Turkish Journal of Agriculture - Food Science and Technology, 10(6): 997-1005, 2022
DOI: https://doi.org/10.24925/turjaf.v10i6.997-1005.4719

Turkish Journal of Agriculture - Food Science and Technology

Available online, ISSN: 2148-127X | www.agrifoodscience.com | Turkish Science and Technology Publishing (TURSTEP)

Genetic Diversity of Indigenous and Exotic Okra [*Abelmoschus esculentus* (L.) Moench] Genotypes at Dire Dawa, Eastern Ethiopia

Anteneh Bekele Melaku[1,a,*], Wassu Mohamed[1,b], Vasantha Kumar[1,c]

[1]*School of Plant Sciences, Haramaya University, P.O.Box: 138, Dire Dawa, Ethiopia*
[*]*Corresponding author*

ARTICLE INFO

Research Article

Received : 24/09/2021
Accepted : 25/03/2022

Keywords:
Genetic diversity
Genetic distance
Cluster
Okra
Indigenous

ABSTRACT

Ethiopia is considered as the possible origin and center of diversity for okra. Therefore, this study was conducted with the objectives of determining the genetic distance between indigenous okra collections and exotic commercial varieties and assessing genetic diversity of okra genotypes. The field experiment was conducted at Dire Dawa in 2016 using 14 indigenous collections and 11 exotic varieties in 5 x 5 triple lattice design. Data were collected on 9 and 29 qualitative and quantitative traits, respectively. The genetic distance measured by Euclidean distance ranged from 3.1 to 12.6 with a mean of 7.2. The highest genetic distances were observed between indigenous okra collections and exotic varieties viz. Guba-12 and NamdHari (12.6) followed by Guba-12 and Vellayani (12.3) and Mythri and Guba-12 (11.8). Dendrogram constructed by Unweighted Pair-group Method with Arithmetic Means grouped the 25 genotypes into seven major clusters in which the three clusters (Cluster II, III and V) were solitary, consisted of one genotype each, Cluster I consisted of six Indian commercial varieties, Cluster IV comprised of seven genotypes (four indigenous okra collections, one variety from USA and two from India), while Cluster VI and VII comprised of 5 and 4 indigenous okra collections, respectively. This study revealed the presence of wide genetic diversity among indigenous okra collections and exotic commercial varieties.

[a] *yitulove@gmail.com* *https://orcid.org/0000-0002-9600-9936*
[b] *wasmoha@yahoo.com* *https://orcid.org/0000-0002-2658-6957*
[c] *vasantkau@gmail.com* *https://orcid.org/0000-0001-6868-4160*

Introduction

Okra [*Abelmoschus esculentus* (L.) Moench] is an annual vegetable that belongs to the Malvaceae family. It was reported that okra is native to North Eastern Africa in the area of Ethiopia and Sudan (Aladele et al., 2008; Santos, 2012). It is a warm-season annual herbaceous vegetable crop and it is self-pollinated, mainly propagated by seeds with the duration of 90-100 days (Tripathi et al., 2011). It is grown primarily for its young immature green fruits and fresh leaves used in salads, soups and stews. Okra is known by many local names in different parts of the world. It is called lady's finger in England, Gumbo in U.S.A., and Bhindi in India (Soni, 2016). In its origin of Ethiopia, it is also called Kenkase (Berta), Andeha (Gumuz), and Bamia (Oromia/Amharic) (Habtamu et al., 2014). Okra has a prominent position among fruits and vegetables due to its multiple virtues like high nutritive and medicinal value, wide adaptability, ease of cultivation, year-round cultivation, good portability, export potential and high returns (Thirupathi et al., 2012a). Okra is a mucilaginous plant suitable for industrial and medicinal applications. The genotypes also need to have many seeds in each pod and produce a high seed yield per plant, because okra seeds are a source of oil and protein. It can be also used as non-caffeinated substitute for coffee after being roasted and ground (Calisir and Yildiz, 2005). The accessions under cultivation over the years in the various regions across the country are landraces (Tesfa and Yosef, 2016), and, therefore, genetic diversity is expected among the landraces. Muluken et al. (2015) and Mihretu et al. (2014b) showed the existence of diversity in okra germplasm in Ethiopia based on agro-morphological traits. However, there is no information about the genetic and morphological divergence or proximity between Ethiopian landraces and improved okra varieties of other countries. Therefore, it is necessary to study the genetic diversity between and among indigenous and exotic okra genotypes for the improvement of the crop. Okra is grown as a wild plant and wide genetic variation is expected. The studies did not provide sufficient information about the genetic distances of the okra collections from Ethiopia and exotic varieties from other countries. Therefore, this study was conducted to determine the genetic diversity between native Ethiopian okra genotypes and exotic okra cultivars.

Materials and Methods

Description of the Study Area

The study was conducted at Dire Dawa, which is located between latitude and longitude of 9°36' N and 41°52' E coordinates with an altitude of 1260 meters above sea level (Hailay et al., 2004). The area has the mean annual temperatures ranging from 21.5°C (December) to 28.4°C (June). The aggregate average annual rainfall is about 604 mm and the annual average humidity is 41.82%. The site has two rain seasons; that is, a short rain season from March to April, and a long rainy season that extends from August to September. The aggregate average annual rainfall that the site gets from these two seasons is about 604 mm. (Levoyageur, 2012).

Treatments and Experimental Design

A total of 25 genotypes were evaluated of which 14 were collected from different okra growing regions of Ethiopia and the remaining 11 were exotic okra varieties. Among the eleven exotic genotypes, two varieties are registered as commercial cultivars in Ethiopia by m Melkassa Agricultural Research Center, one variety was from USA in which the seeds were brought from American Seed Company and eight varieties were introduced from India from the known vegetable seed companies. Genotypes were planted in 5 × 5 triple lattice designs. Each plot was 0.8 m × 7.2 m (5.76 m^2) consisting of one row and a total of 12 plants per row or per plot. The spacing between plots and adjacent replications were 0.8 and 2 m, respectively. The seeds were planted in June 2016 at the start of rainy season and when the soil is becoming moist to support seed emergence. Three seeds per hill were sown and thinned to one plant per hill when plants reached 3-4 leaves stage. Fertilizer was not applied and irrigation water was applied every three days up to the establishment of the crop in the field (3-4 leaves stage) and every week after this period.

Data Collection

International Plant Genetic Resources Institute (IPGRI, 1991) descriptor list for okra species were used to record data on quantitative and qualitative traits. Quantitative traits were recorded from 10 plants per row leaving the two plants grown at both ends of the row as border plants and to collect data for mature fruits traits and seed traits. Five randomly selected tender fruits from each harvest in each plot were used to record tender fruit traits.

Dry matter content of tender fruit (%): Five tender fruits from three harvest were randomly taken from each plot, weighed at harvest, sliced and were dried in oven at 75°C for 72 hours until a constant weight was attained and the dry matter in percent was calculated according to Williams and Woodbury (1968) as follows.

$$\text{Dry matter (\%)} = \frac{\text{weight of sample after drying (g)}}{\text{Initial weight of sample (g)}} \times 100$$

Estimation of mucilage content of okra fruits: A sample of fresh okra fruits harvested from experimental plots was initially dried under shade for 24 hours and further dried in an oven at 50°C for 72 hours until constant weight obtained. Dried fruits were powdered in grinder and mucilage extraction was done in two steps (Uzma et al, 2013).

Step 1: Powdered fruit (200 g) keep in 500 ml distilled water for 6 hours and then heated with continuous stirring at 60°C for 2 hours. The concentrated solution filtered through muslin cloth and allowed cooling.

Step 2: The extract is treated with an equal volume of acetone (100 %) for 30 minutes and filtered through a muslin cloth. The residue which had high fraction of mucilage was dried in oven at 40°C for 12 hours, cool to room temperature; weighed and finally the percentage of mucilage in fruit sample was calculated.

$$\text{Mucilage content (\%)} = \frac{\text{Dried residue mucilage (g)}}{\text{Weight of sample (g)}} \times 100$$

Table 1. List of genotypes, origin of collection and tender fruit yield in 2015

No	Genotype	t ha^{-1}	Origin
1	Guba 12	24.544	Metekel
2	Guba 05	24.44	Metekel
3	Guba 07	20.439	Metekel
4	240204	18.874	Benishangul
5	240609	17.305	Gambella
6	Guba 04	13.588	Metekel
7	Guba 21	13.081	Metekel
8	242443	12.523	Benishangul
9	Guba 47	12.416	Metekel
10	240600	11.797	Gambella
11	Guba 14	10.99	Metekel
12	Guba 08	9.951	Metekel
13	Dangur40	9.482	Metekel
No	Genotype	t ha-1	Origin
14	242444	9.924	Benishangul
15	Vellayani	New	India
16	Mythri	New	India
17	Kiran	New	India
18	Clemson	16.721	USA
19	ArkaAnamica	17.57	India
20	NamdHari	6.192	India
21	Dhenu	2.321	India
22	Anoop	15.064	India
23	SOH 701	11.527	Registered
24	SOH 714	10.578	Registered
25	Arcanamica	New	India

Data Analysis

Heritability and Genetic Advance

Broad sense heritability values were estimated using the formula adopted by Falconer and Mackay (1996) and the heritability percentage was categorized as low, moderate and high as suggested by Robinson et al. (1955). Genetic advance in absolute unit (GA) and as a percent of the mean (GAM), assuming selection of superior 5% of the genotypes was estimated in accordance with the methods illustrated by Johnson et al. (1955) and was categorized as low, moderate and high.

Genetic Distance and Clustering

The genetic distance of 25 okra genotypes was estimated using Euclidean distance (ED) calculated from the 29 quantitative traits after standardization (subtracting the mean value and dividing it by the standard deviation) as established by Sneath and Sokal (1973).

Results

Genetic Distance

The genetic distances of 25 okra genotypes were estimated by Euclidean distance (Sneath and Sokal, 1973) from 29 quantitative traits which is presented in Table 1. The results showed that genetic distance was ranged from 3.1 to 12.6 with 7.2, 2 and 27.85 mean, standard deviation and coefficient of variation, respectively. The highest genetic distance was observed between Guba-12 and NamdHari (12.6) followed by Guba-12 and Vellayani (12.3) and Mythri and Guba-12 (11.8). The genotypes Guba-47 and Guba-08 (3.1) followed by NamdHari and Arcanamica (3.3) as well as Anoop and Arcanamica (3.6) showed the lowest genetic distances.

Euclidean distance of each genotype was calculated by averaging the distances of each genotype to the other 24 genotypes to understand which genotype(s) were most distant or closest to others (Table 2). Guba 12 (8.5) followed by Vellayani and Kiran both with a mean Euclidean distance of 8.4 were the most distant to others. NamdHari (8.3), Guba 04 and Guba 14 both with a mean Euclidean distance of 8 were also distant to others. In contrast, Dhenu (5.9) followed by T240600, Clemson, SOH 701 and T242444 with mean Euclidean distance in between 6 and 6.2 were closest to others. The result indicated that some of the introduced commercial varieties and collections from Ethiopia were most distant to the others. This suggested a higher chance of improving the traits of interest by crossing between commercial varieties and collections from Ethiopia or among collections from Ethiopia.

Cluster Analysis

The distance matrix from 29 phenotypic traits was used to construct a dendrogram based on the Unweighted Pair-group Method with Arithmetic means (UPGMA). The cluster analysis result is presented in the form of a dendrogram (Figure 1). The okra genotypes were grouped into seven major clusters in which the three clusters (Cluster II, III and V) were solitary, consisted of one genotype each. Cluster IV and I comprised of 7 (28%) and 6 (24%), respectively, while Cluster VI and VII consisted of 5 (20%) and 4 (16%), respectively

The three solitary Cluster II and V consisted of okra collections from Metekel and Cluster III was constructed by one Indian origin variety. Cluster I consisted of varieties all from Indian; Cluster IV consisted of seven genotypes (one from Gambella, one from USA, three from India and two from Beneshangul) and Cluster VI was constructed by five genotypes (four from Metekel and one from Beneshangul). Cluster VII consisted of four genotypes of which three were obtained from Metekel and one from Gambella.

Cluster Mean Analysis

The minimum, maximum and mean values of each cluster for the 29 quantitative traits are presented in Table 4 and 5. Cluster I was characterized by consisting of genotypes having similar pod color (green) and position of fruits on the main plant (erect). This cluster was also characterized by early flowering, early pod formation and early maturity less than the overall mean values. In addition, this cluster had mean values lower than overall mean values for all traits except it had long fruits, a greater number of fruits per plant, dry matter and internodes length more than the overall mean values of genotypes.

Three clusters (II, III and V) consisted of one genotype each had an erect position of fruit on the main stem. Cluster II (Guba-04) was characterized by late days to emergence, flowering, pod formation and maturity than the genotypes overall mean values. Mucilage content of tender fruit, leaf length and width and the number of epicalyxes of this cluster was higher than the overall mean values of genotypes. The fresh and dry weight of matured fruit as well as dry matter of this cluster (Guba-04) was much higher than the overall mean values of genotypes. It had the lowest number of matured fruits per plant; fruit yield per plant, per plot and per hectare among clusters and lower than overall mean values of genotypes for many other traits. In contrast, Cluster III (Kiran) had the lowest days to emergence, flowering, pod formation and fruit maturity. It had long fruits and the highest number of fruits per plant, producing high fruit yield per plant, per plot, and per hectare. It had also mean values greater than overall mean values of genotypes for many other traits. Cluster V (Guba-05) had the lowest days to emergence and days to first flowering but had late days to 50% flowering, days to pod formation, days to maturity higher than the genotypes overall mean values. It also had a short internode length, the lowest number of matured pods per plant and dry matter. Mucilage content was high for this cluster. It had also mean values greater than overall mean values of genotypes for many other traits.

Cluster IV consisted of the genotypes having similar flower color (red color at both sides) and leaf petiole color (red above only), it had higher fruit weight and number of matured pod per plant higher than the genotypes overall mean values. It had also average mean values as compared to overall mean values of genotypes for many other traits. Cluster VI consisted of the genotypes having similar flower color (red color at both sides) and leaf color (green with red vein) color which had early days to emergence, lowest dry matter and mucilage content less than the genotypes overall mean values, but it had mean values greater than overall mean values of genotypes for most of the traits. Cluster VII had the genotype similar pod color (green) and was characterized by late days to emergence, days to first flowering, days to 50% flowering, days to pod formation and days to maturity higher than the genotypes overall mean values. It had the longest plant height, and highest number of epicalyxes, number of matured pods, number of seeds per pod and mucilage content higher than the genotypes overall mean values. It had also mean values greater than overall mean values of genotypes for many other traits.

Numbers in parenthesis represented number of genotypes in each cluster, Dem = Days to 50% emergency, DFF = Days to first flowering, DFPF = Days to 50% flowering, DPF= Days to pod formation, DMa = Days to maturity, PH (cm) = Plant height in centimeter, StD (cm) = Stem diameter in centimeter, NPBr = Number of primary branch, Nin = Number of inter node, InLe (cm)= Inter node length in centimeter, LLe (cm) = Leaf length in centimeter, LWd (cm) = Leaf width in centimeter, NEpy = Number of epicalyx, PLe (cm) = Peduncle length in centimeter,

Table 2. Genetic distances of 25 okra genotypes

	T240600	Guba 47	Guba 12	ArkaAnamica	NamdHari	Dangur 40
Mythri	7.63	10.5	11.8	4.0	2.9	9.5
T240600		5.0	5.8	6.2	8.2	5.8
Guba 47			5.0	8.5	11.1	6.8
Guba 12				10.1	12.6	7.8
ArkaAnamica					4.8	7.6
NamdHari						10.3

	Clemson	T240204	Dhenu	Vellayani	Guba 21	Guba 04	T240609
Mythri	5.61	10.0	6.26	6.6	10.8	7.4	10.4
T240600	4.09	4.7	4.45	7.6	6.6	7.0	6.1
Guba 47	6.64	4.1	6.87	11.1	4.8	9.5	6.9
Guba 12	8.01	6.0	8.46	12.3	6.6	10.7	7.7
ArkaAnamica	4.77	7.6	5.29	6.8	9.4	6.9	8.6
NamdHari	6.23	10.4	6.96	7.4	11.6	8.3	11.1
Dangur 40	6.93	5.7	4.90	8.5	8.2	7.9	4.4
Clemson		6.0	4.70	7.3	7.1	6.9	6.8
T240204			5.92	9.6	4.7	8.7	5.2
Dhenu				5.9	7.5	5.5	6.1
Vellayani					11.1	7.0	9.0
Guba 21						9.9	7.6
Guba 04							8.9

	Guba 05	Anoop	T242443	SOH 701	SOH 704
Mythri	8.19	4.3	8.53	6.63	5.94
T240600	5.74	7.5	4.69	4.31	5.62
Guba 47	5.87	10.4	5.84	5.90	6.59
Guba 12	7.74	11.4	6.92	7.34	9.08
ArkaAnamica	6.53	5.1	6.63	5.59	4.75
NamdHari	9.01	3.9	9.16	7.40	6.41
Dangur 40	7.01	9.6	4.66	6.33	7.43
Clemson	5.13	6.1	5.56	3.99	4.38
T240204	5.09	9.5	5.29	5.79	6.58
Dhenu	4.90	6.5	3.81	4.82	4.77
Vellayani	8.69	6.4	8.20	7.99	7.78
Guba 21	5.64	10.4	7.53	6.61	6.99
Guba 04	6.26	7.2	7.39	7.45	7.61
T240609	7.23	10.2	4.56	6.32	7.83
Guba 05		7.8	6.01	6.06	5.91
Anoop			8.72	6.84	6.51
T242443				4.85	5.51

	Arcanamica	Guba 08	Guba 14	Kiran	Guba 07	T242444
Mythri	4.0	10.6	9.4	7.8	10.4	8.03
T240600	7.2	5.4	7.0	6.8	6.2	4.97
Guba 47	9.9	3.1	9.0	7.8	6.1	6.07
Guba 12	11.3	4.9	9.6	9.8	6.5	7.65
ArkaAnamica	4.6	8.8	8.6	7.0	8.8	6.67
NamdHari	3.3	11.4	9.9	7.8	11.4	8.62
Dangur 40	8.9	6.8	5.6	10.2	5.1	5.65
Clemson	6.5	6.9	7.7	6.1	7.3	5.02
T240204	9.5	4.1	7.2	7.5	5.1	5.13
Dhenu	6.0	6.5	6.0	8.2	6.5	3.89
Vellayani	7.0	10.8	8.3	9.6	10.0	7.72
Guba 21	10.6	4.2	9.8	7.9	7.1	7.01
Guba 04	7.6	9.6	8.6	10.8	9.8	5.62
T240609	10.3	6.2	5.9	10.2	3.9	5.39
Guba 05	8.5	5.6	8.9	8.0	7.3	4.52
Anoop	3.6	10.5	9.7	7.5	10.5	7.80
T242443	8.1	5.5	5.9	9.4	5.2	3.81
SOH 701	6.6	6.1	6.7	7.0	6.5	5.41
SOH 704	5.6	7.1	8.2	6.7	8.3	5.92
Arcanamica		10.2	9.5	7.9	10.5	7.92
Guba 08			8.6	8.4	5.3	5.77
Guba 14				10.4	6.6	6.00
Kiran					9.6	8.80
Guba 07						6.19

Table 3. Mean genetic distances of 25 okra genotypes as measured by Euclidean distance from 29 quantitative traits

Genotype	Minimum	Maximum	Mean	SD	CV (%)
Mythri	2.9	11.8	7.8	2.5	32.06
T240600	4.09	8.18	6.0	1.2	19.48
Guba 47	3.1	11.1	7.2	2.3	31.60
Guba 12	4.9	12.6	8.5	2.3	26.99
ArkaAnamica	4.0	10.1	6.8	1.7	25.28
NamdHari	2.9	12.6	8.3	2.7	32.94
Dangur 40	4.4	10.3	7.1	1.8	24.53
Clemson	3.99	8.01	6.1	1.2	19.10
T240204	4.1	10.4	6.6	2.0	29.90
Dhenu	3.81	8.46	5.9	1.2	21.01
Vellayani	5.9	12.3	8.4	1.7	19.90
Guba 21	4.2	11.6	7.9	2.1	26.77
Guba 04	5.5	10.8	8.0	1.5	18.33
T240609	3.9	11.1	7.4	2.1	28.40
Guba 05	4.52	9.01	6.7	1.4	20.23
Anoop	3.6	11.4	7.8	2.3	29.12
T242443	3.81	9.41	6.3	1.7	26.84
SOH 701	3.72	7.99	6.1	1.1	18.40
SOH 704	3.72	9.08	6.5	1.3	20.56
Arcanamica	3.3	11.3	7.7	2.3	30.33
Guba 08	3.1	11.4	7.2	2.4	33.38
Guba 14	5.6	10.4	8.0	1.5	18.84
Kiran	6.1	10.8	8.4	1.3	15.82
Guba 07	3.9	11.4	7.5	2.1	28.50
T242444	3.81	8.80	6.2	1.4	22.91

SD = standard deviation and CV (%) = Coefficient of Variation in Percent.

Table 4. Number of genotypes grouped in 7 clusters, genotype code and collection region of 25 okra genotypes evaluated at Dire Dawa in 2016

C	NG	Genotype code	Collection Region
I	6	Mythri, NamdHari, Anoop, Arcanamica, ArkaAnamica, Vellayani	Indian
II	1	Guba 04	Metekel
III	1	Kiran	Indian
IV	7	T240600, Clemson, SOH 701, SOH 7014, Dhenu, T242443, T242444	Gambella (1), USA (1), India (3), Beneshangul (2),
V	1	Guba 05	Metekel
VI	5	Guba 47, Guba 08, T240204, Guba 21, Guba 12	Metekel (4), Beneshangul
VII	4	Dangur 40, T240609, Guba 07, Guba 14	Metekel (3), Gambella

C: Cluster; NG: Number of Genotypes

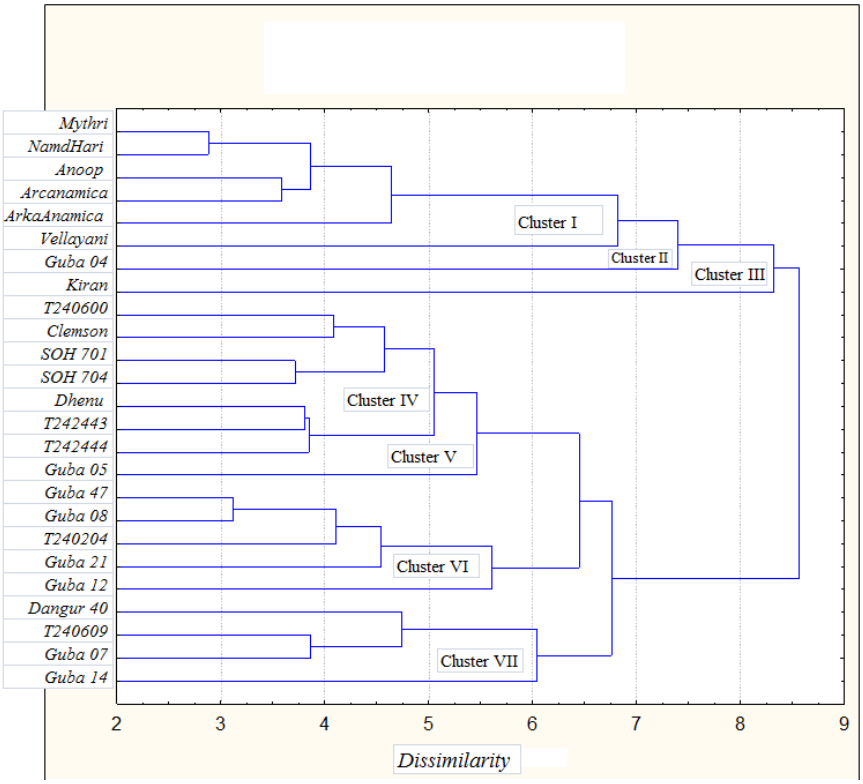

Figure 1. Dendrogram constructed using Unweighted Pair-group Method with Arithmetic means (UPGMA) depicting seven major clusters of 25 okra genotypes.

Table 5. Mean values of seven clusters for 29 traits of 25 okra genotypes

Traits	Cluster								
	I (6)			II (1)	III (1)	IV (7)			V (1)
	Mean	SD	CV (%)	Mean	Mean	Mean	SD	CV (%)	Mean
DEm	7.89	0.72	9.13	8.33	7.00	7.29	0.36	4.91	7.00
DFF	38.45	1.64	4.27	43.33	36.33	42.71	3.09	7.25	40.33
DFPF	45.61	2.16	4.74	48.67	43.33	47.90	2.75	5.73	49.33
DPF	50.06	3.74	7.48	54.00	47.67	52.95	3.12	5.90	55.00
DMa	59.17	4.61	7.80	64.67	56.00	61.76	3.59	5.81	62.00
PH (cm)	96.31	15.68	16.28	34.47	103.67	111.05	22.88	20.60	75.87
StD (cm)	1.42	0.13	9.05	1.69	1.63	1.92	0.11	5.66	1.84
NPBr	2.49	0.97	39.05	3.13	2.40	4.43	0.62	14.09	2.53
Nin	19.47	3.18	16.34	16.00	23.80	22.69	3.05	13.44	18.90
InLe (cm)	5.33	0.55	10.25	3.34	4.53	4.83	0.59	12.30	3.14
LLe (cm)	13.62	2.84	20.85	19.38	17.42	17.52	1.55	8.86	21.73
LWd (cm)	15.24	2.09	13.74	22.42	21.54	21.30	3.73	17.52	17.96
NEpy	10.19	0.47	4.60	11.40	10.27	10.96	0.58	5.30	12.47
PLe (cm)	2.09	0.40	18.99	1.40	2.68	2.52	0.58	23.20	2.46
FLe (cm)	12.29	0.66	5.40	10.23	12.96	10.55	1.15	10.88	12.16
FD (cm)	1.86	0.05	2.49	2.03	1.82	2.32	0.24	10.23	2.11
FWt (g)	15.07	2.26	15.02	22.48	20.72	24.53	1.70	6.95	32.56
NFPP	32.14	2.34	7.27	12.13	59.87	28.93	5.45	18.85	25.87
FR	5.11	0.05	1.03	7.16	5.34	7.03	0.98	13.93	7.75
FYPP (kg)	0.78	0.12	14.86	0.45	1.93	1.06	0.25	23.15	1.28
FYPP1 (kg)	7.78	0.87	11.17	4.45	19.27	10.22	2.24	21.90	12.80
FYPH (t/ha)	16.04	1.45	9.01	9.27	40.15	21.32	4.67	21.89	26.66
NMP	12.89	4.74	36.79	5.00	27.50	15.71	6.86	43.66	6.17
FWMP (g)	48.28	15.56	32.22	78.22	74.20	70.53	5.10	7.23	84.03
DWMP (g)	43.73	15.22	34.79	75.55	68.01	61.34	5.77	9.41	80.65
DM (%)	41.98	7.90	18.81	40.16	38.06	32.63	3.70	11.35	30.99
NSPP	60.09	10.87	18.09	71.50	74.80	88.78	14.45	16.28	100.90
HSW (g)	4.95	0.73	14.71	3.90	5.77	6.08	0.69	11.33	6.87
MuCo (%)	11.25	7.85	69.81	13.43	16.70	13.09	3.56	27.20	12.50

Trait	Cluster						Overall		
	VI (5)			VII (4)					
	Mean	SD	CV (%)	Mean	SD	CV (%)	Mean	SD	CV (%)
DEm	7.07	0.15	2.09	7.67	0.39	5.05	7.46	0.51	6.90
DFF	42.60	2.39	5.60	47.25	1.50	3.17	41.57	3.57	8.59
DFPF	47.67	2.44	5.12	55.08	1.29	2.33	48.23	3.64	7.55
DPF	53.73	2.60	4.83	60.58	1.45	2.40	53.43	4.06	7.60
DMa	62.93	3.38	5.37	70.17	0.84	1.19	62.39	4.43	7.10
PH (cm)	115.99	23.76	20.48	137.14	14.12	10.30	96.36	33.08	34.33
StD (cm)	2.09	0.12	5.59	2.10	0.13	6.18	1.81	0.25	13.79
NPBr	4.68	0.75	15.97	4.65	0.96	20.57	3.47	1.07	30.84
Nin	29.72	5.35	18.01	29.18	1.46	4.99	22.82	5.20	22.78
InLe (cm)	4.19	0.89	21.21	5.87	0.78	13.31	4.46	1.00	22.32
LLe (cm)	23.25	2.25	9.66	21.63	1.54	7.14	19.22	3.31	17.24
LWd (cm)	26.54	3.58	13.50	24.00	5.96	24.82	21.28	3.74	17.58
NEpy	12.41	0.56	4.54	13.82	2.79	20.19	11.65	1.32	11.38
PLe (cm)	2.16	0.50	23.36	2.42	0.46	18.99	2.25	0.43	18.95
FLe (cm)	10.10	1.87	18.49	10.13	0.52	5.12	11.20	1.22	10.89
FD (cm)	2.73	0.47	17.07	2.50	0.13	5.13	2.20	0.34	15.28
FWt (g)	29.72	5.95	20.02	21.49	4.43	20.60	23.80	5.85	24.56
NFPP	35.72	2.47	6.92	30.27	3.27	10.80	32.13	14.35	44.65
FR	8.08	0.39	4.77	7.39	0.74	9.97	6.84	1.16	16.94
FYPP (kg)	1.83	0.21	11.23	1.05	0.38	36.15	1.20	0.54	44.70
FYPP1 (kg)	17.66	1.50	8.47	10.18	3.21	31.51	11.77	5.27	44.77
FYPH (t/ha)	37.46	2.87	7.67	21.08	6.45	30.58	24.57	11.13	45.28
NMP	14.24	3.75	26.34	18.79	4.49	23.88	14.33	7.65	53.38
FWMP (g)	91.57	5.46	5.96	72.79	12.47	17.13	74.23	13.55	18.25
DWMP (g)	82.06	3.42	4.17	62.30	12.16	19.52	67.66	13.42	19.83
DM (%)	29.81	2.61	8.75	31.39	2.30	7.33	35.00	4.94	14.11
NSPP	113.51	7.36	6.48	103.43	3.95	3.81	87.57	19.49	22.26
HSW (g)	7.57	0.71	9.37	6.58	1.12	17.05	5.96	1.23	20.69
MuCo (%)	10.00	2.85	28.45	16.86	7.21	42.76	13.40	2.58	19.25

Table 6. Clusters minimum and maximum values of 29 quantitative traits for 25 okra genotypes evaluated at Dire Dawa in 2016

Traits	Minimum value	Cluster No.	Maximum Value	Cluster No.
Days to emergence	7.00	III, V	8.33	II
Days to first flowering	36.33	III	47.25	VII
Days to 50% flowering	43.33	III	55.08	VII
Days to pod formation	47.67	III	60.58	VII
Days to maturity	56.00	III	70.17	VII
Plant height	34.47	II	137.14	VII
Steam diameter	1.42	I	2.10	VII
Number of branches	2.40	III	4.68	VI
Number of internodes	16.00	II	29.72	VI
Internode length	3.14	V	5.87	VII
Leaf length	13.62	I	23.25	VI
Leaf width	15.24	I	26.54	VI
Number of epicalyxes	10.19	I	13.82	VII
Peduncle Length	1.40	II	2.68	III
Fruit length	10.10	VI	12.96	III
Fruit diameter	1.82	III	2.73	VI
Fruit weight	15.07	I	32.56	V
Number of fruits per plant	12.13	II	59.87	III
Fruit ridge	5.11	I	8.08	VI
Fruit yield per plant	0.45	II	1.93	III
Fruit yield per plot	4.45	II	19.27	III
Fruit yield ha-1	9.27	II	40.15	III
Number of matured pods	5.00	II	27.50	III
Fresh weight of matured pod	48.28	I	91.57	VI
Dry weight of matured pod	43.73	I	82.06	VI
Dry matter	29.81	VI	41.98	I
Number of seed per pod	60.09	I	113.51	VI
100 seed weight	3.90	II	7.57	VI
Mucilage content	10.00	VI	16.86	VII

FLe (cm) = Fruit length in centimeter, FD (cm) = Fruit diameter in centimeter, FWt (g) = Fruit weight in gram, NFPP= Number of fruit per plant, FR = Fruit ridge, FYPP (kg) = Fruit yield per plant in kilogram, FYPPl (kg) = Fruit yield per plot in kilogram, FYPH (t/ha) = Fruit yield per hectare in tones, NMP= Number of mature pod, FWMP (g)= Fresh weight of mature pod in gram, DWMP (g)= Dry weight of mature pod in gram, NSPP = Number of seed per plant, HSW (g) = Hundred seed weight in gram, DM (%) = Dry matter in percent, MuCo (%) = Mucilage content in percent., SD = Standard deviation and CV (%) = Coefficient of variation in percent.

Numbers in parenthesis represented number of genotypes in each cluster, Dem = Days to 50% emergency, DFF = Days to first flowering, DFPF = Days to 50% flowering, DPF= Days to pod formation, DMa = Days to maturity, PH (cm) = Plant height in centimeter, StD (cm) = Stem diameter in centimeter, NPBr = Number of primary branch, Nin = Number of inter node, InLe (cm)= Inter node length in centimeter, LLe (cm) = Leaf length in centimeter, LWd (cm) = Leaf width in centimeter, NEpy = Number of epicalyx, PLe (cm) = Peduncle length in centimeter, FLe (cm) = Fruit length in centimeter, FD (cm) = Fruit diameter in centimeter, FWt (g) = Fruit weight in gram, NFPP= Number of fruit per plant, FR = Fruit ridge, FYPP (kg) = Fruit yield per plant in kilogram, FYPPl (kg) = Fruit yield per plot in kilogram, FYPH (t/ha) = Fruit yield per hectare in tones, NMP= Number of mature pod, FWMP (g)= Fresh weight of mature pod in gram, DWMP (g)= Dry weight of mature pod in gram, NSPP = Number of seed per plant, HSW (g) = Hundred seed weight in gram, DM (%) = Dry matter in percent, MuCo (%) = Mucilage content in percent., SD = Standard deviation and CV (%) = Coefficient of variation in percent.

Discussion

The genetic distances of genotypes showed that the collections from Ethiopia and exotic commercial varieties were more distant than genotypes obtained from the same country. The availability of characterization data and the available information on genetic diversity can help germplasm users to identify genotypes of interest and it also provides data for plant breeders to decide which materials to be used in crop breeding programs (Diers and Osborn; 1994, as cited by Naser, 2014).

The result indicated that some of the introduced commercial varieties and collections from Ethiopia were most distant to the others. This suggested a higher chance of improving the traits of interest by crossing between commercial varieties and collections from Ethiopia or among Ethiopian okra genotypes.

This research showed the presence of diverse genotypes with a wide range of genetic distances which enables the researchers to improve the okra tender fruit yield and other desirable traits either through direct selection of genotypes or hybridization of okra genotypes having desirable traits. Okra has a higher chance of improvement through collection, characterization, evaluation and selection of okra genotypes from different

regions of the country or through hybridization (Muluken et al., 2015). Shujaat et al. (2014) and Pradip et al. (2010) suggested that genetic variation is an important feature to get together the diversified goals of plant breeding including higher yield, resistance to diseases, quality traits and wide adaptation abilities.

Clustering is a multivariate technique that can conveniently show the pattern of genetic relationships or proximity among accessions (Afifi and Clark, 1990). Clustering shows that each group is homogeneous with respect to certain characteristics and each group should be different from the other groups with respect to the same characteristics (Anderson, 1989, as cited Muluken, 2015). Genotypes in solitary clusters diverging from others may serve as potential parents for breeding programs indicating their independent identity and importance due to various unique traits possessed by them and may serve as potential parents in breeding programs (Thirupathi et al., 2102a).

In the current study, genotypes obtained from the same region or country tended to be grouped together, but it was not fully established that clusters were constructed by genotypes obtained from the same geographic region. Prakash et al. (2011), Temesgen et al. (2013) and Amoatey et al. (2015) reported that accessions obtained from the same geographic region fell in different genetic clusters and vice versa. But, Ahiakpa et al. (2013) reported that there was a direct relation between the eco-geographical origins of the okra collections and their clustering patterns. Singh and Singh (1979), Parbhat and Mamta (2012) suggested that forces other than geographical separations are also responsible for divergence. Genetic drift and selection in different environments may cause greater diversity than geographical distance. Patro and Ravisankar, (2004) reported that clusters do not represent their place of origin indicating that the genotypes in a cluster were geographically diverse, while genotypes obtained from the same region were genetically different.

The highest fruit yield may be as a result of long and wide leaves which increase dry matter production and increase fruit yield productions. The highest values in the number of internodes per plant and fruit diameter favor tender fruit yield while the highest values in the number of mature pods per plant increases seed production (Muluken et al., 2015). Therefore, the results suggested crossing of genotypes from Cluster I, III, IV and VII which had the highest number of matured pods per plant and Cluster I and V which had the highest mean values for dry matter content to increase tender fruit yield and seed number per pod. Genotypes in Cluster II and VII can be used for crossing to increase mucilage content.

Tesfa and Yosef (2016) observed a wide range of flowering periods among accessions which implies varying maturity periods that makes difficult for harvesting and practically not feasible for mechanization. The majority of the accessions exhibited compact growth habits. Muluken et al. (2015) and Mihretu et al. (2014a) pointed out that the different clusters have different breeding values that enable breeders to improve different traits and parental selection should be made based on the relative merits of each cluster for each trait depending on the objective of the breeding program.

Conclusion

The results from diversity analysis indicated that the okra collections from Ethiopia and introduced commercial varieties were more distant though some of the collections and introduced varieties were most distant to others. Genotypes obtained from the same geographic regions or countries tend to be grouped together though it was not fully established that clusters were constructed by genotypes obtained from the same geographic region. The results of this study revealed the presence of wide genetic diversity among okra genotypes that could be exploited to develop varieties in Ethiopia. The genotypes that had high tender fruit yield with desirable fruit quality traits could be promoted to multi-location tests to develop varieties. The observed genetic diversity within okra collections in Ethiopia and between collections and exotic commercial varieties is a good indication of the spatial divergence of genotypes within the country and between countries which suggested the importance of conducting molecular characterization to explain genetic diversity in more detail.

Acknowledgements

The authors are grateful to the financial support of the Ministry of Ethiopian Education for the execution of the research. The authors also thank Haramaya University for its unreserved support in facilitating the research activities during the time of conducting the experiment.

Funding

The authors are thankful to Haramaya University for financial support and for providing plant material and other research facilities.

Conflicts of Interest

The authors declare there are no conflicts of interest.

References

Afifi AA, Clark V. 1990. Computer aided multivariate analysis. Van Nostrand Reinhold.NewYork, USA, USA, Pp 505.

Ahiakpa JK, Kaledzi PD, Adi EB, Peprah S, Dapaah HK. 2013. Genetic diversity, correlation and path analyses of okra [*Abelmoschus* spp. (L.) Moench] germplasm collected in Ghana. International Journal of Development and Sustainability, 2(2):1396-1415.

Aladele SE, Ariyo OJ, de Lapena R. 2008. Genetic relationships among West African okra (Abelmoschus caillei) and Asian genotypes (*Abelmoschus esculentus*) using RAPD. Afr. J. Biotech. 7: 1426- 1431.

Amoatey HM, GYP Klu, Quartey EK, Doku HA, Sossah FL, Segbefia MM, Ahiakpa JK. 2015. Genetic diversity studies in 29 genotypes of okra (Abelmoschus spp (L.) using 13 quantitative traits. American Journal of Experimental Agriculture, 5(3): 217-225.

Anderson TW. 1989. An introduction to multivariate statistical analysis. John Wileyand Son, New York. PP 675.

Calisir S, Yildiz MU. 2005. A study on some physico-chemical properties of Turkeyokra (Hibiscus esculenta) seeds. Journal of Food Engineering, 68, 73–78.

Diers BW, Osborn TC. 1994. Genetic diversity of oilseed (*Brassica napus)* germplasm based on restriction fragment length polymorphisms. Theor. Appl. Genet., 88:662-668.

Falconer DS, Mackay TFC. 1996. An Introduction to Quantative genetics. Ed, 4. Printice Hall London. PP 464

Habtamu FG, Negussie R, Gulelat DH, Ashagrie ZW, Fekadu B. 2014. Nutritional Quality and Health Benefits of Okra (*Abelmoschus esculentus*): A Review. Food Science and Quality Management Vol.33.

Hailay DT, Marc L, Awash T, Joel S. 2004. Weather-based prediction of Plasmodium falciparum malaria in epidemic-prone regions of Ethiopia I. Patterns of lagged weather effects reflect biological mechanisms. Malaria Journal 2004, 3:41 doi: 10.1186/1475-2875-3-41

IPGRI. 1991. Okra Descriptor list. International Crop Network Series 5. International Board for plant Genetic Resources (IBPGR), Rome, Italy.

Johnson RW, Robinson HF, Comstock RE. 1955. Estimating genetic and environmental variability in soya bean. Agronomy Journal, 47: 314-318.

Levoyageur Weather: Djibouti. 2012. http://en.wikipedia.org/w/index

Mihretu Y, Weyessa G, Adugna D. 2014a. Multivariate analysis among Okra [*Abelmoschus esculentus* (L.) Moench] Collection in South Western Ethiopia. Journal of Plant Sciences, 9: 43-50.

Mihretu Y, Weyessa G, Adugna D. 2014b. Variability and association of quantitative traits among okra [*Abelmoschus esculentus* (L.) Moench] collection in South Western Ethiopia. Journal of Biological science, 14: 336-342.

Muluken D, Wassu M, Endale G. 2015. Genetic diversity of Ethiopian okra collection through multivariate analysis at Werer, Rift Valley of Ethiopia. The International Journal of Science & Technoledge (ISSN 2321 – 919X).

Naser MS. 2014. Genetic Diversity of okra [*Abelmoschus esculentus* (L.) Monech] landraces from different agro-ecological regions revealed by AFLP analysis. American-Eurasian Journal of Agriculture. & Environmental Science, 14 (2): 155-160.

Parbhat K, Mamta P. 2012. Genetic diversity and its relationship with heterosis in okra. Vegetable Science, 39 (2): 140-143.

Patro TS, Ravisankar C. 2004. Genetic variability and multivariate analysis in okra [*Abelmoschus esculentus* (L.) Moench] Tropical Agricultural Research. 16 : 99-113.

Pradip K, Akotkar DK, De and Pal AK. 2010. Genetic variability and diversity in okra [*Abelmoschus esculentus* (L).Moench]. Electronic Journal of Plant Breeding, 1(4): 393-398.

Prakash K, Pitchaimuthu M, Ravishankar KV. 2011. Assessment of genetic relatedness among okra genotypes [*Abelmoschus esculentus* (L) Moench] using rapd markers. Electronic Journal of Plant Breeding, 2(1): 80-86.

Robinson HF, Comstock RE, Harvey PH. 1955. Estimates of heritability and the degree of dominance in maize. Agronomy Journal, 41: 353-359.

Santos BM, Dittmar PJ, Olson SM, Webb SE, Zhang S. 2012. Okra Production in Florida. University of Florida IFAS extension. pp 163-171.

Shujaat A, Azhar HS, Rehmani G, Habib A, Hasnian N, Sikandar KS. 2014. Morpho-Agronomic Characterization of okra [*Abelmoschus esculentus* (L.) Moench]. World Applied Sciences Journal, 31(3): 336-340.

Singh SP, Singh HN. 1979. Genetic divergence in okra [*Abelmoschus esculentus* (L.) Moench]. Indian Journal of Horticulture, 51(1): 166-170.

Sneath PHA, Sokal RR. 1973. Numerical Taxonomy: the principles and practice of numerical classification. Fransisco USA W.F Freeman, Pp 573.

Soni O. 2016. Genetic Variability, Correlation and Path analysis in Okra. Department of Horticulture College of Agriculture, Jabalpur 482004 Jawaharlal Nehru Krishi Vishwa Vidyalaya Jabalpur, Madhya Pradesh.

Temesgen B, Mebeaselassie A, Million E. 2013. Genetic divergence analysis of garden cress (Lepidium sativum L.). International Journal of Biodiversity and Conservation, 5(11): 770-774.

Tesfa B, Yosef A. 2016. Characterization of Okra (*Abelmoschus esculentus* (L.) Moench) Germplasms Collected from Western Ethiopia. International Journal of Research in Agriculture and Forestry. Volume 3, Issue 2, PP 11-17.

Thirupathi RM, Hari BK, Ganesh M, Chandrasekhar RK, Begum H, Purushothama RB, Narshimulu G. 2012a. Genetic variability analysis for the selection of elite genotypes based on pod yield and quality from the germplasm of okra [*Abelmoschus esculentus* (L.) Moench]. Journal of Agricultural Technology, 8: 639-655.

Tripathi KK, Govila OP, Ranjini W, Vibha A. 2011. Biology of okra [Abelmoschus esculentus (L). (Moench]. Serious of Crop Specific Biology Document. Ministry of Environment and forests government of India and department of biotechnology ministry of science and technology government of India. Pp 22.

Uzma F., Rishabha M. and Pramod KS. 2013 Extraction and Characterization of Okra Mucilage as Pharmaceutical Excipient. Academic Journal of Plant Sciences 6 (4): 168-172, 2013.

William MA, Woodbury GW. 1968. Specific gravity-DM relationship and reducing sugar changes affected