

Original Research Article

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Genetic Diversity Analysis of Okra Genotypes Using Morphological Markers

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ABSTRACT

Genetic divergence of 30 okra genotypes was studied using Mahalanobis D₂ statistics revealed that considerable genetic diversity among genotypes in okra. Thirty diverse genotypes were grouped into six clusters with the highest of 11 genotypes in the cluster II, 10 in the cluster I, 4 genotypes in the cluster III, 3 in cluster V and 1 in each IV and VI cluster. The inter cluster distance was higher than the intra cluster distance indicating wide genetic diversity among the genotypes of different groups. The cluster means of 10 characters among six clusters indicated that high genetic variability range present for fruit yield per plant (174.7 g in cluster V to 350.14 g in cluster III), followed by fruits/plant (20.83 in cluster V to 40.03 in cluster III) and average weight of fruit (7.667 g in cluster IV to 10.033 g in cluster VI). The relative contribution of studied characters indicated that branches per plant had contributed highest (41.61 %) followed by fruit yield per plant (31.49 %), fruits per plant (15.17 %), nodes (1st Flowering node to end) (8.97), stem diameter (1.61). Based on principal component analysis (PCA), the first four components explained 87.83% of total genetic variation. These characters are highly genetic variable and genotype having these characters in different cluster could be used in breeding programme to develop high yielding cultivars in okra.

Keywords

Okra, Genetic diversity, Mahalanobis D₂ statistics, Cluster analysis

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Introduction

Okra [*Abelmoschus esculentus* (L.) Moench] usually denoted as Lady's finger belongs to the Malvaceae family (Kishor *et al.*, 2016) and an important and extensively cultivated, annual crop in both the tropical and sub-tropical provinces of the world (Eshiet and Brisibe, 2015; Ali *et al.*, 2014). It is a vegetable rich in organic and inorganic nutrients like vitamins and mineral salts, including calcium; which are often lacking in

diet (Chattopadhyay *et al.*, 2011; Rahman *et al.*, 2012), further containing 86.1% water, 2.2 % protein, 0.2% fat, 9.7% carbohydrate, 1.0% fiber and 0.8% ash (Saifullah and Rabbani, 2009). The fruits of okra, usually called "pod" which contain digestible fiber, low calories and fat-free contents (Kumar and Sreeparvathy, 2010; Reddy *et al.*, 2013) and consumed as salads, boiled and fried vegetables (Daniela *et al.*, 2012) further the fruits are used for soups and stews thickening due to its mucilaginous and tender texture

nature, (Ijoyah & Dzer, 2012; Das *et al.*, 2013). Tropical Africa is proposed origin of okra from where it spreaded to America, Asia, Southern Europe and other countries (Muhammad *et al.*, 2013). In 2008, India was one of the five top okra producing countries in the world (FAOSTAT, 2010).

The strength and value of germplasm depends on two factors, the number of accessions it contains and the diversity present in those accessions (Ren *et al.*, 1995). For the balanced use of plant genetic resources, characterization and quantification and information on the genetic diversity within and among closely related crop varieties is essential. Genetic diversity is prerequisites for any successful breeding programme. Use of genetically diverse parents in recombination breeding supposed to give maximum heterosis in F1's and the importance of genetic diversity in selecting the parents has been continually emphasized by lot of workers (Murthy and Anand, 1996; Pillai, 2002). Diversity based on morphological characters generally varies with environments therefore evaluation of traits needs growing the plants to full adulthood prior to identification. Omonhinmin and Osawaru (2005) stated that great degree of wide morphological difference exist between accessions of okra, especially in West African type. Hence, estimation of genetic divergence of economically important characters based on sound statistical procedures like Mahalanobis D² statistics is required to identify diverse genotypes for crossing. In determining genetic divergence, cluster analysis is one of the powerful tools among different varieties of crops.

Lack of relationship between the genetic diversity and geographical distance indicated that forces like natural and artificial selection, exchange of genetic materials, genetic drift and spontaneous mutation could lead to genetic diversity instead of geographical

origin (Pradip *et al.*, 2010; Seth *et al.*, 2016). Therefore, selection for outcrossing of okra cultivars ought to base on genetic diversity instead of geographic diversity.

Materials and Methods

Experimental location

The material for the present experimental investigation contained thirty genotypes of okra conserved at the research farm of the Department of Vegetable Science, C.C.S. Haryana Agricultural University, Hisar, during kharif season 2013.

Field evaluation and data collection

The experiment was laid out in randomized complete block design (RCBD) with three replications. In each replication each genotype was grown in a double row plot of size 2.1 m × 1.20 m accommodating 14 plants with row-to-row spacing of 60 cm and plant-to-plant spacing of 30 cm. Two seeds per hill were sown and later thinned to one plant per hill. Recommended package of practices were followed to raise a healthy crop.

The data on ten quantitative characters were recorded on five competitive plants of each genotype selected randomly in each replication. Data were collected on number of nodes (upto end including the first flowering node), days to 50% flowering, plant height (cm), number of branches per plant, stem diameter (cm), diameter of edible fruit (cm), number of fruits per plant, internodal length (cm), fruit weight (g), fruit yield per plant (g).

Data analysis

Genetic diversity between groups was estimated by using D² statistics given by Mahalanobis (1936) following the procedure

given by Rao (1952). The mean values were computed to calculate D2 values between all possible pairs of genotypes. The grouping of genotypes was done using Tocher's method as described by Rao (1952). Genetic diversity in okra germplasm with the practice of cluster analysis had earlier been stated by several researchers (Akotkar *et al.*, 2010; Umrao *et al.*, 2014; Seth *et al.*, 2016).

Results and Discussion

Genetic divergence among 30 genotypes for 10 characters was made by using Mahalanobis D2 analysis as per Rao (1952). Based on Mahalanobis D2 analysis, 30 genotypes were grouped into six clusters, on the basis of observed smaller D2 values among genotypes within a cluster than those belonging to different cluster following Tocher's methods (Fig. 1). Out of the six clusters, Cluster II contains maximum number of 11 genotypes followed by cluster I with 10 genotypes, cluster III with 4 genotypes and cluster V with 3 genotypes while cluster IV and VI have 1 genotype each. The six different clusters with respective cultivars and their numbers are presented in Table 1. It is indicating that Cluster IV and cluster VI are more diverse from resting other clusters. The genotypes in these clusters are more genetically diverse and may be used as potential parents for breeding programmes to develop high yielding cultivars. It was also observed that geographical distance between the genotypes had no relation with the genetic divergence as the genotypes from same source had fallen into different clusters as well as the same cluster contained genotypes from different sources. It indicates that clustering pattern of okra genotypes did not follow their geographic distribution. These findings are in agreement to earlier reports of Bindu *et al.*, (1994), Mishra *et al.*, (1996), Dhaduk *et al.*, (2004), Reddy *et al.*, (2012), Ab.Mazid *et al.*, (2013) in okra.

Widely varied inter-cluster distances in the six clusters of okra cultivars are shown in Table 2. Average intra and inter cluster D2 values, indicating nature of genetic divergence at intra and inter cluster levels, respectively. The D2 values of intra cluster and inter cluster ranged from 0.0 to 71.80 and 35.94 to 360.94 respectively. Maximum intra cluster distance was observed in cluster III (71.80) followed by cluster V (59.37) and minimum intra cluster distance in cluster IV and VI. Inter cluster distance was maximum in between cluster III and cluster V (360.94) followed by cluster IV and V (334.82) and cluster I and VI (263.90) while minimum inter cluster distance was observed in cluster I and IV (35.94) followed by cluster I and II (57.02) and cluster III and VI (128.0). In general, inter cluster distance was much more than intra cluster distances. This suggesting that within cluster genotypes have same genetic constitution i.e., homogeneous are less divergent than those occurred in a different cluster.

Therefore, genotypes belonging to these inter clusters may be used in hybridization programme to obtain transgressive segregants with broad spectrum of genetic variability for yield and other component traits to isolate high yielding genotypes in okra. These results are in accordance with the finding of Vahab *et al.*, (1994), Bisht *et al.*, (1995), Mishra *et al.*, (1996). Outcrossing the cultivars featuring in these clusters could enhance transgressive segregations and generation progress. This has been as earlier opined by Umrao *et al.*, (2014) and Seth *et al.*, (2016). Conclusively, an involvement of highest yielding cultivars, could be exploited directly or hybridized to enhance novel recombinants and exploit transgressive segregates with high genetic yield potentials.

As high yield and earliness is a prime objective in any breeding programme, cluster those having high means for fruit yield per

plant, and its components traits need to be considered for selection of genotypes for breeding programme. The cluster means for 10 characters (Table 3) indicated that considerable variability present in characters among the six clusters. The data showed that

maximum cluster mean variation was observed for fruit yield per plant (174.7 g in cluster V to 350.14 g in cluster III), average weight of fruit (7.667 g in cluster IV to 10.033 g in cluster VI) and fruits/plant (20.83 in cluster V to 40.03 in cluster III).

Table.1 Six different clusters with respective cultivars and their numbers

Sr. No. Cluster	No. of genotypes	Name of genotype										
		HRB-114-1-1	HRB-122-1-1	HRB-109-1-1	HRB-138-1-1	HRB-105-1-1	HRB-147-1-1	HRB-163-1-1	HRB-162-1-1	HRB-151-2-1	HRB-141-2-1	
1.	10											
2.	11	HRB-143-2-2	HRB-140-2-1	HRB-119-1-1	HRB-108-1-1	HRB-151-1-1	HRB-152-1-1	HRB-113-1-1	HRB-140-2-2	HRB-141-1-1	HRB-124-3-1	HRB-106-1-1
3.	4	HRB-146-1-1-2	HRB-108-2-2	HRB-107-4-1	HRB-153-2-1							
4.	1	HRB-141-1										
5.	3	HRB-132-1-1	HRB-130-1-1	HRB-147-2-1								
6.	1	HRB-124-1-1										

Table.2 Average Intra (diagonal) and Inter cluster distance (D2) for okra genotypes

	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster
1 Cluster	20.71	57.02	183.43	35.94	104.27	263.90
2 Cluster		34.30	102.81	101.14	212.47	228.34
3 Cluster			71.80	216.26	360.94	128.00
4 Cluster				0.00	65.86	233.27
5 Cluster					59.37	334.82
6 Cluster						0.00

Table.3 Cluster mean for different characters in 30 okra genotypes by Tocher method

Cluster	Plant Height cm	Branches /Plant	Stem Diameter (cm)	Nodes (1st Flowering Node to End)	Days to 50% Flowering	Diameter of Edible Fruit (cm)	Fruits /Plant	Internodal Length (cm)	Fruit Weight (g)	Fruit Yield/ Plant (g)
1 Cluster	98.960	4.898	1.821	12.497	43.700	1.500	28.493	5.530	8.510	242.037
2 Cluster	99.327	5.279	1.862	14.755	44.636	1.461	35.504	5.258	8.206	291.552
3 Cluster	98.192	3.963	1.770	16.592	43.250	1.217	40.039	5.383	8.775	350.142
4 Cluster	92.633	3.533	1.740	8.000	46.000	1.400	26.467	5.100	7.667	203.367
5 Cluster	97.644	3.422	1.761	9.433	43.333	1.322	20.833	4.989	8.422	174.667
6 Cluster	107.600	2.000	2.593	17.367	47.000	1.467	33.267	5.633	10.033	332.967

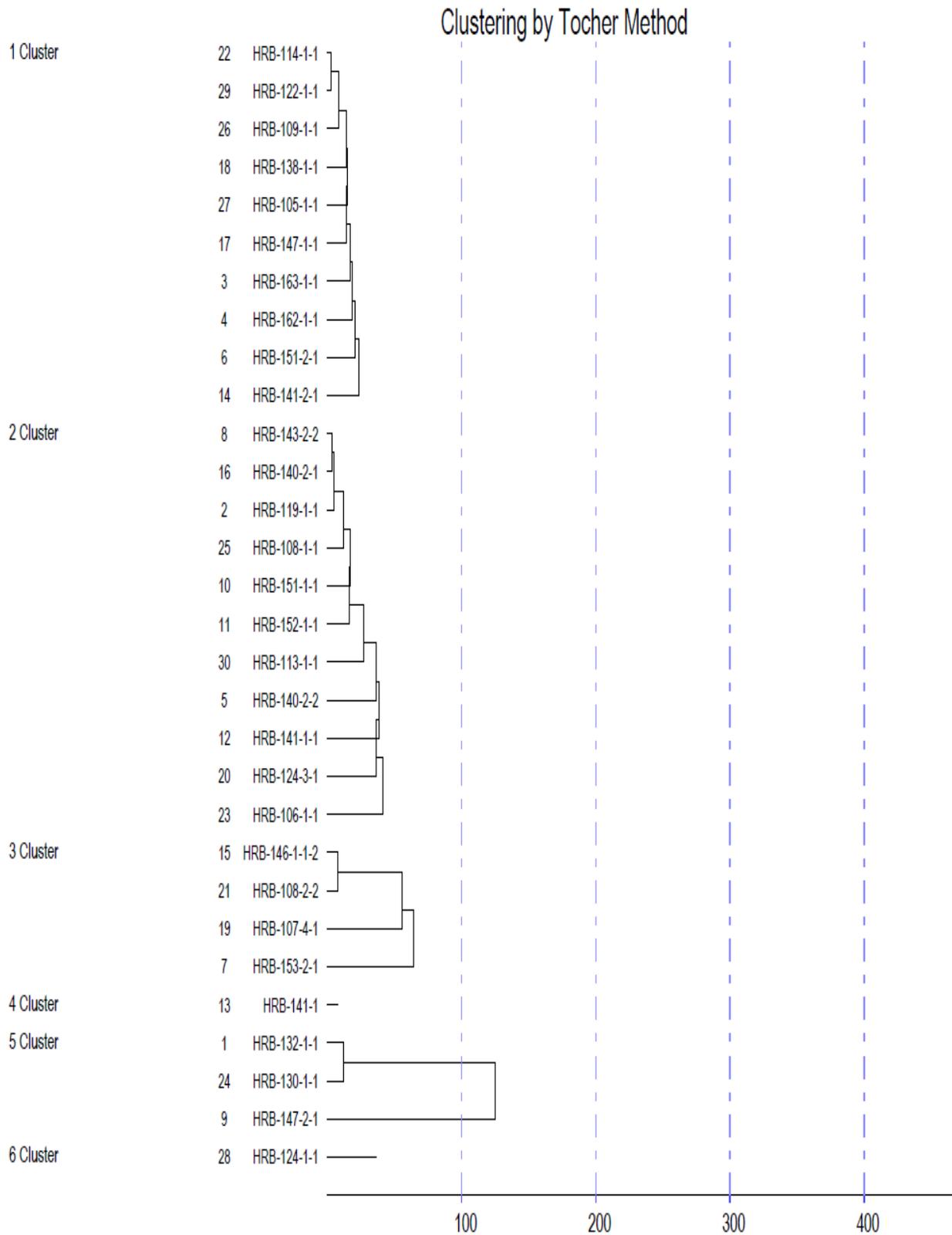
Table.4 Percent contribution of different traits in total variation

Source	Contribution %	Times Ranked 1 st
1 Plant Height cm	0.23	1.000
2 Branches /Plant	41.61	181.000
3 Stem Diameter (cm)	1.61	7.000
4 Nodes (1st Flowering Node	8.97	39.000
5 Days to 50% Flowering	0.69	3.000
6 Diameter of Edible Fruit	0.23	1.000
7 Fruits /Plant	15.17	66.000
8 Internodal Length (cm)	0.01	0.000
9 Fruit Weight (g)	0.01	0.000
10 Fruit Yield/ Plant (g)	31.49	137.000

Table.5 Principal component analysis of the 30 okra genotype showing the factor scores, Eigen values and percentage total variance accounted by the four principal component axes

	PC1	PC2	PC3	PC4
Plant Height cm	0.199	0.052	0.790	0.191
Branches /Plant	0.236	-0.462	-0.052	0.061
Stem Diameter (cm)	-0.072	0.429	0.292	0.305
Nodes (1st Flowering Node to End)	0.432	0.217	0.161	-0.017
Days to 50% Flowering	-0.311	0.381	-0.162	0.133
Diameter of Edible Fruit (cm)	-0.176	0.056	0.321	-0.895
Fruits /Plant	0.445	0.183	-0.277	-0.130
Internodal Length (cm)	-0.397	0.239	-0.085	0.003
Fruit Weight (g)	0.129	0.504	-0.134	-0.101
Fruit Yield/ Plant (g)	0.461	0.244	-0.175	-0.144
Eigene Value (Root)	3.414	3.215	1.239	0.915
Partial variance (%)	34.140	32.153	12.392	9.151
Cum. Var. Exp. (%)	34.140	66.293	78.685	87.836

Fig.1 Dendrogram showing distribution of 30 okra genotype based upon 10 quantitative traits



It was observed that cluster VI genotype has highest desirable cluster mean for six characters followed by cluster III for two characters, one character in each cluster II and cluster. Cluster VI recorded highest mean for plant height (107.60 cm), stem diameter (2.593 cm), number of nodes per plant (1st flowering node to end) (17.36), days to 50% flowering (47.0), internodal length (5.63 cm), and fruit weight (10.03 g). Cluster III recorded highest desirable cluster mean for fruits per plant (40.03), fruit yield per plant (350.14 g). Cluster I and cluster II have desirable cluster mean for diameter of edible fruit (1.50 cm) and branches per plant (5.28) respectively. Therefore, divergent genotypes should be selected from the clusters III and VI for hybridization programme.

An assessment of relative contribution of ten characters towards total genetic divergence (Table 4) revealed that branches per plant had contributed highest (41.61 %) by taking 181 times first ranking followed by fruit yield per plant (31.49 %) by 137 times, fruits per plant (15.17 %) by 66 times, nodes (1st Flowering node to end) (8.97) by 39 times, stem diameter (1.61) by 7 times, It suggested that these characters are highly genetic variable and these characters should be considered while selecting parents for hybridization programmes under studied genotypes. John *et al.*, (1992), Abdul *et al.*, (1994), Kumari and Chaudhury (2006), also observed contribution of plant height, fruit length and weight of fruits towards the genetic divergence. with contrast to this plant height cm, Days to 50% flowering, diameter of edible fruit, internodal length (cm) and fruit weight (g) had very low contribution as 0.23 %, 0.69 %, 0.23 %, 0.01 % and 0.01 % respectively. The cumulative proportion of variation explained by the four PC-axes, 87.836% (Table 5) compared well with observations made by Campos *et al.*, (2005) and Ogunbayo *et al.*, (2005) that the PC-axes contributed 76.62 and 64.5%

variations, respectively. Similarly, Ahiakpa *et al.*, (2013) reported that the first four PC- axis contributed 82.97% of the variations in okra. Branches per plant, nodes (1st flowering node to end), days to 50% flowering, internodal length, fruits per plant and fruit yield contributed to the variation in PC1. Branches per plant, stem diameter, nodes (1st flowering node to end), days to 50% flowering, internodal length, fruit weight and fruit yield accounted for the variations observed in PC2. Plant height, stem diameter, diameter of edible fruit and fruits per plant contributed to the variations in PC3. Stem diameter and diameter of edible fruit contributed to variations in PC4. These variations may suggest the existence of genetic diversity in okra that can be harnessed to improve the crop. Similar observation was made by Yonas *et al.*, (2014).

The present study was carried out to examine the nature and magnitude of genetic divergence in 30 genotypes of okra. A better understanding of the extent of genetic diversity among okra germplasms is necessary for planning selection programme aimed at improvement of yield. Realizing the importance of developing high yielding okra genotypes, the present study was undertaken to assess the genetic diversity of okra germplasms for various agro-morphological traits. From the above findings it can be concluded that, genotypes from high divergent clusters contain wide genetic diversity for different traits under studied, are expected to yield potential F1s and transgressive segregants for further exploitation and hence, these findings are in conformity with earlier reports of Hazara *et al.*, (2002) and Bendale *et al.*, (2003)

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