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Genetic Divergence Analysis Among Sesame (*Sesamum indicum* L.) Germplasm at Werer Ethiopia

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Abstract: This research was conducted to assess the extent and pattern of genetic variability and diversity among sesame accessions. A total of 64 sesame Accessions were evaluated in 8 x 8 lattice design with two replications at Werer Agricultural Research Center. Analysis of variance revealed that there was a statistically significant difference among the accessions for all traits except for 50% days to emergence and the number of seeds per pod. Principal components analysis showed the first five principal components viz. principal component one (21.9%), principal component two (11.00%), principal component three (15.6%), principal component four (18.3%), and principal component five (9.5) with a total contribution of 76.3% variation. The dendrogram was constructed using the Unweighted Pair-group Method with Arithmetic Means to separate Accessions into five distinct clusters. Sesame accessions with high seed yield and high mean values for other desirable traits were grouped into Cluster I and Cluster V. Cluster IV and Cluster V had the highest inter-cluster distance. Accession in Cluster V (Acc.241297) could be crossed with other clusters to come up with promising segregation for further improvement programs.

Keywords: Accessions, Clusters, Principal Component, Sesame

1. Introduction

Sesame (*Sesamum indicum* L.) is the most important oil crop grown well in tropical and sub-tropical climates [1, 2]. It is one of the oldest oil crops and is thought to have originated in Africa [3]. Cultivated sesame belongs to the order Tubiflorae and the family Pedaliaceae, with 37 species described under the genus Sesamum, of which only (*Sesamum indicum* L) has been recognized as a cultivated species [4]. The cultivated species sesame (*Sesamum indicum* L.) is a diploid species with a chromosome number of 2n = 2x = 26 [5] (Morinaga *et al*., 1929).

According to [4], Ethiopia is considered to be the center or origin of sesame and it seems that the crop was taken into cultivation in other African countries and then taken to India. The presence of weedy or wild forms of sesame (S. alatum; 2n = 26 and S. latifolium, 2n = 32) in Ethiopia shows that it is indigenous and considered the center of origin for sesame. Also, the presence of high genetic diversity is serving as a resource for further improvement of the crop [2].

Sesame, locally called '*Selit'*, is a valuable export crop in Ethiopia. Ethiopia is the world's fourth-largest exporter of sesame seeds, after Sudan, India, and Nigeria, and Africa's third-largest exporter, after Sudan and Nigeria [6]. Ethiopian Central Statistics Agency reported the area under production of sesame is estimated to be 375,119.95 and 369,897.32 ha in the 2019/2020 and 2020/2021 cropping seasons, respectively [7, 8]. According to CSA, the total production of sesame was 262, 665.4 and 260, 257.6ton ha^{-1}, in 2019/2020, and 2020/2021 cropping seasons, respectively [7, 8]. Total grain production and productivity are 260, 257.6 ton ha^{-1}, and 700 kg ha^{-1}, respectively 2020/2021 cropping seasons [8]. In Ethiopia average productivity of sesame is low when compared to other sesame-producing countries like china and Nigeria but, it is greater than the world (487.2 kg ha^{-1}) and African (441.9 kg ha^{-1}) sesame productivity [6].

The knowledge of diversity and genetic distances of genotypes helps to identify parental lines for hybridization programs, which can be used to select appropriate parental

genotypes for hybridization to develop a high-yielding potential variety [9]. Principal component analysis (PCA) is the most essential tool in diversity studies. This technique is highly effective and useful for identifying plant features that classify the distinctiveness of promising genotypes [10]. The PCA may give the plant breeder greater flexibility in determining the number of plants to examine, and the plant breeder could apply multivariate approaches by determining the attributes that make up an ideal plant first [11]. A crossing program should be initiated among the genotypes belonging to different clusters [12]. As a result, to begin a crossing program, the parents should be selected from clusters with a large magnitude of genetic distance between them to produce desirable segregates [13]. In addition, Shammoro MH et al. [14] also reported parents chosen from divergent clusters are expected to have the most genetic recombination. To select the desired parent for crossing program and to develop new crop varieties; understanding and knowing genetic diversity is the most crucial in plant breeding. For that reason, the present research was undertaken with the objective to assess genetic distance and clustering among sesame accessions.

2. Materials and Methods

2.1. Description of Experimental Site

The experiment was conducted during 2021 in the summer season at Werer Agricultural Research Center (WARC) in the low land of Ethiopia (middle awash) of Afar Regional State under irrigation condition. Werer is located at latitude of 9° 16' N, the longitude of 40° 9' E, and an altitude of 740 m.a.s.l. The mean annual rainfall of the area is 590 mm and the mean annual minimum and maximum temperature ranges between 26.7 and 40.8°C, respectively (www.eiar.gov.et).

2.2. Experimental Materials

The experimental materials consisted of 64 sesame accessions obtained from Ethiopian Biodiversity Institute (EBI) were used in this study. The origin of those materials was Ethiopian country and which was collected from four regions (Benshungul Gumuz, Tigray, Oromia, and Amhara).

Table 1. *Experimental materials used for the study.*

S№	Accession	Origin	Region	S№	Accessions	Origin	Source
1	9015	Ethiopia	Benishangul	33	28301	Ethiopia	Amhara
2	9017	Ethiopia	Benishangul	34	28302	Ethiopia	Amhara
3	9019	Ethiopia	Benishangul	35	28303	Ethiopia	Amhara
4	9026	Ethiopia	Benishangul	36	28304	Ethiopia	Amhara
5	9027	Ethiopia	Benishangul	37	28305	Ethiopia	Amhara
6	9028	Ethiopia	Benishangul	38	28306	Ethiopia	Amhara
7	9690	Ethiopia	Tigray	39	28307	Ethiopia	Amhara
8	9691	Ethiopia	Tigray	40	28309	Ethiopia	Amhara
9	9692	Ethiopia	Tigray	41	28311	Ethiopia	Amhara
10	9693	Ethiopia	Tigray	42	28312	Ethiopia	Amhara
11	9694	Ethiopia	Tigray	43	28313	Ethiopia	Amhara
12	9696	Ethiopia	Tigray	44	28314	Ethiopia	Amhara
13	9697	Ethiopia	Amhara	45	28316	Ethiopia	Amhara
14	17693	Ethiopia	Oromiya	46	28317	Ethiopia	Amhara
15	17694	Ethiopia	Oromiya	47	28318	Ethiopia	Amhara
16	17695	Ethiopia	Oromiya	48	28319	Ethiopia	Amhara
17	17696	Ethiopia	Oromiya	49	28320	Ethiopia	Amhara
18	17697	Ethiopia	Oromiya	50	28321	Ethiopia	Amhara
19	17698	Ethiopia	Oromiya	51	28322	Ethiopia	Amhara
20	17699	Ethiopia	Oromiya	52	28323	Ethiopia	Amhara
21	17701	Ethiopia	Oromiya	53	28324	Ethiopia	Amhara
22	17702	Ethiopia	Oromiya	54	28325	Ethiopia	Amhara
23	17703	Ethiopia	Oromiya	55	28326	Ethiopia	Amhara
24	17704	Ethiopia	Oromiya	56	28327	Ethiopia	Amhara
25	17705	Ethiopia	Oromiya	57	28328	Ethiopia	Amhara
26	17706	Ethiopia	Oromiya	58	28329	Ethiopia	Amhara
27	17707	Ethiopia	Oromiya	59	28330	Ethiopia	Amhara
28	17708	Ethiopia	Oromiya	60	202286	Ethiopia	Amhara
29	17709	Ethiopia	Oromiya	61	241297	Ethiopia	Amhara
30	17710	Ethiopia	Oromiya	62	241326	Ethiopia	Tigray
31	17711	Ethiopia	Oromiya	63	241338	Ethiopia	Amhara
32	28300	Ethiopia	Amhara	64	241344	Ethiopia	Amhara

Source: Ethiopian Biodiversity Institute

2.3. Experimental Design and Field Management

The experiment was planted in an 8 X 8 simple lattice design. The spacing between plants and rows was 10 cm and 40 cm respectively, and 6 rows were used in each plot. Then the gross plot size was 2.4m * 3m=7.2m^2 and net plot size was 4.8m^2 (four rows). The distance between plots, blocks, and replication was 80cm, 2m, and 3.2m respectively. The

total plot required was 128. According to recommended rate; the seed rate used for planting was 5-7kg/ha which means on average 4 g was required per plot. The plant population was adjusted by thinning after germination according to recommended pant per hectare (25, 0000/ha) and 180 plants per plot.

The experimental field was well prepared by plowing 3 times. After row preparation, accessions were drilled into the rows. After seedlings reached 15-20cm, thinning was made to adjust the distances of 10cm between plants to retain recommended plant stand per hectare. After the seed was drilled, the experimental field was irrigated; second irrigation was carried out after 10 days. Then, until the crops attained physiological maturity, the subsequent irrigation method was carried out with a 15-day gap. There was no fertilizer used in this experiment. Crop management practices such as weeding, thinning, crop protection, and securing it from higher animals and related management used for a crop were done regularly [15].

2.4. Data Collection

To avoid border effects, the data for all of the parameters considered were taken from the net plot area of 1.6 m x 3 m (4.8 m^2). Data were collected for the following parameters using the IPGRI sesame descriptor [16]:

2.4.1. Phenological

1) Days to 50% emergency (DE): the number of days from planting to 50% of the plants in the plot emerged.
2) Days to 50% flowering (DF): the number of days from sowing to 50% of the plants in the plot give flowers.
3) Days to 75% maturity (DM): the number of days from emergence to plant reaching physiological maturity (when parts of a plant are changed to yellow color).

2.4.2. Agronomic (Yield and Yield-Related Parameter)

1) Plant height (PH) (cm): the average length of the plant for 10 randomly selected plants in the plot measured from the base to the tip of the plant at maturity.
2) Length of pod bearing zone (LPBZ) (cm): The average length of the plant from ten randomly selected plants in the plot was measured from the first pod bearing zone to the tip of the plant.
3) A number of primary branches per plant (PBP): The average number of primary branches per plant for ten randomly selected plants in the plot at flowering.
4) Secondary branches per plant (SBP): The average number of secondary branches per plant for ten randomly selected plants in the plot at the flowering stage.
5) Number of pods per plant (NPP): The average number of pods per plant for ten randomly selected plants in the plot at the maturity stage.
6) Pod length (CL) (cm): Ten pods were randomly selected within the middle part of the main stem in a plot from five plants and were measured by a ruler at maturity.
7) Pod width (CW) (cm): Ten pods were randomly selected within the middle part of the main stem in a plot from five randomly selected plants and it was measured by a centimeter at maturity.
8) Biomass yield per hectare (BM) (Kg/ha): Recorded by weighing the total above-ground yield harvested from each experimental plot at the time of harvest and converted to biomass yield per hectare by the formula biomass yield (Kg/ha)= (plot yield (Kg) x 10,000)/plot size in a square meter.
9) Seed yield (SY) (kg/ha): The total seed yield harvested from the net plot area and converted to hectare bases.
10) Thousand seed weight (TSW) (g): The weight of 1000 seeds per plot.
11) Harvest Index (HI) (%): the ratio of seed yield per plot to the above-ground biomass yield per plot expressed in percent.

2.4.3. Quality Parameters

Oil content (OC): oil content was determined by wide line nuclear magnetic resonance (NMR). Bulk seeds were taken from each plot and oven dried at 130°C for 3hr and cooled in desiccators for 30 minutes. Then add a sample of 22g of oven-dried and cooled seed into an NMR sample flask then Record the result delivered by the machine in triplicate and takes the mean value [17].

2.5. Data Analysis

2.5.1. Analysis of Variance

The data were analyzed following procedures appropriate to the simple lattice design used as described by the research [18]. Means of significant treatment effects were separated using Duncan's New Multiple Range Test (DNMRT) test at a 5% probability level. Data collected for each character was subjected to analysis of variance using SAS software version 9.3 [19].

2.5.2. Principal Component Analysis

Principal component analysis (PCA) was computed to identify 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 the correlation matrix was calculated using R- software.

2.5.3. Genetic Distance and Clustering

The genetic distance of 64 sesame accessions was estimated using clustering of genotypes. Euclidean distance (ED) was calculated from quantitative traits after standardization (subtracting the mean value and dividing it by the standard deviation) as established by Sneath, P. H. et al. [20] using Minitab v-17 software as follows:

$$EDik = \sqrt{\sum_{i=1}^{n}(\mathrm{Xij} - \mathrm{Xik})^2}$$

Where, EDjk = distance between genotypes j and k; xij

and xik = phenotype traits values of the i^{th} 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 a dendrogram based on the unweighted Pair-group Method with Arithmetic Means (UPGMA). The results of cluster analysis were presented in the form of a dendrogram.

3. Results and Discussion

3.1. Analysis of Variance

Analysis of variance (ANOVA) for 16 traits revealed that majority of the traits, such as days to 50% flowering, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, pod length, pod width, biomass yield, seed yield, harvest index, thousand seed weight, days to 75% maturity, and oil content showed highly significant (*P<0.01)* variation and length of pod bearing zone and plant height was also significant at (*P<0.05)* (Table 2). This indicates the presence of genotypic variation among the tested sesame accessions. Accessions had recorded a non-significant difference for days to 50% emergence and the number of seeds per pod.

In line with the present findings, different researchers reported the presence of significant variation among sesame genotypes. For instance; the authors [14, 21-24] reported highly significant differences among genotypes for days to 50% flowering, number of primary branches per plant, number of pods per plant, seed yield, thousand seed weight, and days to 75% maturity among 64 sesame genotypes, 75 genotypes, 100 genotypes 30 sesame genotypes and 300 genotypes, respectively. Moreover, the research [14] reported highly significant differences among 100 genotypes for plant height, length of pod bearing zone, pod length, pod width, biomass yield, harvest index, and oil content. Additionally, Singh, A. et al. [22] reported significant differences among 75 genotypes for number of secondary branches per plant.

Table 2. *Mean squares from analysis of variance for 16 traits of 64 sesame accessions.*

SN	Trait	Rep (Df=1)	Block (Df=14)	Genotype (Df=63)	Error (Df=49)	CV (%)
1	Days to 50% emergence	0.28^{ns}	0.36^{*}	0.204^{ns}	0.1557	7.03
2	Days to 50% flowering	164.257^{**}	46.237^{**}	32.73^{**}	11.69	5.64
3	Days to 75% maturity	29.07^{ns}	17.45^{ns}	96.619^{**}	14.348	3.33
4	Plant height (cm)	165.24^{ns}	224.46^{ns}	351.96^{*}	145.027	10.9
5	Length of pod bearing zone (cm)	1316.49^{**}	52.81^{ns}	82.59^{*}	36.61	11.6
6	Primary branch plant-^{1}	0.06^{ns}	0.02^{ns}	0.279^{**}	0.014	4.15
7	Secondary branch plant-^{1}	0.00397^{ns}	0.000^{ns}	0.008^{**}	0.0027	18.8
8	Number of pod plant-^{1}	1774.59^{**}	25.71^{ns}	358.06^{**}	41.36124	14.1
9	Pod length (cm)	0.0009^{ns}	0.0004^{ns}	0.098^{**}	0.0005	0.84
10	Pod width (cm)	0.000078^{ns}	0.0014^{ns}	0.0034^{**}	0.00097	4.3
11	Number of seed pod-^{1}	111.079^{ns}	37.056^{ns}	33.44^{ns}	31.8565	8.99
12	1000 seed weight (g)	0.1069^{*}	0.0056^{ns}	0.273^{**}	0.0073	2.93
13	Biomass yield (kg/ha)	213170.22^{ns}	144248.43^{ns}	1433363.6^{**}	155152.9	10.0
14	Seed yield (kg/ha)	17543.689^{ns}	9777.53^{ns}	87466.8^{**}	11750.05	13
15	Harvest index (%)	3.78^{ns}	3.95^{ns}	16.45^{**}	3.56	8.94
16	Oil content (%)	23.69^{**}	3.145^{*}	4.02^{**}	0.798	1.81

** And *indicates highly significant at (1%), significant at (5%) probability levels respectively, ns= non-significant, CV= coefficient of variations, Df= degrees of freedom.

3.2. Principal Component Analysis

Principal component analysis is the most essential tool in diversity studies. The principal component analysis (PCA) revealed total five principal components (PCs) with Eigen values greater than one (ranging from 1.2 to 4.5) for 14 quantitative traits among the 64 sesame accession (Table 3). The five principal components accounted for percentages of total variance that ranged from 9.5 to 21.9% and accounted for 76.3% of the total variation. First three main PCAs are extracted from the complicated components; with a total cumulative variance of 56.07% with eigenvalues > 1 also reported [11]. Additionally, Tesfaye, T. et al. [24] reported the first five PCAs explained about 75.4% of the variation. According to Brejda J. J. et al. [25], data were considered in each component with an Eigenvalue of >1, which determined at least 10% of the variation. The higher Eigenvalues were considered the best representatives of system attributes in the principal component.

For the present results principal component one (PC1) had a relatively higher value and included the traits namely days to 50% flowering, plant height, number of pods per plant, length of pod bearing zone, and days to 75% maturity. These parameters made a greater impact on total diversity and were responsible for cluster differentiation. Traits like harvest index and seed yield contributed more to total genetic diversity in the principal component (PC2). In principal component three (PC3), the number of primary branches per plant, days to 50% flowering, days to 75% maturity and pod width had relatively greater contributions to the total genetic diversity. The number of primary branches per plant, number of pods per plant, biomass yield, percent oil content, and seed yield all contributed significantly to the total variance in principal component four (PC4). In the principal component five (PC5), characters such as the number of primary

branches per plant, number of pods per plant, and the number of secondary branches per plant had relatively high contributions to the total variance.

In general, the number of pods per plant had the maximum contribution followed by days to 75% maturity, primary branch per plant, and seed yield had relatively high contributions to genetic divergence of accessions. Characters that contributed the most to overall genetic divergence are governed by additive gene action and have a lot of improvement through selection breeding. In a hybridization program, during the selection of parents, the characters contributing the most to the divergence are given greater importance [26]. PCA revealed that different traits contributed to variation in different ways. These differences showed that there is a lot of room for improvement in terms of both qualitative and quantitative characteristics. Important characters coming together in different PCs tend to remain together, which may be kept into consideration during the utilization of these characters in a breeding program to bring about rapid improvement for yield and other associated traits.

Table 3. *Principal components and Eigen values of the first five principal components for 14 quantitative traits of 64 sesame accessions.*

Eigenvectors					
Trait	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**
Days to 50% flowering	0.37	-0.15	0.78	0.16	-0.04
Days to 75% maturity	0.47	0.29	0.70	-0.02	0.12
Plant height (cm)	0.86	-0.02	0.16	0.23	-0.01
Length of pod bearing zone (cm)	0.75	-0.06	-0.32	0.17	0.25
Primary branch per plant	0.20	0.09	0.35	0.53	0.34
Secondary branch per plant	0.14	-0.04	0.02	0.11	0.88
Number of pod per plant	0.66	0.26	0.12	0.36	0.38
Pod length (cm)	-0.34	-0.83	-0.05	-0.05	0.06
Pod width (cm)	-0.26	-0.15	0.73	0.03	0.05
1000 seed weight (g)	-0.75	-0.19	-0.32	0.00	0.02
Biomass yield (kg/ha)	0.17	0.03	0.13	0.8 7	0.14
Seed yield (kg/ha)	0.02	0.36	-0.06	0.87	0.17
Harvest index (%)	-0.27	0.67	-0.41	0.24	0.09
Oil content (%)	0.24	-0.15	-0.08	0.67	-0.40
Eigenvalue (%)	4.5	2.28	1.55	1.22	1.12
Proportion variance (%)	21.9	11.0	15.60	18.3	9.50
Cumulative variance (%)	21.9	40.2	55.8	66.8	76.3

3.3. Genetic Divergence Analysis

3.3.1. Clustering of Accession

Based on the accession mean values for 14 quantitative traits, the 64 sesame accessions were divided into five distinct clusters Table 4 and Figure 1. Cluster II consisted of 25 accessions followed by Cluster I which consisted of 15 accessions, Cluster III had 13 genotypes, Cluster IV had ten accessions and Cluster V had one genotype (Table 4). This finding indicated that accession belonging to the same cluster shared many traits which resemble each other but vary from accession belonging to other clusters in one or more traits. Similarly, the authors [24, 26, 27, 28] reported six, five, three, and twelve, clusters for three hundred, fifty genotypes, thirty-three and two hundred eighty-four respectively.

3.3.2. Intra and Inter Cluster Distance of Accessions

The intra- cluster and inter-cluster distances of 64 accession were listed in the Table 5, with Cluster IV and Cluster V having the highest inter-cluster distance, followed by Cluster III and Cluster V. Cluster V and the other clusters (clusters II, III, and IV) had a ranged from (6.45-8.88) an ED. Cluster V had a high dissimilarity level with all the other clusters. This means that the accession included in cluster V could be used as a parent during hybridization for the rest accession included in the other four clusters. The inter-cluster distance between Cluster I and Cluster II was the smallest of all (2.49). Because the accession in this group had a high similarity level or a low dissimilarity level, the effectiveness of hybridization and segregation will be low. Present result revealed that intra-cluster distances were lower than inter-cluster distances. This suggests that wider diversity among the accession of different groups and accession within the same cluster were closely related. Similar results were also reported [12, 26]. The intra-cluster distances had a ranged from (0 to 2.95) an ED. High intra cluster distance was recorded for cluster IV followed by Cluster I, cluster II, cluster III and cluster V.

Table 4. *The Distribution of 64 sesame accessions into five clusters.*

Clusters	**№ of accession**	**Accession list**
Cluster I	15	9015, 9019, 9026, 9028, 17708, 17709, 17710, 28304, 28309, 28312, 28313, 28316, 28321, 28326, 28329
Cluster II	25	9017, 17693, 17694, 17695, 17696, 17697, 17698, 17699, 17701, 17702, 17703, 17704, 17705, 17706, 17707, 17711, 28301, 28302, 28314, 28319, 28322, 28323, 28330, 202286, 241344
Cluster III	13	9027, 9693, 9696, 28300, 28305, 28306, 28307, 28318, 28320, 28327, 28328, 241326, 241338
Cluster IV	10	9690, 9691, 9692, 9694, 9697, 28303, 28311, 28317, 28324, 28325
Cluster V	1	241297

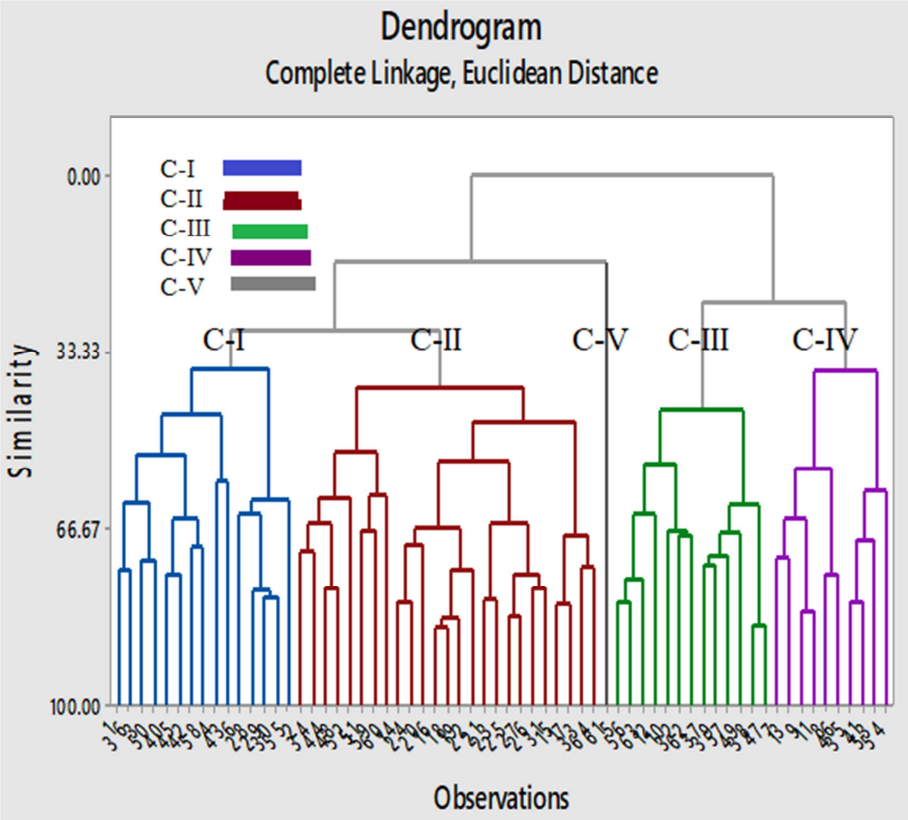

Figure 1. *Dendrogram generated based on UPGMA clustering method depicting genetic relationships among 64 sesame accessions based on 14 quantitative traits. *note: numbers in horizontal axis indicate accessions listed in table 1.*

Table 5. *Average intra (bold) and inter (off) diagonal cluster distance among 64 sesame accessions.*

Cluster	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V
Cluster-I	*2.92*	2.49	4.51	4.31	6.45
Cluster-II		*2.79*	3.37	4.51	6.61
Cluster-III			*2.75*	3.4	8.75
Cluster-IV				*2.95*	8.88
Cluster-V					*0*

3.3.3. Cluster Mean Analysis

The mean values of the 5 clusters for 14 quantitative traits are presented in Table 6. The distinguishing features of Cluster I have higher mean values than overall mean values of accession for all traits except for 1000 seed weight and pod length. Also, Cluster V had higher mean values than the overall mean values of accession for all traits including for seed yield except for 1000 seed weight and harvest index. Cluster II had higher mean values for pod length, pod width, and 1000 seed weight. Cluster III had a high mean value for five traits, viz., and days to 50% flowering, plant height, primary branch per plant, oil content, and days to 75% maturity. Cluster IV had a high mean value for three traits namely plant height, length of pod bearing zone, and harvest index.

According to the mean values of the clusters, selection of accession from Cluster I could be possible to obtain accession with the highest seed yield and other desirable traits. It is also suggested that accession from Cluster I and other Clusters be crossed to combine desirable traits and search for better-performing accession in subsequent segregating generations. The genotypes with the highest cluster mean value could be used as a parent in a future hybridization program for higher yield [26].

Table 6. *Cluster mean values for 14 quantitative traits of 64 sesame accessions.*

Trait	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V	Grand mean
DF	61.73	58.85	61.63	59.69	61.23	60.62
DM	114.77	110.12	114.88	113.15	115.23	113.60
PH	117.57	98.06	112.38	113.47	114.03	110.87
LPBZ	54.94	49.37	50.25	52.43	55.83	52.28
PBP	3.05	2.53	2.92	2.61	2.91	2.80

Trait	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V	Grand mean
SBP	0.30	0.27	0.26	0.28	0.29	0.28
NPP	55.13	35.70	43.40	41.85	55.27	45.58
CL	2.73	2.91	2.76	2.65	2.75	2.76
CW	0.74	0.73	0.71	0.72	0.72	0.72
1000 SW	2.86	3.18	2.87	2.85	2.87	2.93
BM	5395	2793	3813	3400	4582	3926
SY	1150	547	794	751	956	830
HI	21.33	20.66	20.74	22.06	20.91	21.12
OC	50.46	48.08	49.62	49.09	49.37	49.30

Where, DF= Days to 50% flowering, DM=Days to 75% maturity, PH=Plant height (cm), LPBZ=Length of pods bearing zone (cm), PL= Pod length (cm), PW= Pod width (cm), PBP=Primary branch per plant, SBP=Secondary branch per plant, NPP= Number of pods per plant, BM= Biomass yield (kg/ha), 1000 SW=Thousand seed weight (g), SY= Seed yield (kg/ha), HI=Harvest index (%), and OC= Oil content (%).

4. Conclusion

From this study it can be concluded that: 1) Five main components accounting to 76.3% total variation. 2) for 64 sesame accessions, five distinct clusters were identified. 3) Highest inter-cluster distance between Cluster IV and Cluster V identified. Based on the present finding, Accessions from divergent clusters, such as cluster IV and cluster V, and cluster III and cluster V are suggested as a source of parental material for sesame improvement through segregation and hybridization of which cluster V could be crossed to other clusters followed by further segregation and selection. 4) cluster I and cluster V had higher mean values over all mean values except for few traits as a result from those two clusters it could be possible to obtain accession with the highest seed yield and other desirable traits. Finally, we suggest that this study has to be repeated for most the promising accessions in multi-season and multi-location to verify the present finding due to the fact that quantitative traits are polygenic and highly influenced by the environment.

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