

Characterisation of promising okra genotypes on the basis of Principal Component Analysis

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Abstract

Twenty selected genetically diverse okra strains were evaluated using Principal Component and cluster analysis for the extent of variability and relationship between various economically important traits for the purpose of genetic improvement. The trial was laid out in a randomized block design (RBD). Positive significant correlation for days to 50% flowering (DF) with days to first harvest (DFH), number of pod per plant (NP) with pod yield per plant (PY) and pod yield per plot (PYP) ($P \leq 0.001$) and PY with PYP ($P \leq 0.001$) and negative correlation was observed for pod weight (PW) with NP ($P \leq 0.01$). The analysis of extracted components, component pattern and Eigen values revealed that the first two principal components alone accounted for 53.25% of variance. First component was found heavily loaded with days to 50% flowering (DF), days to first harvest (DFH), pod length (PL), pod diameter (PD) and pod weight (PW), which comprised of fourteen genotypes in three clusters. The matrix obtained from principal component analysis revealed that the genotype Pb- 57 and HRB-9-2 found their positions in same cluster in principal space. Dominating similar prominent phenotypic characters formed separate place in principal space as coherent cluster. Cluster based inter breeding of genotypes would exhibit high heterosis and is also likely to produce new recombinants with desired characters in okra.

Key words: Okra, *Abelmoschus esculentus*, correlation, variance, principal component.

Introduction

Okra [*Abelmoschus esculentus* (L.) Moench] is one of the oldest cultivated vegetable crops. *Abelmoschus* genus contains about 150 known species with *esculentus* as the species of okra (Thompson and Kelly, 1957), also known as lady's finger or gumbo in England (Tindall, 1986) and bhindi in India, is believed to be native to tropical Africa and belongs to family Malvaceae. It is grown in all parts of the tropics during spring, summer and rainy season as kharif crop (Baloch, 1994). It is available all year-round, with a peak season during the summer months (Anon., 2003).

The crop is highly nutritious and also considered as power house of valuable nutrients. This vegetable provides protein, carbohydrate and an important input of vitamins and mineral salts, including calcium; which are often lacking in diet of developing countries. The young tender pods of okra are used in different ways; as boiled vegetables (Magness *et al.*, 1971), fresh, canned, frozen or dried and used as soup thickeners (Tindall, 1986) or cooked in curries, stewed and used in soups. Considerably high quantity of both soluble and insoluble fibre is present in okra. Nearly half of which is soluble fibre in the form of gums and pectin, which helps in lowering the serum cholesterol and thus reducing the risk of coronary heart diseases. The other half is insoluble fibre, which helps to keep the intestinal tract healthy (Jeff, 2002) and prevent the symptom of irritable bowel syndrome (IBS). The mucilaginous extract of okra is often used for clearing the cane juice from which jaggery or brown sugar is manufactured (Prasad and Nath, 2002). The stem of plant provides non digestible strong linear fiber, which finds uses in the paper, packaging and textile industries (Baloch, 1994).

Stability with consistent performance under predictable and unpredictable environment is the main concern in screening

of phenotypically stable genotypes. Large variations among important traits are desirable. To improve particular attribute including yield characteristic information on genetic variability and inter-relationship among different traits is necessary as improvement is proportional to its magnitude of genetic variability present in the germplasm. Genetic diversity is one of the important tools to qualify genetic variability in both cross- and self-pollinated crops (Murty and Arunachalam, 1966; Gaur *et al.*, 1978). Therefore, the present study was undertaken to analyze the genetic divergence in 20 okra genotypes, based on multivariate approach, which is not possible through univariate analysis. The aim was also to find out the characteristic pattern prevailed so as to get divergence information that may be useful for the varietal improvement.

Materials and methods

In pursuance of the envisaged objectives, the present study was carried out with twenty okra genotypes collected from different agro climatic regions of India. Seeds of selected genotypes were planted in randomized block design at three different sowing time scattered uniformly of twenty days interval during the kharif season starting from mid June with three replications. Standard techniques were adopted in data collection for 5 competitive plants in each genotypes on 10 characters *viz.*, plant height (PH), number of branches per plant (NB), days to 50% flowering (DF), days to first harvest (DFH), number of pods per plant (NP), pod length (PL), pod diameter (PD), pod weight (PW), pod yield per plant (PY) and pod yield per plot (PYP).

The data on various genotypes of okra under kharif season was processed using MINITAB v 13.2 and SPSS v 11.0 for multivariate analysis and Microsoft Excel v 2000 for descriptive statistics. The

Principal component and Hierarchical cluster analysis was applied to analyze characteristic pattern to classify the selected genotypes.

Results and discussion

The comparative performance of twenty okra genotypes for variability in different traits was compared as the overall mean response of genotypes in respect of overall performance of genotypes as mean line (Fig. 1). The analysis of variance revealed that the differences in genotypes were significant for characters indicating the presence of variability among them. The results indicated that genotypes, HOE-202 (XIV), BO-2 (X) and Sel.-10 (XII) had the highest plant height (PH) with mean of 133.68, 134.14 and 138.67 cm, respectively. Highest values of number of branches (NB) for Sel.-7, days to 50% flowering (DF) and days to first harvest (DFH) for HOE-301, number of pods per plant (NP) for HRB-9-2, pod length (PL) for Sel. 10, pod diameter (PD) for Pb-57, pod weight (PW) for 71-14 and pod yield per plant (PY) & pod yield per plot (PYP) for HRB 9-2 (Fig. 1). These results may support the varietal improvement program in selecting parents.

Positive significant correlation could be observed (Table 1) for days to 50% flowering (DF) with days to first harvest (DFH), number of pod per plant (NP) with PY and PYP ($P \leq 0.001$) and PY with PYP ($P \leq 0.001$) and negative correlation was observed for pod weight (PW) with NP ($P \leq 0.01$). The strong correlation is indicative for the genotypic character association and the feeble correlation is influenced by environmental factors and limiting the yield (Subramanyan *et al.*, 1995). The results are in agreement with earlier studies on *Hibiscus sabdariffa* L (Banarjee *et al.*, 1988).

The data of observed measurements was subjected to Principal Component Analysis (PCA). The Eigen values given in Table 2 indicate that four principal components (PCs) account for 80.45% of the total variance in the

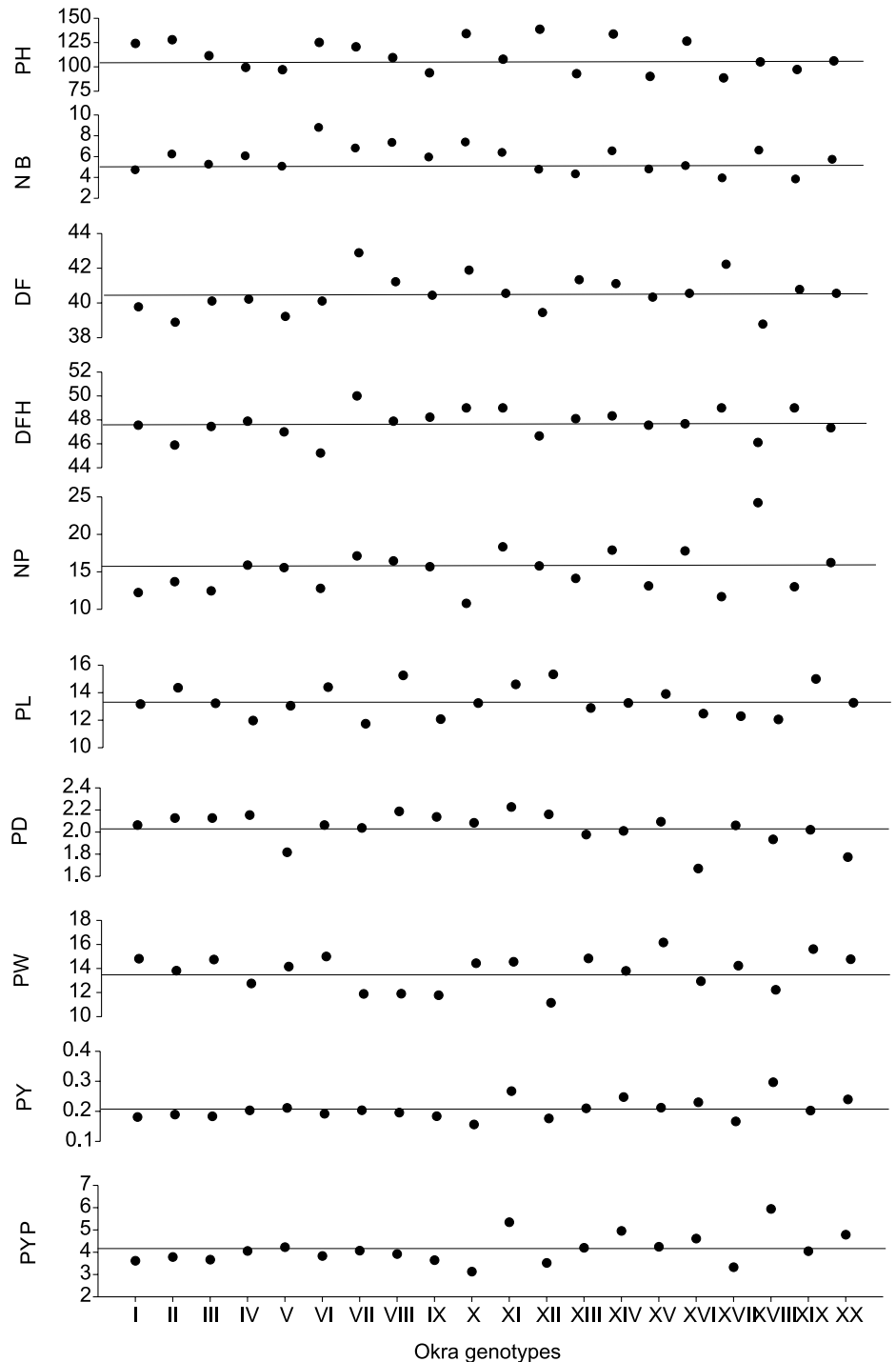


Fig. 1. Characteristic performance of twenty okra genotypes

Table 1. Correlation Matrix of performance variables of okra genotypes

Variables	PH	NB	DF	DFH	NP	PL	PD	PW	PY	PYP
PH	1.000									
NB	0.441	1.000								
DF	-0.077	0.041	1.000							
DFH	-0.211	-0.241	0.816***	1.000						
NP	0.014	0.228	-0.259	-0.120	1.000					
PL	0.264	0.062	-0.236	-0.254	-0.226	1.000				
PD	0.028	0.210	0.066	0.128	-0.258	0.368	1.000			
PW	-0.265	-0.250	0.020	0.004	-0.544**	0.198	-0.109	1.000		
PY	-0.126	0.126	-0.271	-0.116	0.853***	-0.130	-0.354	-0.034	1.000	
PYP	-0.121	0.128	-0.268	-0.116	0.852***	-0.127	-0.356	-0.031	0.999***	1.000

Table 2. Eigen values and their contribution in variation

No.	Eigen value	Individual Percent
1	3.249	32.50
2	2.075	20.75
3	1.666	16.66
4	1.054	10.54
5	0.912	9.12
6	0.656	6.56
7	0.301	3.01
8	0.081	0.81
9	0.003	0.04
10	0.001	0.01

Table 3. Distribution of 20 okra genotypes among four clusters

Group/ cluster No.	No. of genotypes	Genotypes in different cluster
1	3	Vaishali Vadhu (IV), HOE-3019 (VII), HRB-55 (IX)
2	4	BO-1 (II), Sel.-7 (VI), Sel.-4 (VIII), Sel.-10 (XII)
3	7	AROH-1 (I), Sel.-2 (III), BO-2 (X), KS-3 (XIII), 71-14 (XV), NDO-25 (XVII), Sel.-8 (XIX)
4	6	H-1-87-16 (V), Pb-57 (XI), HOE-202 (XIV), D-1-87-5 (XVI), HRB-9-2 (XVIII), Pusa Sawani (XX)

data. The loading of component on principal axes indicated a high degree of genetic diversity among the selected genotypes (Fig. 2). To study the pattern of the attributes and to identify factors that are substantively meaningful, a multivariate approach was used. The loading plots are shown in Fig. 2, for the three principal components. It can be seen that the first component explaining 32.50 % of variance is highly correlated both positively (PD, DF and DFH) and negatively (NP, PY and PYP). Thus it classifies and distinguishes the score of okra genotypes on the basis of these components. The second principal component explaining 20.75% of total variance is highly correlated with DF and DFH in positive direction and with PH, NB, and PL in negative direction. While, the third component has explained only 16.66% of total variance is positively correlated with PW and negatively with PH, NB and DF. Fig. 2 illustrates the biplot of scores and loadings of the three principal components of observed parameters of okra genotypes, which further affects their positions according to their characteristics with respect to the extracted principal components. The Biplot of PC1 and PC2 shows the separation of the okra genotypes according to their respective scores. First and fourth quadrant of the plot contains samples having positive PC1 scores. The genotypes of this quadrant are heavily loaded with days to 50% flowering (DF), days to first harvest (DFH), pod length (PL), pod diameter (PD) and pod weight (PW), which comprised of fourteen genotypes of cluster 1, 2 and 3 (Table 3). Second and third quadrant is expressing samples with negative PC1 scores and heavily loaded mainly with the phenotypic and yield related characters and contains the high yielding promising genotype HRB 9-2. The loading pattern thus obtained with respect to the position of the genotype in principal space may be considered as one of the imperative indicator for finding out the characteristic divergence or similarity, which is essentially required for genetic improvement through breeding.

Hierarchical cluster analysis (HCA) using Ward’s minimum variance using Euclidean distance method (Ward, 1963) as dendrogram is shown in Fig. 3. As a result of applying HCA to

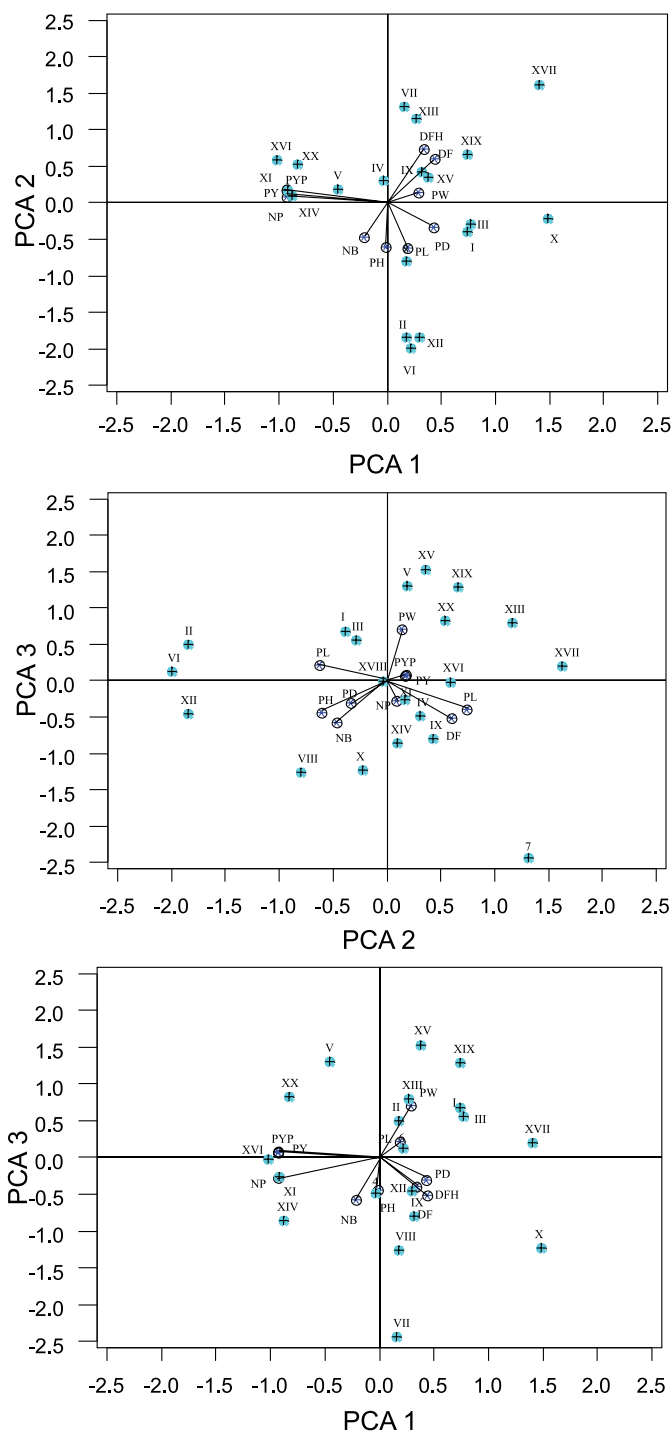


Fig. 2. Biplot of loadings and scores for okra genotypes on principal axes 1, 2 and 3

the principal component score matrix, the okra genotypes were grouped into four different clusters (Table 3). It was revealed that clusters 1, 2, 3 and 4 have 3, 4, 7 and 6 genotypes in clusters, respectively. The genotype Pb -7, a high yielding and promising genotype, showed complete resistance to yellow vein mosaic virus and fell in the cluster 4 where another high yielding variety HRB 9-2 occupied the position in the space. Clustering pattern of okra genotypes showed considerable genetic diversity among themselves by occupying four clusters. The data pertaining to the phenotypic characters showed diverse nature towards various parameters studied. The combination of all quality attributes in single genotype as presented in Fig. 1 does not give a firm output on univariate analysis. Thus the above characterizations

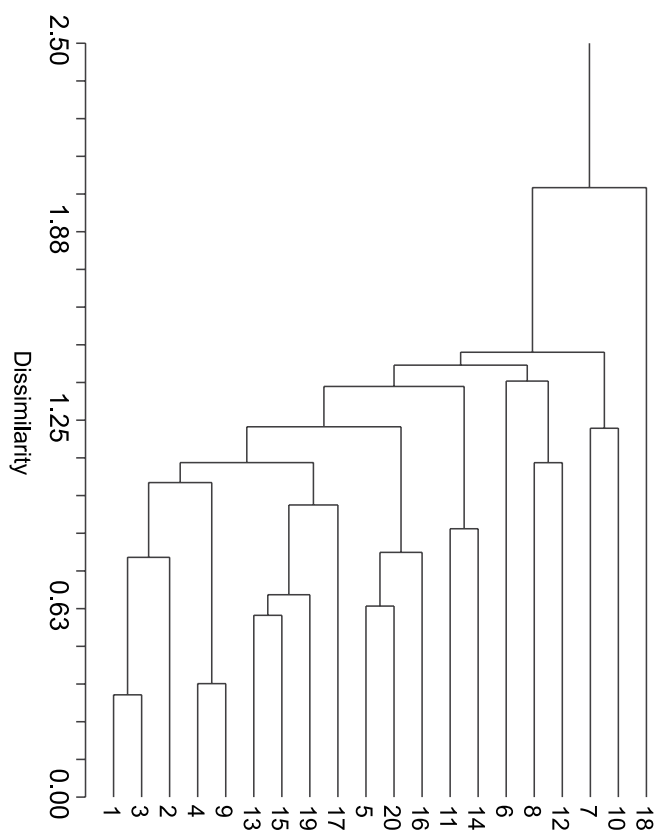


Fig. 3. Dendrogram of cluster analysis for selected okra genotypes

of okra genotypes on the basis of dissimilarity in scores with respect to extracted principal components indicates the existence of variability and confirm the same among the clusters for the selected attributes.

From the results obtained it was concluded that genetic variation existed among the genotypes in all characters. Genotypes Pb-57 and HRB 9-2 showed a greater potentials in terms of yielding attributes as it out performed the other cultivars, indicating the usefulness as promising genotypes in kharif crop and crosses

among the other clusters would exhibit high heterosis and is also likely to produce new recombinants with desirable characters in okra.

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