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# Genetic diversity in nine commercial okra (*Abelmoschus esculentus* L. Moench) genotypes

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## Abstract

Nine commercial cultivars of okra were evaluated for a number of agro-botanical traits. The analysis of variance for all the traits showed highly significant variations among the genotypes. The phenotypic coefficient of variation (PCV) was found higher than the genotypic coefficient of variation (GCV) for all characters. Maximum GCV and PCV were observed for branches/plant (42.54 and 42.60) and leaves/plant (27.93 and 27.99) respectively. Heritability as well as genetic advance was found maximum for branches/plant recorded as 99.72 and 87.50 respectively. Based on $D^2$ statistics 9 genotypes were grouped into 4 clusters, namely cluster I, II, III and IV. Highest inter-cluster distance (1.18) was observed between cluster II and cluster IV. The genotypes of cluster IV possessed heterogeneous nature and showed highest intra-cluster distance (0.65). Titanic-1, BARI Derosh-1 and Green Finger genotypes were found superior to the rest of the genotypes due to their highest cluster mean for yield/plant (955.8g), plant height (208cm), leaves/plant (60.8) and fruits/plant (31.4). These information could be useful in recombination breeding programme.

**Key words:** Okra, genetic variability, genetic diversity, $D^2$ statistics.

## INTRODUCTION

Okra (*Abelmoschus esculentus* (L.) Moench) commonly known as lady's finger is a perennial flowering plant belonging to Malvaceae. It is extensively grown in temperate, subtropical and tropical regions of the world, including Indian sub-continent and East Asia (Rashid, 1990). In Bangladesh, it is known as Derosh that provides an important source of vitamins, calcium, potassium and other mineral matters (Lamont, 1999). This nutritious fruit plays an important role to meet the demand of vegetables in the country. Although the acreage production of okra increased gradually from 38715 M tons in 2006-2007 to 43000 M tons in 2010-2011 (BBS, 2011), the yield per unit area is very low compared to other developing countries namely India, Nigeria, Sudan and Iraq.

In spite of its multiple virtues, okra is being neglected because of the non-availability of high yielding, improved and locally adapted cultivars. Improvement of okra requires a broad spectrum of genetic variability from where useful characters can be selected for improved hybridization programme (Lester *et al*., 1990; Hammond & Charrier, 1983).

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The present investigation was therefore, undertaken to evaluate the genetic variability of different characters in nine okra genotypes to select suitable parents for improved breeding programme.

## MATERIALS AND METHODS

The experimental material for the present study comprised of nine genotypes that include both the local and hybrid cultivars namely Boishaki, Derosh Orka, Green Finger, Titanic-1, Erri, Iron, Masum-1, BARI Derosh-1 and Choice Bendi. Seeds of the cultivars (genotypes) were collected from different seed markets, certified seed companies and national research institution of Bangladesh. The genotypes were evaluated through a field experiment conducted in a Randomized Complete Block Design (RCBD) with three replications at the Botanical Garden of Jahangirnagar University during Kharif season (March to June) in 2013. The soil of the experimental field was sandy loam in texture. Each genotype was raised in a single plot of 4×4 square feet maintaining a plant spacing of 1×1 square feet. A distance of 2 feet in the form of drain was maintained between the block and between the plots within a block. Genotypes were randomly assigned in different blocks. The fertilizer and manure were applied as per recommended dose for the commercial cultivation of okra and the cultural practice were followed when required. Biometric data were recorded on ten randomly selected plants from each genotype in each replication for quantitative traits namely plant height (cm), branches/plant, leaves/plant, length of internode (cm), fruit diameter (cm), fruit length (cm), days to first flowering, days to first fruiting, fruits/plant, fresh weight/fruit (g) and yield/plant (g).

The collected data were compiled and tabulated in proper forms for statistical analysis. Analysis of variance was performed with the help of a MSTAT-C program (Freed, 1986). To test the differences between genotypes, Duncan's Multiple Range Test (DMRT) was performed according to the method of Steel & Torrie (1960).The variance components namely phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability and genetic advance were determined following Kumar *et al*. (1985).

The genetic divergence among the germplasms was assessed following Mahalanobis $D^2$ statistics (Mahalanobis, 1936). The Mahalanobis disance ($D^2$) values were calculated from transformed uncorrelated means of characters according to Singh & Chaudhary (1979). Mean data for each character was subjected to multivariate Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CLSA) and Canonical Variate Analysis (CVA) using GENSTAT 5.5 (Mahalanobis 1936; Digby *et al.*,1989). Scattered diagram obtained for first three principal component scores were done by R 3.0.2 software.

## RESULTS AND DISCUSSION

Analysis of variance indicated significant variation among the genotypes under study for different morphological characters (Table 1). Wide range of variations was observed

among the genotypes in respect to leaves/plant, fruit length (cm), yield/plant (g) and Fresh weight/fruit. Titanic-1 genotype showed maximum yield/plant recorded as 1007g followed by Green Finger (944.3g) and BARI Dedosh-1 (916g) respectively. Rest of the genotypes showed moderate yield while minimum yield was observed in the genotype Masum-1 (369.9g). Titanic-1 genotype also showed superiority over BARI Dedosh-1 and Green Finger in respect to plant height, branches/plant, length of internode (cm) and fruits/plant.

Coefficient of variation (CV%) is a measure of variability in a sample and is useful in comparison of variability for a character among the genotypes. In the present study, among the 11 characters fruit length with CV 0.84% represented lowest variance. However highest variability among genotypes was observed for fruit diameter with CV 5.7% followed by yield/plant (5.24%), fruits/plant (3.80%) and plant height (3.31%) respectively (Table 1).

The magnitude of the phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV) for all characters under study (Table 1). Maximum GCV and PVC were observed for branches/plant (42.54 and 42.60) followed by yield/plant (31.42 and 31.86) and leaves/plant (27.93 and 27.99) respectively which were an indication of high variability for these traits and can be regarded as highly heritable character for selection in further breeding programme. The highest difference between PCV and GCV was found for fruit diameter (2.12). There are two probable reasons for this difference, either due to environmental effect or phenotypic plasticity of this character. Vijay & Manohar (1990) observed similar type of results.

Estimation of heritability serves as an index of the relative contribution of genotype and environment to the phenotypic variance for the concerned trait in a population. The highest heritability was recorded for branches/plant (99.72), followed by leaves/plant (99.61), fruit length (98.66), fresh weight/fruit (97.37), yield/plant (97.30), length of internode (95.50), fruits/plant (95.25) indicates a relatively low contribution of the environmental factors to the phenotypic variance and the selection would be reliable and effective for these characters (Table 1). The highest genetic advance as percentage of mean was observed for branches/plant (87.50) followed by yield/plant (63.85) and leaves/plant (57.43) respectively.

Panse (1957) concluded that a character with high heritability in association with high genetic advance is an indication of expression of additive gene action. Characters without such combination appear generally because of non-additive gene action (Liang & Walter, 1968). In the present study the high estimates of heritability, GA, PCV and GCV recorded for branches/plant, leaves/plant, yield/plant could be explained by additive gene action, hence their improvement can be done through mass selection. Similar kinds of observations in okra were reported earlier (Randhawa & Sharmar 1972, Ibrahim & Hussein 2006).

**Table 1. Mean values and genetic variability parameters for different characters in nine okra genotypes**

| Serial no. | Genotypes | Plant height (cm) | Branches/ plant | Leaves / plant | Length of internode (cm) | Fruit diameter (cm) | Fruit length (cm) | Days to first flowering | Days to first fruiting | Fruits / plant | Fresh weight / fruit (g) | Yield / plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | Boishaki | 170.3c | 1.66c | 44.93f | 8.43b | 7.83ab | 16.55f | 46a | 49a | 25.17cd | 20.17e | 506.9e |
| 2 | Derosh Orka | 166.2c | 0.99d | 38.44g | 8.18bc | 8.42a | 19.33c | 44.67b | 48.67a | 26.17c | 29.43bc | 771.1c |
| 3 | Green Finger | 203b | 1.03d | 51.75d | 6.9d | 7.5bc | 20.72b | 40.33e | 43.33c | 29.33b | 32.17a | 944.3ab |
| 4 | Titanic-1 | 216.1a | 2.33a | 68.79a | 9.16a | 7.5bc | 19.11cd | 43.67bc | 47.67a | 34.42a | 29.25bc | 1007a |
| 5 | Erri | 176.6c | 1.66c | 48.55e | 8.16bc | 7.42bcd | 18.79e | 43c | 46b | 25.58c | 24.77d | 632.7d |
| 6 | Iron | 195.3b | 1.99b | 58.06c | 7.01d | 6.75cd | 19.16cd | 41.67d | 45.33b | 23.75d | 28.53c | 678.1d |
| 7 | Masum-1 | 176.7c | 0.66e | 32.27h | 9.33a | 6.67d | 18.72e | 40e | 44c | 20.17e | 18.3f | 369.9f |
| 8 | BARI Derosh-1 | 205b | 1.66c | 61.77b | 9.01a | 7.25bcd | 18.89de | 39.33e | 43.33c | 30.42b | 30.08b | 916b |
| 9 | Choice Bendi | 173.7c | 0.66e | 28.91i | 8.03c | 7cd | 21.55a | 39.67e | 43c | 21.33e | 23.68d | 505.8e |
| Grand mean | | 186.98 | 1.40 | 48.16 | 8.24 | 7.37 | 19.20 | 42.04 | 45.59 | 26.26 | 26.27 | 703.56 |
| Standard error (± SE) | | 3.49 | 0.11 | 2.49 | 0.16 | 0.13 | 0.27 | 0.46 | 0.46 | 0.86 | 0.90 | 41.91 |
| LSD (0.05) | | 10.70 | 0.05 | 1.46 | 0.32 | 0.73 | 0.28 | 1.22 | 1.32 | 1.73 | 1.36 | 63.81 |
| CV% | | 3.31 | 1.75 | 1.75 | 2.28 | 5.70 | 0.84 | 1.67 | 1.67 | 3.80 | 2.98 | 5.24 |
| PCV | | 10.02 | 42.60 | 27.99 | 10.70 | 8.74 | 7.25 | 5.88 | 5.38 | 17.45 | 18.37 | 31.86 |
| GCV | | 9.46 | 42.54 | 27.93 | 10.46 | 6.62 | 7.20 | 5.64 | 5.12 | 17.03 | 18.13 | 31.42 |
| $H^2$ BS | | 89.11 | 99.72 | 99.61 | 95.50 | 57.35 | 98.66 | 91.91 | 90.38 | 95.25 | 97.37 | 97.30 |
| GA% | | 18.39 | 87.50 | 57.43 | 21.05 | 10.33 | 14.74 | 11.14 | 10.02 | 34.24 | 36.85 | 63.85 |

Legend: LSD (0.05) = Least significant difference design, CV = Coefficient of variation%, PCV= Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, $H^2$ BS = Heritability in broad sense, GA% = Genetic advance as % of mean. In a column means followed by common letter are not significantly different at 5% level by DMRT (Duncan's Multiple Range Test).

The Principal Component Analysis (PCA) yielded Eigen values of each principal component axes of ordination of genotypes with the first axes totally accounting for the variation among the genotypes (Table 2). The result revealed that the first axis largely accounted for the variation among the okra genotypes (42.74%) followed by second axis (30.56%) and third axis (14.96%) respectively (Table 2). The first three axes accounted for 88.26% of the total variation among 11 characters describing in nine okra accessions. Thus the character plant height, branches/plant and leaves/plant will offer a good scope for improvement through selection. According to Chahal & Gosal (2002) character with largest absolute values closer to unity within the first principal component influence the clustering more than those with lower absolute values closer to zero.

**Table 2. Eigen values and contributing percentage of variation for corresponding characters in okra**

| Principle component axis | Eigen values | Variability percent |
|---|---|---|
| Plant Height (cm) | 4.701 | 42.74 |
| Branches/Plant | 3.361 | 30.56 |
| Leaves/Plant | 1.646 | 14.96 |
| Length of Internode (cm) | 0.886 | 8.05 |
| Fruit Diameter(cm) | 0.232 | 2.11 |
| Fruit Length(cm) | 0.112 | 1.02 |
| Days to First Flowering | 0.059 | 0.53 |
| Days to First Fruiting | 0.002 | 0.02 |
| Fruits/Plant | 0 | 0 |
| Fresh Weight/Fruit(g) | 0 | 0 |
| Yield/Plant(g) | 0 | 0 |

On the basis of principal component scores, a three dimensional scatter diagram using component score 1 as X-axis, 2 as Y-axis and 3 as Z-axis was constructed (Fig.1). The distribution of genotypes in scattered diagram revealed that considerable diversity exists among the genotypes. Bisht *et al.* (1995) showed the diversity of 260 okra germplasm of Indian subcontinent following PCA.


**Fig. 1. Three dimensional scattered diagram of nine okra genotypes based on their principal component score 1, 2 and 3 showing considerable diversity**

A two dimensional scatter diagram was developed by using principal component score 1 and 2 that accounted for 73.3% of the total variation among the genotypes (Fig. 2). The main aim of clustering of genotypes was selection as well as rejection of genotypes for hybridization programme. Cluster II and cluster IV contained three genotypes and cluster III had two genotypes while cluster I was found to be monogenotypic. Distribution of nine genotypes into four clusters represented genotypic diversity obtained by the application of non-hierarchical clustering using co-variance matrix based on eleven different morphological characters (Fig. 2).

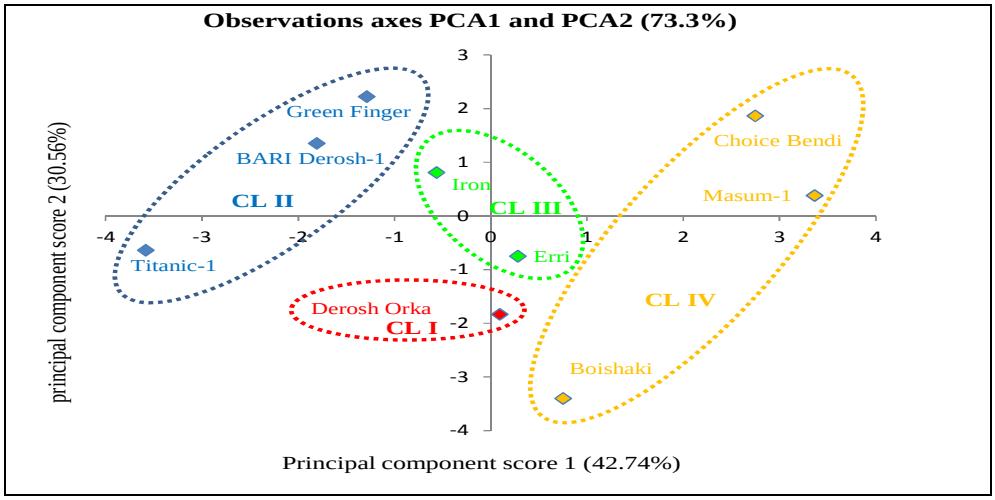


**Fig. 2. Scatter distribution of nine okra genotypes based on their principal component scores superimposed with clusters. (CL=Cluster)**

Average inter cluster distances were found much higher than those of intra cluster distances (Table 3), suggesting homogeneous and heterogeneous nature of the germplasm lines within and between the clusters. These results are in accordance with the findings of Partap *et al*. (1980), Mandal & Dana (1993) and Vahab *et al*. (1994).

Inter genotypic distance as obtained from principal coordinate analysis showed highest inter cluster distance (1.18) between cluster II and cluster IV which implies a great number of contrasting alleles at the desired loci. Lowest inter cluster distance (0.57) was observed between cluster I and cluster III represented little genetic diversity between these clusters and would not effective for future hybridization programme. The genotypes of cluster IV would be effective for recombination breeding because of the highest intra cluster distance (0.65) whereas cluster I had the lowest distance (0.00) since consisted of only one genotype (Table 3).

Cluster means for fruit yield per plant and its major components were considered for selection of genotypes. The cluster means for different quantitative characters indicated considerable differences among the clusters and all the traits studied (Table 4). The genotypes of cluster II produced highest mean for yield/plant (955.8g), fruits/plant (31.4),

fresh weight/fruit (30.5g), fruit length (19.6cm) followed by cluster I, III and IV respectively. The above results of cluster mean clearly revealed that genotypes of cluster II viz. Titanic-1, BARI Derosh-1 and Green Finger could be regarded as superior because of highest cluster mean and thus selected as potential parents for future recombination breeding programme.

**Table 3. Average Intra and Inter cluster distance ($D^2$) for okra genotypes**

| Cluster | I | II | III | IV |
|---|---|---|---|---|
| I | 0.0 | | | |
| II | 0.69 | 0.48 | | |
| III | 0.57 | 0.60 | 0.17 | |
| IV | 0.77 | 1.18 | 0.80 | 0.65 |

**Table 4. Cluster mean for different characters in nine okra genotypes**

| Characters | I | II | III | IV |
|---|---|---|---|---|
| Plant Height (cm) | 166.2 | 208 | 186 | 173.6 |
| Branches/Plant | 1 | 1.7 | 1.8 | 1 |
| Leaves/Plant | 38.4 | 60.8 | 53.3 | 35.4 |
| Length of Internode (cm) | 8.2 | 8.4 | 7.6 | 8.6 |
| Fruit Diameter(cm) | 8.4 | 7.4 | 7.1 | 7.2 |
| Fruit Length(cm) | 19.3 | 19.6 | 19 | 18.9 |
| Days to First Flowering | 44.7 | 41.1 | 42.3 | 41.9 |
| Days to First Fruiting | 48.7 | 44.8 | 45.7 | 45.3 |
| Fruits/Plant | 26.2 | 31.4 | 24.7 | 22.2 |
| Fresh Weight/Fruit(g) | 29.4 | 30.5 | 26.6 | 20.7 |
| Yield/Plant(g) | 771.1 | 955.8 | 655.4 | 460.9 |

Greater genetic variation and the magnitude of genetic diversity among okra genotypes for different botanical traits would be effective for generating superior recombinants. Yield/plant is a polygenically controlled complex quantitative character. Thus, degree of inter relationship existing among different component characters with yield is important for devising an efficient selection criterion for improved breeding programme in future.

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