, at any stage, the increase in average D^2 value exceeded the average of previously included genotypes, that genotype was deleted. The first cluster consisted of genotypes that were already in that group. This procedure was repeated until the D^2 values of the remaining genotypes were exhausted, excluding those that were already in the previous cluster and grouping them into a different cluster. The average intra- and inter-cluster average D^2values were calculated by the formula given by [19,20]

Table 1. List of genotypes and their source

Sr.	Genotypes	Crop	Source	Origin
1.	HB-9-35	*Abelmoschus esculentus* (L.) Moench	CCS HAU, Hisar	India

2.	HB-9-37	*Abelmoschus esculentus* (L.) Moench	CCS HAU, Hisar	India
3.	HB-9-38	*Abelmoschus esculentus* (L.) Moench	CCS HAU, Hisar	India
4.	HB-9-43	*Abelmoschus esculentus* (L.) Moench	CCS HAU, Hisar	India
5.	HBT-1	*Abelmoschus esculentus* (L.) Moench	CCS HAU, Hisar	India
6.	Punjab-8	*Abelmoschus esculentus* (L.) Moench	PAU, Ludhiana	India
7.	Pusa Sawani	*Abelmoschus esculentus* (L.) Moench	IARI, New Delhi	India
8.	Punjab Padmini	*Abelmoschus esculentus* (L.) Moench	PAU, Ludhiana	India
9.	HB-9-29	*Abelmoschus esculentus* (L.) Moench	CCS HAU, Hisar	India
10.	HB-06-46-1-1	*Abelmoschus esculentus* (L.) Moench	CCS HAU, Hisar	India
11.	HB-S-4	*Abelmoschus esculentus* (L.) Moench	CCS HAU, Hisar	India
12.	HB-25-2-1	*Abelmoschus esculentus* (L.) Moench	CCS HAU, Hisar	India
13.	HBBT-19	*Abelmoschus esculentus* (L.) Moench	CCS HAU, Hisar	India
14.	HBT-48	*Abelmoschus esculentus* (L.) Moench	CCS HAU, Hisar	India
15.	HB-08-3-1	*Abelmoschus esculentus* (L.) Moench	CCS HAU, Hisar	India
16.	Prabhani Kranti	*Abelmoschus esculentus* (L.) Moench	MAU, Prabhani	India
17.	HBT-11-1	*Abelmoschus esculentus* (L.) Moench	CCS HAU, Hisar	India
18.	HBT-42	*Abelmoschus esculentus* (L.) Moench	CCS HAU, Hisar	India
19.	HBT-49-1	*Abelmoschus esculentus* (L.) Moench	CCS HAU, Hisar	India
20.	HBT-15	*Abelmoschus esculentus* (L.) Moench	CCS HAU, Hisar	India
21.	JNDOL-05	*Abelmoschus esculentus* (L.) Moench	AAU, Gujrat	India
22.	HB-691-08	*Abelmoschus esculentus* (L.) Moench	CCS HAU, Hisar	India
23.	HBTC-6-7-1	*Abelmoschus esculentus* (L.) Moench	CCS HAU, Hisar	India
24.	HBT-53	*Abelmoschus esculentus* (L.) Moench	CCS HAU, Hisar	India
25.	Arka Abhay	*Abelmoschus esculentus* (L.) Moench	IIHR, Banglore	India
26.	Hisar Unnat	*Abelmoschus esculentus* (L.) Moench	CCS HAU, Hisar	India
27.	Varsha Uphar	*Abelmoschus esculentus* (L.) Moench	CCS HAU, Hisar	India
28.	Hisar Naveen	*Abelmoschus esculentus* (L.) Moench	CCS HAU, Hisar	India
29.	HB-9-27	*Abelmoschus esculentus* (L.) Moench	CCS HAU, Hisar	India
30.	HBT-12-1	*Abelmoschus esculentus* (L.) Moench	CCS HAU, Hisar	India

3. RESULTS AND DISCUSSION

The results of analysis indicated that there were significant differences present among the genotypes. To find extent of diversity among the genotypes, Mahalanobis D^2 statistics [21] as described by Rao were used.Grouping of genotypes into different clusters were done by the method suggested by the Tocher and described by the Rao. The thirty genotypes were grouped into five clusters using Tocher's method, as shown in Table 2. The maximum number of genotypes was found in the cluster number I (18) followed by cluster number III (5) and cluster number V (5) while the clusters II and IV consist of one genotype each.

Table 2. Grouping of genotypes into different clusters using Tocher's method

Cluster	**No. of**	**Name of Genotypes**

	Genotypes	
Cluster I	18	HB-691-08, HBTC-6-7-1, HBT-15, Hisar Naveen, HBT-11-1, Arka Abhay, HB-08-3-1, Punjab-8, HB-9-27, Punjab Padmini, Prabhani Kranti, HB-9-38, HB-9-29, HB-06-46-1-1, HB-S-4, Hisar Unnat, HBT-1, HB-9-43
Cluster II	1	HB-25-2-1
Cluster III	5	HBT-49-1, JNDOL-05, HB-9-35, HBT-12-1, HB-9-37
Cluster IV	1	Varsha Uphar
Cluster V	5	Pusa Sawani, HBT-48, HBT-53, HBT-42, HBBT-19

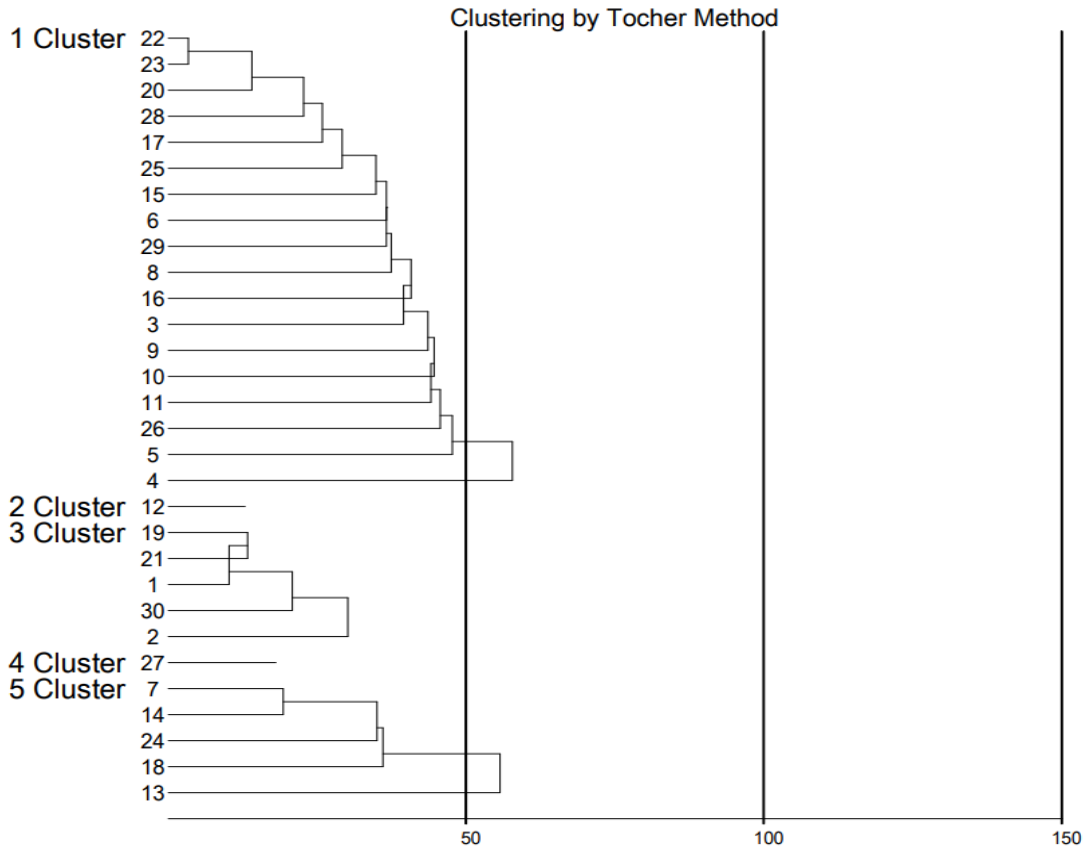

Fig .1 Dendrogram showing the clustering pattern of thirty genotypes of okra

The inter-cluster and intra-cluster distance was given in table 3. The maximum intra-cluster distance was recorded for cluster V (7.4) followed by Cluster I (6.7), cluster III (5.2). The maximum inter-cluster distance was recorded for cluster III and cluster V (16.7) followed by cluster II and cluster III (16.5), cluster IV and cluster V (12.5), cluster I and cluster III (11.2), cluster II and cluster IV (11.2), cluster III and cluster IV (9.2), cluster I and cluster V (8.9), cluster I and cluster IV (8.2), cluster I and cluster II (8.0), cluster II and cluster V (6.9).

Table 3. Intra (diagonal) and inter-cluster (below diagonal) average D^2 values

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	6.7				

Cluster II	8.0	0.0			
Cluster III	11.2	16.5	5.2		
Cluster IV	8.2	11.2	9.2	0.0	
Cluster V	8.9	6.9	16.7	12.5	7.4

The cluster means value of five clusters for eleven characters were studied and presented in the Table 4. The values of cluster means indicated that the cluster III had maximum cluster value of plant height (100.7 cm), branches per plant (3.2 cm), fruit length (9.8cm), number of fruits per plant (38.9), yield per plant ((285.3g), minimum days taken to 50% flowering (42.8), internodal length (4.3), first fruit node (3.7) and fruit diameter (1.1). Cluster I had maximum value of fruit weight (9.8g) and cluster IV for fruit diameter (1.5 cm).Branches per plant had maximum value in Cluster III (3.2 cm) and minimum value in Cluster IV (2.6 cm).Minimum days to 50% flowering were found in Cluster III (42.8) and maximum value in Cluster II (54.0).Maximum fruit length was found in Cluster III (9.8cm) and minimum in Cluster V (8.8 cm).Maximum fruit yield per plant was observed in Cluster III (285.3 g) and minimum in Cluster II (222.1g).Maximum fruit weight (9.8g) were found in cluster I and minimum value of fruit weight found in cluster V (8.9 g).

Table 4. Cluster mean value of thirty genotypes of okra for eleven characters

Sr. no.	Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
1	**PH (cm)**	68.0	46.6	100.7	59.0	59.0
2	**BPP**	2.7	2.7	3.2	2.6	2.5
3	**DFF**	48.6	54.0	42.8	51.6	50.6
4	**PL (cm)**	16.8	14.7	17.5	19.1	15.6
5	**INL (cm)**	5.2	5.6	4.3	4.4	5.4
6	**FFN**	5.2	4.9	3.7	4.4	6.7
7	**FL (cm)**	9.0	9.3	9.8	8.9	8.8
8	**FD (cm)**	1.3	1.1	1.4	1.5	1.3
9	**FW (g)**	9.8	9.7	9.1	9.0	8.9
10	**FPP**	32.0	32.9	38.9	31.8	32.8
11	**FYPP (g)**	253.1	222.1	285.3	232	243.2

PH-Plant height, BPP- Branches per plant, DFF- Days to 50% flowering, PL- Petiole length, INL- Inter-nodal length, FFN- First fruit node, FL- Fruit length, FD- Fruit diameter, FW- Fruit weight, FPP- Fruits per plant, FYPP- Yield per plant

The results of contribution of individual character towards genetic divergence were depicted in the Table 5. The per cent contribution of yield and its attributing characters in genetic divergence were reported maximum for number of fruits per vine (46.4%) followed by first fruit node (16.3%), fruit diameter (10.8%), plant height (10.3%), fruit length (3.9%), yield per plant (3.04%), days taken to 50% flowering (2.3%), internodal length (2.3%), fruit weight (2.0%), petiole length (1.65).

Table 5. Contribution of individual Character towards genetic divergence

Sr. no.	Source	Contribution %

1.	Plant height (cm)	10.3
2.	Branches per plant	0.4
3.	Days to 50% flowering	2.3
4.	Petiole length (cm)	1.6
5.	Inter-nodal length (cm)	2.3
6.	First fruit node	16.3
7.	Fruit length (cm)	3.9
8.	Fruit diameter (cm)	10.8
9.	Fruit weight (g)	2.0
10.	Fruits per plant	46.4
11.	Yield per plant	3.4

From the above results, it was observed that the cluster III had maximum plant height (100.7), branches per plant (3.2), fruit length (9.8),fruits per plant (38.9), yield per plant (285.3) and minimum days taken to 50% flowering (42.8), inter-nodal length (4.3), first fruit node (3.2). The above finding was in consonance with the finding of [22,23,24].

Analysis of contribution of the characters to genetic diversity revealed that characters like plant height (10.3%), branches per plant (0.4%), fruit weight (2.07%), yield per plant (3.4%) contributed to parameters of yield and different scientist also observed almost similar level of contribution for various growth and yield contributing characters[23, 25, 26, 27, 28, 29, 30].

4. CONCLUSION

The study conclude that the maximum intra-cluster distance was recorded for cluster V, which suggested that the cluster V had maximum genetic heterogeneity among the genotypes present in this cluster, whereas, the maximum inter- cluster distance was recorded for cluster III and cluster V, which indicated that the genotypes present in these two clusters had highest genetic diversity. The maximum inter-cluster distance was observed in cluster III and cluster V, followed by cluster I and cluster III. So, the genotypes present in these clusters contains maximum genetic diversity, which can be exploited for further crop breeding programmes. The genotypes HB-691-08, HBT-49-1, JNDOL-05, Hisar Unnat, HBTC-6-7-1, Varsha Uphar, Arka Abhay were superior for overall yield and yield attributing characters.

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