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Genetic Divergence Studies for Yield, Yield Attributes and Quality Traits in Okra [*Abelmoschus esculentus* (L.)]

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ABSTRACT

The present experiment was conducted during October, 2021 to January, 2022 in the Department of Vegetable Science, College of Horticulture, Mojerla, Wanapathy District, Sri Konda Laxman Telangana State Horticultural, University, Mulugu, Siddipet, Telangana, (509 382), India on the genetic divergence studies in Okra (*Abelmoschus esculentus* L.) genotypes. 37 okra diverse okra genotypes were evaluated in a randomized block design (RBD) with three replications using various yield attributes. The cluster VI showed maximum intra-cluster distance (752.33) followed by cluster V (491.19) and Clusters IV (434.85). The inter-cluster D^2 values of the nine clusters recorded that the highest inter-cluster generalized distance (5966.95) was between cluster VIII and cluster IX. The per cent contribution of different characters towards genetic divergence of genotypes of cluster IX registered maximum fruit length (14.35 cm). Fruit diameter exhibited maximum in cluster II (1.95 cm). Early days to first picking were recorded in cluster VI (42.05 days). Number of fruits plant^{-1} was highest in cluster IX (52.90) and lowest in cluster II (18.53). Fruit yield plant^{-1} was recorded maximum in cluster IX (0.44 kg), while it was minimum in cluster VIII (0.16 kg) showed the highest yield contributing characters towards total diversity among the genotypes, IC33823, IC42490, EC329422, IC42484 and IC42470 are more genetically diverse among the genotypes and can be used in hybridization programme, for obtaining superior and desirable recombinants.

KEYWORDS: Clusters, genetic divergence, okra, percent contribution and genotypes

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Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

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1. INTRODUCTION

Okra (*Abelmoschus esculentus* L. Moench) is a widely cultivated vegetable crop in tropical and subtropical regions, with a chromosome number of 2n=2x=130 (Patil et al., 2015). It is generally known as 'bhendi' or lady's finger in India. Okra flowers are hermaphroditic and heavily self-pollinated. Cross-pollination also occurs depending on frequency of pollen transfer by the insects. (Fufa, 2019). Vegetables being a rich source of minerals and vitamins, while low in calories and free of fat are playing a vital role not only in human nutrition and health but also in the livelihood of the farming community in rural and urban areas (Aboyeji et al., 2021). India is the largest global producer of okra, contributing over 72% (6.47 mt) from an area of 0.5 mha, as per the National Horticulture Board Report Anonymous (2022). It accounts for 60% of the total fresh vegetable export from India (Chaudhary et al., 2023) and is known for its immature green seed pods, which are consumed as a cooked vegetable, fresh or sundried (Liu et al., 2021). Immature okra pods are utilized for making pickles (Chavan, et al., 2021). Okra is cooked and consumed in a variety of ways. A dry seed of okra contains 13–22% edible oil and 20–24% crude protein (Thamburaj and Singh, 2004).

According to (Yadav et al., 2016), the fruits of okra contain many nutrients in 100 g of edible portion viz., water 88%, carbohydrates 7.7%, protein 2.2%, fat 0.23%, fiber 1.2%, mineral matters 0.7%, calcium 0.09%, phosphorus 0.04%, iron 0.15%, vitamin 'A' 88 IU. Vitamin 'B' 0.07 mg and vitamin 'C' 16 mg. Several experts have noted the medicinal and nutritional value of okra, including mineral components, protein, fibre, antioxidants, and vitamins (Adetuyi et al., 2011). Flavonoid and antioxidants such beta carotene, xanthein, and lutein are abundant in okra pods (Dilruba, et al., 2009). To overcome the yield limitations of existing open-pollinated okra varieties, the implementation of a hybridization-based breeding strategy is deemed essential (Waghmare, 2022). Exploiting heterosis in okra plays a crucial role in enhancing yield and related traits within crop improvement programs. Being a cross-pollinated crop, it has a high level of genetic diversity (Duggi et al., 2013), making it important to evaluate the germplasm for genetic variability as the first step in okra improvement (Singh et al., 2012). The second step is to generate crosses using a suitable mating design, to understand the extent of heterosis for various economic traits and the inheritance pattern of desired characters (Das et al., 2020). Yield is a pivotal trait in both okra cultivars and hybrids, prompting extensive endeavours have been undertaken to enhance yield, production and quality characteristics (Singh et al., 2017).

The freshly harvested seed of okra hybrid, Uphar, with different seed vigour levels after subjecting to accelerated ageing at 40+10°C and 85+5% relative humidity for 4, 8, 12 and 16 days to study the effect of seed vigour on initial seed quality, field performance and yield (Keshavulu et al., 2012). Genetic variability plays an important role in crop breeding for selecting the elite genotypes for making rapid improvement in yield and other desirable characteristics as well as selecting the potential parent for hybridization programmes (Mishra et al., 2015). The D^2 statistic, which calculates two levels of genetic divergence, namely; inter-cluster and intra-cluster levels, aids in choosing genetically diverse parents for use in hybridization programmes. (Mahalanobis, 1936). The objectives of the study were to analyse the genetic diversity of 37 okra genotypes, determine the genetic relationships among different traits which contribute more towards growth, yield and quality determine the promising excellent genotypes which could be parents in okra breeding program.

2. MATERIALS AND METHODS

The present experiment was conducted at the PG research block in the department of Vegetable Science, College of Horticulture, Mojerla, Wanaparthy district, Sri Konda Laxman Telangana State Horticultural University, Mulugu, Siddipet, Telangana (509 382), India during *rabi* (October, 2021 to January, 2022). It is situated at an altitude of 401 m above mean sea level on 77°.96' East longitude and 16°.36' North latitude and climate is semi-arid. The monthly mean maximum temperature ranged from 24.9°C to 32.4°C with an average of 30.50°C while the monthly mean minimum temperature ranged from 12.7°C to 21.4°C with an average of 17.5°C during the crop growth period. Relative humidity forenoon and afternoon fluctuated between 86% to 90% and 38% to 71% respectively rainfall received during the crop growth period. The monthly mean sunshine hours varied from 3.3 to 8.2 with an average of 5.6 hours' day^{-1} and mean evaporation ranged from 2.8 to 5.1 mm with an average of 4.1 mm day^{-1}. The mean wind speed ranged from 2.8 to 11.2 km hr^{-1} with an average of 5.4 km $hr^{-1.}$ Mahanalobis D^2 statistics were used to assess the genetic divergence between the groups.

2.1. Source of seed materials

The 37 genotypes of okra were collected from NBPGR, Regional station, New Delhi. IC33823, IC33853, IC34124, IC39132, IC39133, IC39134, IC39135, IC39136, IC39137, IC39143, IC40289, IC42451, IC42456, IC42464, IC42470, IC42472, IC42484, IC42490, EC329362, EC329364, EC329365, EC329366, EC329367, EC329368, EC329369, EC329370, EC329371, EC329372, EC329384, EC329384, EC329406, EC329418, EC329420, EC329421, EC329422, EC329423, Kashi Lalima (Check), IIVR, Varanasi and Arka Anamika

(Check) IIHR, Bangalore the data was recorded on following parameters.

2.2. Experimental design

The experiment was under taken on 37 genotypes of okra using randomized block design (RBD) with three replications at College of Horticulture, SKLTSHU, Mojerla, Wanaparthy district. The crop was sown during Rabi season, in the year 2021–2022.

2.3. Preparation of experimental plot

The experiment field was brought to fine tilth by ploughing thrice followed by harrowing. Before final harrowing, FYM @ 25 t ha^{-1} was applied at the time of last ploughing and incorporated well into the soil. Ridges and furrows were formed at a spacing of 45 cm. The recommended basal dose of fertilizer at the rate of 25 kg Nitrogen, 50 kg Phosphorus and 50 kg Potash ha^{-1} was applied in the form of urea, single super phosphate and muriate of potash and mixed with soil. The seeds of each accession were dibbled on one side of ridges at a spacing of 30 cm at the rate of two seeds per hill in a plot size of 3.9×3.6 m^2. Gap filling was done a week after sowing. After establishment, the seedlings were thinned out to one plant $hill^{-1}$. Thirty days after sowing, 25 kg of Nitrogen ha^{-1} was applied as top dressing. Other cultural operations including plant protection measures were done regularly. The mean values were computed to calculate D^2 values between all possible pairs of genotypes. The grouping of genotypes was done using Tocher's method as described by Rao (1952).

3. RESULTS AND DISCUSSION

3.1. Genetic divergence (D^2 statistic)

The quantitative assessment of genetic divergence was made by adopting Mahalonobis D^2 statistic for yield and its seed quality characteristics.

3.2. Grouping of genotypes into different clusters (D^2 analysis)

The D^2 values between any two genotypes were calculated as the sum of squares of the differences between the mean values of all the nineteen characters and used for the final grouping of the genotypes.

The procedure suggested by Tocher (Rao, 1952) has been used to group thirty-seven genotypes into nine clusters by treating the estimated D^2 values as the square of the generalized distance.

Based on D^2 values, the thirty-seven genotypes were grouped into nine highly divergent clusters shown in Table 1 and Figure 1. Some of the genotypes were so divergent in all the characters, hence, every single genotype formed a separate cluster. Thus, five clusters *viz.*, II (IC33823), III (IC42490), VII (EC329422), VIII (IC42484) and IX

Table 1: Clustering pattern of thirty seven genotypes of okra by Tocher's method

Cluster	No. of genotypes	Name of genotype
I	17	IC42472, EC329365, IC39136, Arka Anamika, EC329423, IC42451, EC329418, IC39135, IC40289, EC329421, EC329420, IC39137 and EC329369
II	1	IC33823
III	1	IC42490
IV	5	EC329372, EC329406, Kashi Lalima, IC42464 and IC34124
V	5	IC39133, IC39143, IC39134, IC39132 and EC329371
VI	5	IC42456, EC329362, EC329366, EC329367 and EC329368
VII	1	EC329422
VIII	1	IC42484
IX	1	IC42470

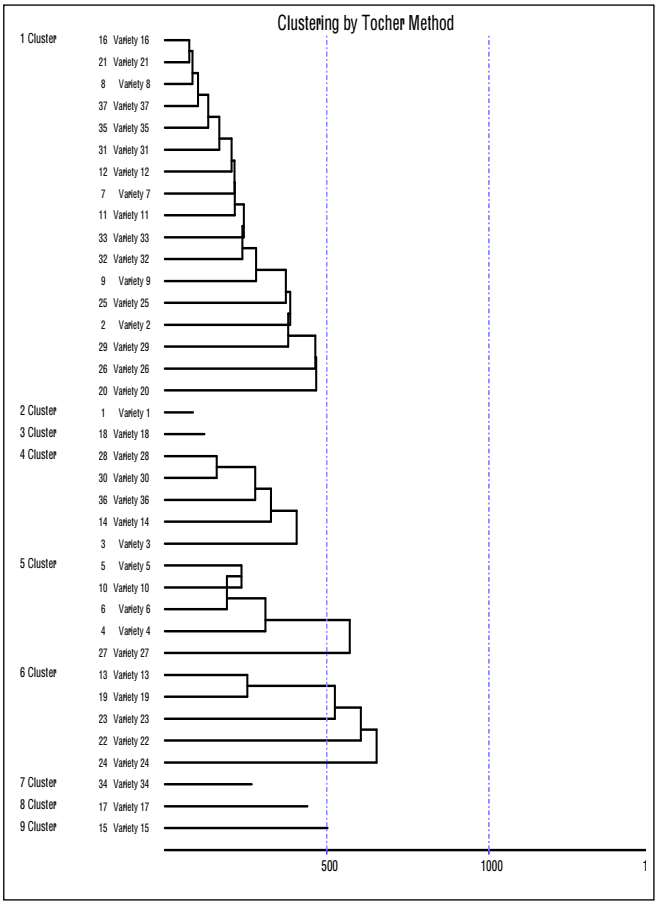

Figure 1: Dendrogram showing clustering pattern for divergence of okra

(IC42470) were solitary with one genotype in each cluster.

The remaining four clusters had a maximum number of genotypes. Cluster I was biggest with 17 genotypes *viz*., IC42472, EC329365, IC39136, Arka Anamika, EC329423, IC42451, EC329418, IC39135, IC40289, EC329421, EC329420, IC39137, EC329369, IC33853, EC329384, EC329370 and EC329364 followed by cluster IV (EC329372, EC329406, Kashi Lalima, IC42464 and IC34124), Cluster V (IC39133, IC39143, IC39134, IC39132, EC329371) and Cluster VI (IC42456, EC329362, EC329366, EC329367 and EC329368) with 5 genotypes are represented in Figure 2 in three-dimensional plot diagram.

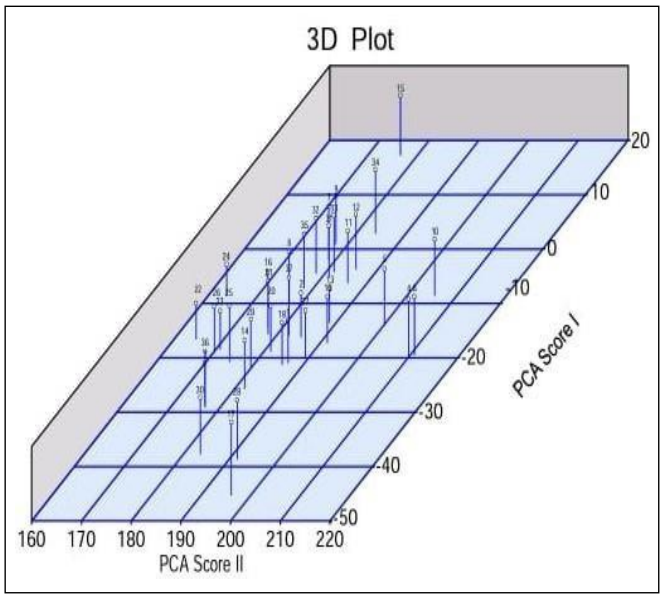

Figure 2: 3D plot showing clustering pattern for divergence of okra genotypes

3.3. Cluster means of characters in a cluster

The cluster means for the nineteen characters studied in okra genotypes revealed considerable differences among all the clusters shown in Table 2 From the present data, it is evident that plant height was highest in cluster IX (71.28 cm) and lowest in cluster IV (38.74 cm). Maximum number of primary branches plant^{-1} was recorded in cluster IX (5.53), whereas+minimum was recorded in cluster IV (2.26).

The cluster IX noticed the maximum internodal length (5.94 cm), whereas cluster VIII noticed the minimum internodal length (1.83 cm). The cluster IX had the early days to 50% flowering (40.50 days), whereas cluster V had the late day to 50% flowering (51.63 days).

The genotypes of cluster IX registered maximum fruit length (14.35 cm), whereas genotypes of cluster IV (10.70 cm) recorded minimum fruit length. Fruit diameter exhibited maximum in cluster II (1.95 cm) and minimum in cluster VII (2.26 cm). Early days to first picking were recorded in cluster VI (42.05 days) and late days to first picking were registered in cluster VIII (56.46 days).

A maximum number of locules fruit^{-1} was recorded in cluster VI (8.07) and it was minimum in cluster IX (5.04). Number of seeds fruit^{-1} was highest in cluster IX (60.87) and lowest in cluster VIII (19.73). Number of fruits plant^{-1} was highest in cluster IX (52.90) and lowest in cluster II (18.53). Fruit yield plant^{-1} was recorded as maximum in cluster IX (0.44 kg), while it was minimum in cluster VIII (0.16 kg). Maximum seed weight fruit^{-1} was recorded in cluster IX (4.17 g), while minimum in cluster VIII (2.20 g). Maximum test weight was noticed in cluster IX (75.83 g), while minimum in both cluster III and cluster IV (56.93 g). Maximum germination percent was observed in cluster IX (91.70 %), whereas it was minimum in cluster VI (75.96 %).

Table 2: Mean values of clusters for nineteen characters in thirty seven genotypes of okra

Cluster	Plant height (cm)	No. of primary branches plant^{-1}	Internodal length (cm)	Days to 50% flowering	Fruit length (cm)	Fruit diameter (cm)	Days to first picking	No. of locules fruit^{-1}	No. of seeds fruit^{-1}	No. of fruits plant^{-1}
I	54.00	3.35	3.96	41.55	12.75	1.42	46.12	5.76	53.69	36.92
II	45.72	2.47	3.63	43.20	14.24	1.95	46.35	5.15	48.20	18.53
III	52.13	2.50	3.54	43.53	13.51	1.66	46.18	5.62	55.53	21.63
IV	38.74	2.26	2.27	42.47	10.70	1.65	46.82	5.41	38.59	24.24
V	51.62	3.09	4.23	51.63	13.43	1.59	55.13	6.34	54.05	34.23
VI	46.25	2.39	3.12	45.35	12.32	1.47	42.05	8.07	53.27	30.23
VII	62.10	3.60	4.98	43.17	13.59	1.26	49.38	6.19	39.53	48.76
VIII	40.79	2.33	1.83	41.83	11.51	1.49	56.46	5.35	19.73	19.21
IX	71.28	5.53	5.94	40.50	14.35	1.41	45.44	5.04	60.87	52.90

Table 2: Continue...

Cluster	Fruit yield plant^{-1} (kg)	Seeds weight fruit^{-1} (g)	Test weight (g)	Germination (%)	Seedling length (cm)	Seedling dry weight (g)	Vigour index I	Vigour index II	Chlorophyll content (mg 100 g^{-1})
I	0.28	3.49	64.47	89.18	10.18	0.03	906.95	2.80	0.80
II	0.25	3.41	65.77	85.11	8.29	0.03	705.49	2.87	0.73
III	0.23	3.75	56.93	89.97	10.58	0.03	952.03	2.59	0.35
IV	0.21	3.28	56.93	87.58	9.96	0.03	871.49	2.27	0.30
V	0.25	3.58	65.51	85.61	10.24	0.03	872.00	2.50	0.67
VI	0.25	3.92	58.88	75.96	8.86	0.03	683.85	1.95	0.67
VII	0.42	4.09	64.17	88.87	13.79	0.03	1225.7	2.86	1.46
VIII	0.16	2.20	67.83	88.87	13.68	0.03	1071.8	2.72	0.26
IX	0.44	4.17	75.83	91.70	12.05	0.04	1105.3	3.25	1.95

Highest seedling length was recorded in cluster VII (13.79 cm), while the minimum was in cluster II (8.29 cm), seedling dry weight was recorded highest in cluster IX (0.04 g), while the lowest in cluster I, II, III, IV, V, VI, VII, VIII (0.03 g). Maximum vigour index I was noticed in cluster VII (1225.76) and minimum in cluster VI (683.85).

Vigour index II was registered maximum in cluster IX (3.25), while it was minimum in cluster VI (1.95). Chlorophyll content was highest in cluster IX (1.95 mg) and lowest in cluster VIII (0.26 mg).

Cluster mean values showed a wide range of mean values among the characters studied indicating the presence of wide variation among the genotypes studied. Cluster III was the largest containing genotypes followed by cluster VIII with four genotypes. Composition of clusters indicated non-existence of correspondence between genetic diversity and geographical distribution. fruit yield, plant height and length of edible pod were the major characteristics contributing towards divergence. Cluster VII and X was the most divergent followed by cluster V and X as supported by the findings of reported by Ramya and Senthilkumar (2009); The genotypes which was in the cluster V, III and II also exhibited significant performance for fruit yield plant^{-1}, number of fruits plant^{-1} and plant height sequentially has been employed in various studies as a multivariate technique to analyze diversity in Akotkar et al. (2010); Fluorescent organic nanoparticles (FONs) were prepared from pyrene-containing guanine analogues has evolved in Reddy et al. (2012); High heritability coupled with high genetic advance as percent of mean for the characters like plant height, fruits plant^{-1}, fruit weight, equatorial fruit diameter, seeds fruit^{-1} and fruit yield plant^{-1} similar Koundinya et al. (2013); Cluster analysis based on Canberra, Furthest Neighbour Similarity Matrix grouped the accessions into two major clusters and subsequently into four sub-clusters, with no duplications, based on the characters studied. Seven pairs of quantitative traits were positive and significantly correlated ($p \leq 0.05$) while three were highly significantly associated ($p \leq 0.01$). Amoatey et al. (2015) and Balai et al. (2015).

It is rich in nutrients and active ingredients (i.e. dietary fiber, vitamins, oils, poly-saccharides, polyphenols), which makes it have antioxidant, anti-inflammatory, hypoglycemic, hypolipidemic and other functions shown in Kumar et al. (2020); Selection based on these characters would result in an increase in total yield plant^{-1}, and it is also very useful to develop high yielding genotypes through hybridization programme with the combination of characters above similar characters of Sravanthi et al. (2022); India ranks first in the world with 72% of the total world production of okra. In India, the total area covered under okra is 0.509 million ha which has produced 6.094 mt green fruits with the productivity of 12.0 t ha^{-1} in the year 2017–18 in similar results Maurya and Yadav (2021); The use of diverse genotypes from the clusters with high inter cluster distance (clusters IV and V, III and IV, I and IV and II and IV) in hybridization is expected to result in high heterosis and throw desirable transgressive segregants has evolved in the use of diverse genotypes from the clusters with high inter-cluster distance (clusters IV and V, III and IV, I and IV and II and IV) in hybridization is expected to result in high heterosis and throw desirable transgressive segregants as similar of Nanthakumar et al. (2021); Seven major clusters in which the three clusters, was solitary, consisted of one genotype each, Cluster I consisted of six Indian commercial varieties, Cluster IV comprised of seven genotypes (four indigenous okra collections, one variety from USA and two from India), while Cluster VI and VII consist of 5 and 4 indigenous okra collections, respectively. This study revealed the presence of wide genetic diversity among indigenous okra collections and exotic commercial varieties. Mahalanobis D^2 analysis (Mahlanobis, 1928) was used to measure the genetic divergence among 30 genotypes similar to Melaku et al. (2022).

3.4. Average intra and inter cluster distances

The mean intra and inter cluster D^2 values among the nine clusters are given in the Table 3 Figure 3. The intra cluster D^2 value ranged from nil (cluster II, cluster III, cluster VII, cluster VIII and cluster IX) to 752.33 (cluster VI). The cluster VI had the maximum D^2 value (752.33) followed by cluster V (491.19), clusters IV (434.85) and cluster I (348.49).

The inter cluster D^2 values of the nine clusters recorded that highest inter cluster generalized distance (5966.95) was between cluster VIII and cluster IX, while the lowest (196.60) was between cluster II and cluster III.

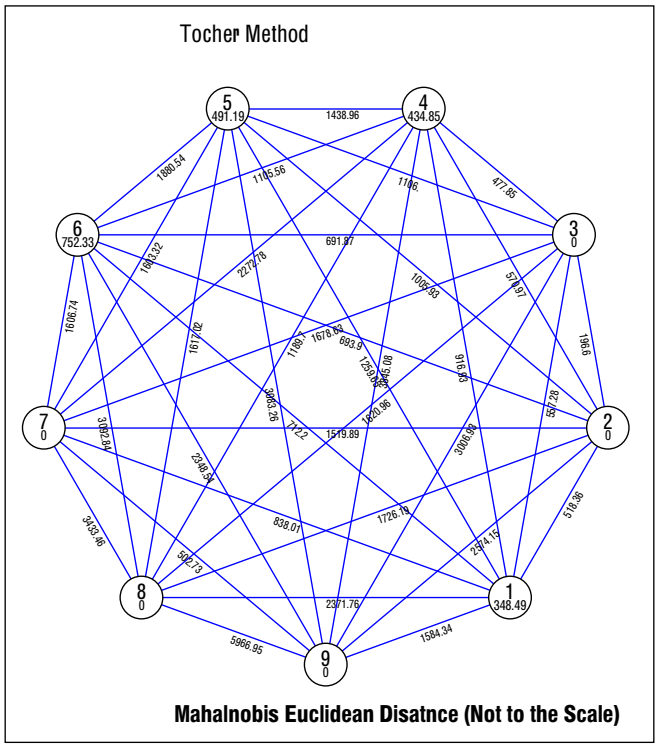

Figure 3: Cluster diagram showing average intra and inter-cluster D^2 values of okra genotypes

The inter cluster distance was minimum between cluster II and III indicating narrow genetic diversity, whereas maximum recorded between clusters VIII and IX indicating wider genetic diversity between these groups.

The nearest and distant clusters from each of the cluster based on D^2 values are presented in Table 4 and Figure 3. Cluster I was nearest to cluster II (518.36) and distant from cluster VIII (2371.76). Cluster II exhibited close proximity with cluster III (196.60) and maximum divergence with cluster IX (2574.15). Cluster III was nearest to cluster II (196.60) while it was farthest from cluster IX (3006.93).

Cluster IV was nearest to cluster III (477.85) and distant from cluster IX (3845.08). Cluster V exhibited intimate relation with cluster II (1005.930) and wide diversity with cluster IX (3083.26). The nearest and farthest clusters for cluster VI are cluster III (691.87) and cluster VIII (3092.84).

Cluster VII was nearest to cluster IX (502.73) and distant from cluster VIII (3433.46). Cluster VIII exhibited close proximity with cluster IV (1189.70) and maximum divergence with cluster IX (5966.95). Nearest and farthest clusters for cluster XI are cluster VII (502.73) and cluster VIII (5966.95).

3.5. Relative contribution of different characters towards divergence

The per cent contribution of each character towards divergence is presented in Table 5 and Figure 4. It was observed that days to 1st picking contributed maximum (37.99 %) towards divergence taking 253 times first ranking followed by chlorophyll content (27.93%) by 186 times, number of fruits plant^{-1} (9.76%) by 65 times, days to 50% flowering (8.41%) by 56 times, fruit length (3.45%) by 23 times, plant height (3.30%) by 22 times, seedling length (2.40 %) by 16 times, number of seeds fruit^{-1} (1.50%) by 10 times, germination percent (1.20%) by 8 times, inter nodal length (1.05%) by 7 times, number of locules fruit $^{-1}$ (0.90%) by 6 time, fruit yield plant $^{-1}$ (0.75%) by 5 time, vigour index

Table 3: Average intra (bold) and inter-cluster D^2 values for nine clusters in thirty seven genotypes of okra

cluster s	I	II	III	IV	V	VI	VII	VIII	IX
I	348.49	518.36	557.28	916.93	1259.65	712.20	838.01	2371.76	1584.34
II		0.00	196.60	570.97	1005.93	693.90	1519.89	1726.19	2574.15
III			0.00	477.85	1106.00	691.87	1678.63	1620.96	3006.93
IV				434.85	1438.96	1105.56	2272.78	1189.70	3845.08
V					491.19	1880.54	1603.32	1617.02	3083.26
VI						752.33	1606.74	3092.84	2348.54
VII							0.00	3433.46	502.73
VIII								0.00	5966.95
IX									0.00

Table 4: The nearest and farthest clusters from each Cluster based on D^2 values in okra genotypes

Cluster number	Nearest cluster with D^2 values	Farthest cluster with D^2 value
I	II (518.36)	VIII (2371.76)
II	III (196.60)	IX (2574.15)
III	II (196.60)	IX (3006.93)
IV	III (477.85)	IX (3845.08)
V	II (1005.930)	IX (3083.26)
VI	III (691.87)	VIII (3092.84)
VII	IX (502.73)	VIII (3433.46)
VIII	IV (1189.70)	IX (5966.95)
IX	VII (502.73)	VIII (5966.95)

Table 5: Percent contribution of different characters towards genetic divergence in thirty-seven genotypes of okra

Sl. No.	Characters	Times ranked 1st	Per cent contribution
1.	Plant height	22	3.30 %
2.	No. of primary branches	0	0.00 %
3.	Internodal length (cm)	7	1.05 %
4.	Days to 50% flowering	56	8.41 %
5.	Fruit length (cm)	23	3.45 %
6.	Fruit diameter (cm)	0	0.00 %
7.	Days to 1st picking	253	37.99 %
8.	Number of locules $fruit^{-1}$	6	0.90 %
9.	Number of seeds $fruit^{-1}$	10	1.50 %
10.	Number of fruits $plant^{-1}$	65	9.76 %
11.	Fruit yield $plant^{-1}$ (kg)	5	0.75 %
12.	Seeds weight $fruit^{-1}$	2	0.30 %
13.	Test weight (g)	2	0.30 %
14.	Germination (%)	8	1.20 %
15.	Seedling length (cm)	16	2.40 %
16.	Seedling dry weight (cm)	0	0.00 %
17.	Vigour index I	4	0.60 %
18.	Vigour index II	1	0.15 %
19.	Chlorophyll content	186	27.93 %

1 (0.60%) by 4 time, seeds weight $fruit^{-1}$ (0.30%) by 2 time, test weight (0.30%) by 2 time, vigour index 2 (0.15%) by 1 time. In contrast, the remaining traits *viz.*, number of primary branches, fruit diameter and seedling dry weight did not contribute to the total divergence. Apart from the high divergence, the performance of the genotypes and the characters with maximum contribution towards divergence

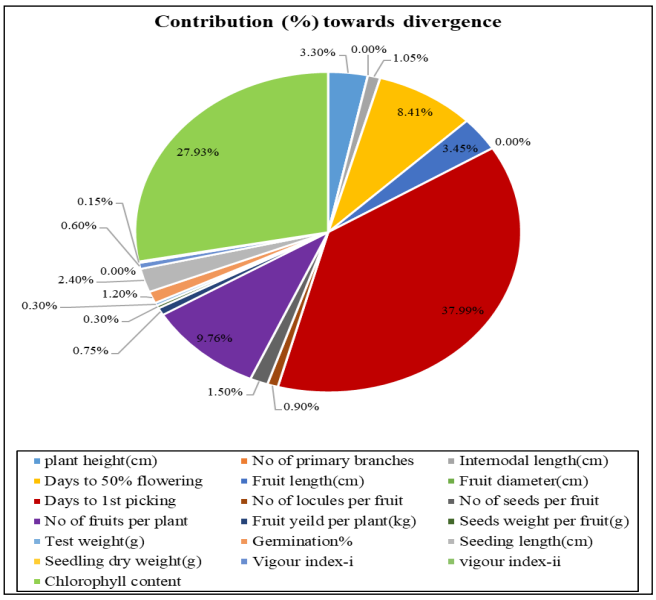

Figure 4: Direction and contributions of variables parameters in influencing genetic divergence

should also be given due consideration which appears as desirable for inclusion in okra improvement.

Mahalanobis D^2 statistics, a powerful tool has been used to quantify the genetic divergence between the genotypes and to identify diverse parents for crossing. This also helps to relate clustering pattern with the geographical origin. This technique has been employed widely to resolve divergence at inter varietal, species and subspecies levels in classifying problems in crop plants (Anonumous, 1997). In the present study, thirty-seven germplasm lines of okra were grouped into nine clusters. The magnitude of D^2 values confirmed that there was considerable amount of diversity in the experimental material evaluated.

Statistical distance represents the extent of genetic diversity among clusters. The inter cluster distance was minimum between cluster II and cluster III indicating close relationship and similarity for most of the characters of the genotypes included in these clusters. The maximum inter cluster distance was observed between clusters cluster VIII and IX indicating wider genetic diversity among the genotypes included in these groups.

Selection of parents from these diverse clusters for hybridization programme would help in achieving novel recombinants. Maximum intra cluster distance was recorded in cluster VI, this might be due to limited gene exchange or selection practices among the genotypes for diverse characters.

Emphasis should be laid on characters contributing maximum D^2 values for choosing the cluster for further selection and choice of parents for hybridization. The highest contribution towards divergence in this regard

was put forth by days to 1st picking contributed maximum, chlorophyll content, number of fruits plant^{-1}, days to 50% flowering, fruit length, plant height, seedling length, number of seeds fruit^{-1}, germination percent, internodal length, number of locules fruit^{-1}, fruit yield plant^{-1}, vigour index I, seeds weight fruit^{-1}, test weight and vigour index II. Thus, these were the major traits contributing to divergence. Hence, selection for divergent parents based on these characters will be useful for further breeding programmes in okra.

4. CONCLUSION

Genetic diversity was assessed for nineteen quantitative characters. Grouping of genotypes in the formation of nine clusters. The inter-cluster distance minimum between clusters II and III indicated narrow genetic diversity, whereas maximum was recorded between clusters VIII and IX indicating wider genetic diversity between these groups.

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