



Morphological Characterization and Diversity Studies of Okra Genotypes for Different Yield Contributing Traits

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Abstract

Abelmoschus esculentus (L) is an essential vegetable crop that belongs to the Malvaceae family. It is one of the important summer vegetables of Pakistan. Pakistan is far behind in production from many okra-producing countries. There is a need for a breeding program to increase its yield. The availability of genetic diversity in germplasm is necessary for a successful breeding program. The present study assessed the genetic variability among 40 okra genotypes obtained from the Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan. Analysis of variance, cluster analysis, and principle component analysis were employed to estimate genetic diversity. The experiment was conducted in a randomized complete block design using two replications. Different yield-related parameters i.e. fruit length, fruit diameter, fruits per plant, fruit weight, plant height, internodal length, leaves per plant, stem diameter, fruiting habit, fruit pubescence, stem pubescence, and no. of ridges/fruit were measured by using the standard protocols. The analysis of variance demonstrated significant variation among genotypes based on the analyzed traits. Principal component analysis (PCA) revealed genetic diversity among 40 okra genotypes. The first 3 PCs out of eight principal components displayed >1 eigenvalues and had maximum share to total variability. PC-I, II and III had share of 35.86%, 20.34%, and 13.0369% in total variability respectively. Among genotypes G19, G28, and G36 were proved to be good for most of the traits. This study shows that a great range of genetic diversity is present in assembled accessions which may be used in the breeding of high-yielding okra cultivars.

KEYWORDS

Morphological characterization, Diversity, Analysis of variance, Principal component analysis, Cluster analysis

1 | INTRODUCTION

Okra (*Abelmoschus esculentus* L. Monech) is economically an important vegetable crop that belongs to Malvaceae family. It is indigenous to tropical Africa (Joshi et al. 1974). It has the chromosome number varying from $2n = 66$ to $2n = 144$. In Pakistan locally it's known as "Bhindi" (Benchasr et al. 2018). In Pakistan the mean okra production is approximately 2.7 million tons from an area of 14658 acres. Its primary cultivation areas are found in tropical and subtropical zones (Adekoya et al. 2014). This plant has an annual growth pattern. Okra is very useful, its fruit contain water (90.19

g), carbohydrate (7.45 g), sugars (1.48 g), dietary fiber (3.2 g), fat (0.19 g), protein (2 g), vitamin A (7%), thiamine b1 (17%), riboflavin b2 (5%), niacin b3 (7%), vitamin C (28%), vitamin E (2%), vitamin K (30%), calcium (8%), iron (5%), magnesium (16%), potassium (6%) and zinc (6%). It can reduce blood cholesterol levels. It has Potential to lower heart disease and especially cancer (Saleem et al. 2018).

As an anti-diabetic, anti-coagulant, anti-cancer, and antioxidant agent, okra possesses pharmaceutical properties. As a moisturizing agent and demulcent, okra

root and leaf extracts are utilized. Additionally, leaves are utilized as cattle fodder. Okra is also beneficial in the medical industry due to the presence of mucilage. (Gemede et al. 2015). High cholesterol levels and the removal of toxic substances are both treated with mucilage. For healthiness of joints and remedy of ulcer it is mostly used. (Kumar et al. 2013).

The economy of Pakistan depends upon its agriculture sector. Agriculture shares approximately 19.5% to our national gross domestic yield of the Pakistan among this, 9.5% is contributed by sector of field crops. In Pakistan production of okra per unit area is not satisfactory due to non-availability of satisfactory germplasm (Amjad et al. 2001). The loss in production is due to lack of better okra cultivars with significant attractive user-facing characteristics (Kumar et al. 2013). Cultivars from many countries have gain some extra ordinary traits especially in the country to which they belong (Siemonsma 2018).

For breeding of okra, it is necessary to understand the morphological characterization of okra (De Vicente et al. 2005). The variety that exists among distinct morphological features should be explored for crop improvement (Memon et al. 2017). Characterization is a process for analyzing different varieties according to their characters. It provides information about diversity within the variety as well as between crops. Evaluation of okra traits require to grow the plant until it becomes full mature. Morphological variation of high degree is present among accessions of okra. Characterization-related information is either unavailable or inaccessible. It is one of the vegetables having huge diversity among different varieties grown in different parts of the country. Morphological traits and study about diversity are compulsory for clearing the path for making any improvement at the genetic level. Among okra cultivars specifically grown in Pakistan and generally all over the world there is a great variation among fruiting and flowering periods among all accessions. (Oppong-Sekyere et al. 2011). Diversity studies provide a gate way for plant breeders to introduce uniformity in morphological characters. The present study was conducted to assess the genetic variability among 40 okra genotypes.

2 MATERIAL AND METHOD

Description of Material and Site

The present study was conducted to assess the genetic variability among 40 okra genotypes these genotypes were planted in March 2023 (Table 1). Cultural practices were kept constant during the whole season and plant protection measures were adopted to keep the crop disease-free.

Experiment Design

The experiment was conducted in a randomized complete block design using two replications. Row-to-row and plant-to-plant distance was maintained at 45 cm and 15cm respectively. Ten plants of each genotype were sown in each row in two replications.

Table 1: Genotypes used in the experiment.

Sr. No.	Genotypes	Sr. No.	Genotypes
1	Okra-3A	21	G20
2	Nirali	22	G21
3	Anmol	23	G22
4	Krishna	24	G18
5	G2	25	G23
6	G3	26	G24
7	G4	27	G25
8	G6	28	G26
9	G7	29	G27
10	G8	30	G28
11	G9	31	G29
12	G10	32	G30
13	G11	33	G31
14	G12	34	G32
15	G13	35	G33
16	G14	36	G34
17	G15	37	G35
18	G16	38	G38
19	G17	39	G39
20	G19	40	G40

Soil

The texture of the soil was clay loam at which this experiment was conducted. Sufficient drainage was provided in the experimental area. From sowing to maturity of the plant all agricultural practices like rousing, fertilization, and watering were maintained.

Data Collection

Growth-related Traits

All the growth-related traits like plant height (cm), leaves per plant, internodal distance (cm), diameter of stem (cm), were calculated by tagged plants. Plant height was measured after two months of sowing at maturity. Plant height was measured in centimeters utilizing a measuring tape. The measurement of plant height was taken from the tip of the bud to the ground. The mean plant height was determined for each genotype across all replicates. The number of leaves per plant were counted at the maturity of the plant. Leaf counting was done after 65 days of the sowing. The means of the individual genotypes were computed. On maturity, internodal length was measured as the distance between two consecutive nodes (5th and 6th node) and then the average was calculated. From one foot above the ground, the stem diameter of five okra plants was

obtained using a digital caliper.

Fruit and Quality-Related Traits

The data for traits related to the fruits was collected from tagged fruits after about 60 to 70 days of sowing. Fruits after 7 days from flowering were harvested and all parameters were calculated. From each genotype, five fruits were selected at random, and the length of each fruit was determined using a measuring tape. The fruits of the fourth picking were chosen for getting the fruit per plant for each genotype. Tags with specific dates were used and fruits of seven to eight days were taken to get average weight. The average weight of fruits was calculated for each genotype in a replication. For each okra genotype, the pubescence on fruits was physically evaluated and classified as either absent, slight, or abundant using the provided groupings of 1, 2, and 3. A visual inspection of fruiting habit revealed different characteristics distributed as erect, slightly falling, horizontal, and drooping. The mean value of a number of ridges was observed on five fruits selected at random and the average was calculated for each replication. Five fruits of marketable size were selected at random, and their girths were calculated using a vernier caliper.

Statistical Analysis

Collected data was subjected to analysis of variance (Steel et al. 1997) to find genotype differences among studied genotypes. Basic statistics for forty genotypes of *Abelmoschus esculentus* (L) for exhibiting distinct morphological characteristics were estimated. For assessment of genetic diversity principal component analysis and cluster analysis of variance was used.

3 RESULTS AND DISCUSSION

Growth Related Traits

Analysis of variance revealed significant differences for the studied attributes among the genotypes (Table 2). There is a significant difference recorded among genotypes for phenology and growth traits (Muluken et al. 2015), Comparison of genotypes mean showed that maximum plant height (114.67cm) at maturity was recorded in 'G33' followed by 'krishna' (114.25). However, minimum plant height (38.00cm) at maturity was observed in 'G18'. The mean of the plant height was 76.75cm. The value for coefficient of variation was 13.81%. These findings are parallel with those of Khan et al. (2015), who have conducted similar research. Comparison of treatment means revealed that maximum number of leaves (24.33) was shown by 'G10' followed by 'G26' (24.00). Minimum number of leaves (8.00) was observed in 'G18'. The mean value for the number of leaves was 16. These findings are consistent

to the results reported by Amanullah et al. (2016), who found considerable variations in the number of leaves per plant. The value for coefficient of variation for this trait was 13.83%. While maximum internodal length (11.81cm) was shown by 'G6' followed by 'G7' (11.24cm) and G33 (11.80cm). Minimum internodal length (4.3cm) was observed for 'G18'. The analysis of variance (ANOVA) conducted on stem diameter revealed significant differences ($P < 0.05$) among the okra genotypes, with Karishna demonstrating the highest value at 20.48cm. Least stem diameter (4.8 cm) was recorded for 'G18' followed by Anmol (18.22cm) and G2 (16.67cm). The mean value for stem diameter was 12.51mm. The value for the coefficient of variation for this trait was 9.82%. Most of the genotypes showed slight pubescence on the stem except Krishna which exhibited abundant pubescence on stem.

Fruit Related Traits

Significant variation was presented by analysis of variance among the various okra accessions for fruit related traits. All fruit related traits like no. of fruits, fruit girth, fruit length, and fruit weight showed significant and highly significant results for genotypes. These results revealed the need to choose genotype that has a high variation for yield and other contributory traits for attaining desired results in breeding trials.

The highest number of fruit (13.00) per plant has been observed for 'G34', which is statistically comparable to G6 and 'G19'. Similarly, the minimum number of fruits per plant (4.00) demonstrated by genotype G30 (Table 3). These findings are parallel with those of Binalfew and Alemu (2016) and Khan et al. (2015), who have conducted similar research. It is statistically comparable to 'G24'. There was a statistically significant maximum fruit girth of 6.8 cm observed by G13. In contrast, 'G20' yielded okra determining a minimum of 3.5 cm in diameter. The mean of the fruit girth was 4.60cm. Comparison of treatment means revealed that maximum fruit length (15.8cm) was shown by 'G26' followed by 'G20'. Minimum fruit length (9.5cm) was observed for 'G3'. These findings are consistent with that of Amanullah et al. (2016). The maximum fruit weight (19.81) was shown by 'G26'. Minimum fruit weight (8.53) was observed for 'G6'. Fruit weight also had the lowest CV%. The value for coefficient of variation for this trait was 6.7%. Most of the genotypes showed slight pubescence on fruits except Krishna which exhibited abundant pubescence on fruits. Only two genotypes G30, G34 exhibited erect type of fruiting habit, while all other genotypes slightly falling fruiting habit. All studied genotypes showed five number of ridges per fruit. Similar results have been reported by (Sawant et al. 2014; Bagwale et al. 2016; Patil et al. 2016; Khajuria et al. 2015; Chandra et al. 2014.

Table 2: Mean square of forty genotypes of morphological attributes *Abelmoschus esculentus*(L)

Source	DF	PH	NL	IL	SD	NF	FG	FL	FW
Rep	1	74.83**	0.01**	0.005**	0.82**	34.60**	0.11**	1.99**	2.61**
Gen	40	533.49**	22.7**	6.76**	20.63**	12.86**	0.20**	2.84**	7.08**
Error	40	124.36**	5.97**	0.35**	1.06**	3.23**	0.08**	0.76**	0.78**
Total	81								

** Highly significant ($P < 0.001$), *Significant ($P < 0.005$), PH= Plant height, NL= Number of leaves, IL= Internodal length, SD= Stem diameter, NF= Number of fruits, FG= Fruit girth, FL= Fruit length, FW=Fruit weight,

Table 3: Estimation of basic statistics for forty genotypes of *Abelmoschus esculentus* (L) for exhibiting distinct morphological characteristics

Variables	Maximum	Minimum	Mean	SD	CV%	Variance
PH	114.25	38	76.75	16.3323	13.81	28.04
NL	24	8	16	3.3746	13.83	102.15
IL	11.81	4.3	8.93	1.8387	7.48	27.46
SD	20.48	4.8	12.51	3.2119	9.82	28.69
NF	13	4	8.81	2.5360	18.33	148.74
FG	5.8	3.5	4.60	0.3179	5.34	28.04
FL	15.8	9.5	12.65	1.1928	7.37	102.15
FW	19.81	8.34	14.07	1.8828	6.7	27.46

PH= Plant height, NL= Number of leaves, IL= Internodal length, SD= Stem diameter, NF= Number of fruits, FG= Fruit girth, FL= Fruit length, FW=Fruit weight,

Among genotypes G19, G28, and G36 were proved to be good for most of the fruit related traits. These genotypes can be selected for future breeding program for getting high yielding okra cultivars.

Principle Component Analysis

PCA is the efficient mean of measuring variation present among genotypes for yield and its related traits. Typically, it is implemented to decrease the complexity of enormous data sets. It reduces data sets with a significant number of variables to smaller ones that contain nearly all the information from the larger data set. It facilitated the detection of genotypes exhibiting improved yield related characteristics that boost the yield of okra (Rathinavel, 2018; Munir et al. 2020).

With the help of PCA on the mean values of all examined characteristics, the genetic divergence between forty okra genotypes was investigated. The variance has been divided into eight components. PC-I, II and III had share of 35.86%, 20.34% and 13.03% to total variability respectively (Table 4). These 3 PCs imparted 69% to total variability among studied genotypes. Rest of the PCs had <1 eigen value therefore was not discussed further. Contribution of PC-I and PC-II were primarily associated with plant height, leaf count, and internodal length; (Table 4) however, PC-II yielded greater and positive results for fruit count and fruit weight (Table 4). Higher levels for PC-I were observed in the G4, G35, and G36 genotypes, whereas genotypes associated with PC-II were G9, and G28. PC-III exhibited positive results for various attributes, such as fruit weight, plant height,

and leaf count, fruit girth and Stem diameter (Table 4). PC1 had main contribution from plant height, and fruit length while the least contribution was recorded for number of leaves and stem diameter. PC-II had contribution to main variation due to number of leaves. Similarly, PC-III got main contribution from stem diameter and internodal length. Characters with high variability as identified by the PCA are expected to respond more to selection during breeding programs (Aliyu et al. 2000).

Table 4: Contribution of the first three principal component axes to variation in okra genotypes

	PC1	PC2	PC3
PH	23.12	5.60	0.0072
NL	0.55	45.66	1.74
IL	9.12	15.71	28.54
SD	5.86	3.54	57.61
NF	15.99	4.71	0.50
FG	12.31	5.86	8.94
FL	17.57	16.55	1.44
FW	15.44	2.33	1.19
Eigenvalue	2.8693	1.6279	1.0430
Variability (%)	35.8664	20.3489	13.0369
Cumulative %	35.8664	56.2153	69.2522

PH= Plant height, NL= Number of leaves, IL= Internodal length, SD= Stem diameter,

NF= Number of fruits, FG= Fruit girth, FL= Fruit length, FW=Fruit weight.

Biplot Analysis for Morphological Attributes

Biplot indicated that the variables were physically represented as vectors on the plot (Figure 1). The percentage of overall variation in the genotypes was denoted by the variables. The distance taken from the

point of origin to the extremity of the plot provides an Understanding the genetic variation that exists between genotypes. The variety that is at maximum distance from the origin had higher variation as compared to other varieties (Rathinavel 2018).

Fruit weight and Stem diameter varied least due to its closeness to the origin, whereas the number of leaves varied considerably, fruit girth and the high variations in fruit length were observed at increasing distances from the point of origin. It showed that variation was present among different characters and each shared differently to the total variability. This information about existing variability among the studied genotypes for different traits is essential for fruitful breeding experiments.

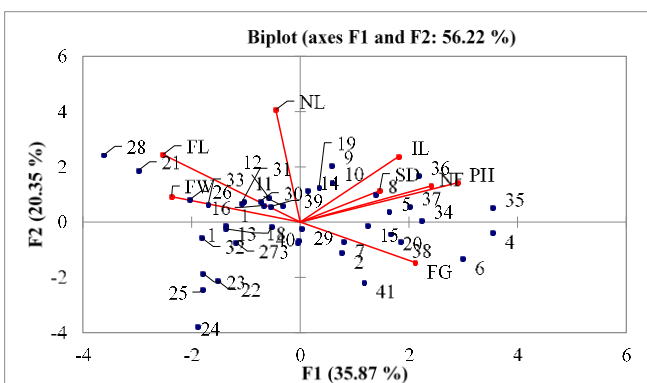


Fig. 1: Principal component biplot for contribution of traits

Relationships among Agronomic and Growth Traits

Correlation Analysis

Correlation analysis studied the type of association among the attributes under study and which attribute should be selected to increase the okra yield. It determined traits that may be able to increase the yield of the crop. Correlation study is an important factor in development of selection strategy for breeding program.

Correlation Analysis provided the relationship between traits under study. Plant height showed a positive correlation with internodal length, number of fruits, stem diameter, and fruit girth. However, plant height was negatively correlated with fruit length (-0.368) and fruit weight. The number of leaves was negatively correlated with fruit length. Internodal length showed a positive correlation with the number of fruits. Similarly, fruit girth was found negatively correlated with fruit length and fruit length showed a high positive correlation (0.529) with fruit weight. A non-significant correlation was also present between the traits under study. Correlation present in traits of interest was highly significant and significant. Through correlation analysis, direct and indirect selection of traits for improvement can be made, present in our germplasm.

Table 5: Phenotypic correlation of morphological traits

Traits	PH	NL	IL	SD	NF	FG	FL
NL	0.148						
IL	0.505**	0.21					
SD	0.381*	0.151	0.01				
NF	0.506**	0.076	0.405**	0.185			
FG	0.321*	-0.224	0.037	0.214	0.39		
FL	-0.49**	0.43**	-0.128	-0.067	-0.226	-0.465**	
FW	-0.368*	0.21	-0.271	-0.256	-0.284	-0.18	0.529**

PH= Plant height, NL= Number of leaves, IL= Internodal length, SD= Stem diameter, NF= Number of fruits, FG= Fruit girth, FL= Fruit length, FW=Fruit weight.

Cluster Analysis

The purpose of cluster analysis is to group comparable objects together and distinguish diverse objects in another group. The corresponding factors of PCs were further analyzed by cluster analysis. It is an efficient method to group similar object together. The variable clustered in one group were similar and differentiated from other variables. (Rathinavel 2018).

Cluster III contained the greatest number of genotypes, as shown (Table 6); clusters II, I, V, and IV proceeded pattern. Cluster I had genotypes with high values for plant height number of leaves. Cluster II displayed highest value for number of leaves and for stem diameter. Cluster III had highest mean value for fruit weight while cluster IV had genotypes with highest values for plant height (Table 6). Genotype in a group is more similar than genotypes from different clusters.

Table 6: Cluster wise distribution of okra genotypes in 5 clusters

Class	Frequency	Genotypes
1	7	okra3A, Nirali, Anmol, G27, G30, G31, G32
2	8	G4, G5, G6, G35, G36, G37, G38, G41
3	16	G7, G9, G10, G11, G12, G13, G14, G15, G16, G17, G19, G20, G29, G34, G39, G40
4	5	G8, G18, G21, G26, G33
5	5	G22, G23, G24, G25, G28

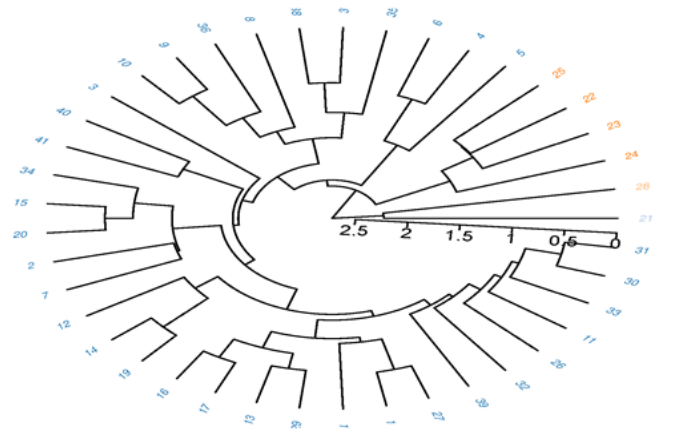


Fig. 2: Distribution of 40 okra genotypes into 5 clusters

Dendrogram classified 40 genotypes into five clusters. The characters being studied are represented by these clusters. The genotypes being displayed by these clusters could be used according to the magnitude of their genetic diversity (Fig. 2)

Conclusions

Pakistan is far behind in production from many okra-producing countries. There is a need for a breeding program to increase its yield. The availability of genetic diversity in germplasm is necessary for a successful breeding program. Our experiment assessed the genetic variability among different okra genotypes.

Significant variation was presented by analysis of variance among the various okra accessions for all the characters. All traits under study showed significant and highly significant results for genotypes, revealing the need to choose genotype that has a high variation for yield and other contributory traits for attaining desired results in breeding trials. Genotype G33 showed the highest plant height (114.25cm), while parent G19 produced the most fruits per plant (13). Genotypes exhibited diverse leaf production, with some showing robust growth. Fruit weight differed significantly, with some genotypes. Internodal length showed notable variation, with some genotypes displaying more elongated stems. Fruit girth also varied, with some genotypes having more slender fruits and others more vigorous ones. Analysis of variance, cluster analysis, and principal component analysis were employed to estimate genetic diversity. Analysis of variance revealed significant differences for the studied attributes among the genotypes. There was considerable variation present for all eight traits within the genotypes. Among genotypes G19, G28, and G36 were proved to be good for most of the traits. These genotypes can be efficiently employed in future okra breeding program to improve okra crop yield. The outcomes of this research will be convenient for genetic improvement and conservation of the genetic diversity of the crop.

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