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Genetic Diversity of Ethiopian Okra Collections through Multivariate Analysis at Werer, Rift Valley of Ethiopia

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Abstract:
Okra[Abelmoschus esculentus (L.)Moench] is the most popular multipurpose vegetable and it belongs to Malvaceae family. It flourished before date palm in the tropical climate of Ethiopia. Therefore, this study was initiated with the objectives determining genetic distance of okra collections from different regions of Ethiopian and generated information about genetic diversity of Ethiopian okra collections to other country okra varieties.The field experiment was conducted at Werer Agricultural Research Center in 2014 using 23 local okra collections obtained from Ethiopian Biodiversity Institute and two exotic varieties obtained from Melkassa Agricultural Research Center using in simple lattice design with five incomplete blocks. Data were recorded from 25 quantitative and 10 qualitative traits. Principal component analysis showed eight principal components (PC1 to PC8) with eigen values ranged from 1.0 to 9.07 and with total contribution of 81.3% variation. Genetic distances were estimated using both quantative and qualitative traits. Genetic distance dissimilarity ranged from 3.89 to 18.24 with mean of 9.57. The two introduced varieties exhibited highest genetic distances than local collections. Exotic varieties were grouped in one cluster while the local collections were distributed in nine clusters. This study revealed the presence of genetic diversity among local okra collections and between local okra collections and introduced varieties that can be exploited for future breeding program. Since agro-morphology traits are highly influenced by environment, it is necessary to conduct agro-morphology traits along with a molecular study to determine the genetic diversity within Ethiopian okra collections and between other countries okra varieties.

Keywords: *Prinicipal component, genetic distance, cluster*

1. Introduction

Okra [*Abelmoschus esculentus* (L.) Moench] is the most popular vegetables and it belongs to Malvaceae family.It used for as a garden crop as well as on large commercial cultivation (Moekchantuk and Kumarn, 2004). Okra is native to North Eastern Africa in the area of Ethiopia and Sudan (Santos, 2012). It flourished before date palm in the tropical climate of Ethiopia (William, 1999). Okra is an annual plant, mainly propagated by seeds and has duration of 90-100 days (Tripathi *et al.*, 2011). The plant is cultivated in tropical, subtropical, and warm temperate regions around the world (Yuan *et al*., 2014).It is a multipurpose crop due to its various uses. Okra has a prominent position among fruits, vegetables due to its multiple virtues like high nutritive and medicinal value, ease of cultivation, wide adaptability, year round cultivation, good portability, export potential and bountiful returns (Thirupathi *et al*., 2012,). Okra seeds contain abundant mineral elements, oil and protein source which can be used as a coffee additive (i.e. in place of drinking coffee) (Yuan *et al*., 2014). Okra has found medical application as a plasma replacement or blood volume expander (Benchasri, 2012). Genetic diversity is a key factor for crop improvement (Thirupathi *et al*., 2012). Genetic diversity among okra germplasm will play significant role in breeding program as it helps to develop varieties with desired traits (Prakash *et al*., 2011). The existence of large diversity in okra for quantitative characters, implying the need for further collection of germplasm from the untouched geographical areas of the country to broaden the genetic base for future breeding program in Ethiopia (Mihretu et al., 2014b).Even though, the potential contribution of okra for food security and export purpose is very well, there is no improved varieties development so far for cultivation in Ethiopia. There is no information about the genetic and morphological divergence or proximity of Ethiopian landraces or improved okra varieties of other countries is also unavailable. The present study assessed genetic diversity among Ethiopia okra collections and exotic varieties based on agro-morphological traits. Thus the objectives of this study were determining genetic distance of okra collections from different regions of Ethiopian and generated information about genetic diversity of Ethiopian okra collections to other country okra varieties.

2. Materials and Methods

2.1. Description of the Study Area

The study was conducted at Werer Agricultural Research Center (WARC). The site is located in the Afar National Regional State, which is 280 km in the northeast of Addis Ababa and at an altitude of 740 m.a.s.l. The center is characterized has total annual rainfall of 564 mm and total annual average evapotranspiration of 2050 mm. The soil is light textured alluvial and black soil with a pH of 8.4. The mean annual temperature is 34.1 °C with a minimum of 18.9 °C and maximum of 38 °C, respectively (WARC, 2007).

2.2. Treatments and Experimental Design

In this experiment 23 okra genotypes obtained from Ethiopian Biodiversity Institute (EBI) and two introduced varieties from Melkassa Agricultural Research Center were used. Genotypes were evaluated on field at Werer Agricultural Research Center in the simple lattice design with 5 x 5 and spaced 2 m between blocks. Three seeds per hill was sown at 1 x 0.60 m and thinned to one plant per hill when plants reached 3-4 leaves stage.

2.3. Data Collection

International Plant Genetic Resources Institute (IPGRI, 1991) descriptor list for okra species were used to record the quantitative and qualitative traits. Quantitative traits were recorded from 12 plants per row leaving the two plants grown as boarder plants. Mature fruit from two plants next to border plant in each row were used to estimate mature fruits characters and 100 seeds weight while the remaining10 plants grown at each row used to record growth, phenology and tender fruits characters and to estimate tender fruit yield. Five randomly selected tender fruits from each harvest in each plot were used to record tender fruit characters.

- Quantative traits: Phenology and growth traits recorded from days to 50%emergence, days to first flowering, days to 50% flowering, days to maturity, plant height (cm), stem diameter (mm), number of primary branches per stem, number of internodes, internodes length (cm), leaf length (cm), leaf width (cm) and number of epicalyxes. Fruit and yield traits were recorded from peduncle length (cm), fruit length (cm), fruit diameter (mm), average fruit weight (g), number of tender fruits per plant, number of ridges on fruit, yield per plot (kg), yield per hectare (t/ha), number and weight of matured pods per plant, dry weight of matured pods per plant (g/plant), number of seeds per pod and hundred seed weight (g).
- Qualitative traits: recorded according to International Plant Genetic Resources Institute (IPGRI, 1991) descriptor list for okra species from plant habit, flower color, leaf color, leaf petiole color, pod color, stem color, leaf shape, fruit position on main stem, fruit pubescence and fruit shape

2.4. Data Analysis

2.4.1. Principal Component Analysis

The data were standardized to mean zero and variance of one before computing principal component analysis. The Principal component based on correlation matrix was calculated using SAS software.

2.4.2. Genetic Distance and Clustering

Euclidean distance (ED) was computed from quantative and qualitative traits of okra accessions after standardization (subtracting the mean value and dividing it by the standard deviation) using the formula suggested by Sneath and Sokal 91973). 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 was presented in the form of the dendrogram. In addition, mean ED was calculated for each accession by averaging of a particular clone to the other 24 accessions.

3. Results and Discussion

3.1. Principal Component Analysis

Principal components analysis (PCA) results of 25 quantitative traits are presented (Table 1). The PCA analysis results includes the factor scores of each character among the 25 okra accessions, eigen values, percentage total variance accounted for by eight principal components (PCs).

This analysis resulted eight principal components (PC1 to PC8) with eigen values ranged from 1.0 to 9.07. The eight principal components accounted varied percentage of total variance ranged from 3.6 to 32.4% which accounted a total 81.3% variation. The total contribution of the eight principal component axes of this study result was higher (81.3%) than observations made by other workers. Nwangburuka *et al.* (2011) and Ahiakpa (2012) who reported that principal component axes contributed 64.32% and 78.51% variation, respectively. There was no guideline to determine the significance of eigenvectors (Duzyaman, 2005). The higher coefficients for traits substantiated the relatedness of that trait with respective PC axes (Broschat, 1979). The first eight components were retained in analysis because eigen values are >1. The others factors having eigenvalue < 1 were ignored due to Gutten's lower bound principle that eigen values <1 should be ignored (Kumar *et al*., 2011).The first three principal components PC1, PC2 and PC3 with values of 32.4%, 16.7% and 8.2%, respectively, contributed more to the total of 57.3% variation. Similar result was reported by Amoatey *et al*. (2015) and Ahiakpa (2012) that the first principal component (PC1) recording the highest (32.44%) variance. According to Chahal and Gosal (2002), characters with largest absolute values closer to unity within the first principal component

influence the clustering more than those with lower absolute values closer to zero. Therefore, in the present study, differentiation of the genotypes into different cluster was because of a cumulative effect of a number of characters rather to the small contribution of each character (± 0.001-0.524).

	Eigenvectors							
Characters	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
DEM	0.053	0.082	0.264	-0.059	0.440	-0.371	0.173	0.362
DPF	0.289	-0.109	0.094	0.062	0.101	0.028	0.103	-0.083
DFF	0.212	-0.189	0.102	0.098	0.296	0.006	0.047	0.079
DFPF	0.252	-0.205	0.095	-0.095	0.133	0.083	0.067	0.029
DM	0.260	-0.191	0.117	-0.133	0.179	-0.102	0.099	-0.002
PH	0.246	-0.105	-0.189	0.006	0.055	-0.025	-0.345	-0.038
StD	0.180	-0.135	0.272	0.237	-0.073	-0.119	-0.384	-0.121
NBr	0.219	-0.247	-0.015	0.178	-0.038	0.043	0.075	0.195
NIn	0.274	-0.094	-0.157	-0.049	-0.124	0.072	-0.241	0.169
InLe	0.148	0.095	-0.320	-0.208	0.205	-0.198	-0.363	-0.286
LLe	0.194	0.250	-0.123	0.148	-0.143	0.073	0.173	-0.081
LWd	0.175	0.085	0.241	0.209	-0.057	-0.175	-0.042	-0.524
NEp	0.181	0.154	-0.060	-0.178	-0.188	0.199	0.017	0.280
PL	0.079	0.259	-0.316	0.169	0.174	-0.088	0.179	0.185
FL	-0.069	0.345	0.018	0.210	0.058	0.172	-0.251	0.095
FD	0.253	-0.012	0.020	-0.170	-0.243	-0.175	0.169	0.129
FW	0.195	0.311	0.118	0.042	-0.106	0.001	-0.085	0.168
NFP	0.117	-0.264	-0.284	0.316	-0.069	-0.032	0.070	0.068
FR	0.268	0.183	0.011	-0.060	-0.004	-0.073	-0.109	0.015
FY	0.195	0.0001	-0.267	0.415	-0.145	-0.067	0.017	0.158
NMP	0.087	-0.175	-0.085	0.065	-0.003	0.301	0.433	-0.349
FWMP	0.154	0.303	0.213	0.039	-0.006	0.209	0.030	-0.003
DWMP	0.211	0.278	0.022	-0.064	0.077	0.042	0.189	-0.097
NSP	0.243	0.203	0.053	-0.173	0.068	-0.028	0.122	-0.210
SW	-0.069	0.172	0.013	0.412	0.164	0.078	0.104	-0.102
Eigenvalue	9.067	0.203	2.306	2.064	1.416	1.138	1.088	1.000
Difference	4.389	0.172	0.243	0.647	0.279	0.050	0.088	0.122
Total variance %	0.324	0.167	0.082	0.074	0.051	0.041	0.039	0.036
Cumulative total variance %	0.324	0.491	0.573	0.647	0.698	0.738	0.777	0.813

Table 1: Principal component values of the first eight principal components from 25 quantative traits for 25 okra genotypes evaluated at Werer in 2014.

Dem= Days to 50% Emergency, DPF= Days to first Pod Formation, DFF= Days to first flowering, DFPF = Days to 50 % flowering, DM= Days to maturity, PH= Plant height, StD= Stem diameter, NBr= No. of branch, NIn= No. of inter node, InLe= Inter node length, LL = Leaf length, LWd = Leaf width, NEp = No. of epicalyx, PL= Peduncle length, FL= Fruit length, FD= Fruit diameter, FW= Fruit weight, NFP= No. of fruit/plant, FR= Fruit ridge, FY= Fruit yield, NMP= No. of mature pod, FWMP= Fresh weight of mature pod, DWMP= Dry weight of mature pod,NSP= No. of seed/plant, SW= Seed weight

This result showed relative contribution of different characters towards the genetic divergence of genotypes. Leaf width had a maximum contribution, others, viz. days to 50% emergence, number of mature pod per plant, tender fruit yield t ha^{-1}, 100 seed weight, stem diameter, internode length, fruit length, plant height, peduncle length, number of tender fruit per plant, fruit weight and fresh weight of mature pod per plant had relatively high contribution to genetic divergence of genotypes. Similar results were reported by Pradip *et al.* (2010) for that plant height, number of nodes on main stem and ridges per fruit, Nwangburuka *et al.* (2011) for plant height, fruit length, number of fruit per plant and 100 seed weight. However, the results reported by Nwangburuka*et al*. (2011) disagreed with the results in the current study for days to flowering, branches per plant, fruit diameter and seeds per podhad relatively high in the principal axes. Ahiakpa (2012) also reported that plant height, 50% germination and number of pods per plant were relatively high in the principal axes. The characters which had more contribution to total genetic divergence are under the control of additive gene action and will offer a good scope of improvement through selection breeding. The current study result indicates that direct selection can be practical for achieving desirable results. The output of PCA revealed that different traits contributed differently to the variation. These differences indicated the present of variability and considerable opportunity for improvement of different qualitative and quantitative traits. Principal component analysis (PCA) proved to be a better tool which provided genetic variability among okra progenies (Aremu *et al*., 2007 Rezwan*et al*., 2014).

3.2. Genetic Diversity Analysis

3.2.1. Genetic Distance

Genetic distance of 25 okra accessions was measured using Euclidean distance based on 25 quantitative and 10 qualitative traits and the result is presented in Table 2. Euclidean distance developed by Sneath and Sokal (1973) has been used to classify the divergent genotypes into different groups.

The genetic distances for all possible pairs of 25 okra accessions ranged from 3.89 to 18.24 with mean and standard deviation of 9.57 and 3.44, respectively. The most distant accessions were SHO714 and T242448 (18.24) followed by SHO714 and T92203 (17.39) and SHO714 and T240786 (17.17). The lowest genetic distance was exhibited between T240209 and T240587 (3.89) followed by T240209 and T245157 (4.24) and, T240587 and T240615 (4.36). The most distant pairs of accessions were Indian okra varieties and Benishangul okra accessions. The more close pairs of accessions were obtained from Metekel and Gambella okra collection respectively. Ethiopia okra collections exhibited wide genetic distances in the range between 5.16 and 11.14 while exotic varieties had 11.95 to 13.78. This suggested that the higher chance of improving the crop production through collection, characterization, evaluation and selection or hybridization of okra genotypes from different regions of Ethiopian other than introducing okra varieties from other countries. The extent of diversity present between genotypes determines the extent of improvement gained through selection and hybridization. The more divergent the two genotypes are the more will be the probability of improving through selection and hybridization (Prakash *et al*., 2011, Kamalpreet *et al*., 2013, Mihretu *et al*., 2014a).

The mean distance of each accession was computed to generate information which accessions were most and closest to other 24 accessions. On the basis of mean Euclidean distance, SHO714 (13.78) followed by SHO701 (11.95) and T92203 (11.14) were the most distant accessions to others, whereas, T245157 (5.16), T240209 (6.87) and 240587 (7.38) were found the closest to others which had mean distances much lower than accessions overall mean distance. The introduced okra varieties were the most distant to others than the Ethiopian okra collections. More than half of the Ethiopian okra collections (13 out of 23) had mean distance less than accessions overall mean distance (<9.57) indicating that majority of the Ethiopian okra collections were more close each other as compared to introduced varieties. However, considerable number of Ethiopian okra collections had mean distance that can be considered as distant to others. This showed that considerable number of local accessions are genetically distant each other and with exotic varieties. The exotic varieties being most distant to others might be due to genetic differences by origin or differences brought by the rigorous selection of varieties for production as compared to the local accessions which have not been subjected for selection of desirable traits.

Genetic distance or diversity of genotypes is considered as a good start in plant breeding to improve crops either by means of hybridization or direct selection of genotypes for their desirable traits. The high yielding varieties in okra has been developed by exploiting the genetic diversity available in the crop. Genetic diversity is importance for selecting parents in combination breeding of different autogamous crops to obtain transgressive segregants (Pradip*et al.*, 2010). Shujaat *et al*., 2014).Crossing of genotypes not genetically diverse or with little genetic diversity might not give higher heterotic value in F_1 and narrow range of variability in the segregating F_2 population. Thus, selection of genotypes for hybridization between the genetically diverse parents in further breeding programs may produce large variability and better recombinants in the segregating generations. Therefore, the observed genetic distance among Ethiopian okra collections that grouped as most distant and close to others is suggesting the higher possibility of improving the crop either through selection or crossing of distant accessions (Mihretu *et al*., 2014a)

	SOH701	SOH714	T92203	T240204	T240207	T240209	T240583	T240586	T240587	T240591	T240592	T240599
SOH701												
SOH 714	5.62											
T92203	15.85	17.39										
T240204	12.49	14.62	12.36									
T240207	14.06	15.59	6.05	9.19								
T240209	11.02	13.18	11.64	5.63	9.32							
T240583	9.10	10.51	12.81	7.14	10.61	4.87						
T240586	10.32	12.34	12.16	7.76	9.94	5.16	5.28					
T240587	10.22	12.21	12.03	5.64	9.18	3.89	4.79	4.55				
T240591	11.58	13.32	12.98	7.40	10.53	4.53	5.44	5.55	5.18			
T240592	12.54	14.18	15.50	7.14	12.72	6.48	8.02	8.00	7.17	8.27		
T240599	10.83	12.08	12.82	7.46	11.15	5.73	4.72	5.53	5.40	6.39	8.51	
T240602	11.37	13.76	13.65	7.26	11.97	5.20	6.57	5.67	6.04	5.85	6.88	5.20
T240609	9.45	11.47	15.55	8.09	13.12	7.03	6.57	6.03	7.01	7.21	6.23	7.19
T240615	9.98	11.62	13.11	5.54	10.23	4.90	5.48	5.71	4.36	5.97	6.00	5.79
T240784	11.12	12.21	13.37	7.52	11.12	6.27	6.35	5.90	5.40	7.37	6.34	5.31
T240786	16.05	17.17	5.52	12.93	7.88	12.52	13.11	13.11	12.38	13.27	16.48	12.94
T2420203	12.36	13.47	11.79	6.67	9.48	5.02	6.88	7.03	5.46	6.90	7.31	6.39
T242433	13.96	15.25	5.83	10.96	5.69	10.08	10.57	10.67	10.28	10.86	14.38	11.47
T242443	9.70	11.39	13.39	7.28	10.82	5.83	4.89	5.68	4.37	6.62	7.12	6.38
T242445	13.67	14.40	6.97	13.87	8.45	12.71	12.24	12.16	12.26	13.18	16.34	12.68
T242448	17.01	18.24	6.80	13.62	8.05	11.94	13.26	12.36	12.84	11.85	15.86	13.42
T242451	13.78	15.08	7.07	10.08	4.95	9.19	10.11	9.31	8.83	9.40	12.46	10.67
T245157	11.85	13.09	11.50	6.55	9.40	4.24	5.90	6.69	5.47	6.36	7.98	6.09
T245162	12.87	14.47	12.24	6.42	9.95	4.87	7.22	6.66	5.66	6.24	7.07	7.68
Mean	11.95	13.78	11.14	8.29	9.73	6.87	7.63	7.68	7.38	8.38	9.93	8.55

Table 2: Genetic Euclidean distances and mean Euclidean distance of 25 genotypes based on 25 quantative and 10 qualitative traits

	T240602	T240609	T240615	T240784	T240786	T2420203	T242433	T242443	T242445	T242448	T242451	T245157	T245162
T240609	5.78												
T240615	5.32	5.25											
T240784	5.53	5.57	4.78										
T240786	14.32	16.43	13.72	14.20									
T2420203	7.08	8.82	5.64	6.99	12.32								
T242433	12.55	13.92	11.64	12.02	6.93	11.19							
T242443	6.72	6.37	5.54	5.38	13.55	7.20	11.45						
T242445	14.29	15.06	13.54	13.08	7.40	13.54	6.81	12.79					
T242448	13.99	15.60	13.93	14.03	8.18	13.23	7.33	14.13	7.82				
T242451	11.62	12.39	9.91	10.62	7.60	9.67	6.79	10.21	8.08	6.56			
T245157	7.02	8.89	6.00	7.07	12.13	4.87	9.59	7.76	12.94	12.40	9.80		
T245162	6.98	8.50	5.55	7.69	12.58	5.24	11.52	7.51	14.13	12.77	9.58	5.16	
Mean	9.27	10.62	9.02	10.12	10.08	9.28	8.92	10.48	10.74	10.57	9.69	5.16	8.69

Table 2: Genetic Euclidean distances and mean Euclidean distance of 25 genotypes based on 25 quantative and 10 qualitative traits

3.2.2. Cluster Analysis

The distance matrix from 35 agro-morphological traits was used to construct dendrograms based on the Unweighted Pair-group Method with Arithmetic means (UPGMA). The cluster analysis result was presented in the form of dendrogram in Figure 1. The 25 okra accessions were grouped under ten major clusters. The four clusters are solitary while six clusters consisted of more than one, up to the maximum 10 accessions. Number of accessions and accessions included in each cluster with the region where accessions were collected presented in Table 3. Clustering is multivariate technique that can conveniently show the pattern of genetic relationships or proximity among accessions (Afifi and Clark, 1990) such that each group is homogeneous with respect to certain characteristics and each group should be different from other groups with respect to the same characteristics (Anderson, 1984).

Cluster III consisted of 10, IV consisted three, I, VI, Vand VII consisted two accessions each, other clusters VI, II, IX and X are solitary each represented one growing area of Asossa region. This result is in agreement with Pradip*et al* (2010), Reddy *et al*. (2012) who reported that major clusters consisted of solitary clusters. This study result is supported by Thirupathi *et al*. (2102) who reported that genotypes in solitary clusters being diverge from others may serve as potential parents for breeding programmes and this indicate their independent identity and importance due to various unique characters possessed by them. In general, the genotypes grouped together in one cluster are less divergent than those which are placed in a different cluster. The geographic and genetic diversity are not necessarily related; viz. accessions collected from the same geographic region fell in different genetic clusters, whereas those collected from different geographic regions tended to be grouped in the same cluster. This finding is in supported by Prakash *et al*. (2011), Temesgen *et al*. (2013) and Amoatey *et al*. (2015) who reported that accessions collected from the same geographic region fell in different genetic clusters and vice versa. The current study results, partly agreed with results reported by Ahiakpa *et al*. (2013) that there was a direct relation between the eco-geographical origins of the okra collections and their clustering patterns.

However, it is not possible to overlook the importance of geographic origin since the two exotic varieties fell in one cluster, four clusters are constructed each with single accession from same growing region and two Gambella okra collections constructed one cluster. Hence,this result indicates that geographical diversity may not be used as an index of genetic diversity. This result suggested is supported by Singh and Singh (1979), Parbhat and Mamta (2012) who reported 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. Biotypes originating in particular habitat have different utility, only for certain traits for which selection has been practiced. Therefore the varieties originating at the same place may have different genetic architecture or vice versa

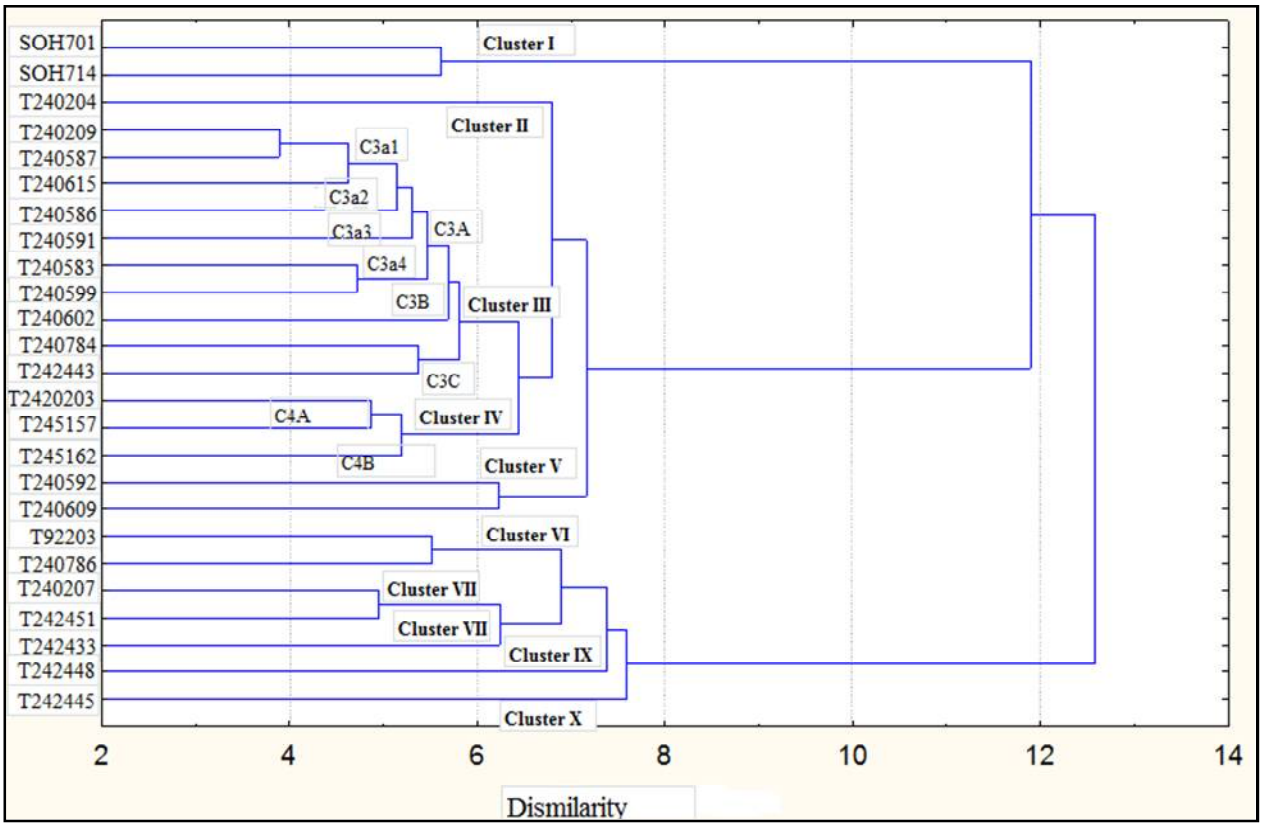

Figure 1: A Dendrogram Showing Genetic relationships using Euclidean distance

Cluster	Number of Accessions	Accession code	Collection Region/Country
I	2	SOH701, SOH714	Indian
II	1	T240204	Benishangul (Metekel)
III	10	T240209,T240587,T240615,T240586, T240591,T240583, T240599, T240602,T240784, T242443	Benishangul (Metekel, Asossa), Gambella(Zone3,Zone1,Zone2)
IV	3	T2420203, T245157,T245162	Benishangul (Metekel), Gambella (Zone3)
V	2	T240592, T240609	Gambella (Zone3,Zone1)
VI	2	T92203 , T240786	Oromia(Wellega), Benishangul (Metekel)
VII	2	T240207, T242451	Benishangul (Metekel, Asossa)
VIII	1	T242433	Benishangul (Asossa)
IX	1	T242448	Benishangul (Asossa)
X	1	T242445	Benishangul (Asossa)

Table 3: Number of accessions grouped in 10 clusters, accession code and collection region 25 okra genotypes evaluated at Werer in 2014

	Cluster									
Traits	I	II	III	IV	V	VI	VII	VIII	IX	X
DEm	5.00	5.50	5.40	5.00	5.50	5.25	5.00	5.00	5.50	5.50
DPF	25.75	40.50	39.90	42.83	39.25	43.75	39.50	39.50	39.50	39.50
DFF	37.75	52.00	53.95	61.00	50.75	63.25	49.50	49.50	51.50	55.50
DFPF	41.75	68.00	70.35	75.50	61.75	83.50	71.75	85.00	82.50	68.00
DM	50.88	79.79	85.56	86.43	75.23	95.75	80.88	87.25	98.20	85.45
PH	123.78	190.04	223.33	300.17	162.28	258.81	235.49	212.25	229.75	130.28
StD	19.92	37.19	31.58	35.45	30.38	34.49	33.33	35.56	34.87	25.20
NBr	3.01	8.82	6.86	8.44	6.40	12.33	7.78	9.75	8.64	6.00
NIn	26.04	44.41	40.19	48.85	36.66	45.93	42.35	44.40	50.50	34.11
InLe	4.28	6.27	5.69	5.90	4.69	4.72	5.62	5.01	5.38	4.22
LLe	19.33	26.91	22.03	23.96	24.62	23.49	23.74	21.77	20.55	20.66
LWd	25.11	36.54	33.35	33.04	33.79	31.56	33.69	30.88	28.90	30.21
NEp	9.20	10.30	10.20	10.54	10.51	9.86	10.33	9.94	11.07	9.95
PL	2.59	3.21	2.75	3.20	3.44	2.34	3.09	1.97	2.48	1.94
FL	17.96	17.14	14.69	14.04	20.02	10.17	18.04	12.50	13.59	6.95
FD	20.09	29.46	30.04	31.03	28.22	30.10	29.06	30.55	32.61	27.56
FW	29.68	62.18	52.65	50.63	67.39	36.21	58.63	44.69	56.05	25.65
NFP	48.11	91.28	57.12	72.78	43.49	96.48	70.52	81.20	54.55	70.50
FR	5.21	8.15	8.06	8.16	7.92	6.98	8.30	7.18	8.24	5.59
FY	186.50	484.72	281.42	366.27	293.11	377.54	365.82	288.26	269.43	193.00
NMP	20.78	22.00	28.94	35.17	26.81	41.28	41.50	59.75	31.75	32.78
FWMP	29.47	64.19	54.65	54.70	87.80	32.08	57.06	43.66	62.03	32.42
DWMP	6.17	17.78	16.21	15.51	18.89	10.48	15.27	12.34	14.27	10.40
NSP	51.13	101.30	110.44	107.95	109.14	78.45	104.33	95.25	107.90	81.05
SW	7.53	6.90	6.40	6.60	7.08	6.55	7.28	4.70	4.55	5.50

Table 4: Cluster mean value for 25 quantative characters of 25 okra genotypes evaluated at Werer in 2014.

Dem= Days to 50% Emergency, DPF= Days to first Pod Formation, DFF= Days to first flowering, DFPF = Days to 50 % flowering, DM= Days to maturity, PH= Plant height, StD= Stem diameter, NBr= No. of branch, NIn= No. of inter node, InLe= Inter node length, LL = Leaf length, LWd = Leaf width, NEp = No. of epicalyx, PL= Peduncle length, FL= Fruit length, FD= Fruit diameter, FW= Fruit weight, NFP= No. of fruit/plant, FR= Fruit ridge, FY= Fruit yield, NMP= No. of mature pod, FWMP= Fresh weight of mature pod, DWMP= Dry weight of mature pod, NSP= No. of seed/plant, SW= Seed weight.

4. Conclusion

The characters which had more contribution to total genetic divergence, are under the control of additive gene action and will offer a good scope of improvement through selection. Leaf width had a maximum contribution while tender fruit yield had a relatively low contribution. The local collections from different okra growing regions fall in different cluster except few constructed separate groups. The result suggested that the presence of wide genetic difference between introduced varieties and local okra accessions as well as the presence of genetic distance among Ethiopian okra collections. This result indicated the presence of wide genetic diversity among tested okra genotypes. This result suggested the importance of further study on genetic diversity of okra genotypes in the country. However, further agro-morphology study along with the molecular study since agro-morphological characteristic of the genotypes is mostly influenced by environment for measuring genetic distance between Ethiopian and other country okra genotypes.

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