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Evaluation of Okra [*Abelmoschus esculentus* (L.) Moench] Genetic Variability at Melkassa, Central Ethiopia

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Abstract

Okra [*Abelmoschus esculentus* (L). Moench] is one of the indigenous genetic resources of western Ethiopia. However, only a few studies were carried out to assess its diversity and performance throughout the country, and specifically, no research was conducted to assess the diversity of okra within a regional state. Therefore, this study was conducted to determine the genetic divergence of okra genotypes collected from a regional state. A total of 36 genotypes of which 33 okra genotypes were collected from different areas of Benishangul Gumuz Regional State, 3(three) checks, of 2 introduced and 1(one) released were evaluated for 24 quantitative traits at MARC in 2018/19 using simple lattice design (6 x 6). The results from the study were revealed that four principal components (PC1 to PC4) with eigenvalues ranged from 1.83 to 7.58 which accounted for a total of 71.34% cumulative contributions of which the PC1 and PC2 had a larger contribution of 31.591 and 18.397%, respectively, while PC3 and PC4 contributed 13.754 and 7.596%, respectively. The genetic distance of genotypes ranged from 2.83 to 12.24 with mean, standard deviation, and coefficient of variation 6.73, 1.63, and 24.18(%), respectively. All the 36 genotypes clustered in 13 distinct clusters consisting of 11 (30.56%) in cluster I to seven clusters in which genotypes are solitarily clustered. Among cluster, cluster VII had the highest fruit yield by leading the other seven clusters greater than overall cluster means. The result observed in this study was the presence of a wide genetic variation among genotypes collected from Benishangul Gumuz Regional State.

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Keywords

Clustering analysis, Genetic distance, Genetic divergence, Principal component

Introduction

Okra [*Abelmoschus esculentus* (L.) Moench] belongs to the family Malvaceae and it is a very important vegetable crop grown in tropical and sub-tropical parts of the world (Kisher *et al.,* 2016). Okra is proposed to be originated in Tropical Africa and it is native to North Eastern Africa in the area of Ethiopia and Sudan from where it extensively spread to Asia, America, Southern Europe, and other countries (Santos *et al.,* 2012). It is self-pollinated, mainly propagated by seeds with a duration of 3 to 4 months (Muhammad *et al.,* 2013; Osawaru *et al.,* 2014). Cultivated okra fruit has a considerable area under cultivation in Africa, America, and Asia in particular because of its contribution to the human diet by supplying fats, proteins, carbohydrates, minerals, and vitamins. Its mucilage is suitable for medicinal and various industrial applications (Lamont, 1999; FAO,

2004; Saifullah and Rabbani, 2009; Haruna *et al*., 2016). The unripe green finger-like seed capsule of okra, usually called "pod" is processed and consumed as stews and salads, soups, sliced, boiled, and fried vegetables (Akanbi *et al.*, 2010; Daniela *et al.*, 2012). Okra typically differs from most other common vegetables in having high mucilage content (Jideani and Bello, 2009). The seed is used as a coffee additive or substitute (Moekchantuk and Kumar, 2004).

The collection of desirable plant germplasm relies on the proven accession features and genetic divergence, which are essential in genetic resource utilization (Olaoye*et al.*, 2009; AdeOluwa and Kehinde, 2011). Genetic diversity denotes the variability in different crop species, and its links with accession identification which is important in genebank curators and improvements (Osekitar and Akinyele, 2008; Bello *et al.*, 2011). Improvement in plant breeding scheme leans on high genetic differences in the population and the magnitude of inheritance of favorable attributes (Olawuyi*et al.*, 2015). Progress and gain from the selection in any breeding program depend upon the magnitude of useful variability present in the population and the degree to which the desired traits are heritable. Therefore, the efficiency of selection in any breeding program mainly depends upon the presence of genetic variationsbased on study traits.

The recently conducted research tried to characterize and reported the presence of diversity in okra collection in Ethiopia (Miheretu *et al*., 2014a and b; Muluken *et al*., 2015 and 2016; Tesfa and Yosef, 2016; Wassu*et al*., 2017). However, these studies did not focus to assess the genetic variability among okra genotypes in each major okra growing region in Ethiopia. Geographic distances and environment differences are the two major causes of genetic diversity among plant populations (Slatkin, 1987; Nosil*et al*., 2009). Moreover, Benishangul Gumuz Regional State one of the potential producers of okra among the major producers and many genotypes collected from regional state and no one can try to investigate the genetic diversity of okra in the regional state. Therefore, research focusing on the assessment of diversity among okra genotypes collected from Benishangul Gumuz Regional State is important to generate additional information and fill the gap of insufficient information generated on okra genotypes in the region. The information generated from such study also helps to design appropriate okra breeding and germplasm conservation strategies in the region. Therefore, this research is initiated and intended to determine the genetic divergence of okra genotypes collected from the Benishangul Gumuz Regional State.

Materials and Methods

Description of study area

The study was conducted at Melkassa Agriculture Research center (MARC), Ethiopia in the 2018/19 main cropping season. Malkasa is located $8^0$24'N latitude and $39^0$21'E by having a distance of around 112 K.M from Addis Abeba on the Eastern direction at an altitude of 1550m.a.s.l. The area is characterized by low and erratic rainfall with a mean annual rainfall of 763 mm with peaks in July and August. The dominant soil type of the center is andosol of volcanic origin with pH that ranges from 7 to 8.2. The mean annual temperature is 21.2^0C with a minimum of 14^0C and a maximum of 28.4^0C (MARC, 2019 http://www.eiar.gov.et/marc).

Experimental materials and design

A total of 36 genotypes were evaluated of which 33 okra genotypes were collected from different areas of Benishangul Gumuz Regional State of Ethiopian by the Ethiopian Biodiversity Institute and 2 (two) of the varieties were introduced from India and now registered as a commercial variety in Ethiopia by one company and 1 (one) variety is released from Humera research center. The okra genotypes were collected at different altitudes ranging from 661 to 1518 m.a.s.l. The three registered varieties will be used as the standard checks. Genotypes were evaluated on the field in 6 x 6 simple lattice designs. Each plot had 0.8 m x 5.4 m (4.32 m^2) consisting of one row and a total of 12 plants per row or plot. The spacing between plant, plots, and adjacent replications was 0.45, 0.8, and 2m, respectively. Three seeds were sown and thinned to one plant per hill when plants reached 4-5 leaves stage.

Data collections

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 the two border plants were used for mature pod and seed traits measurement. Five randomly selected tender fruits from each harvest in each plot were used to record tender fruit characters.

Crop phenology and growth traits

Days to emergence (50%), days to first flowering, days to 50% flowering, days to 90% maturity, number (frequency) of harvest, plant height (cm), stem diameter (cm), number of primary branches, number of internode, internodes length (cm), leaf length (cm), leaf width (cm), number of epicalyxes, and peduncle length (cm) was measured properly.

Pod yield and yield component

Fruit length (cm), fruit diameter (mm), average fruit weight (g), number of tender fruit per plant, fruit yield per plant (kg), fruit yield per hectare (t/ha-1), number of seed per fruit, hundred seed weight (g), seed yield per plant (g), and seed yield per hectare (kg) was taken accordingly.

Tender fruit quality related traits

Dry matter content of tender fruit (%) and estimation of mucilage content of fruit (%) were also employed at the laboratory.

Data analysis

Principal component analysis

Principal component analysis (PCA) was computed to find out the characters, which accounted more for the total variation. The data was standardized to mean zero and variance of one before computing principal component analysis. The principal component based on a correlation matrix was calculated using XLSTAT software (2014).

Genetic distance and clustering

Euclidean distance (ED) was computed from all data collected for okra accessions after standardization (subtracting the mean value and dividing it by the standard deviation) as:

$EDjk = \sqrt{\sum_{i=1}^{n}(Xij - Xik)^2}$ (Sneath and Sokal, 1973), Where $EDjk$ = distance between accessions j and k; Xij and Xik = phenotype traits values of the ith character for genotypes j and k, respectively; and n = number of phenotype traits used to calculate the distance. The distance matrix from phenotype traits was used to construct dendrograms based on the Unweighted Pair-group Method with Arithmetic Means (UPGMA). The results of cluster analysis were presented in the form of dendrograms. Besides, mean ED was calculated for each accession by averaging of a particular genotype to the other 35 genotypes. The calculated average distance (ED) was used to estimate which genotype(s) is closest or distant to others.

Results and Discussions

Principal component analysis

The principal component analysis (PCA) of 24 quantitative traits are presented in (Table 1). The results were also included the factor score of each trait among the 36 okra genotypes, Eigenvalues, and the percentage of contribution to the total variability accounted for 4 principal components. Principal component analysis (PCA) was computed to find out the traits which accounted more to the total variation (Chahal and Gosal, 2002).

This principal component analysis resulted in four principal components (PC1 to PC4) with eigenvalues ranged from 7.582 to 1.832. The four principal components accounted for the varied percentage of the total variance of 31.591%, 18.397%, 13.754%, and 7.596% for PC1, PC2, PC3, and PC4, respectively. These four components accounted for a total of 71.34% cumulative contributions. In PCA principles, if >50% of the variations catches with the PCs in which each contribution is having >10% contribution and Eigenvalue >1, it is acceptable (Table 1). Therefore, since the total variation of PC1 to PC4 > 50%, the other could be ignored. There was no guideline to determine the significance of eigenvectors (Duzyaman, 2005). The higher coefficients for traits substantiated the relatedness of that trait with the respective PC axis (Broschat, 1979).

The total contribution of the four principal component axis of this study result was higher and similar to the results reported by other authors. Osawuru *et al.,* (2014) reported the variation observed up to five principal component axis ranges from 6.90 to 22.97% for PC1 to PC5, respectively. They also reported the cumulative variation of five PCA was accounted for 70.2% of the variation. Mihretu *et al.,* (2014b) reported six principal components for 20 traits of 25 okra genotypes in which eigenvalues were 10.65, 3.04, 2.41, 1.7, 1.62, and 1.32 which accounted 83% of the cumulative variation. Mulukene*t al.,* (2016) reported the first three principal

components PC1, PC2, and PC3 with values of 32.4%, 16.7%, and 8.2%, respectively, and contributed more to the total of 57.3% variation. Asare and Asare-bediako (2016) also reported eigenvalues of four PCs 3.42, 1.34, 1.11, and 1.06 from PC1 to PC4 respectively that accounted for 77% of cumulative variations. Davinder*et al.,* (2018) reported four principal components for ten quantitative traits and the eigenvalues of each component were 3.414, 3.215, 1.239, and 0.915 from PC1 to PC4, respectively which accounted for 87.84% of the cumulative variation. Ahiakpa (2012) reported that the principal component axis contributed 64.32% of the cumulative variation.

According to Chahal and Gosal (2002), traits with the largest absolute values closer to unity with in the first principal component influence the clustering more than those with lower absolute values closer to zero. Therefore, in the present study, the differentiation of the traits was due to the cumulative effect of the number of traits rather thanto the small contribution of each trait ($\pm$ 0.006 to 0.923).

The traits that highly contributed to differentiation were in principal component (PC-I) was number (frequency) of the fruit harvest, number of tender fruit per plant, number of primary branches, seed yield per plant, pod yield, days to first flowering, days to 50% flowering, number of internode, and days to 90% maturity had a relatively high contribution. For PC-2 average fruit weight, number of fruit ridge, number of seed per pod, fruit length, fruit diameter, and fruit yield had relatively higher contributions (Table 1).

Mihretu *et al.,* (2014b) reported that days to first flowering, number of seed per pod, number of tender fruit per plant, internode length, and number of internodes were major contributors of diversity in the okra plant and they confirm the presence of genetic diversity for further improvement programs. Pradip *et al.,* (2010) reported plant height, number of internode, and fruit ridges as a major contributor to okra diversity. On the contrary Muluken *et al.,* (2015) reported the maximum contributors on component axis were leaf width followed by days to 50% flowering, pod yield per plant, hundred seed weight, stem diameter, internode length, fruit length, plant height, peduncle length and the number of tender fruit per plant. Relative reports by Ahiakpa *et al.,* (2014) reported that the first four PC-axis contributed for 82.97% of the variations in okra was a number of branches per plant, days to 50% flowering, intermodal length, number of fruits per plant and fruit yield contributed to the variation in PC1. Stem diameter, days to 50% flowering, internodal length, fruit weight, and fruit yield accounted for the variations observed in PC2. Plant height, stem diameter, fruit diameter, and fruits per plant contributed to the variations in PC3. Stem diameter and fruit diameter contributed to variations in PC4. These variations may suggest the existence of genetic diversity in okra that can be an input to improve the crop.

Davinder *et al.,* (2018) reported an assessment of the relative contribution of ten characters towards total genetic divergence revealed that branches per plant had contributed highest (41.61%) followed by fruit yield per plant (31.49%), fruits per plant (15.17%) and stem diameter (1.61). He also suggests characters with the highest genotypic variability should be considered while selecting parents for hybridization programs.

In general, this result implied that traits such as number of harvests, number of tender fruit per plant, number of primary branches, seed yield, pod yield, days to flowering, number of internodes, maturity date, average fruit weight, fruit length, and fruit diameter which associated with PC1 and PC2 are implicated for being responsible for the phenotypic divergence observed in the cultivars and can be used for cultivar discrimination for the improvement program. The traits which contributed much in each PC1 to PC4 were also presented in the figure for visual observation (Figure 1).

Clustering and genetic distances of okra genotypes

Clustering of genotypes

The Euclidean distance matrix of 630 pairs of genotypes estimated from 24 phenotypic traits was used to construct dendrograms based on the Unweighted Pair-group methods with Arithmetic Means (UPGMA). Accordingly, all 33 local collections and 3 checks are grouped into 13 distinct clusters (Figure 2). The highest number of genotypes were grouped in the first Cluster contained 11 genotypes (30.56%) which included 3 checks, 1 from Guba, 2 from Menge, 3, from Kurmuk and 2 from Assosa woredas followed by Cluster VIII which consisted of 6 (16.67%) genotypes and all genotypes were collected from Assosa woreda. Cluster IX consisted of 4 (11.11%) genotypes of which 2 each from Mandur and Assosa woredas, while Cluster X and III had 3 and 2 genotypes, respectively. The other

clusters (IV, V, VII, XI, XII, and XIII) were all solitary and each consisted of genotype (Figure 2).

Wassu *et al.,* (2017) grouped 25 okra genotypes into seven major clusters in which the three clusters (Cluster II, III, and V) were solitary consisted of one genotype and each cluster had distinct characters. Tesfa and Yosef (2016) from Melkasa have grouped 50 okra accession collected from four major okra growing areas of the country into IV clusters. Muluken *et al.,* (2016) reported 25 okra accessions grouped into ten major clusters and four clusters were solitary that each cluster consists of one accession. They also reported that the other six clusters consisted of more than one up to the maximum 10 accessions. Mihretu *et al.,* (2014) were also able to group 25 okra genotypes collected from two regions into five major clusters. Davinder *et al.,* (2018) from India reported 30 okra genotypes are clustered into six groups based on 10 quantitative characters. Clustering is a multivariate technique that can conveniently show the pattern of genetic relationships or proximity among accessions (Afifi and Clark, 1990). Each group is homogeneous for certain characteristics and each group should be different from other groups for some characteristics (Anderson, 1989).

Genetic distances of genotypes

The genetic distances of 630 pairs of okra genotypes are presented in (Appendix Table 1). The mean genetic distance of 36 okra genotypes was calculated to generate information about the most distant and closest genotypes (Table 2). The genetic distance for all possible pairs of 36 genotypes ranged from 2.83 to 12.24 with the mean, standard deviation, and coefficient of variation of 6.73, 1.63, and 24.18, respectively. The highest genetic distances (Euclidean distance) were computed between accession 29618 and 29417 (12.24) followed by genotype [29618 to 29408 (12.04), 29409 (11.92) and 29411 (11.48)], respectively. Whereas, the lowest was computed between genotypes 29625 and 29412 (2.83) followed by SOH714 and Bamia Humera (2.88), 242433A, and 240209A (2.87), 29620 and 29623 (3.051), respectively. The largest proportion 312 (49.52%) of pair of genotypes had Euclidean distances of $\leq$6.73 (overall mean ED), a small percentage 25(3.97%) pair of genotypes had Euclidean distances of >9.56, and the remaining 293(46.51%) pair of genotypes had Euclidean distances in between 6.73 to 9.56 (Table 2). The result suggested that the presence of a considerable number of distant okra genotypes to others that could be used in the crossing program to combine the desirable traits of the genotype.

The genotype 29618 which collected from Assosa woreda on 1419 m.a.s.l. and two genotypes 29416 and 29415 collected from Balojiganfoy Woreda on 1195 and 1192 m.a.s.l. had higher genetic distance among evaluated genotypes as well as checks (Table 2). Since most genotypes had greater genetic distance than released variety and introduced varieties, there is a higher chance of improving fruit yield and fruit related traits through the selection and/or crossing of okra genotypes from the regional state. Wassu *et al.,* (2017) reported that Euclidean distances of 300 pairs of 25 genotypes evaluated at Dire Dawa and reported the genetic distance ranged from 3.1 to 12.6 with 7, 2.2, and 27.85% mean, standard deviation, and coefficient of variation, respectively. They also reported the presence of a high genetic distance between Ethiopian accessions. Muluken *et al.,* (2015) reported that Ethiopian okra collections exhibited wide genetic distances in the range between 5.16 and 11.14. Mihretu *et al.,* (2014b) were also reported a very high genetic distance among local collections.

The genotype 29618 had the highest mean Euclidean distance of 8.94 followed by 29416 (7.93), T240204 (7.63), and 29415 (7.62). Whereas genotypes 242433A (5.47) followed by genotypes 242445A (5.61) and 240209A (5.66) and 29413 (5.73) had the lowest Euclidean distance compared all other genotypes (Table 2). The genotypes with high genetic distances between them have the potential to produce heterotic hybrids through crossing made among genotypes. Among tested 33 local collections, 20 (60.6%) genotypes had mean genetic distances greater than the overall mean genetic distance of genotype (Table 2). The results indicated that the genotypes were highest distant to others or/and had genetic distance above the average to other genotypes and 13 (39.4%) of the new collection had less than the overall mean Euclidean distance. Whereas, the released variety Bamia-Humera (6.05), and the two other introduced checks viz. SOH701 (5.98) and SOH714 (6.37) had a distance lower than the mean Euclidean distances.

These results revealed the presence of diverse okra 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 or crossing of okra genotypes having different desirable traits. The availability of genetically broad-

based variation for yield and its component traits is a prerequisite for the development of new cultivars of okra. Okra breeders all over the world have been utilizing the available genetic resources to modify the varieties (Reddy *et al.,* 2012). Maximum genetic recombination is expected from the hybridization of the parents selected from divergent combinations (Mihretu *et al.,* 2014).

Table.1 The principal component values of four principal components from 24 quantitative traits for 36 okra genotypes evaluated at Melkassa in 2018/19

No	Trait	Eigenvectors			
		PC1	**PC2**	**PC3**	**PC4**
1	Days to 50% emergence	0.469	-0.164	0.370	0.015
2	Days to first flower	0.634	-0.231	0.641	-0.169
3	Days to 50% flowering	0.611	-0.233	0.667	-0.151
4	Days to 90% maturity	0.559	-0.223	0.687	-0.086
5	Stem diameter (mm)	0.232	0.348	0.351	0.549
6	Plant height (cm)	0.170	0.323	0.469	0.597
7	Number of primary branches	0.891	0.191	-0.147	-0.098
8	Number of internodes	0.578	0.023	0.100	0.565
9	Internode length (cm)	-0.247	0.363	0.337	0.090
10	Peduncle length (cm)	-0.190	-0.160	0.627	-0.540
11	Fruit length (cm)	-0.541	0.652	-0.052	-0.012
12	Fruit diameter (mm)	0.083	0.639	0.491	0.213
13	Average fruit weight (g)	-0.317	0.847	0.224	0.006
14	Number of tender fruit per plant	0.902	-0.123	-0.301	-0.034
15	Number of fruit ridge	-0.470	0.701	0.091	-0.147
16	Pod yield per plant (g)	0.682	0.638	-0.182	-0.148
17	Pod yield per hectare (tons)	0.682	0.638	-0.182	-0.148
18	Number of seed per pod	-0.218	0.675	-0.016	-0.215
19	Hundred seed weight (g)	0.157	0.476	-0.072	-0.251
20	Seed yield per pod (g)	0.876	0.296	-0.281	-0.173
21	Seed yield per hectare (Kg)	0.876	0.296	-0.281	-0.173
22	Number of harvests	0.923	0.031	-0.074	0.076
23	Dry matter content (%)	0.025	0.046	0.445	-0.399
24	Mucilage content (%)	0.380	-0.280	-0.360	0.180
	Eigenvalue	7.582	4.415	3.301	1.823
	Difference	3.167	1.114	1.478	0.503
	Contribution to Variability (%)	31.591	18.397	13.754	7.596
	Cumulative contribution %	31.591	49.988	63.742	71.338

PC = Principal Component.

Table.2 Range, mean, standard deviation, and Coefficient of variation Euclidean distances of 36 okra genotypes estimated from 24 quantitative traits evaluated at MARC in year 2018/19

No	Genotype	Minimum	Maximum	Mean	SD	Cv (%)
1	29408	4.66	12.03	7.07	1.79	25.25
2	29409	4.03	11.92	7.06	1.84	26.14
3	29410	4.89	10.14	6.89	0.94	13.62
4	29411	3.92	11.48	6.74	1.93	28.66
5	29412	2.83	10.83	6.52	1.92	29.39
6	29622	3.65	11.29	6.79	1.89	27.88
7	29414	3.83	8.93	6.71	1.38	20.63
8	29415	5.49	10.14	7.62	0.98	12.80
9	29416	4.97	9.78	7.93	1.26	15.85
10	29418	3.59	9.36	7.06	1.43	20.27
11	29616	3.13	8.99	6.31	1.52	24.15
12	29618	4.35	12.24	8.94	1.99	22.29
13	29052	4.06	9.62	6.85	1.52	22.15
14	T240204	4.47	9.66	7.63	1.41	18.53
15	29417	4.13	12.24	7.44	1.72	23.10
16	T242443	3.84	9.06	7.02	1.29	18.45
17	240207A	3.83	9.07	6.77	1.26	18.67
18	240209A	2.87	8.81	5.66	1.10	19.41
19	242433A	2.87	8.15	5.47	0.99	18.07
20	242449A	5.04	9.51	6.99	1.20	17.15
21	242445A	3.99	8.05	5.61	1.25	22.24
22	29051	3.81	9.13	5.95	1.09	18.31
23	29413	3.65	9.90	5.73	1.57	27.43
24	29615	3.13	9.90	7.11	1.65	23.21
25	29625	2.83	10.52	6.66	1.78	26.76
26	29617	4.54	9.24	7.45	1.27	17.10
27	29624	4.24	9.78	7.30	1.15	15.80
28	29620	3.05	9.63	6.70	1.46	21.76
29	29621	3.71	9.24	6.41	1.40	21.84
30	29623	3.05	8.89	6.06	1.36	22.51
31	29619	3.72	9.58	6.74	1.44	21.44
32	242451A	3.74	9.26	6.87	1.27	18.49
33	T242444	3.81	8.72	6.00	1.39	23.21
34	SOH701	3.36	9.91	5.98	1.57	26.26
35	SOH714	2.88	10.16	6.37	1.90	29.78
36	BamiaHumera	2.88	8.92	6.05	1.57	25.93
	Overall	**2.83**	**12.24**	**6.73**	**1.63**	**24.19**

Table.3 Mean values of 13 clusters for 24 quantitative traits of 36 okra genotypes evaluated at Melkassa in year 2018/19

	Cluster													
Traits	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**IX**	**X**	**XI**	**XII**	**XIII**	**Means**
Eme	7.86	7.50	8.25	8.50	8.0	8.83	9.50	9.75	9.38	8.83	10.50	10.50	9.50	8.99
Dflo	48.00	54.50	48.25	61.0	60.5	64.50	58.50	59.42	51.63	49.67	54.0	71.0	60.50	57.04
Flo	52.73	60.0	52.0	66.0	67.0	70.33	63.50	65.08	56.25	54.0	59.50	77.50	67.0	62.38
Mat	80.86	87.50	81.0	92.0	102.5	95.83	87.50	94.67	85.25	81.50	89.50	103.0	96.0	90.55
SD	19.41	30.50	17.75	21.0	28.6	21.67	18.50	20.25	22.25	21.17	24.0	22.50	18.2	21.98
PH	117.02	178.0	137.50	155.5	148.5	104.35	115.50	126.53	164.21	88.30	186.50	194.50	141.0	142.88
PB	2.24	3.70	7.50	6.30	6.25	7.38	12.70	4.0	5.3	4.03	4.95	5.0	4.7	5.70
NI	21.23	29.00	29.75	18.50	39.0	26.67	30.50	28.33	27.75	23.83	32.50	31.50	26.50	28.08
IL	5.18	7.40	4.75	10.25	3.4	3.02	3.70	3.73	6.08	3.03	5.85	6.60	6.40	5.34
PL	2.13	2.10	1.75	3.30	2.3	1.93	1.90	2.41	1.93	2.04	1.53	1.88	3.45	2.20
FL	14.26	9.87	10.77	18.80	13.25	8.18	5.77	6.85	14.17	15.79	12.15	12.45	5.50	11.37
FD	26.04	35.15	23.08	26.34	35.2	27.20	24.10	26.89	33.35	27.79	29.39	28.95	29.10	28.66
AFW	39.09	39.66	23.36	60.32	55.9	30.85	17.04	23.14	55.46	47.0	46.12	25.36	23.66	37.46
NTFPP	13.27	20.40	37.25	17.0	24.4	33.63	55.20	22.70	18.65	19.73	26.80	24.90	22.0	25.84
NR	6.96	6.90	5.75	7.0	7.2	6.20	5.70	5.52	7.30	6.93	6.0	6.30	6.50	6.48
YPP	473.89	670.23	977.77	1016	869.66	993.69	1183.6	502.65	957.41	872.13	924.80	541.91	556.10	810.76
Yhaton	13.16	18.62	27.16	28.22	24.16	27.60	32.88	13.96	26.59	24.23	25.69	15.05	15.45	22.52
NSPP	82.07	63.20	64.55	94.0	106.0	81.87	60.50	66.10	95.18	92.07	80.70	65.20	63.50	78.07
SDW	5.75	5.28	5.90	6.84	5.96	5.55	6.02	5.92	6.19	6.31	7.16	5.24	6.24	6.03
SYPP	63.31	65.46	139.93	109.23	154.08	152.26	198.04	87.51	109.31	114.69	150.53	84.79	87.46	116.66
Syph	1758.7	1818.4	3887.1	3034.1	4280.1	4229.5	5501	2431	3036.5	3185.8	4181.3	2355.3	2429.3	3240.6
Nha	5.94	7.30	7.95	6.80	7.50	8.0	8.0	7.13	7.03	6.97	7.60	7.70	7.40	7.33
DMC	25.85	24.56	25.58	30.20	32.48	26.99	22.56	25.87	24.59	24.82	27.88	22.04	34.55	26.77
PMC	11.15	11.02	13.84	12.01	7.17	13.89	20.01	16.43	11.59	19.91	19.93	16.01	7.85	13.91

Eme= Days to 50% emergence, Dflo= Days to first flower, Flo= Days to 50% flowering, Mat= Days to 90% maturity, SD=Stem diameter (mm), PH= Plant height (cm), PB= Number of primary branch, NI= Number of internode, IL= Internode length (cm), PL= Peduncle length (cm), FL= Fruit length (cm), FD= Fruit diameter (mm), AFW= Average fruit weight (g), NTFPP= Number of tender fruit per plant, NR= Number of fruit ridge, YPP= Pod yield per plant (g), Yhaton= Pod yield per hectare (tons), NSPP= Number of seed per pod, SDW= Hundred seed weight, SYPP= Seed yield per pod (g), Syph= Seed yield per hectare (Kg), Nha= Number of harvest, DMC= Dry matter content (%), PMC= Mucilage content

Figure.1 Biplot (axes PC1, PC2, PC3, AND PC4) OF 24 quantitative traits of 36 okra genotypes evaluated at Melkassa 2018/19

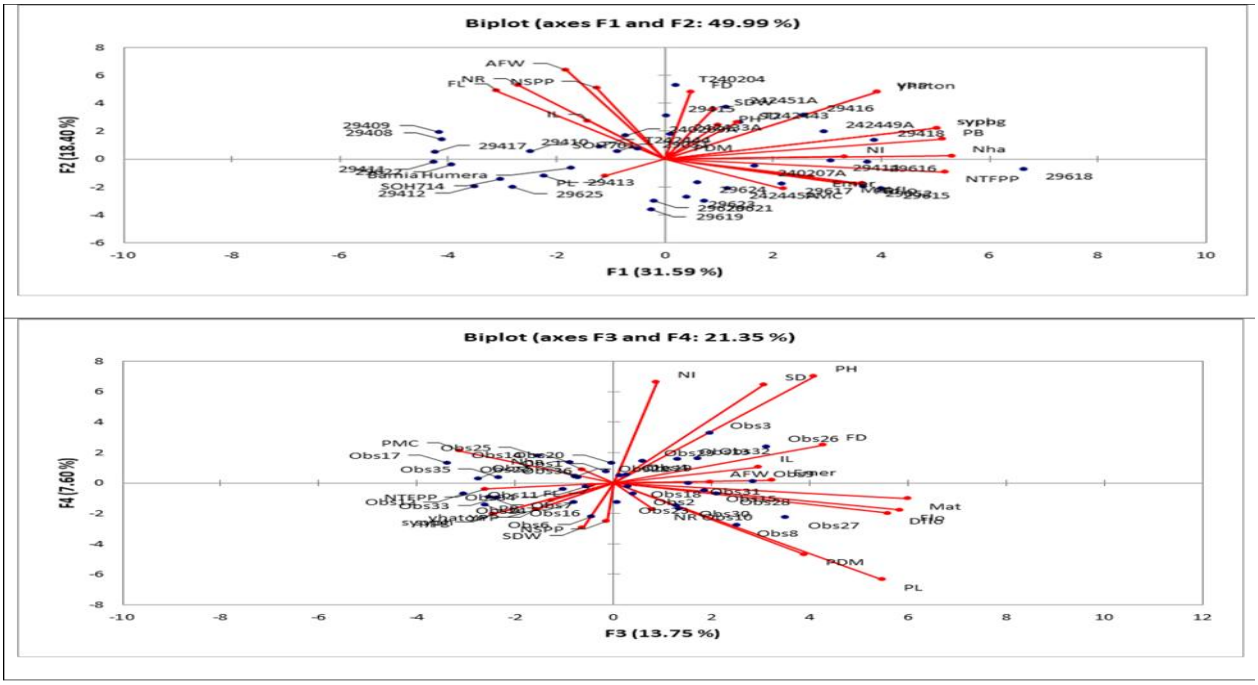
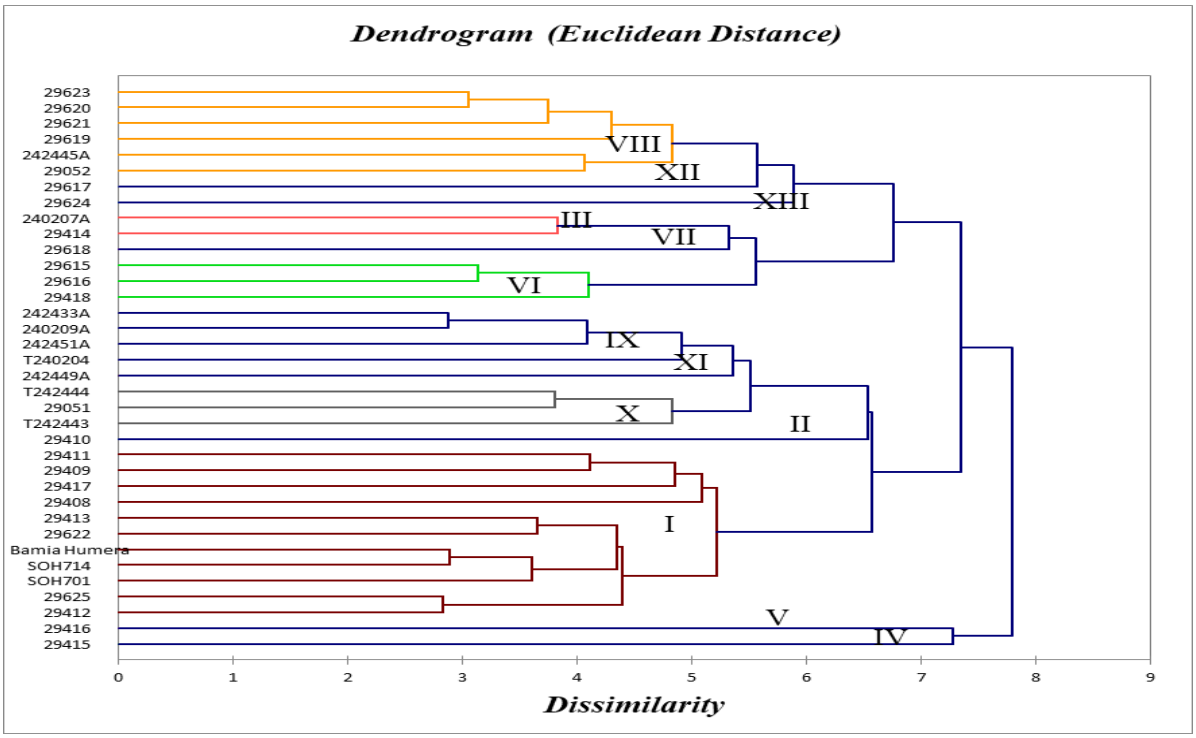


Figure.2 The dendrogram shows the dissimilarity of 36 okra genotypes based on 24 quantitative traits by using UPGMA



Cluster mean analysis

The mean values of the 13 clusters for 24 quantitative traits were presented in (Table 3). The unique features of a cluster for plant phenology and growth traits are as follows. Among the overall mean of thirteen clusters, Cluster I had the lowest mean values for days to first flowering, days to 90% maturity, and a number of primary branches. Days to 50% emergence are early in cluster II and III while late in cluster VIII, XI and XII. Cluster III had the lowest stem diameter from others. A number of internode and internode length are poor traits of cluster IV and VI, respectively. Whereas cluster XII shows the highest plant height but too late for flowering and maturity as compared to other clusters. Cluster II, IV, V, and VII had the highest mean values for stem diameter, internode length, number of internodes, and number of primary branches, respectively among other clusters. The shortest plant height was observed for cluster X. Hence, among thirteen okra clusters; clusters I, II, III, VII, IX, and X contain almost early maturing genotypes. This indicates it is better to develop early maturing varieties through further selection and/or crossing from these clusters accompanied by further evaluation. But in contrary to this cluster V, XII, and XIII are too late as compared to the overall mean values.

The clusters having a distinguishing character in pod yield and related traits among other clusters and also in comparison with the overall mean values of quantitative traits. Therefore, genotypes in cluster IV, X, I, and IX had longer fruit length, and the highest fruit diameter was observed in cluster V followed by cluster II, IX, and XI. Cluster IV, V, IX, X, and XI are distinguished by higher average fruit weight. Cluster VII had the highest number of tender fruit per plant, pod yield, seed yield, and also mucilage contents and the lowest average fruit weight as compared to other clusters. Cluster (III and IV), (IV, VI, III, and X), (V, VI, and XI), and (XI, X, and VIII) had also better in a number of tender fruit per plant, pod yield, seed yield and percentage of mucilage contents than the overall mean values of clusters. Whereas the number of seed per pod is higher in cluster V followed by IX, IV, and X respectively. The percentage of dry matter content is higher in cluster XIII followed by IV and V respectively. On the other hand cluster VII was characterized by the lowest average fruit weight, a number of seed per pod, and percentage dry matter contents. Whereas, seed and pod yield, number of harvests as well as the number of tender fruit per plant are lowest in cluster I.

Wassu *et al.,* (2017) grouped 25 genotypes under seven clusters each cluster having distinguishing characters. Muluken *et al.,* (2015) were reported that 25 okra accession were clustered into ten distinct groups based on their quantitative and qualitative similarity of genotypes. Therefore, each cluster had unique features among other clusters. Mihretu *et al.,* (2014a) were also reported that different clusters had distinguishing traits from others. Davinder *et al.,* (2018) reported 30 okra genotypes grouped into six clusters in which all clusters had their distinguishing traits

Summary and conclusion

Okra *(Abelmoschus esculentus*) is mainly known for its edible pod around southwestern and western parts of Ethiopia. It is grown traditionally around Benishangul Gumuz Regional State mainly for its edible pod which had cultural value. Even though it is an important vegetable throughout the world it's negligible for our country as well as the regional state in terms of export and domestic use. This may arise due to lack of appropriate agricultural technology for okra plant i.e. agricultural packages and improved varieties. Therefore, this study was conducted to assess the genetic divergence in okra genotypes collected from Regional states that are bases for improvement programs.

This research identified the presence of significant variation among analyzed genotypic traits in which the four principal components (PC1 to PC4) accounted for a total of 71.34% cumulative contributions to total variations, and the PC1 and PC2 had the larger contribution of 31.591 and 18.397%, respectively, while PC3 and PC4 contributed 13.754 and 7.596%, respectively.

The genetic distance of 36 okra genotypes ranged from 2.83 to 12.24 with the mean, standard deviation, and coefficient of variation of 6.73, 1.63, and 24.18, respectively. The largest proportion 312 (49.52%) of pair of genotypes had Euclidean distances of $\leq$6.73 (overall mean ED), a small percentage 3.97% (25) Pair of genotypes had Euclidean distances of >9.56, and the remaining 293 (46.51%) pair of genotypes had Euclidean distances between 6.73 to 9.56. Among genotypes under study 20 (55.56%) had a mean genetic distance of >6.73 (overall mean distances of genotypes) and 16 (44.44%) including all the three checks had a mean genetic distance of <6.73 (overall mean distances of genotypes). The Euclidean distance matrix of 630 pairs of genotypes estimated from 24 quantitative traits was used to construct dendrograms and accordingly, 33 local genotypes and 3 checks are grouped into 13 distinct

clusters. The highest number of genotypes is grouped in the first cluster and contains 11 genotypes (30.56%) followed by cluster VIII which consisted of 6 (16.67%) genotypes and cluster IX accommodates 4 (11.11%). Cluster X and III consisted of 3 and 2 genotypes, respectively. The rest clusters IV, V, VII, XI, XII, and XIII are all solitary consisted of each one genotype. The 13 clusters varied for a varying number of traits such as the eight of clusters (III, IV, V, VI, VII, XI, X, and XI) had higher fruit yield performance >22.52 t ha^{-1} (overall mean performance of clusters for fruit yield) as compared to all other clusters. The study revealed the presence of wide genetic variations among okra genotypes for all agro morphology traits except for three traits. This suggested a higher chance of developing varieties either through the selection and/or hybridization of okra genotypes for the Benishangul Gumuz regional state. It is recommended to conduct a similar experiment over seasons and locations since this research was conducted for one season and at one location.

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Appendix Table 1. Euclidean distances of 36 okra genotypes based on 24 quantitative traits evaluated at Melkassa in 2018/19

	29409	29410	29411	29412	29622	29414	29415	29416	29418	29616	29618	29052	T240204	29417	T242443	240207A	240209A	242433A
29408	5.465	6.589	4.690	5.350	4.863	8.851	7.889	8.304	9.085	8.664	12.035	9.222	7.391	5.112	7.823	7.658	6.102	5.524
29409		6.935	4.115	4.962	4.389	8.672	6.691	8.748	8.836	8.794	11.915	9.619	6.693	5.564	7.625	8.592	4.409	5.441
29410			6.107	6.816	7.722	8.049	7.859	6.908	7.259	6.820	10.141	6.320	7.092	6.671	8.139	7.004	5.621	4.893
29411				4.170	4.290	8.351	7.609	9.781	9.361	8.609	11.477	8.570	8.064	4.133	7.959	7.904	4.795	5.409
29412					4.130	7.700	8.556	9.640	9.034	7.788	10.826	8.185	8.764	5.826	8.281	6.814	5.653	6.056
29622						8.109	7.590	9.110	8.339	8.007	11.293	9.175	8.736	4.853	7.418	8.186	5.494	5.664
29414							7.732	8.293	5.763	3.852	4.349	5.769	7.209	8.928	5.720	3.831	5.889	5.541
29415								7.276	6.619	7.698	10.140	8.074	6.808	7.003	7.314	8.656	5.485	6.189
29416									4.972	6.217	9.685	7.245	6.999	9.564	8.014	8.477	7.280	5.988
29418										3.591	6.680	5.887	7.591	9.149	5.970	7.420	6.208	5.141
29616											4.897	4.448	7.521	8.995	5.624	5.258	5.618	4.793
29618												6.432	9.658	12.242	7.391	6.300	8.805	8.145
29052													8.786	9.299	7.894	5.951	6.782	5.961
T240204														8.490	6.180	7.171	5.219	5.055
29417															8.830	9.070	5.612	6.131
T242443																6.635	4.910	4.351
240207A																	6.650	6.053
240209A																		2.870
242433A																		

Appendix Table 1.Continued

	242449A	242445A	29051	29413	29615	29625	29617	29624	29620	29621	29623	29619	242451A	T242444	SOH701	SOH714	BamiaHumera
29408	8.375	7.073	5.275	4.811	9.559	5.353	9.210	8.506	7.507	7.817	7.439	8.186	6.945	5.260	5.007	4.656	5.893
29409	8.483	7.482	6.084	5.096	9.729	6.237	8.947	7.964	7.798	8.164	7.344	7.824	7.181	5.917	4.032	5.742	5.476
29410	7.276	5.658	6.478	6.367	8.112	6.484	6.059	7.365	7.360	6.515	7.130	6.944	5.467	7.292	6.090	6.838	6.780
29411	8.763	6.637	6.295	4.596	9.298	5.280	7.862	7.861	6.636	6.679	6.581	6.925	7.577	5.748	3.920	4.555	5.193
29412	8.627	5.518	5.191	3.822	8.262	2.833	7.912	7.448	6.315	6.028	5.710	5.540	8.171	5.758	4.840	3.713	4.100
29622	9.475	6.460	5.555	3.650	8.324	5.489	8.992	7.755	6.707	7.267	6.134	6.986	8.270	4.797	4.764	4.629	4.934
29414	5.943	4.938	6.706	7.051	4.799	7.896	7.501	7.500	7.745	6.609	6.017	7.279	7.030	5.948	6.521	6.834	5.764
29415	6.842	7.871	6.821	7.041	8.866	9.018	8.484	6.433	8.223	9.244	7.196	7.889	6.432	7.233	7.128	8.801	8.133
29416	6.623	7.376	6.906	7.811	7.411	9.485	8.146	7.383	8.278	8.598	8.017	9.144	5.022	8.199	8.454	9.520	8.842
29418	6.382	5.758	6.745	7.296	4.595	9.111	6.618	6.816	7.558	7.175	6.252	7.741	5.897	7.035	7.948	9.011	8.112
29616	5.495	4.181	5.934	6.638	3.129	7.729	5.973	7.153	6.581	5.474	5.390	6.842	5.901	6.155	7.159	7.567	6.412
29618	7.366	6.928	9.130	9.903	5.389	10.516	8.795	9.779	9.633	8.325	8.351	9.375	9.255	8.716	9.907	10.163	8.920
29052	5.399	4.064	6.862	7.119	4.951	7.575	4.543	6.370	5.720	4.906	5.361	5.390	6.896	7.619	7.886	8.020	7.442
T240204	5.692	8.049	6.119	7.983	9.611	8.648	9.238	9.386	9.606	8.918	8.889	9.579	4.471	6.306	6.371	7.969	6.885
29417	9.508	7.691	6.781	5.824	9.903	6.956	8.327	7.756	7.533	7.705	6.984	7.066	7.586	6.429	5.629	6.226	6.912
T242443	5.759	6.193	5.812	6.614	6.921	8.011	8.954	9.059	8.226	7.518	7.417	8.762	6.371	3.842	6.119	7.490	6.392
240207A	6.046	4.270	5.925	6.510	5.927	6.039	8.233	8.062	7.965	6.818	6.772	7.185	7.377	5.896	6.147	5.367	4.670
240209A	5.525	5.468	4.930	4.825	7.219	6.418	6.459	6.815	6.022	5.674	5.480	6.480	4.443	4.268	3.738	5.862	4.941
242433A	5.165	4.758	4.485	4.858	6.480	6.177	6.195	6.985	6.217	5.430	5.677	6.694	3.735	3.974	4.454	5.839	5.282

Appendix Table 1.Continued

	242445A	29051	29413	29615	29625	29617	29624	29620	29621	29623	29619	242451A	T242444	SOH701	SOH714	BamiaHumera
242449A	5.908	5.944	7.431	7.085	7.950	7.112	7.695	7.345	6.817	6.990	7.527	5.036	6.414	7.071	8.239	7.358
242445A		4.841	4.323	3.990	4.800	5.933	5.991	4.979	3.998	4.035	4.258	7.061	4.975	5.278	4.920	4.557
29051			4.319	7.215	4.425	7.502	7.454	6.264	5.778	5.485	5.800	6.062	3.808	5.626	5.300	4.233
29413				6.971	4.387	7.884	5.460	4.262	5.394	4.059	5.102	7.126	4.280	3.719	3.719	4.286
29615					8.120	6.733	7.248	6.722	5.955	5.569	6.920	8.164	7.068	7.810	7.862	7.075
29625						8.021	8.207	6.752	6.036	6.334	5.453	8.369	5.465	5.550	3.816	4.133
29617							7.371	6.370	4.723	5.728	6.104	7.007	8.521	8.238	8.753	8.167
29624								5.135	6.836	4.242	5.262	7.694	8.129	6.814	7.736	7.930
29620									3.713	3.051	4.630	7.713	6.577	6.222	6.456	6.750
29621										3.785	4.553	7.229	6.112	6.280	6.177	5.956
29623											3.723	7.532	5.954	5.757	5.863	5.778
29619												8.490	6.833	6.710	6.334	6.288
242451A													6.664	6.651	8.225	7.550
T242444														4.126	4.509	3.998
SOH701															3.362	3.849
SOH714																2.882