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ASSESSMENT OF GENETIC DIVERGENCE THROUGH MAHALANOBIS D^2 STATISTICS FOR YIELD AND QUALITY TRAITS IN OKRA (*Abelmoschus Esculentus* L. MOENCH.)

Rahul Kumar[1]*, Keshav Arya[1], Vishal Yadav[1], Rohit Rawat[1], Krishan Kumar[1], Subham Singh[1], Ankita Tiwari[1] and Ankul Kumar[2].

[1]Department of Vegetable Science, Chandra Shekhar Azad University of Agriculture & Technology, Kanpur, Uttar Pradesh, (208002), India.

[2]Department of Fruit Science, Chandra Shekhar Azad University of Agriculture & Technology, Kanpur, Uttar Pradesh, (208002), India.

*Corresponding author email: rahulskb150798@gmail.com

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ABSTRACT

The main aim of the study was to estimate genetic divergence among various okra genotypes based on yield and yield contributing traits. The experiment comprised of 44 genotypes of okra which were shown in Randomized Block Design with three replications at Vegetable Research Farm, Department of Vegetable Science, CSAUA&T, Kanpur. The forty four genotype of okra were grouped into five cluster using Tocher's method. The cluster IV and cluster V were comprise highest thirteen number of genotypes, cluster III comprise ten genotypes, while minimum number of genotypes were comprised in cluster II followed by cluster I respectively. The range of intra cluster distance was from 1.363 to 2.712. The result showed that the maximum intra cluster distance was recorded in cluster V (2.712) followed by cluster IV (2.591), cluster II (2.135) and cluster III (2.093) while minimum intra cluster distance was found in cluster I (1.363). The range of inter cluster distance was from 1.363 to 8.852. The maximum inter cluster distance was observed in cluster III & I (8.852) followed by cluster IV & I (7.673), cluster V & I (6.968) and cluster II & I (6.042) whereas the minimum inter cluster distance was recorded in cluster I & I (1.363).

***Key words*:** Genetic Divergence, Mahalanobis D^2 Statistics, Yield and Yield Contributing Traits, Okra (*Abelmoschus Esculentus* L. Moench.

Introduction

The cultivated okra (*Abelmoschus esculentus* L.) is a most important vegetable crop in India which belongs to Malvaceae family. The main center of origin of okra is Africa Vavilon (1951). It is often cross pollinated crop due to protogyny with chromosome number of 2n=2x=130. Previously, the cultivated bhindi was known as *Hibiscus esculentus* L. which has been renamed as *Abelmoschus esculentus* (L.) Moench., to distinguish it from *Hibiscus* which has a persistent calyx. This is because the calyx, corolla and staminal column in bhindi are fused together at the based and fall together after anthesis Thumburaj and Singh 2018. The cultivated species *Abelmoschus esculentus* is an amphidiploid and a genome size range of 3897 Mb to 17321 Mb. Mostly eight *Abelmoschus* species occurs in India; out of those four, *Abelmoschus esculentus* and *Abelmoschus caillei* (West African okra) are grown for their fruit and used as vegetable, *Abelmoschus manihot* (aibika) used as leafy vegetable, and *Abelmoschus Moschatus* (ambrette, musk mallow) used for its aromatic seed and other species of okra are used for ornamental purposes Kute *et al*., 2023.

The okra is mostly used as a green vegetable crop which widely grown in tropical and subtropical region of the world. The tender fruits of okra are rich source of

carbohydrate, protein, vitamin (A, B & C), calcium, potassium and other minerals Sravanthi *et al*., 2022. Okra has a growing importance due to its nutritional, medicinal and industrial values as well as its contribution to rural farmer's subsistence and income generation in developing countries like India Prakash *et al*., 2023.

The success of any crop improvement programme depends primarily on the magnitude of genetic divergence present in the base population, which serves as prerequisite for exploiting heterosis. Hybridization involving genetically distant parent is widely recognized to generate superior hybrid vigour and transgressive segregation in subsequent generations. Therefore, precise identification of divergent genotypes is vital for designing effective hybridization strategies. Mahalanobis (D^2) statistic technique for quantitative traits establishes itself as a powerful to find out degree of divergence among populations. According to Rao (1952), this methodology effectively pinpoint promising parents for targeted breeding a strategy that has historically facilitated the successful development and commercial release of numerous elite okra varieties.

Material and Methods

The experiment was conducted using Line × Tester mating design at Vegetable Research Farm, Department of Vegetable Science, CSAUA&T, Kanpur by using Randomized Block Design (RBD) with three replications during *summer season* 2024-25. The experimental material was comprised 10 lines viz., IC-12891, IC-691-10-3, IC-1754, IC-015537, IC-43746, IC-045857, IC-282236, IC-200, VRO-6, Arka Anamika and 3 testers viz., Kashi Kranti, Pusa Makhmali and Pusa Sawani which presented in Table 1. For the estimation of genetic divergence there are 15 yields and quality parameters *viz*., Days to first flowering, Days to 50% flowering, Days to first picking, Node at which first flower appears, Length of internodes (cm), Number of primary branches per plant, Number of nodes per plant, Plant height at final harvest (cm), Length of fruits (cm), Fruit diameters (cm), Average fruit weight (g), Number of fruits per plant, Self life of fresh fruit, Fruit yield per plant (g), Fruit yield per plot (kg) were recorded during the experimental period. All of the fifteen observations were recorded from each plot and each replication by five randomly selected plant of each genotype. The row to row and plant to plant spacing of the crop was maintain during the cropping season which was 60 cm and 20 cm respectively. Analysis of variance for all traits was performed accordance with the methodology outlined by Panse and Sukhatme (1978). Genetic divergence was evaluated via multivariate analysis using Mahalanobis (D^2) statistic.

Table 1: List of Lines, Testers and sources.

Sr.	Name of genotypes	Source
LINES		
1.	IC- 12891	Indian Institute of Vegetable Research, Varanasi
2.	IC-691-10-3	Indian Institute of Vegetable Research, Varanasi
3.	IC-1754	Indian Institute of Vegetable Research, Varanasi
4.	IC-015537	Indian Institute of Vegetable Research, Varanasi
5.	IC-43746	Indian Institute of Vegetable Research, Varanasi
6.	IC-045857	Indian Institute of Vegetable Research, Varanasi
7.	IC-282236	Indian Institute of Vegetable Research, Varanasi
8.	IC-200	Indian Institute of Vegetable Research, Varanasi
9.	VRO-6	Indian Institute of Vegetable Research, Varanasi
10.	Arka Anamika	Indian Institute of Horticultural Research, Bengaluru
TESTERS		
1.	Kashi Kranti	Indian Institute of Vegetable Research, Varanasi
2.	Pusa Makhmali	Indian Agricultural Research Institute, New Delhi
3.	Pusa Sawani	Indian Agricultural Research Institute, New Delhi

Genotype were subsequently grouped into distinct cluster using Tocher's optimization procedure and relative contribution of individual traits toward total divergence was estimated following Singh and Chaudhary (1985).

Results and Discussion

Cluster mean

The cluster mean for fifteen distinct characteristics under investigation have been shown in Table 2. The result revealed that highest mean value were observed for days to first flowering in cluster IV (39.70) followed by cluster III (38.02), cluster V (34.43) and cluster II (32.67) while lowest mean value was recorded in cluster I (28.57). For days to 50% flowering, the highest mean value were found in cluster (49.52) followed by cluster III (48.23), cluster II (43.91) and cluster V (43.81) while lowest mean value was observed in cluster I (38.66). For days to first picking, the highest mean value were recorded in cluster IV (63.12) followed by cluster V (62.18), cluster III (61.93) and cluster II (57.28) whereas lowest mean value was exhibited in cluster I (56.45). For node at which first flower appear, the highest mean value were observed in

Table 2: Cluster mean of different genotypes of Okra (*Abelmoschus esculentus* L.).

Clusters		DFF	D50%	DFP	NFFA	LI	NPBPP	NNPP	PHFH	LF	FD	AFW	NFPP	SLFF	FYP	FYPP
I	Mean	28.57	38.66	56.45	3.46	7.04	3.99	23.67	169.01	17.60	1.51	19.94	21.67	5.08	432.01	10.80
	SE±	1.40	0.96	1.91	0.35	0.17	0.19	0.61	6.77	0.55	0.15	1.06	0.65	0.28	24.61	0.61
II	Mean	32.67	43.91	57.28	3.66	6.23	2.18	20.86	131.37	13.27	1.33	16.88	16.99	5.10	176.49	4.55
	SE±	4.09	4.34	0.97	0.59	0.69	0.76	2.26	31.68	0.19	0.05	1.14	1.81	0.23	7.36	0.43
III	Mean	38.02	48.23	61.93	4.59	4.26	2.25	20.80	91.65	11.05	1.49	15.08	12.90	3.12	169.12	4.23
	SE±	2.91	1.99	1.77	0.60	0.51	0.38	1.33	19.48	1.20	0.15	1.17	1.28	0.59	18.13	0.45
IV	Mean	39.70	49.52	63.12	5.04	4.67	2.09	19.91	94.82	13.44	1.52	15.86	18.86	3.24	298.55	7.46
	SE±	2.30	2.50	1.66	0.67	0.56	0.44	2.21	14.59	1.60	0.18	2.36	1.32	0.66	47.01	1.18
V	Mean	34.43	43.81	62.18	4.44	4.61	2.61	18.83	88.93	12.51	1.54	15.33	19.10	3.08	285.42	7.11
	SE±	2.98	2.48	1.46	0.55	0.58	0.55	2.75	15.07	2.19	0.20	1.90	1.09	0.42	57.27	1.49

DFF - Days to first flowering; **NPBPP -** Number of primary branches per plant; **AFW-** Average fruit weight (g);
D50% - Days to 50% flowering; **NNPP -** Number of nodes per plant; **NFPP-** Number of fruits per plant;
DFP - Days to first picking; **PHFH -** Plant height at final harvest (cm); **SLFF-** Shelf life of fresh fruit;
NFFA - Node at which first flower appears; **LF -** Length of fruits (cm); **FYP-** Fruit yield per plant (g);
LI - Length of internodes (cm); **FD** – Fruit diameter (cm); **FYPP-** Fruit yield per plot (kg)

cluster IV (5.04) followed by cluster III (4.59), cluster V (4.44) and cluster II (3.66) while lowest mean value was found in cluster I (3.46). For length of internode, the highest mean values were recorded in cluster I (7.04) followed by cluster II (6.23), cluster IV (4.67) and cluster V (4.61) whereas the lowest mean value was observed in cluster III (4.26). For number of primary branches per plant, the highest mean value were observed in cluster I (3.99) followed by cluster V (2.61), cluster III (2.25) and cluster II (2.18) while lowest mean value was found in cluster IV (2.09). For number of nodes per plant, the highest mean value were recorded in cluster I (23.67) followed by cluster II (20.86), cluster III (20.80) and cluster IV (19.91) while lowest mean value was exhibited in cluster V (18.83). For plant height at final harvest, the highest mean value were observed in cluster I (169.01) followed by cluster II (131.37), cluster IV (94.82) and cluster III (91.65) while lowest mean value was found in cluster V (88.93). For length of fruit, the highest mean value were recorded in cluster I (17.60) followed by cluster IV (13.44), cluster II (13.27) and cluster V (12.51) while lowest mean value was found in cluster III (11.05). For fruit diameter, the highest mean value was observed in cluster V (1.54) followed by cluster IV (1.52), cluster I (1.51) and cluster III (1.49) whereas the lowest mean value was found in cluster II (1.33). For average fruit weight, the highest mean value were observed in cluster I (19.94) followed by cluster II (16.88), cluster IV (15.86) and cluster V (15.33) while the lowest mean value was exhibited in cluster III (15.08). For number of fruit per plant, the highest mean value were recorded in cluster I (21.67) followed by cluster V (19.10), cluster IV (18.86) and cluster II (16.99) while the lowest mean value was found in cluster V (12.90). For self-life of fresh fruit, the highest mean value were observed in cluster II (5.10) followed by cluster I (5.08), cluster IV (3.24) and cluster III (3.12) while the lowest mean value was exhibited in cluster V (3.08). For fruit yield per plant, the highest mean value were recorded in cluster I (432.01) followed by cluster IV (298.55), cluster V (285.42) and cluster II (176.49) whereas lowest mean value was found in cluster III (169.12). For fruit yield per plot, the highest mean value were observed in cluster I (10.80) followed by cluster 4 (7.46), cluster V (7.11) and cluster II (4.55) and lowest mean value was found in cluster III (4.23). These findings are in close agreement with the findings of Keerthana *et al*., (2024), Pattanaik *et al*., (2023), Rai *et al*., (2022), Verma *et al*., (2018), Waskar *et al*., (2017), Goswami *et al*., (2017).

Intra and inter distance

The average intra and inter cluster distance are shown in Table 3. The range of intra cluster distance was from 1.363 to 2.712. The result showed that the maximum intra cluster distance was recorded in cluster V (2.712) followed by cluster IV (2.591), cluster II (2.135) and cluster III (2.093) while minimum intra cluster distance was found in cluster I (1.363). The range of inter cluster distance was from 1.363 to 8.852. The maximum inter cluster distance was observed in cluster III & I (8.852) followed by cluster IV & I (7.673), cluster V & I (6.968) and cluster II & I (6.042) whereas the minimum inter cluster distance was recorded in cluster I & I (1.363). Similar results were also reported earlier by Keerthana

Table 3: Average Inter and Intra-cluster (D^2 Value) distances in 44 Genotypes of okra (*Abelmoschus esculentus* L.):

Clusters	I	II	III	IV	V
I	**1.363**				
II	6.042	**2.135**			
III	8.852	4.588	**2.093**		
IV	7.673	5.053	3.188	**2.591**	
V	6.968	4.477	3.253	2.229	**2.712**

Table 4: Number of Genotypes in each cluster on the basis of Mahalanobis D^2 statistics.

Clusters	No of genotypes	Genotypes
I	5	IC-12891 x Kashi Kranti, IC-1754 x Kashi Kranti, IC-015537 x Kashi Kranti, IC-015537 x Pusa Makhmali, IC-43746 x Pusa Makhmali.
II	3	IC- 12891, IC- 1754, IC- 015537
III	10	IC- 691-10-3, IC-43746, IC-045857, IC- 282236, IC- 200, VRO-6, Arka Anamika, Kashi Kranti, Pusa Makhmali, Pusa Sawani
IV	13	-691-10-3 x Pusa Makhmali, IC-691-10-3 x Pusa Sawani, IC-1754 x Pusa Sawani, IC-015537 x Pusa Sawani, IC-43746 x Kashi Kranti, IC-43746 x Pusa Sawani, IC-045857 x Kashi Kranti, IC-045857 x Pusa Makhmali, IC-045857 x Pusa Sawani, IC-200 x Pusa Sawani, VRO-6 x Pusa Sawani, Arka Anamika x Kashi Kranti, Arka Anamika x Pusa Sawani.
V	13	IC-12891x Pusa Makhmali, IC-12891x Pusa Sawani, IC-691-10-3x Kashi Kranti, IC- 1754 x Pusa Makhmali, IC- 282236 x Kashi Kranti x Pusa Makhmali, IC- 282236 x Pusa Sawani, IC- 200 x Kashi Kranti, IC- 200 x Pusa Makhmali, VRO-6 x Kashi Kranti, VRO-6 x Pusa Makhmali, Arka Anamika x Pusa Makhmali, Azad Bhindi-1

et al., (2024), Abhilash *et al*., (2024), Singh *et al*., (2023), Pattanaik *et al*., (2023), Kumar *et al*., (2023), Nanthakumar *et al*., (2021), Karthika *et al*., (2019), Priyanka *et al*., (2017).

Cluster pattern

Forty four genotype of okra were examine in this study for the estimation of genetic diversity, which were grouped into five cluster using Tocher's method presented in Table 4. The cluster IV were comprise highest 13 number of genotypes *viz*., IC-691-10-3 × Pusa Makhmali, IC-691-10-3 × Pusa Sawani, IC-1754 × Pusa Sawani, IC-015537 × Pusa Sawani, IC-43746 × Kashi Kranti, IC-43746 × Pusa Sawani, IC-045857 × Kashi Kranti, IC-045857 × Pusa Makhmali, IC-045857 × Pusa Sawani, IC-200 × Pusa Sawani, VRO-6 × Pusa Sawani, Arka Anamika × Kashi Kranti, Arka Anamika × Pusa Sawani. The cluster V were also comprise highest 13 number of genotypes *viz*., IC-12891x Pusa Makhmali, IC-12891x Pusa Sawani, IC-691-10-3x Kashi Kranti, IC-1754 × Pusa Makhmali, IC- 282236 × Kashi Kranti × Pusa Makhmali, IC- 282236 × Pusa Sawani, IC- 200 × Kashi Kranti, IC- 200 × Pusa Makhmali, VRO-6 × Kashi Kranti, VRO-6 × Pusa Makhmali, Arka Anamika × Pusa Makhmali, Azad Bhindi-1 and cluster III comprise ten genotypes *viz*., IC- 691-10-3, IC-43746, IC-045857, IC-282236, IC- 200, VRO-6, Arka Anamika, Kashi Kranti, Pusa Makhmali, Pusa Sawani while minimum number of genotypes comprised in cluster II *viz*., IC- 12891, IC-1754, IC- 015537 followed by cluster I viz., IC-12891 × Kashi Kranti, IC-1754 × Kashi Kranti, IC-015537 × Kashi Kranti, IC-015537 × Pusa Makhmali, IC-43746 × Pusa Makhmali. Similar results were also indicated to support the study with earlier findings of Bhardwaj *et al*., 2025, Abhilash *et al*., (2024), Singh *et al*., (2023), Sravanthi *et al*., (2022), Karthika *et al*., (2019), Verma *et al*., (2018), Ranpise *et al*., (2018).

Conclusion

The present investigation revealed the substantial genetic variability among forty four genotype of okra evaluated for yield and quality traits. Mahalanobis D^2 analysis successfully classified the genotypes into five cluster using Tocher's method with cluster IV and cluster V being highest 13 number of genotypes while the minimum number of genotypes were comprised in cluster II. The result revealed that the highest intra cluster distance was recorded in cluster V while cluster I having lowest intra cluster distance which exhibited the highest mean values for several economically important traits. The maximum inter cluster distance was observed in cluster III & I indicating that genotypes grouped in these clusters are genetically the most diverse from one another. Notable, the pattern of clustering did not align strictly with the geographical origin of the genotypes, suggesting that genetic diversity in this material is influenced more by selection and genetic drift than by geographical distance alone. Given its high inter-cluster distance from cluster III & I followed by cluster IV & I, cluster V & I can be effectively hybridized with genotypes from these divergent clusters to maximize heterotic expression and generate transgressive segregants in subsequent generations. Such crosses between genetic distant, high performing parents are expected to broaden the genetic base and support the development of superior okra varieties combining high yield with desirable quality traits.

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