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Article · January 2018

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DOI No. 10.5958/2395-146X.2018.00023.6

MULTIVARIATE ASSESSMENT OF YIELD AND ITS COMPONENTS IN OKRA [*Abelmoschus esculentus* (L.) Moench] GENOTYPES

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Okra [*Abelmoschus esculentus* (L.) Moench] is a valuable vegetable in many regions of the world, especially in the tropics and sub-tropics. It is not only a nutrient-rich vegetable but also an important medicinal herb (Yuan *et al*., 2014). Although India is the largest producer of okra with 6.35 million tonnes production (72.9% of total world production) from 0.53 million hectare area (Anonymous, 2015), its productivity potential is low. A major constraint in okra productivity is the low genetic potential of the present okra varieties.

Improvement of okra requires a broad spectrum of genetic variability from which useful characters can be selected for developing broad-based populations to be used in hybridization programme (Lester *et al*., 1990; Hammond and Charrier, 1983). Genetic distance estimates form the basis for selecting parental combinations. Genetic distance estimates for population can be estimated by different methods. One of the approaches is to apply multivariate analysis as it has extensive use in summarizing and describing the inherent variation among crop genotypes. Multivariate statistical tools include Mahalanobis D^2 analysis, cluster analysis, principal component analysis (PCA) and discriminate analysis (Oyelola, 2004). Mahalanobis D^2 multivariate analysis (Mahalanobis, 1936) for obtaining quantitative estimates of genetic divergence and Tocher's method for grouping of different genotypes of a particular crop are more valuable tools in choosing suitable parents for heterosis breeding. PCA can be used to uncover similarities between variables and classify the genotypes. With this backdrop, an attempt was made in the present study to assess the nature and magnitude of genetic divergence of some okra genotypes consisting of advanced breeding elite lines developed at Indian Institute of Horticultural Research (IIHR), Bangalore using various multivariate analysis tools.

Experimental material consisted of seven elite okra genotypes (IIHR-285, IIHR-291, IIHR-294, IIHR-296, IIHR-299, GMS-1 and GMS-4) developed at IIHR and five popular varieties (VRO-6, Parbhani Kranti, Arka Anamika, JNDO-5 and Varsha Uphar). GMS-1 and GMS-4 were genic male sterility lines. In total, twelve genotypes were raised in randomized block design (RBD) with three replications at spacing of 20cm X 30cm in paired row at vegetable breeding plot, IIHR, Bangalore during Kharif season of 2013. Recommended agronomic practices and need based plant protection measures were followed. Data were recorded on five random plants for fifteen characters namely days to first flowering (DFF), days to first harvest (DFH), node at first flower appeared (NFF), plant height (PH) (cm), internodal length (INL) (cm), number of branches per plant (NB/P), final stem girth (FSG) (cm), average fruit weight (AFW) (g), number of fruits per plant (NF/P), total yield per plant (TY/P) (g), marketable yield per plant (MY/P) (g), marketable yield/ha (MY/ha) (t), fruit length (FL) (cm), fruit girth (FG) (cm) and number of ridges per fruit (NR/F). Mean values of five plants were used for multivariate analysis using Windostat Biometrical Tool version 12. The genetic divergence in the experimental material was assessed by applying Mahalanobis D^2 statistic (Mahalanobis, 1936). Grouping of genotypes into different clusters was carried out by adopting Tocher's procedure (Rao, 1952). The PCA analysis reduces the dimensions of multivariate data to a few principal axes, generates an Eigen vector for each axis and produces component scores for the characters (Ariyo *et al.,* 1991).

On the basis of Mahalanobis D^2 analysis, 12 genotypes were grouped into 4 clusters (Table 1). Cluster 1 was the largest group that included 7 genotypes followed by cluster 3 comprising of 3 genotypes. Cluster 2 and 4 remained monogenotypic. All the genotypes and varieties released from the same institute did not fall into same cluster, instead they distributed among different clusters. Cluster 1 accommodated most of the elite genotypes developed at IIHR along with VRO 6 and Varsha Uphar which are respectively from IIVR, Varanasi and HAU, Hissar. Genotypes IIHR-299 and IIHR-294 although developed from the same institute formed two different clusters. It indicated that genotypes of cluster 2 and cluster 4 are more diverse from other clusters. It was also observed that geographical distance between the genotypes had no relation with the genetic divergence because the genotypes from same source had fallen into different clusters as well as the same cluster contained genotypes from different sources. These findings are in agreement with earlier reports of Akotkar *et al*. (2010) and Reddy *et al*. (2012) on okra.

Average intra and inter cluster distances (Table 2, Fig. 1) indicated nature of genetic divergence. The values of intra cluster and inter cluster distances ranged from 28.27 to 37.82

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Date of receipt : 12.07.2017, Date of acceptance : 29.12.2017

Table 1. Clustering of 12 okra genotypes using Tocher's method

Cluster No.	Number of okra genotypes	Name of genotype
Cluster 1	7	GMS -4, Varsha Uphar, VRO 6, IIHR -285, IIHR -291, GMS -1, IIHR -299
Cluster 2	1	IIHR -296
Cluster 3	3	Arka Anamika, JNDO 5, Parbhani Kranti
Cluster 4	1	IIHR -294

and 43.02 to 109.74, respectively. In general, inter cluster distance was much more than intra cluster distance suggesting that genotypes within the cluster were less divergent than those in a different cluster. Reddy *et al*. (2012) and Prakash and Pitchaimuthu (2010) also estimated higher inter cluster distances compared to intra cluster distances. Maximum intra cluster distance was observed in cluster 3 (37.82), while inter cluster distance was maximum between cluster 2 and cluster 3 (109.74) followed by cluster 1 and cluster 3 (98.17). Cluster 2 was monogenotypic with IIHR-296, while cluster 3 composed of Arka Anamika, JNDO 5 and Parbhani Kranti, which were developed at different institutes and contributed to their maximum intra and inter cluster divergence. The cluster means of 15 quantitative characters (Table 3) also revealed that cluster 3 showed the highest mean values for characters like TY/P (160.1g), MY/P (131.56g), MY/ha (15.55t), AFW (19.28g) and PH (118.87cm) and lowest mean values for earliness characters like DFF (39.89), DFH (43.33) and NFF (3.15). Selection of genotypes from divergent clusters with high mean values for earliness, yield and its components for use in crossing programme would give greater chances of obtaining high heterosis and high genetic variability for quantitative and other desirable traits in segregating generations. In the present investigation, it was revealed that hybridization between the genotypes of divergent cluster 2 and cluster 3 would give high yielding cultivars in okra.

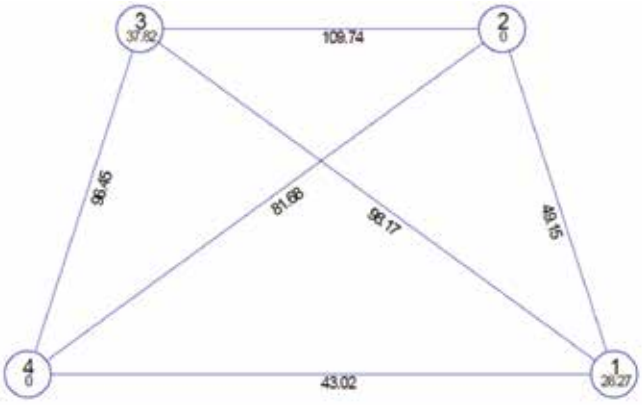

Fig. 1. Mahalanobis Euclidean distances (not to the scale)

Principal component analysis measures the importance and contribution of each component to total variance. Principal components (PCs) with Eigen value > 1.0 are considered more informative than a single variable. Different morphological traits contribute for total variation calculated for each component. In the present investigation, PCA reduced the original 15 morphological characters to 5 PCs with Eigen values > 1 (Table 4). These five PCs explained 92.06% of total existing variability. PC1 (42.50%) contributed more than PC2 (22.68%), PC3 (10.30%), PC4 (8.76%) and PC5 (7.82%). First 3 PCs contributed 75.48 % of the total variation. Characters like DFF, INL, FSG, TY/P, FL and FG were important contributors for PC1; FSG, MY/ha and NR/P for PC2 and NFF, NB/P, TY/P and MY/P were important for PC3. Thus the results of PCA used in the study have revealed high level of genetic variation and the traits contributing for the variation were identified. Ijaz *et al.* (2015) and Shivaramegowda *et al.* (2016) also identified the above mentioned traits playing prominent role in classifying the variation in their studies conducted on okra.

In the present study, genotypes from the same institute accommodated into different clusters and those from different sources formed single cluster indicating prevalence of sufficient genetic variability among the okra genotypes under study. Principal component analysis identified that characters like DFF, INL, FSG, TY/P, FL and FG were important contributors to the variation. Inter cluster distances and cluster means revealed that cluster 2 and cluster 3 were most divergent. Therefore, hybridization between the genotypes of cluster 2 (IIHR-296) and 3 (Arka Anamika, JNDO 5, Parbhani Kranti) would give high heterosis for hybrid development and high genetic variability for selection of desirable traits in segregating generations to develop high yielding cultivars in okra.

Table 2. Intra (diagonal bold) and inter (off diagonal) cluster distances of okra genotypes

Cluster No.	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Cluster 1	**28.27**	49.15	98.17	43.02
Cluster 2	49.15	**0.00**	109.74	81.68
Cluster 3	98.17	109.74	**37.82**	96.45
Cluster 4	43.02	81.68	96.45	**0.00**

Table 3. Cluster means of okra genotypes for 15 charaters

Trait*	Cluster 1	Cluster 2	Cluster 3	Cluster 4
DFF	40.48	40.33	36.89	38
DFH	48.9	49.67	43.33	45.33
NFF	3.48	3.28	3.15	4.18
PH	97.38	102.1	118.87	102.87
INL	4.85	3.13	4.98	4.2
NB/P	3.41	3.13	3.24	3.13
FSG	1.95	1.7	1.89	1.86
AFW	19.5	15.2	19.28	17.88
NF/P	17.97	21.67	16.48	21
TY/P	139.34	132.75	160.1	101.97
MY/P	110.76	94.74	131.56	89.17
MY/ha	13.09	11.2	15.55	10.54
FL	14.24	16.19	13.9	16.27
FG	2.06	2.06	1.91	2.13
NR/F	5.17	5.6	5.2	5

*Days to first flowering (DFF), days to first harvest (DFH), node at first flower appeared (NFF), plant height (PH) (cm), internodal length (INL) (cm), number of branches per plant (NB/P), final stem girth (FSG) (cm), average fruit weight (AFW) (g), number of fruits per plant (NF/P), total yield per plant (TY/P) (g), marketable yield per plant (MY/P) (g), marketable yield/ha (MY/ha) (t), fruit length (FL) (cm), fruit girth (FG) (cm) and number of ridges per fruit (NR/F)

Table 4. Eigen value, percent of total variation and component matrix for the principal component axes

Principal components	PC1	PC2	PC3	PC4	PC5	PC6
Eigen value (Root)	6.37	3.40	1.54	1.31	1.17	0.46
% Var. Exp.	42.50	22.68	10.30	8.76	7.82	3.08
Cum. Var. Exp.	42.50	65.18	75.48	84.23	92.06	95.14
Component matrix						
DFF	0.31	0.11	0.12	0.00	0.43	0.27
DFH	0.29	0.28	-0.15	-0.03	0.22	-0.31
NFF	0.24	0.25	0.41	-0.15	0.18	-0.20
PH	-0.29	0.29	0.09	0.06	0.36	-0.06
INL	0.30	-0.27	0.02	0.25	0.21	-0.03
NB/P	0.08	-0.28	-0.45	0.25	0.37	-0.51
FSG	0.31	-0.31	0.07	-0.09	0.07	0.13
AFW	-0.27	-0.14	0.07	-0.50	-0.07	-0.37
NF/P	0.22	0.10	0.03	0.53	-0.45	-0.02
TY/P	-0.33	-0.12	-0.33	0.21	-0.02	0.15
MY/P	-0.04	-0.29	0.56	0.30	-0.15	-0.41
MY/ha	0.13	-0.44	-0.07	-0.34	-0.13	-0.08
FL	0.36	0.08	0.00	-0.18	-0.26	0.01
FG	0.33	-0.05	-0.27	-0.19	-0.11	0.12
NR/F	-0.11	-0.43	0.28	0.05	0.29	0.39

*Days to first flowering (DFF), days to first harvest (DFH), node at first flower appeared (NFF), plant height (PH) (cm), internodal length (INL) (cm), number of branches per plant (NB/P), final stem girth (FSG) (cm), average fruit weight (AFW) (g), number of fruits per plant (NF/P), total yield per plant (TY/P) (g), marketable yield per plant (MY/P) (g), marketable yield/ha (MY/ha) (t), fruit length (FL) (cm), fruit girth (FG) (cm) and number of ridges per fruit (NR/F)

Authors' contribution

Conceptualization of research work and designing of experiments (MP, KMI, HBL); Execution of field/lab experiments and data collection (MB, PGR); Analysis of data and interpretation (PGR, KMI); Preparation of manuscript (MB, MP, PGR)

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