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Analyzing patterns of genetic divergence and clustering among okra [Abelmoschus esculentus (L.) Moench.] genotypes

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Abstract: Okra cultivation across India aligns with warm season windows, notably spring and monsoon period. Despite its economical and nutritional significance, productivity remains major concerns in okra. In the valley regions of Uttarakhand, the identification of superior genotypes with desirable horticultural traits is crucial for enhancing growth, yield potential and quality. However, limited research has been conducted on the genetic divergence and hybridization potential of okra under the valley conditions of Uttarakhand. Hence, this particular research was undertaken to assess the genetic diversity in the selected okra genotypes using D^2 analysis, in order to categorize the genotypes into distinct clusters according to their horticultural traits and to identify potential parental lines from the most divergent clusters for future hybridization programme to obtain superior recombinants in segregating generations. The trial was conducted during summer 2019 on the premises of H.R.C a horticultural research farm of H.N.B.G.U., Srinagar, (Garhwal) Uttarakhand where 26 okra genotypes were evaluated under Uttarakhand valley conditions, and Arka Anamika served as the check. Based on inter-cluster distances, clusters VI and II exhibited the highest inter-cluster distance, subsequently between clusters V and II and then clusters IV and II. Using Mahalanobis D^2-based diversity metrics, the 26 okra entries were partitioned into six distinct clusters; the greatest distance was observed between clusters VI and II, making crosses among their members strong candidates for generating superior recombinants in subsequent segregating generations

Keywords: Genotypes • Genetic diversity • Hybridization • Okra and Uttarakhand.

Introduction

Vegetables possess a vital part in the human diet as they are known to supply all the essential components that are required by the human body *viz.,* carbohydrates, proteins, vitamins, dietary fiber, trace elements, and some medicinal properties. Regular consumption of vegetables has been linked to improved health, prevention of chronic diseases and overall well-being (Choudhary 2015). Okra is a major vegetable with economic value that thrives across warm regions globally, particularly throughout the tropics and subtropics. It is valued not only for its nutritional benefits but also for its adaptability to diverse agro-climatic conditions, making it an important crop for food security and income generation (Ramgiry & Singh 2017). It is an important rainy and spring-summer crop chiefly grown for its raw and tender green fruits. These fruits are highly nutritious, widely consumed and contribute significantly to both household supply and the local economy (Akotkar et al., 2010). It is widely regarded as originating from Africa, particularly in the regions of Ethiopia and Sudan, before spreading to other parts of the

world, including India, which is now the largest producer of okra globally. Over time, okra has become an important vegetable crop in many countries due to its nutritional value, adaptability and economic significance (Joshi et al., 2021; Kumar & Joshi 2024).

Okra is highly valued for its tender green pods which comprises of 89g water, 7.6g carbohydrate, 2-4g protein, 0.3g fat and nutrients like 249 mg potassium, 92mg calcium, 51mg phosphorus, 0.6 mg iron, and vitamins like 13 mg vitamin-C, 88IU vitamin-A and 0.6 mg nicotinic acid per 100g fresh weight. These nutritional qualities make okra an excellent addition to the human diet, supporting overall health and providing essential nutrients (Choudhary 2015; Joshi et al., 2020). Furthermore, okra contributes to the food industry as a reservoir of edible oil, medicinal compounds and industrial mucilage enhancing its economic importance (Priyanka et al., 2017). Although, at present, numerous commercial hybrids and improved cultivars of okra have been developed (Shaikh et al., 2013), most of them still perform inconsistently across environments. However, the accessible cultivars are less profitable as their productivity is constrained by the absence of locally adapted varieties resistant to key pests and diseases, particularly the fruit and shoot borer (*Earias vitella*) and yellow vein mosaic virus (YVMV) (Gangopadhyay et al., 2017; Rajesh et al., 2018). This highlights the importance of developing region-specific high-yielding and pest-resistant genotypes.

Hence to sustain production, and improve profitability, it is essential to develop high yielding, stress tolerant and region-specific cultivar that perform well under diverse agro-ecological conditions (Koundinya et al., 2016). Despite its high economic and nutritional value, okra cultivation faces challenges such as low genetic diversity, susceptibility to biotic and abiotic stresses and limited improvement in yield potential (Singh et al., 2018). Addressing these challenges requires the exploration and utilization of diverse germplasm to identify superior genotypes. Consequently, understanding the genetic diversity among okra genotypes is essential for breeding programs aimed at developing high-yielding, stress-tolerant, and disease-resistant cultivars. For a plant breeder, insights on the genetic divergence prevalent among the genotypes under study are crucial while selecting diverse parents for the hybridization process. The selection of genetically diverse parents enhances the likelihood of obtaining superior recombinants and heterotic F_1's exhibiting wide variability in segregating populations (Akotkar et al., 2010). To quantify the genetic diversity among genotypes, the Mahalanobis D^2 statistics has proven to be an effective multivariate approach, allowing simultaneous consideration of multiple morphological and yield traits (Gadekar et al., 1992). Accordingly, this study set out to profile genetic diversity among okra genotypes collected from multiple Indian locations, with the goal of pinpointing highly divergent parents for use in future crop improvement breeding programmes.

Material and methods

The study was conducted during the summer of 2019 at the H.R.C. (An Experimental unit of Department of Horticulture), Chauras campus, Department of Horticulture, School of Agriculture and Allied Science, H.N.B. Garhwal University, Srinagar (Garhwal), Uttarakhand, India. A randomized block (R.B.D.) design constituting three replications was employed for the field experiment to obtain precise and dependable results. A total of 25 genotypes, along with one check cultivar (Arka Anamika), were evaluated. These genotypes were sourced from different regions across India to capture a wide range of genetic diversity. During the experiment, five plants from each treatment per replications were selected randomly and tagged for the collection of data and measurement. Observations were recorded on various

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morphological and quality traits and the average values were calculated for all the studied characteristics. Quality parameters were analyzed following standard procedures outlined by AOAC (1990) and Ranganna (2015).

The analysis of the statistical parameters was conducted using the software like MS Excel and SPSS version 26 to validate the data for all the observed characters. Genetic divergence among the 26 okra genotypes were assessed using Mahalanobis D^2 statistics, as proposed by Rao (1952). The computation of D^2 values followed the methodology outlined by Murty and Arunachalam (1966), which involved calculating generalized distances to quantify genetic diversity. Based on these D^2values, genotypes were grouped into clusters following Mahalanobis (1936) approach, using non-hierarchical Euclidean cluster analysis to categorize the lines into distinct groups. This clustering approach effectively determined the genetic relationships among the genotypes, providing valuable insights for future breeding programmmes.

Results and discussion

For breeders, understanding how diverse the available germplasm is, helps in selecting parents for crosses; choosing more genetically distant parents typically increases heterosis in the F_1 and broadens variability among the resulting segregating progeny. (Akotkar 2010; Singh et al., 2018). Among available techniques, Mahalanobis D^2 offers a multivariate distance that groups germplasm using all measured traits jointly, rather than relying on single index comparisons from morphology, eco geography or phylogeny. (Priyanka et al., 2017; Harish 2018). This approach enables the identification of superior genotypes and optimizes parental selection for breeding programs. Therefore, D^2 analysis is widely used to enhance crop improvement by exploiting the maximum genetic variability present in the germplasm.

Partitioning of the okra genotypes into distinct clusters based on D^2 analysis

The entire series of the okra germplasm was partitioned into six distinct clusters, as presented in Table 1. Singh et al (2018) also highlighted similar sort of results in some okra genotypes. Out of the six distinct clusters studied under present investigation, the cluster III was the biggest cluster that comprised of 10 genotypes subsequently, cluster I comprising 6 genotypes, cluster V comprising 5 genotypes, cluster IV and cluster VII consisting of 2 genotypes each and cluster II consisting of 1 genotype. These observations align with the findings of Shaikh et al (2013), Krishna & Begum (2016), Priyanka et al (2017) and Singh et al (2018) in okra. The distribution of genotypes into clusters did not correspond to their geographic locations. Genotypes did not consistently group by their collection regions, indicating no clear, direct association between geographic origin.

Table 1: Distribution of 26 okra genotypes into clusters according to their genetic differences

Clusters	No of genotypes	Genotypes
I	6	Agri Bahar, Chanda, LC-4, Lucky-666, Vandana-241 and Varsha Uphar
II	1	VL Bhindi-2
III	10	Hisar Naveen, LC-3, Pusa A-4, Kashi Kranti, Super Anamika, Kashi Pragati, Pusa Sawani, Kaveri, LC-6 and Hisar Unnat
IV	2	Kashi Mohini and Kashi Vibhuti
V	5	King Bhindi, LC-5, Parbhani Kranti, Punjab-8 and Arka Anamika
VI	2	LC-1 and LC-2

Intra and Inter-cluster distance

Intra and inter-cluster average D^2 values are shown in the Table 2 and depicted in the Fig 1. Among the six clusters, the intra-cluster D^2 values ranged from 2.050 to 3.210. Cluster I consisted of 6 distinct genotypes which was seen with the maximum intra-cluster diversity (D^2 = 3.210) followed by cluster V (D^2 =

3.141), cluster III (D^2 = 3.054), cluster VI (D^2 = 2.444), cluster V (D^2 = 2.425) while, the least intra-cluster distance was observed in cluster II (D^2 = 2.050). Maximum intra-cluster diversity in the first cluster highlighted that the genotypes included in the cluster I were very diverse which was also reported by Akotkar et al (2010), Shaikh et al (2013), Balai et al (2015) and Ramgiry et al (2017) in okra. The highest inter-cluster distance in okra genotypes was observed between clusters VI and II (D^2 = 10.409), followed by cluster V and II (D^2 = 8.817) and cluster IV and II (D^2 = 8.613). The lowest inter-cluster distance was found between cluster III and I (D^2 = 2.802). Maximum inter-cluster D^2 values between the clusters VI and II indicated that the genotypes within these clusters can be utilized as parental lines in breeding programs to develop hybrids with greater heterosis, thereby enhancing the probability of obtaining improved segregants in the F_1 and later generations. Such genetically distant parents are likely to contribute complementary traits, increasing variability and potential performance in the progeny. This information can guide breeders in selecting optimal parent combinations for improving yield, quality, and stress tolerance in okra. The present findings corroborated with the findings of Akotkar et al (2010), Priyanka et al (2017) and Singh et al (2018) in okra.

Table 2: Mean genetic distances within and among clusters ((D^2)

Clusters	I	II	III	IV	V	VI
I	**3.210**					
II	7.792	**2.050**				
III	2.802	8.110	**3.054**			
IV	5.684	8.613	4.791	**2.425**		
V	5.520	8.817	3.439	5.237	**3.141**	
VI	8.469	10.409	6.756	6.694	4.917	**2.444**

Cluster means for all the growth yield and quality parameters under investigation

Cluster means for twenty traits across six groups are summarized in Table 3, and the marked differences among these averages demonstrate substantial inter-genotypic diversity. The largest value of the cluster mean for days taken to first germination was noticed in the cluster IV. The lowest value of the cluster mean was observed in cluster V. Highest cluster means for plant height was noticed in the cluster V, subsequently in the cluster III, Cluster I, cluster VI and cluster IV, while the lowest cluster means for plant height was observed in cluster II. These results were also line with the findings of Akotkar et al (2010), Shaikh et al (2013) and Balai et al (2015) in okra. The number of primary branches per plant recorded maximum cluster mean in cluster VI followed by cluster V, cluster III, cluster II and cluster IV. The lowest cluster mean for this trait was recorded in cluster I in okra. Lowest cluster mean for days to first flowering was observed in cluster I followed by cluster III, cluster II, Cluster V and cluster IV, and the highest cluster mean was observed in cluster VI. Lowest cluster mean for the number of nodes at first flowering was noticed in cluster I followed by cluster IV, cluster III, cluster II and cluster VI, while the highest cluster mean was observed in cluster V.

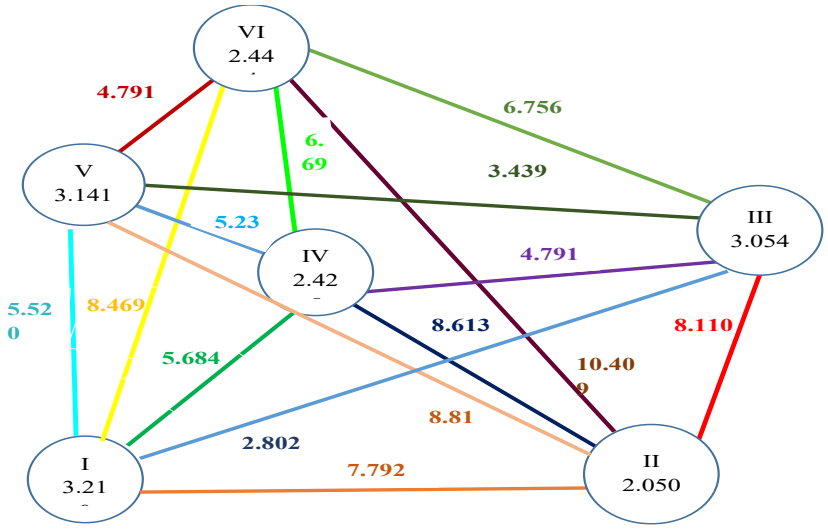

Fig. 1: Intra and inter cluster distance diagram for different characters in okra

Table 3: Cluster-wise specific mean values for various traits in 26 distinct okra genotypes

SN	Traits	Clusters					
		I	II	III	IV	V	VI
1	Days taken to first germination	5.67	5.33	5.70	7.67	5.27	6.00
2	Plant height (cm)	213.49	138.20	226.54	201.13	247.92	208.30
3	Number of primary branches per plant	4.12	4.80	5.15	4.20	6.91	10.77
4	Days taken to first flowering	45.83	48.87	48.48	51.37	50.75	53.63
5	Number of nodes at first flowering	5.78	6.33	6.05	5.83	6.89	6.80
6	Fruit length (cm)	17.57	22.32	17.74	18.39	17.31	16.97
7	Fruit diameter (mm)	15.89	18.26	15.29	16.31	15.41	16.13
8	Average fruit weight (g)	19.29	23.16	19.77	18.41	19.72	18.55
9	Number of fruits per plant	57.36	59.73	53.79	58.43	50.73	45.20
10	Number of ridges per fruit	5.08	5.00	5.02	5.53	5.25	6.00
11	Days taken to first fruit set	47.31	49.67	50.29	52.40	52.26	54.73
12	Days taken to first fruit harvest	53.33	56.27	56.01	57.83	58.07	60.60
13	Flesh thickness (mm)	1.60	1.87	1.55	1.67	1.56	1.65
14	Number of seeds per fruit	58.21	83.27	64.46	53.30	68.29	83.73
15	Seed index	6.48	7.40	6.29	6.72	6.39	5.43
16	Yield per plot (Kg)	8.11	10.02	6.97	6.16	4.98	4.55
17	Total soluble solids (°Brix)	10.20	9.90	10.66	10.55	11.84	12.17
18	Chlorophyll content (SPAD)	56.17	54.67	58.21	61.27	58.62	57.07
19	Ash content (%)	9.11	10.73	9.53	10.79	10.30	9.60
20	Physiological loss	5.17	3.33	5.53	4.50	4.07	4.67

Highest cluster mean for fruit length was observed in the cluster II followed by cluster IV, cluster III, cluster I and cluster V. The lowest cluster mean was observed in cluster VI. Highest cluster mean for fruit diameter was observed in the cluster II followed by cluster IV, cluster VI, cluster I and cluster V. Lowest cluster mean was observed in cluster III. Highest cluster mean for average fruit weight was observed in the cluster II followed

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by cluster III, cluster V and cluster VI, while the lowest cluster mean was observed in cluster IV. Similar results were also obtained by Prakash et al (2011), Priyanka et al (2017) and Ramgiry et al (2017) in okra. Highest cluster mean for the number of fruits per plant was observed in the cluster II followed by cluster IV, cluster I, cluster III and cluster V. Lowest cluster mean for this trait was observed in cluster VI. The number of ridges per fruit recorded maximum cluster mean in cluster VI followed by cluster IV, cluster V, cluster I and cluster III. The lowest cluster mean for this trait was recorded in cluster II. Lowest cluster mean for days taken to first fruit set was observed in cluster I followed by cluster II, cluster III, cluster V and cluster IV, while the highest cluster mean was observed in cluster VI. Lowest cluster mean for days taken to first fruit harvest was noted in cluster I which was at par with cluster III, cluster II, cluster IV and cluster V, while the highest cluster mean was observed in cluster VI which was in line with the findings of Akotkar et al (2010), Ramgiry et al (2017) and Singh et al (2018) in okra.

Flesh thickness recorded maximum cluster mean in cluster II followed by cluster IV, cluster VI, cluster I and cluster V. The lowest cluster mean for this trait was recorded in cluster III. The number of seeds per fruit recorded maximum cluster mean in cluster VI followed by cluster II, cluster V, cluster III and cluster I. The lowest cluster mean for this trait was recorded in cluster IV. Similar results were also obtained by Prakash et al (2011), Shaikh et al (2013) and Ramgiry et al (2017) in okra. Yield per plot recorded maximum cluster mean in cluster II followed by cluster I, cluster III, cluster IV and cluster V. The lowest cluster mean for this trait was recorded in cluster VI. Highest cluster mean total soluble solids was observed in the cluster VI followed by cluster V, cluster III, cluster IV and cluster I. Lowest cluster mean for total soluble solid was observed in cluster II. Highest cluster mean for chlorophyll content was observed in the cluster IV followed by cluster V, cluster III, cluster VI and cluster I. Lowest cluster mean for this trait was observed in cluster II. Ash content recorded maximum cluster mean in cluster IV followed by cluster II, cluster V, cluster VI and cluster III. The lowest cluster mean for ash content was recorded in cluster I. Highest cluster mean for physiological loss was observed in the cluster III followed by cluster I, cluster VI, cluster IV and cluster V. Lowest cluster mean for physiological loss was observed in cluster II. Earlier workers like Akotkar et al (2010), Shaikh et al (2013), Balai et al (2015), Ramgiry et al (2017) and Singh et al. (2018) also came up with the similar findings in okra.

Conclusion

In the present investigation, twenty-six genotypes were grouped into six clusters according to their genetic divergence. The resultant six clusters showcased genetic diversity, and the maximum number of genotypes was seen in cluster III (10 genotypes). The average intra cluster distance was maximum in cluster I and was minimal in cluster II; the crossing of genotypes belonging to the same cluster will not expect to yield superior hybrids segregates. At the same time, the greatest inter-cluster distances observed between clusters VI and II indicate that genotypes from these clusters may be utilized as parents in breeding programs to develop hybrids with enhanced heterosis in the progeny. The significant genetic diversity observed among the genotypes suggests the potential for improving okra yield and other desirable traits through strategic selection and hybridization. The genotypes from clusters VI and II can be exploited to produce superior hybrids due to the higher probability of heterosis. These findings provide valuable insights for the development of improved okra cultivars with better yield potential, disease resistance and adaptability to diverse environmental conditions.

WoS Indexing

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