



## Artificial Selection Of Elite Okra Accessions (*Abelmoschus Esculentus* (L.) Moench) Via Cluster Analysis

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### Abstract

Forty-eight okra accessions were subjected to a replicated field trial arranged in a Randomized Complete Block Design (RCBD) to examine the genetic dissimilarity and distances pertaining to quantitative traits. Mahalanobis  $D^2$  analysis partitioned the genotypes into ten separate clusters. Cluster II constituted the largest group followed by cluster III. Also three solitary clusters (VII, IX, and X) were reported. In compliance with genetic distances, cluster IV, VIII and VI had broad divergent genotypes within them along with wide genetic dissimilarity was between the clusters VII and X, following I and X, I and IX. Cluster IX had genotypes with high cluster means for fruit yield than others. Among various morphological characters, fruit yield per plant alone contribute nearly 36 per cent toward divergence preceded by days to first flower, and plant height at 80 per cent maturity. Therefore, top priority in artificial selection of diverse parents might be given to the genotypes in clusters I, II, VII and IX for attempting improvement of complex traits in okra.

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**Keywords:** clustering,  $D^2$  statistic, parent selection, okra

### Introduction

At the core of crop improvement lays the concept of artificial selection that has reshaped the genetic landscape of countless species, including okra (*Abelmoschus esculentus* (L.) Moench). The pivotal role of artificial selection in okra breeding approaches includes the strategic augmentation of desirable traits within okra populations, targeted trait improvement of okra genotypes with the needs of both producers and consumers and balancing the preservation of natural genetic diversity with the pursuit of improved cultivars ensures the continued resilience and adaptability of okra in the face of changing environmental and market dynamics (Nizar *et al.* 2007 and Seth *et al.* 2016).

Okra is the quintessential multi-cuisine vegetable, but its origins are a bit murky. According to Vavilov (1924), okra's origin centre was claimed at Abyssinian region with important gene pools in Ethiopia (Engels and Hawkes, 1991). Various gene banks and germplasm repositories around the world maintain collections of okra accessions representing reservoirs of genetic diversity. With its distinctive green pods and striking hibiscus-like flowers, okra is a nutritional powerhouse and a culinary delight (Samiksha *et al.* 2020). Its resilience to heat, adaptability to various soil types and relatively low resource requirements make it an ideal candidate for breeding and genetic improvement (Verma *et al.* 2018).

Selection, either phenotypic or genotypic, is the essential and crucial step which the breeder should not skip to evolve superior crossbreeds'. Selecting diverse genotypes ensures access to a wide range of gene variants, including rare or unique alleles that can be valuable for breeding (Rathod and Patel, 2017). Clustering technique employs Mahalanobis distance as a distance metric and dendrogram displays the level of divergence and associations among them (Sravathi *et al.* 2022). The main focus of this research activity was to measure the genetic distance and find out the degree of diversification among collected okra accessions. Cluster analysis supported the differentiation of okra genotypes into distinct clusters based on genetic similarity. This grouping indicated the presence of different phenotypic patterns all through the population.

## Materials and methods

A total of forty-eight diverse okra accessions and cultivars were received from National Bureau of Plant Genetic Resource (NPGR), New Delhi and several locations in and across India respectively which were evaluated at the Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Chidambaram, India during *Kharif* season. The experimental materials were laid out in a randomized complete block design with three replications at the row to row and plant to plant spacing of 60 cm and 30 cm, respectively.

Healthy plant samples from every single replication were taken for recording quantitative data in an unbiased way for fifteen plant, fruit and seed related agronomic traits in okra *viz.*, Plant height at 80% maturity (cm), Number of branches per plant, Number of internodes, Days to first flower (days), Fruit length (cm), Fruit diameter (mm), Average fruit weight (gm), Number of fruits per plant, Number of seeds per fruit, Hundred seed weight (gm), Days to first harvest (days), Harvest duration (days), Total number of pickings, Plant duration at 80% maturity (days) and Fruit yield per plant (gm).

The degree of genetic diversity is worked out in the collected genetic materials based on the characters taken into count for the study. Replication data collected were brought to statistical analysis for accounting average genotype performance and their clustering pattern. Cluster analysis was done by the use of AGRISTAT software package.

## Results and discussion

### I) Clustering of genotypes

Cluster analysis upon forty-eight okra genotypes for fifteen quantitative characters distilled into ten non-overlying clusters (Table 1). Cluster II followed by cluster III, cluster V each hold twenty-four, six, and five genotypes respectively. The smallest clusters VII, IX, and X each had single genotypes and clusters VI and VIII was the second smallest with only two genotypes each. Compared to genotypes in distinct clusters, genotypes within the same cluster share a greater degree of genetic similarity for the majority of plant traits taken. Several mono and poly genotypic clusters were resulted for immense researchers such as Asha *et al.* 2015; Mohammad and Marker, 2017; Ranpise *et al.* 2018; Karthika and Maheshwari, 2019, Kumar *et al.* 2020; Sravanthi *et al.* 2022; Murtadha *et al.* 2023 and many.

**Table 1. Cluster groups separated for forty-eight okra genotypes**

Cluster groups	No. of genotypes	Genotypes name
I	4	Okra 26, Okra27, Parbhani kranti, Kashi kranti
II	24	EC 329363, EC 329365, EC 329367, EC 329369, EC 329371, EC 329373, EC 329379, EC 329381, EC 329383, EC 329386, EC 329396, IC 44572, IC 45728, IC 45747, IC 45796, IC 45800, IC 45819, African type okra, Red short okra, Green okra, Tree okra, White velvet, White okra, Multi branch okra
III	6	IC 45817, IC 90174, EC 329377, IC 44529, Clemson spineless, Arka anamika
IV	2	Hill okra, Double color okra
V	5	Pink okra, Cow horn okra, Elephant tusk okra, Green round okra, Red long okra
VI	2	Emerald, Okra 28
VII	1	Okra29
VIII	2	IC45806, IC45813
IX	1	IC45790
X	1	IC45804

Cultivars gathered from different regions were pooled into a single cluster, while genotypes from the same area were sorted into different groups (Ariyo, 1987), for instance, Clemson spineless from Africa and Arka anamika from India; Emerald from Africa and Okra 28 from India were categorized into the same cluster (Cluster III and VI respectively). Even while geographic diversity seems to be a crucial element, the lack of connection between spatial and genetic diversity in the study results suggested that additional factors such as population heterogeneity, different genetic architects, natural and artificial selection, exchange of genetic materials, genetic drift, and spontaneous mutation could cause genetic diversity rather than place of origin. Okra findings of Kumar *et al.* 2016, Singh *et al.* 2018, Nandhakumar *et al.* 2021, Ranga and Darvhankar, 2022 and so on had no indication for their link.

## II) Intra and inter cluster genetic distance

Genetic distance of ten clusters is stated in table 2. As the clusters VII, IX, and X were mono genotypic clusters, they showed zero intra cluster distance. Maximum distance within clusters was covered by IV<sup>th</sup> cluster (466.94), cluster VIII (441.06) and cluster VI (435.65) as follows. The genotypes found within clusters IV, VIII and VI were more diverse in traits than those in other groups, as evidenced by the greater genetic distance between them. The range of inter cluster genetic distance was recorded between 4216.31 and 514.70. The farthest genetic distance was observed between cluster VII and X (4216.31) followed by I and X (3478.42), I and IX (2957.73) while shortest distance was between cluster III and VI (514.70) backed by cluster II and VI (553.27), cluster II and III (553.61). Genetic distance of genotype clustering varied over ranges for several okra works based on the genetic materials used for study. Priyanka *et al.* 2017; Patra *et al.* 2018; Kumari *et al.* 2019; Kumar *et al.* 2020; Mohammed *et al.* 2022; Saleem *et al.* 2023 and numerous studies were in consistent.

**Table 2. Intra and inter cluster distances of ten clusters**

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	<b>381.59</b>	2665.88	795.82	1274.76	1891.55	503.67	628.10	1121.64	2957.73	3478.42
II		<b>429.74</b>	553.61	598.11	2173.87	553.27	1120.56	2051.64	2261.69	1342.21
III			<b>330.78</b>	588.31	1459.08	514.70	628.37	1275.92	1756.89	2369.30
IV				<b>466.94</b>	1214.71	608.57	763.53	1141.74	1221.19	2165.18
V					<b>385.08</b>	1738.78	875.77	642.14	631.30	926.90
VI						<b>435.65</b>	564.77	1330.85	2283.76	1179.41
VII							<b>0.00</b>	587.48	1579.52	4216.31
VIII								<b>441.06</b>	1363.21	1205.93
IX									<b>0.00</b>	2302.69
X										<b>0.00</b>

(The bold letters indicate intra cluster distance)

The genotypes with zero intra cluster distance evince wide divergence as juxtaposed with others. A collection of two or more genotypes is considered to be in an acceptable cluster if their within-cluster genetic distance is lower than the aggregate average genetic distance and their between-cluster distance is higher than the distance between their respective within-cluster distances (Alemu and Mohammed, 2022). Highly distinctive and diverse genetic materials were present in those farthest clusters and these genotypes might be put forward as the parental choice for hybridization events to gain segregants and hybrids with best possible heterosis

additionally obtaining a wide range of quantitative trait variability in generations of segregating individuals in order to choose worthy recombinants (Mudhalvan and Senthilkumar, 2018; Melaku *et al.* 2022).

### III) Average cluster performance

The cluster mean performance for 15 plant characters evinced comparable differentiation among the ten clusters divided (Table 3). Plants with more mean height and number of internodes was observed in cluster X and short heighted plants with less intermodal number were in cluster VI. More branchy and less branchy plants were presented in cluster V and II respectively. Earlier flowering was noted in cluster I and late flowering by cluster X. Clusters II and IX showed minimum and maximum mean for fruit length. Low fruit diameter was appeared in the cluster III and high values in cluster X. Cluster IX had the more weighted fruits while cluster II hold the least.

**Table 3. Average of ten clusters for twenty characters**

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X
PH	129.46	102.79	123.51	125.34	191.99	94.08	179.26	133.32	206.23	215.51
NoB	5.17	3.92	4.06	4.44	7.13	4.22	4.67	6.00	6.33	5.33
NoI	27.83	22.04	24.72	32.50	34.80	20.68	28.33	28.83	33.67	36.67
DFE	45.58	58.71	56.71	68.00	83.07	48.86	48.30	65.41	70.19	92.58
FL	19.14	15.99	16.41	16.03	21.75	16.64	19.86	20.03	23.77	18.30
FD	23.15	22.46	21.16	23.36	25.39	22.84	23.40	29.38	26.92	29.91
FW	22.89	18.73	19.34	20.84	29.65	21.64	28.15	25.38	29.23	24.89
NoF/P	30.97	19.39	25.68	21.52	25.52	27.91	40.28	30.52	32.77	19.39
NoS/F	76.30	62.50	78.86	60.91	79.88	61.08	89.33	70.10	88.25	65.04
HSW	6.48	5.51	6.37	5.01	6.92	5.91	7.33	6.63	4.38	5.56
DFH	55.09	69.61	67.77	80.49	92.83	62.08	59.43	75.36	80.30	101.02
HD	50.38	48.54	48.24	57.01	53.99	49.14	51.12	50.48	59.41	46.64
NoP	15.59	10.66	12.50	10.64	12.61	14.9	18.36	15.52	17.51	7.62
PD	93.26	91.20	88.98	100.04	113.16	96.54	100.46	97.42	105.44	122.06
FY/P	737.20	310.80	500.82	403.24	775.23	630.10	844.95	748.61	852.30	525.92

[PH-Plant height at 80% maturity (cm); NoB-Number of branches per plant; NoI-Number of internodes; DFF-Days to first flower; FL-Fruit length (cm); ); FD-Fruit diameter (mm); FW-Average fruit weight (gm); NoF/P-Number of fruits per plant; NoS/F-Number of seeds per fruit; HSW-Hundred seed weight (gm); DFH-Days to first harvest; HD-Harvest duration (days); NoP-Total number of pickings; PD-Plant duration at 80% maturity (days); FY/P-Fruit yield per plant (gm)]

Both clusters II and X hold genotypes that bore fewer fruits, while cluster VII genotypes had more fruiting capacity. Fruits from the cluster VII had more seeds and least seed count was in cluster IV. Mean seed weight was low in cluster IX and high in cluster VII. Mean for first fruit harvest was earlier touched by members of cluster I while late fruits were obtained from cluster X. The characters number of fruit pickings and harvest duration were averaged maximum in cluster VII and IX in respect while minimum in cluster X. More plant duration was attained by cluster X and less optimum in cluster II. The cluster mean of fruit yield per plant was high in cluster IX and low in cluster II. The result outcomes are in accordance with a lot of okra researchers [Sood *et al.* 2017; Verma *et al.* 2018; Samiksha *et al.* 2020; Singh *et al.* 2023].

From the cluster mean data and cluster distance, it is assumed that the genotypes present in the clusters X, VII, IX may be chosen as parents for different trait improvement breeding in addition to fruit yield and cluster I may be selected as parents for earliness trait improvement and hybridization between clusters I, VI, VII, IX and X may be beneficial and effective for development of superior crossbred performers because of proportionate broad genetic diversity (Nandhakumar *et al.* 2021). Even though the cluster X resulted in high inter cluster distance, it may not be reward for crossing due to high mean values for most of the long duration and low yielding traits which might cause unfavorable impacts on production performance.

### IV) Percent contribution of traits towards divergence

Analysis of relative contribution of fifteen characters to genetic diversity was estimated in table 4. Fruit yield per plant (35.82%) contributed highest percentage succeeded by days to first flower (22.07%), plant height at 80% maturity (12.68%), number of branches per plant (8.87%), 100 seed weight (8.16%), harvest duration (4.88%), plant duration at 80% maturity (4.26%), number of seeds per fruit (4.17%), fruit diameter (2.31%) and others in the order contributed smaller percentage.

**Table 4. Relative contribution of characters to divergence**

S. No.	Plant characters	Percent contribution (%)
1.	Plant height at 80% maturity (cm)	12.68
2.	Number of branches per plant	8.87
3.	Number of internodes	0.36
4.	Days to first flower (days)	22.07
5.	Fruit length (cm)	1.95
6.	Fruit diameter (mm)	2.31
7.	Average fruit weight (gm)	0.44
8.	Number of fruits per plant	1.33
9.	Number of healthy seeds per fruit	4.17
10.	100 seed weight (gm)	8.16
11.	Days to first harvest (days)	1.24
12.	Harvest duration (days)	4.88
13.	Total number of pickings	0.27
14.	Plant duration at 80% maturity (days)	4.26
15.	Fruit yield per plant (gm)	35.82

The traits fruit length, number of fruits per plant, days to first harvest, Average fruit weight, number of internodes, and total number of pickings devoted inconsequential difference to divergence. This relative trait contribution suggested highly genetic variable traits which should be contemplated while selecting parents for hybridization work. Parallel findings were claimed by Waskar *et al.* 2017; Ragavendra and Hadimani, 2017; Mudhalvan and Senthilkumar, 2018; Nandhakumar *et al.* 2021; Gurve *et al.* 2022.

## Conclusion

The current research study is summarized that the geographic location has no bearing on the genotypic clustering behaviour on the basis of separated ten clusters. The parental choice for hybridization may be selected from the distant clusters I, VI, VII, IX and X which possess wide genetic diversity between them for the traits under analyzed genotypes. Adopting individuals from these clusters for subsequent crossing experiments would increase the probability of achieving substantial heterosis in segregating generations. Moreover, elite parents are selected based upon comparative strengths of each clusters as accordance with breeding targets such as earliness, pest and disease resistance, quality upgrades, *etc.*, thereby the genotypes from moderately distant clusters can also be taken for trait based okra improvement program to develop new and improved varieties.

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