Bangladesh J. Bot. **45**(1): 47-53, 2016 (March)

GENETIC DIVERGENCE FOR YIELD AND YIELD COMPONENTS IN ADVANCED BREEDING LINES OF OKRA

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Key words: Okra, Principal component analysis, Genetic diversity

Abstract

Fourty okra genotypes were subjected to the principle component analysis (PCA) and hierarchical cluster analysis (HCA) to estimate the existed genetic diversity for yield contributing characters. The first six principle components having Eigen value more than one and cumulatively contributing 74.93% to the total variability were selected. The PC1 added highly 26.72% to the total variability with significant loading of days to 50% flowering, days to first harvest and days to first flowering indicating these characters contributed maximum to the total variance. HCA revealed that the okra genotypes had considerable diversity and were classified into five divergent clusters. Among the five clusters, cluster 2 had highest number of genotypes (13) whereas cluster 5 had least number of genotypes (3). Clusters 1, 3 and 4 were having 10, 6 and 8 genotypes, respectively. It also indicated that geographical origin had no role in the diversity among the available germplasm.

Introduction

Okra is one of the important vegetables of the tropical and subtropical regions of the world and is native to tropical Africa. Okra is highly nutritious and grown during summer and rainy seasons in all parts of the country. India is the largest producer of okra with area, production and productivity of 0.23 mha, 6.35 mt and 27.5 t/ha, respectively for the year 2012-2013 (Anon. 2014). The young tender pods of okra are being used as fresh vegetable, canned, dehydrated and frozen products. When ripe, the black or white eyed seeds are sometimes roasted and used as a substitute for coffee in Turkey (Sharma and Prasad 2010). The mucilaginous extract of okra is used for clarification of sugarcane juice while manufacturing brown sugar (Prasad and Nath 2002). Genetic diversity is one of the important tools to quantify genetic variability in both cross and self pollinated crops (Sharma and Prasad 2010). Numerous approaches are being used in estimation of genetic diversity among various genotypes. Principle component analysis (PCA) is a descriptive method which shows the pattern of covariation of characters among the individuals (Rhodes and Martins 1972). PCA produces Eigen vectors for each principle component axis and removes highly inter-correlated nature of prevalent variations. Thereby reduces the dimensions of multivariate data. The character loadings will be useful in determination of component scores and allows a multidimensional relationship to be plotted on two or three principle axes (Hayman 1967, Ariyo 1993, Nwangburuka *et al.* 2011). However, PCA alone is not sufficient to study the genetic diversity among the available germplasm unless it is accompanied with cluster analysis which classifies the genotypes into different divergent clusters. Such a study permits the selection of genetically divergent parents to obtain highly heterotic hybrids (Moll *et al.* 1962) and desirable recombinants in the segregating generations (Sharma and Prasad 2010). Moreover, it allows confirming the role of geographic origin in diversity among the available germplasm. Hence, the

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present work was undertaken with the objective of identifying potential parental lines employing the combined technique of PCA and cluster analysis through Ward's minimum variance technique.

Materials and Methods

The present study was carried out at the research farm of the Department of Vegetable Science, Chaudhary Charan Singh Haryana Agricultural University, Hisar during summer season 2011 and 2012 laid out in RBD with three replications. The genetic material consists of 40 okra advanced breeding lines (Table 2) developed by using parents collected from different places as well as lines collected from different localities. In each replication each genotype was grown in a double row plot accommodating 18 plants with row-to-row spacing of 30 cm and plant-to-plant spacing of 10 cm. Due to low vegetative growth during summer and non branching habit of genotypes lesser spacing was followed between the plants. Two seeds per hill were sown and later thinned to one plant per hill. The recommended package of practices was followed. Necessary plant protection measures were carried out uniformly to safe guard the germplasm lines. Observations were taken on 15 quantitative characters. The data on quantitative characters were recorded on five competitive and randomly selected plants in each genotype and in each replication, except days to first flowering, days to 50% flowering, days to first harvesting, number of fruits per plant, fruit weight and fruit yield per plant which were recorded on whole genotype basis. The principle components (PCs) were calculated by using the method suggested by Gower (1966). The mean genotype scores were applied to the hierarchical cluster analysis (HCA) by Ward's minimum variance method to classify the genotypes into clusters (Ward 1963). The software employed were SAS v 9.3 for calculating the PC scores and MINITAB v 16 for clustering of genotypes.

Results and Discussion

The Eigen values, per cent contribution of variance and variable loading of six PCs were presented in Table 1. It was observed that the first six PCs accounted for 74.93% cumulative variance were considered out of 15 and remaining were discarded as they were having Eigen values less than one as per Kaiser criterion given by Kaiser (1960). Thus, the reduced dimensionality descriptor space was six and the characters associated with these were used in differentiating the okra accessions. These observations were supported by Ariyo (1993), Sharma and Prasad (2010) and Nwangburuka *et al.* (2011). The relative discriminating power of the PCA as revealed by the Eigen values was high in PC1 (4.009) and lower in PC6 (1.031). The PC1 added highly 26.72% to the total variability with significant loading of days to 50% flowering (0.459), days to first harvest (0.459) and days to first flowering (0.453) which were positively correlated. Hence, it can be said that these characters contributed maximum to the total variance. The PC 2 contributed 14.24% to the total variance having positive correlation with fruit yield per plant (0.496), fruits per plant (0.473) and plant height (0.382) and first fruiting node (0.375), which were loaded significantly. PC3 donated 10.35% variance to the total variance. The character, seeds per fruit (0.352) was loaded significantly with PC3 and was positively correlated. While the characters branches per plant (–0.553) and fruit diameter (–0.452) loaded and correlated negatively. PC4 loaded and correlated positively with intermodal length (0.553) and test weight (0.500) and it had 9.27% of total variation. PC5 with 7.48% of total variation significantly loaded with fruit weight (0.677), which was positively correlated. PC6 made least contribution of 6.87% to the total variance among six PCs. Fruit length (0.555) significantly loaded and positively correlated while stem diameter (–0.598) loaded and correlated negatively with PC6. These

observations were in agreement with Ariyo (1993), Sharma and Prasad (2010) and Nwangburuka *et al.* (2011).

Table 1. Eigen values, percentage of variation and variable loadings of six PCs among 40 genotrypes of okra.

PCs	Eigen value	Variation (%)	Variable loadings
1	4.009	26.72	Days to 1st flowering (0.453), days to 1st harvesting (0.459), days to 50% flowering (0.459)
2	2.136	14.24	Plant height (0.382), first fruiting node (0.375), fruits per plant (0.473), fruit yield per plant (0.496)
3	1.552	10.35	Seeds per fruit (0.352), branches per plant (–0.553), fruit diameter (–0.452)
4	1.390	9.27	Internodal length (0.553), 100 seed weight (0.500)
5	1.122	7.48	Fruit weight (0.677)
6	1.031	6.87	Stem diameter (–0.598), fruit length (0.555)

Loading of 15 characters and component scores of genotypes on principle axes 1 and 2 were presented in Figs 1 and 2, respectively. By comparing the loading and score plot one can identify the relationship between characters and genotypes as these two plots are complimentary and superimposable to each other. On loading plot sit together behavior of similar characters was observed. Similarly sit together behavior of similar genotypes was also observed in scoring plot.

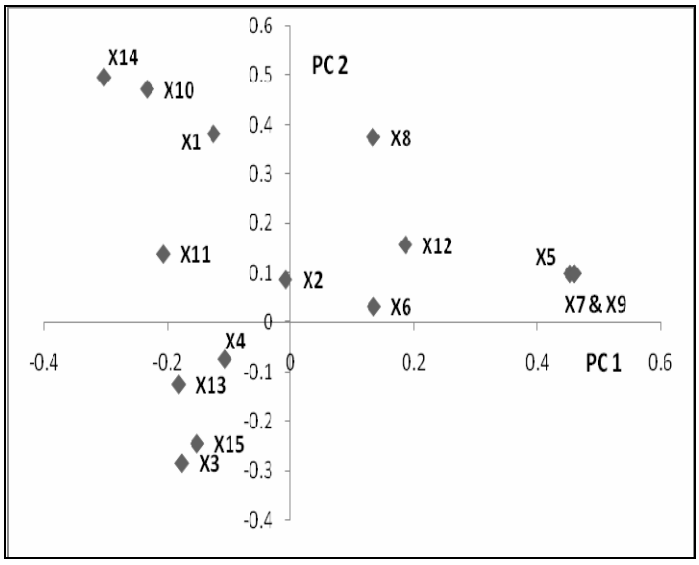

Fig. 1. Loading of 15 variables (Characteristics) on principle axes 1 and 2 (loading plot).
X1: Plant height, X2: Stem diameter, X3: Seeds per fruit, X4: Intermodal length, X5: Days to first flowering, X6: Branches per plant, X7: Days to first harvesting, X8: First fruiting node, X9: Days to 50% flowering, X10: Fruits per plant, X11: Fruit weight, X12: Fruit diameter, X13: Fruit length, X14: Fruit yield per plant, X15: Test weight

Maturity characters *viz.*, days to first and 50% flowering, days to first harvest and first fruiting node were present in 1st quadrant of loading plot. Correspondingly in the first quadrant of scoring plot genotypes with late flowering Raj-12 and HB-02-14-1-1 and maximum first fruiting node HBT-49-1, HB-02-17-1 and Raj-12 were present. Second quadrant of loading plot contains important yield characters such as plant height, fruits per plant, fruit weight and fruit yield per plant. Genotypes with maximum fruits per plant HBT-21, HBT-19-1, genotype with high fruit weight HBT-47 and genotype with maximum plant height and fruit yield per plant HBT-21 was present in the analogous 2nd quadrant of scoring plot. Seed characters such as seeds per fruit and test weight were present in 3rd quadrant of loading plot. Genotypes with maximum number of seeds per fruit and test weight Lam Selection-1 and Parbhani Kranthi were present in the equivalent 3rd quadrant of scoring plot.

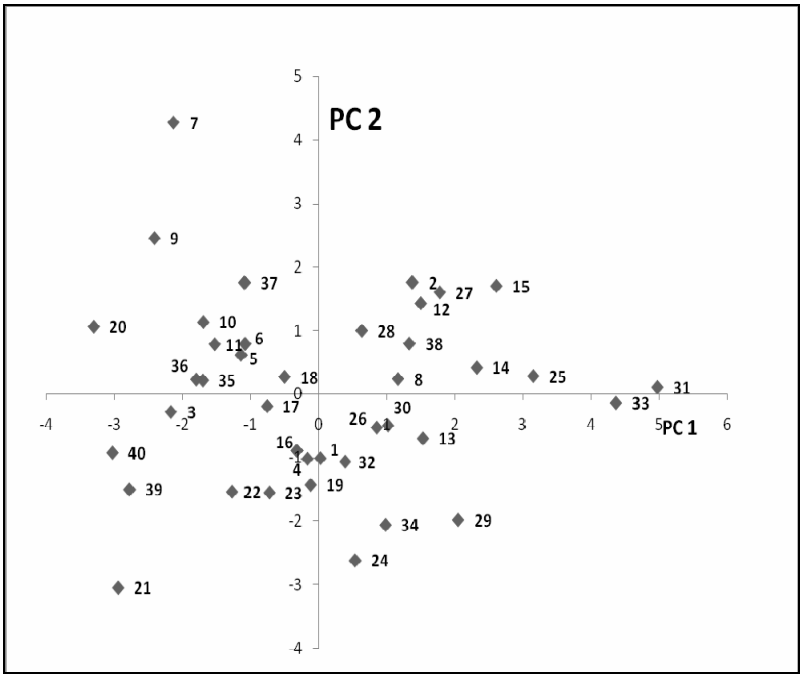

Fig. 2. Loading of okra genotypes component scores on principle axes 1 and 2 (score plot).
In score plot numbers 1 to 40 indicate the genotypes in Table 2.

Classification of okra genotypes was done by applying the principle component scores of the genotypes to the HCA. The dendrogram (Fig. 3) showed that at 100% similarity, all the genotypes were fallen in different clusters and when near about 40% similarity was considered all the fourty genotypes were classified into five divergent clusters (Table 2) indicating the existence of considerable diversity among the genotypes under study. Sharma and Prasad (2010) also classified 20 okra genotypes into five clusters by applying HCA to the PC scores. Among the five clusters, cluster 2 had highest number of genotypes (13) where as cluster 5 had least number of genotypes (3). Clusters 1, 3 and 4 were having 10, 6 and 8 genotypes, respectively. The clustering pattern of genotypes indicated that genotypes developed by using parents from different sources and genotypes collected from different places had the tendency to fall in different clusters. Moreover,

certain genotypes probably having same pedigree were merged into different clusters. This indicated there was no association between clustering pattern and eco-geographical distribution of genotypes, which was supported by the previous studies of Ghai *et al.* (2005), Ramya and Senthil kumar (2009) and Koundinya *et al.* (2013).

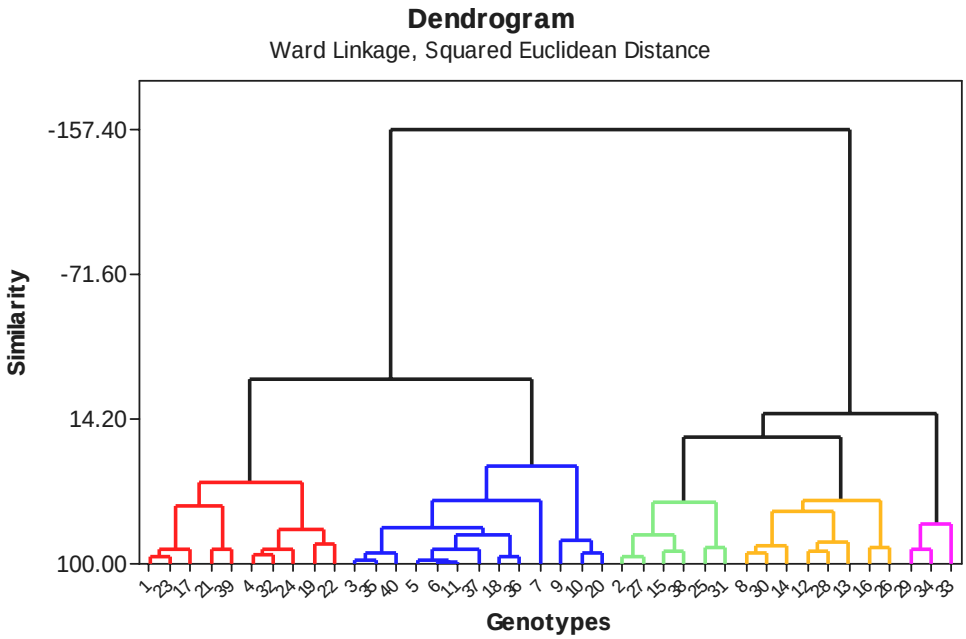

Fig. 3. Ward's minimum variance dendrogram classifying 40 genotypes of okra.

Statistical distance represents the extent of genetic diversity among clusters. The inter- and intra-cluster squared ecluidean distances of five clusters were presented in Table 3. The least intra cluster distance was observed in cluster 5 followed by cluster 3 signifying the genotypes within these clusters were less variable genetically and the highest intra cluster distance was found in cluster 2 followed by cluster 1. The highest inter cluster distance was observed between clusters 2 and 5 followed by cluster 2 and 4 and clusters 1 and 2 revealing the existence of divergence genotypes that fall in these clusters. The involvement of genotypes belonging to these clusters in hybridization would help in achieving highly heterotic hybrids or novel recombinants in segregating generations. Similar observations were reported in okra by Ghai *et al.* (2005), Dhankhar *et al.* (2008) and Koundinya *et al.* (2013). The least inter-cluster distance was found between clusters 1 and 4 followed by clusters 4 and 5 indicating close relationship among the genotypes included in these clusters.

Cluster-wise mean values of various characters were presented in Table 4. Cluster 2 had highest mean values for all the important yield components like plant height, number of fruits per plant and fruit yield plant and lower values for earliness characters like days to flowering and harvesting. Cluster 5 had the lowest mean values for number of fruits per plant, average fruit weight, fruit length and fruit yield plant and late maturity.

Table 2. Classification of genotypes into five clusters.

Clusters	Genotypes	Genotypes
1	10	HB-02-14-2 (Hisar), HB-02-14-1 (Hisar), HBT-36 (Hisar), Lam Selection-1 (Guntur), Parbhani Kranthi (Parbhani), HB-03-23-1 (Hisar), Pusa Sawani (New Delhi), HB-03-20-5-1 (Hisar), HB-03-29-7C (Hisar), HB-57 (Hisar)
2	13	HB-03-26-1 (Hisar), HRB-146-2-1 (Hisar), Varsha Upahar (Hisar), HBT-19-1 (Hisar), HBT-6 (Hisar), HBT-15 (Hisar), HB-06-1 (Hisar), VRO-6 (Varanasi), HBT-21 (Hisar), HBT-47 (Hisar), HBT-16 (Hisar), HB-92 (Hisar)
3	6	HB-02-17-1 (Hisar), HB-06-1-6 (Hisar), HB-03-20-5 (Hisar), HBT-49-1 (Hisar), JNDOL-05 (Junagarh), HB-02-14-1-1 (Hisar), Raj-12 (Rajasthan)
4	8	HBT-40 (Hisar), JNDOL-03 (Junagarh), HBT-3 (Hisar), HBT-1 (Hisar), HB-03-20-5-3 (Hisar), HBT-1-1 (Hisar), HCT (Hisar),HB-03-20-5-2 (Hisar)
5	3	HBT-1-19-1 (Hisar), HB-03-25-1-5 (Hisar), HB-03-25-1 (Hisar)

Table 3. Average inter- and intra-cluster (bold) distances.

Clusters	1	2	3	4	5
1	**4.012**				
2	7.988	**4.756**			
3	6.067	6.921	**3.434**		
4	5.163	8.151	6.230	**3.845**	
5	5.504	8.491	6.570	5.340	**2.687**

Table 4. Cluster-wise mean values of 15 characters in okra.

Cluster No.	Plant height (cm)	Stem diameter (cm)	Internodal length (cm)	Branches per plant	Days to 1st flowering	Days to 50% flowering	Days to 1st harvesting
1	119.7	1.10	5.03	2.41	41.2	44.0	50.0
2	132.4	1.11	5.01	2.54	40.6	43.4	49.4
3	123.1	1.09	4.78	2.64	46.1	48.9	54.9
4	110.6	1.12	4.01	2.66	42.6	45.8	51.8
5	115.0	1.16	5.78	2.82	45.7	48.4	54.4

First fruiting node	No. of fruits per plant	Avg. fruit weight (g)	Fruit length (cm)	Fruit diameter (cm)	Fruit yield per plant (g)	No. of seeds per fruit	100 seed weight (g)
4.0	12.9	7.70	9.03	1.34	99.6	61.5	6.51
4.2	17.3	7.88	8.96	1.37	135.9	56.1	6.56
4.6	13.5	7.96	8.82	1.40	107.5	49.9	5.95
4.3	14.3	7.41	8.83	1.45	105.4	54.3	5.87
3.8	12.9	6.76	8.62	1.41	87.5	52.2	7.35

It could be concluded from the present experiment that the first 6 PCs contributed maximum to the total variability and these could be used in distinguishing okra genotypes. Loading of days to 50% flowering, days to first harvest and days to first flowering on to the PC1 with 26.72% variability indicated that these characters contributed maximum to the variability and selection of

genotypes based on these characters would be reliable. The genotypes with maximum values for a given character can be selected from loading and score plots as the characters on loading plot were matched with the genotypes on corresponding quadrant of score plot. Considerable genetic diversity was present among the experimental material as they were classified into five highly divergent clusters and geographic origin did not have any prominent role in the diversity among the available okra germplasm. Involving the genotypes from cluster 2 and 5; 2 and 4; and 1 and 2 in hybridization could yield highly heterotic hybrids and maximum recombination in segregating generations could be expected.

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(Manuscript received on 3 March, 2015; revised on 30 June, 2015)