# Morphological Characterization of Selected Sesame (*Sesamum Indicum* L.) Genotypes in Western Kenya

Koitilio B.*, Kinyua M., Kiplagat O., Pkania K., Chepkoech E., and Kimno S.

Department of Biotechnology, University of Eldoret,
P.O BOX 1125-30100 Eldoret
*Corresponding author, E-mail: koechbill90@gmail.com

**Abstract**

*Sesame is one of the most important oilseed crops in the tropical and subtropical regions of the world. Despite its importance, sesame yields in Kenya are very low due to lack of improved and high yielding varieties as well as insufficient variety information regarding genetic diversity. The objective of this study was to evaluate the diversity in morphological characters of sesame in Western Kenya. A high level of genetic diversity based on morphological traits was observed which could be attributed to a wide range of environmental conditions which induces variability through genotype by environment interaction. The dendrogram based on UPGMA cluster analysis did not separate the genotypes based on their geographical distribution instead grouped them according to their morphological differences. PCA showed that the first four principal components were important and indicated that number of capsule/plant, number of fruiting branches/plant, seed yield/plant, leaf arrangement, leaf hairiness and flower color were the most important characters and hence were most useful for distinguishing sesame genotypes. Genotypes UG1 and KSS showed better yield performance across the three environments. The use of these genotypes in breeding programs would contribute to improving sesame varieties with a high seed yield and hence improved food security. This research study, therefore, provides important insights into the diversity in morphological traits of sesame genotypes in Western Kenya and constitutes a set of useful genetic background information that can be used as a basis for future breeding strategies and sesame improvement programs.*

**Keywords:** breeding, diversity, environment genotype, sesame, variability.

## INTRODUCTION

Sesame (*Sesamum indicum* L.) in the family Pedaliaceae is one of the most ancient oilseeds crop known to mankind (Nupur *et al*., 2011). It was cultivated and domesticated on the Indian subcontinent during Harappan and Anatolian eras about 5000 years ago (Bedigian *et al.,* 2003; Pathak *et al.,* 2015) but now it is being grown in more than 60 countries in the world (FAO, 2011). Sesame originated from Africa; therefore tropical and sub-tropical regions are best suited for its cultivation (Salah *et al*., 2013; Wang *et al.,* 2014). Its cultivation is much cheaper than other crops and requires little care hence represents a significant crop for small-holders. It is predominantly considered a self-pollinated and drought-resistant plant (Islam *et al.,* 2016).

Sesame is one of the highest oil content (up to 64%) and quality plant among major oilseed crops in the world (Wei *et al.,* 2015; Dossa *et al.,* 2017). Due to its high quality, sesame is referred to as the "Queen of oilseed crops" (Eskandari *et al.,* 2015) and occupies the fifth position in production after soybean, groundnut, sunflower and mustard (Pathak *et al*., 2014). Its oil has medicinal, pharmaceutical and insecticidal value and is being used in many healthcare products (Alege *et al*., 2014). It contains medically important antioxidant lignans,

namely; sesamin, sesamolin, and sesamol (Dar *et al.*, 2014). It is widely used as a source of food, feed, and edible oil. Besides its industrial and medicinal properties, it is an important component in crop rotation and intercropping (Renuka *et al*., 2011; Abdel-Galil *et al.*, 2014). Sesame seeds when added as an ingredient form highly nutritious components of the dessert in cakes (Iman *et al*., 2011). According to FAOSTAT (2016), a total of 6.1 million tons of sesame seeds were produced annually with Sudan, Myanmar, India, China, and Tanzania accounting for more than 60% of the total tonnage worldwide. Africa contributes more than 40% of the world's sesame seed production with Sudan as the leading producer in the continent (FAOSTAT, 2016). The total area under sesame cultivation in Kenya has grown at a slow proportion stretching from 20,000 ha in 1980 to 26,556 ha in 2016 with a concomitant low seed yield production ranging from 8,000-12,874 tons in 1980 to 2011 respectively (FAOSTAT 2016). Its production is currently restricted to lower midlands in Western and Nyanza provinces with its seed yields being low averaging 400 kg $ha^{-1}$ compared to research seed yield of 2230 kg $ha^{-1}$ (Ong'injo and Ayiecho, 2009) and other sesame-growing areas such as Northern Uganda at 673 kg $ha^{-1}$ (Munyua *et al*., 2013) and Ethiopia at 735 kg $ha^{-1}$ (Geleta *et al*., 2015). Despite its significance, sesame is considered an orphan crop since it has received very minute attention from scientists, manufacturers, and lawmakers. As a concern, it lags behind other major oilseed crops in terms of genetic improvement (Dossa *et al.*, 2016).

The reasons for low seed production are associated with lack of improved varieties, poor yield potential associated with cultivated genotypes (Ram *et al.*, 2006; Ogbonna and Ukaa, 2012) and insufficient variety information regarding exploitable genetic diversity (Were *et al*., 2006). Moreover, genetic diversity of sesame landraces in Kenya remains largely unexplored and research has been scarce (Bedigian, 2010a). Cultivated sesame still has some wild characters including seed shattering, indeterminate growth habit and asynchronous capsule ripening resulting in low seed yield of less than 400 Kg $ha^{-1}$ (Islam *et al.*, 2016). Sesame germplasm has revealed a wide and valuable morphological diversity present for different desirable traits (Alemu *et al.*, 2013; Pathak *et al*., 2014; Abate *et al.*, 2015; Pandey *et al.*, 2015) but this variations in traits has not been fully harnessed for genetic improvement of the existing cultivars (Wei *et al.*, 2015; Dossa *et al.*, 2016a).

The low seed production can be corrected by selecting sesame varieties of good quality and those that can highly adapt to the diverse climatic conditions (Salah *et al*., 2013). Its success is subsequently dependent on the nature and magnitude of genetic variability present in this crop (Wei *et al.*, 2015). This knowledge is of immense value for planning efficient breeding programs to improve yield potential, resistance to phyllody disease and selection of desirable genotypes (Salah *et al*., 2013; Pathak *et al*., 2014). Genetic diversity in sesame plays an important role in sustainable development and food security and sesame germplasm collected from the local sources can furnish useful traits to provide greater genetic variability and broaden the genetic base of sesame species (Pervaiz *et al.*, 2010). These sesame landraces could provide useful genes for genetic improvement since they harbor wide genetic diversity (Yue *et al.*, 2013; Wang *et al.*, 2014a; Wei *et al*., 2015). Information on genetic diversity is remarkable when working to improve the profile of sesame accessions and this majorly depends on germplasm characterization (Yogranjan *et al*., 2015). Intensive research on genetic diversity and breeding of sesame is therefore needed to improve its worldwide productivity (Abberton *et al.*, 2015). The wide diversity in a sizeable number of sesame characteristics as revealed by IPGRI (2004), will enable plant breeders to understand the diversity in morphological characters in sesame genotypes for continued improved production in Western Kenya.

## MATERIAL AND METHODS

### Experimental Material

The experimental material consisted of 10 sesame genotypes; one released, seven advanced and two landraces of sesame genotypes. The advanced lines included KK4, KLI, KL2, KL3, KL4, UG1 and SUDSIM. ABL and AWL genotypes were the local landraces while genotype KSS was the released variety.

### Experimental Sites

The experiment was carried out in three agro-ecological zones of Western Kenya, namely: Agricultural Training Center (ATC) Busia which is located within Busia County at longitude 34° 6'E, latitude 00°, 20° N and altitude of 1220 M above sea level. It lies in lower midland one (LM1) agro-ecological zone with medium dark clay ferralsols soils. It receives mean annual rainfall and temperature range between 1200mm-1800mm and 14.7 °C - 30.4 °C respectively (Jaetzold *et al*., 2009). Agricultural Training Center (ATC) Siaya is located within Siaya County between latitude 0° 26' to 0° 18' north, longitude 33° 58' east and 34° 33' west at 1256 M above sea level. It receives mean annual rainfall and temperature range between 1400-1550mm and 21.5°-22.3°C respectively. It lies in lower midland two (LM2) agro-ecological zone and has dystric Nitisols and ferralsols soils (Jaetzold *et al*., 2009). Kimwanga Farmers' demonstration field is located in Bungoma County at an altitude of 1593 M above sea level. It receives mean annual rainfall and temperature range between 1300-1600mm and 20.4-21.7 °C respectively. It falls in Upper Midland 2 (UM2) agro-ecological zone and has mainly Mollic Nitisols soils.

### Experimental Design

The experiment was laid down in a Randomized Complete Block Design with three replications in each environment. The unit plot size in a replication measured 9 rows of 2 m in length and 3.6 m in width keeping inter and intra row spacing of 40 cm and 10 cm, respectively. To reduce border effects, data were recorded from the five central rows. The recommended agronomical practices and plant protection measures were adopted for raising a good crop.

### Data Collection

Morphology of all selected sesame accessions was determined and recorded on twenty-five (25) randomly selected plants per variety in each block. A total of 26 morphological characters were recorded for each plot following to Descriptors of Sesame (IPGRI and NBPGR, 2004).

### Statistical Analysis

Descriptive statistics was performed on quantitative variables to determine minimum, maximum, average, variance, LSD and coefficient of variation among the variables. The means of the genotypes and environments were compared based on the mean grouping test according to Fisher`s protected Least Significant Difference (LSD) whenever the genotypes and location effects were significant at 95% confidence level. Variability of qualitative traits was analysed by GenStat software, 14th edition. Selected morphological descriptors were arranged and analysed using Principal Component Analysis (PCA) in GenStat software, 14th edition. The PCA of the traits was used to examine the percentage contribution of each trait to total genetic variation. A dendrogram was constructed by ascending hierarchical clustering based on quantitative and qualitative data to examine morphological diversity and relatedness among the genotypes.

The following linear models were used during the study:
$Y_{ijkl} = \mu + G_i + E_j + R_{(j)} + GE_{ij} + \varepsilon_{ijkl}$ .....Combined over Environments/locations.
Where:
$Y_{ijkl}$ = observation on $i^{th}$ genotype in the $k^{th}$ replicate and $j^{th}$ environment
$\mu$ =overall mean. $G_i$ =effect of the $i^{th}$ genotype. $E_j$ =effect due to $j^{th}$ environment
$R_{k(j)}$= effect of the $k^{th}$ replicate within $j^{th}$ environment,
$GE_{ij}$ =effect of the $i^{th}$ genotype in $j^{th}$ environment. $\varepsilon_{ijkl}$ =residual

## RESULTS AND DISCUSSIONS

### Morphological qualitative traits

**Table 1: Variability of qualitative traits in 10 sesame genotypes**

| Variability | Variable | Rate | Variability | Variable | Rate |
|---|---|---|---|---|---|
| SH | Glabrous | 30% | FC | White With Deep Violet | 10% |
| | Sparse/Weak | 60% | | White With Light Violet | 70% |
| | Hairy | 10% | | White | 10% |
| SC | White | 70% | LH | Hair Absent | 50% |
| | Brown | 10% | | Sparse | 30% |
| | Grey | 20% | | Hairy | 20% |
| LA | Mixed | 60% | BH | Branching | 100% |
| | Alternate | 40% | | Non-Branching | 0% |
| F/LA | One | 100% | PGT | Indeterminate | 100% |
| | More Than One | 0% | | Determinate | 0% |
| CH | Sparse Hair | 40% | CDR | Completely Shattering | 100% |
| | Hair Absent | 40% | | Partially Shattering | 0% |
| | Strong/Profuse | 20% | | | |
| C/C | Bicarpellate | 70% | | | |
| | Tetracarpellate | 30% | | | |

**S**tem Hairiness (SH), Seed Color (SC), Leaf Arrangement (LA), Number of flowers per Leaf Axil (F/LA), Capsule Hairiness (CH), Flower Color (FC), Leaf Hairiness (LH), Branching Habit (BH), Plant Growth Type (PGT), Capsule Dehiscence at Ripening (CDR), No of carpels per capsule (C/C).

Table 1 above showed that there was no variability among the genotypes in four traits. All the plants had one flower per leaf axil, indeterminate growth habit, branching pattern and a complete shattering of the capsule at ripening. Sixty percent (60%) of the genotypes had sparse/weak stem hairs whereas 70% of the genotypes had white with light violet flower color and white seed coat color. It was also observed that 60% of the genotypes had mixed leaf arrangement. Moreover, 60% of the genotypes had both strong and sparse hair capsules. Fifty percent (50%) of the genotypes had no leaf hairs. The study also showed that 70% of the genotypes had a bicarpellate structure of carpels per capsules.

A range of variations was observed among the accessions for 11 qualitative descriptors. These variations did not exist for branching habit, plant growth type, number of flowers per leaf axil and capsule dehiscence at ripening among the accessions. These results were in agreement with the finding of Uzun and Cagirgan, (2009) who reported that all the landraces grown throughout Turkey consisted of sesame plants with branching, shattering and

indeterminate growth habit. Grichar *et al.* (2012) reported that the majority of the world's sesame is shattering and 99% of the harvest is manual.

There were mostly white flower colors with light violet shading. This type of flower color was quite similar to results obtained by Furat & Uzun, (2010) on Indian sesame collection. Hairiness is a distinctive character of sesame which is found in many parts of the plant such as the stem, leaf, corolla and capsule. Leaf hairiness has a positive effect in terms of preventing water loss, a desirable trait in breeding. Capsule hairiness is a desired feature as it increases tolerance against plant diseases, pests and drought. There were large variations in stem, leaf and capsule hairiness among the genotypes. Majority of the accessions either had sparse or glabrous hairs on stem, leaf and capsule. Strong or profuse hairs were observed in a few accessions. However, genotype UG1 exhibited strong stem, leaf, and capsule hairiness. This could be evaluated as an advantage for insect pests. Genotypes UG1, KSS and KL3 had tetracarpellate capsule structure. These type of capsules enlarge the space for more seeds to fit and a structural modification converting the two extra-floral nectaries to a capsule.

**Morphological Quantitative Characterization**

A considerable level of diversity was observed among the 10 sesame genotypes for most of the quantitative traits measured. The degree of genetic diversity described here is similar to diversity reported for some sesame genotypes grown in India as well as germplasm from other countries such as Turkey (Frary *et al*., 2015; Uncu *et al*., 2015), Cambodia and Vietnam (Pham *et al.,* 2009), China (Zhang *et al*., 2010), Korea (Park *et al.,* 2015) and Indian (Kumar *et al.,* 2011).

The pattern of variation among the genotypes was different for different agro-morphological traits. Genotypes differed significantly *($P \leq 0.05$)* for the majority of the traits except for days to emergence and stem height. The pooled data of environments revealed that genotypes exhibited highly significant *($P \leq 0.001$)* difference for all the traits except capsule length as shown in Table 2 below. Moreover, highly significant *($P \leq 0.001$*) difference among genotypes was observed across the three environments except for stem height. The interactions between genotypes and environments were highly significant *($P \leq 0.001$)* for all the characters except for the number of capsules per plant and plant height. The CV (%) ranged from 3.2% for the number of fruiting branches to 17.5% for the number of capsules per plant. Genotypes UG1 and KSS had the highest seed yield per hectare at 1838 kg $ha^{-1}$ and 1819 kg $ha^{-1}$ respectively across the environments. Genotype ABL had the lowest yield at 409 kg $ha^{-1}$. The largest variation among genotypes was observed for seed yield per hectare, number of seeds per capsule, plant height and number of capsules per plant. The variances for the said traits were 385042, 137.2, 123.6 and 108.8 respectively. The mean values of the sesame genotypes for days to flower initiation, days to 50% flowering and days to maturity were 49, 54.56 and 109.82 respectively. Sesame cultivar KK4 showed low values for these three traits while many other genotypes showed late maturity in this study. Both earliness and lateness in maturity of sesame genotypes are important for plant breeding programs trying for adaptation of sesame germplasms to various ecological regions as well as for researches on photoperiod and thermo-sensitivity (Akbar *et al*., 2011). Days to flower initiation, days to 50% flowering and days to maturity traits should be assessed to recognize for early and late maturing genotypes.

The plant height ranged from 64.1cm to116.3cm, number of fruiting branches per plant varied from 3.24 and 8.36, number of capsules/plant ranged from 14 to 57, number of

seeds/capsule ranged from 14.96 to 62.08, seed yield per plant ranged from 0.57g to 10.68 g and 1000-seed weight was 2.6 g and 3.47 g. The mean seed yield per hectare of 1151 $kgha^{-1}$ was recorded with a range of 141.8 kg $ha^{-1}$ to 2670 kg $ha^{-1.}$ The estimation of different morphological characters among the sesame genotypes in our study has revealed the existence of some level of morphological diversity. This result was in agreement with that obtained by Bandila *et al.* (2011) and Sharma *et al.* (2014) in sesame. Plant height, number of fruiting branches, number of capsules per plant, number of seeds per capsule, 1000-seed weight and seed yield per plant showed extensive genetic variation and accessions with such a large level of genetic diversity often used for the determination of best genotypes for diverse ecological conditions. The means for genotypes, environment and genotype by environment interaction showed a highly significant difference ($p<0.001$) for the majority of the morphological traits. Zerihun *et al.* (2011) also found similar results for Genotypes, Environment and Genotype by Environment interaction in barley landraces. Adjebeng-Danquah *et al.* (2017) also observed significant Genotype by Environment interaction on quantitative traits of cassava. The highly significant difference observed across the three locations could be attributed to a wide range in environmental conditions such as temperature, soil and rainfall which has been reported to induce variability in sesame (Basu *et al.*, 2009).

**Table 2: Means of quantitative traits of sesame genotypes across the three sites in Western Kenya**

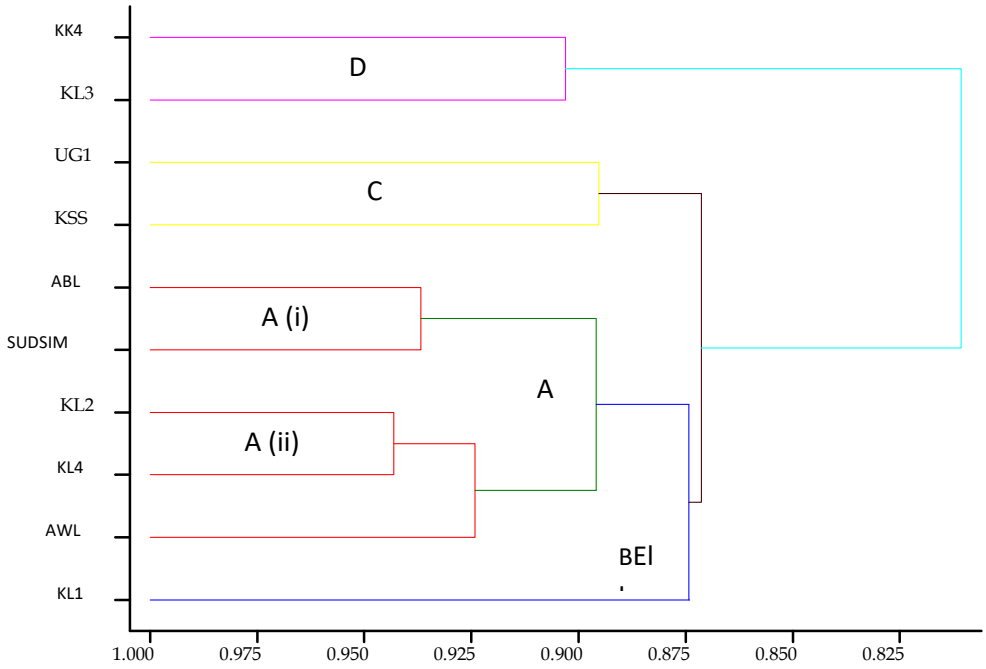
| | TRAITS | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| GENOTYPE | DTE | DFI | 50%F | DCI | DM | SH | PH | CL | CD | NFB | C/PLANT | S/C | 1000SW | SY/P | SY/HA |
| ABL | 6.56d | 54.33c | 63.44c | 70.56c | 115.1f | 48.32ab | 83.71a | 2.498b | 5.471a | 3.684a | 26.5a | 20.29a | 2.8a | 1.264a | 409a |
| KL2 | 5.33a | 48.44ab | 53a | 58a | 110.1e | 49.57abc | 93.93bc | 2.587bcd | 6.36c | 4.96c | 26.82a | 28.57c | 2.927b | 2.238b | 560ab |
| KL1 | 5.56ab | 48.67ab | 52.78a | 57.78a | 109.7de | 47.63a | 93.51bc | 2.358a | 5.764b | 4.711b | 27.16a | 33.97cd | 3.06cd | 2.728c | 682b |
| KL4 | 5.77ab | 47.67a | 51.67a | 50.86a | 109.7de | 52.61c | 100.35de | 2.524bc | 6.298c | 5.213d | 35.11b | 36.52cd | 3.008bc | 3.912d | 978c |
| KK4 | 5.89bc | 47.22a | 52.89a | 57.89a | 110de | 52.11bc | 104.93e | 2.575bcd | 6.596d | 7.538h | 38.02bc | 39de | 2.987bc | 4.496e | 1124cd |
| SUDSIM | 6.33cd | 47.44a | 52.67a | 58a | 109.44cd | 51.82bc | 96.46cd | 2.577bcd | 6.298c | 7.107fg | 38.77bc | 39.11de | 3.19ef | 5.057f | 1264de |
| AWL | 5.78ab | 50.56b | 57.56b | 62.78b | 108.44ab | 50.03abc | 89.73b | 2.618cd | 6.653d | 6.773e | 40.04bc | 45fd | 3.06cfg | 5.454ef | 1364ef |
| KSS | 6bc | 48.11ab | 53.89a | 59.22a | 109bc | 49.92abc | 103.66e | 2.64d | 6.702d | 7.267g | 43.04cd | 42.56ef | 3.18ef | 5.87g | 1468f |
| UG1 | 6.56d | 47.78a | 53.67a | 58a | 108.33a | 46.94abc | 93.82bc | 2.533bcd | 6.929e | 7.604h | 42.33cd | 50.7ff | 3.222h | 7.274h | 1819g |
| Mean | 5.78ab | 49.78ab | 54a | 58.33a | 108.33a | 52.16bc | 91.64bc | 2.904e | 6.9e | 6.938ef | 46.98d | 49.63f | 3.124de | 7.351h | 1838g |
| LSD (0.05) | 5.956 | 49 | 54.56 | 59.74 | 109.82 | 50.11 | 95.17 | 2.581 | 6.405 | 6.18 | 36.48 | 38.53 | 3.056 | 4.564 | 1151 |
| | 0.9267 | 4.716 | 4.556 | 4.473 | 1.0654 | 7.151 | 10.15 | 0.192 | 0.3601 | 0.3229 | 9.19 | 7.515 | 0.1561 | 0.849 | 2650 |

| | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CV (%) | 9.5 | 5.9 | 5.1 | 5.3 | 6 | 8.7 | 11.8 | 4.6 | 3.4 | 3.2 | 17.5 | 11.9 | 5.5 | 11.4 | 14.1 |
| Variance | 0.695 | 15.8 | 24.97 | 31.92 | 11.27 | 34.93 | 123.6 | 0.0417 | 0.339 | 2.14 | 108.8 | 137.2 | 0.046 | 6.3 | 385042 |
| Minimum | 5 | 43 | 47 | 53 | 106 | 35.24 | 64.11 | 2.164 | 5.08 | 3.24 | 14.72 | 14.96 | 2.6 | 0.57 | 141.8 |
| Maximum | 8 | 63 | 70 | 79 | 122 | 66.44 | 116.3 | 3.752 | 7.44 | 8.36 | 57.24 | 62.08 | 3.47 | 10.68 | 2670 |
| Ms. G | 1.51*** | 41.53*** | 109.8*** | 152.9*** | 35.26*** | 37.11 | 375.39*** | 0.17159*** | 2.035*** | 17.6467*** | 489.5*** | 786.42*** | 0.155*** | 77.68*** | 222702*** |
| Ms. E | 5.91*** | 34.2** | 73.89*** | 77.34*** | 293.4*** | 303.22*** | 1527.4*** | 0.02056ns | 2.707*** | 6.6885*** | 1040.4*** | 1257.9*** | 0.265*** | 37.96*** | 454095*** |
| Ms. G*E | 2.83*** | 26.68*** | 33.19*** | 45.48*** | 3.83*** | 54.10*** | 82.03ns | 0.0732*** | 0.196*** | 0.8869*** | 66.24ns | 75.35*** | 0.091*** | 2.66** | 199153*** |

DTE=Days to emergence. DFI=days to flower initiation, 50%F=Days to50% flowering, DCI=days to capsule initiation, DM=days to maturity, SH=stem height. CD=capsule diameter. SY/HA=Seed Yield per Hectare, CL=Capsule Length, S/C=number of Seeds per Capsule, C/P=Capsule per Plant, NB=Number of Fruiting Branches, PH=Plant Height, SY/P=Seed Yield per Plant, 1000SW=1000 Seed Weight. LSD=Least Significant Difference, CV=Coefficient of Variation, Ms. G=Means square of Genotypes, Ms. E=Mean square of Sites/Environment, Ms. G*E=Mean square of Genotype Environment Interaction

**Genetic Relatedness Based on Morphological Clustering.**

UPGMA-based dendrogram depicting genetic relationships among 10 sesame genotypes based on Euclidean dissimilarity estimates for morphological traits was constructed as showed below.




It is observed from the figure above that both quantitative and qualitative traits were grouped by ascending hierarchical clustering into four groups at 0.885 Euclidean distances. Group A contained two sub group (i and ii). This group consisted of genotypes AWL, KL4, KL2, SUDSIM, and ABL. The first pair of genotypes in subgroup (ii) (KL2 and KL4) represents the most closely related genotypes while subgroup (i) contained ABL and Sudsim. Generally, genotypes in group A were characterized by weak or no stem hairs, white flower color, mixed mode of leaf arrangement, early maturing genotypes, low number of seeds per capsule and low seed yield per hectare. Group B consisted of genotype KL1. These genotypes were characterized by grey seed color, sparse hairiness on leaves and stem but no hairs on the capsules, early emergence but late maturity, low number of capsule per plant and seeds per capsule and a concomitant low seed yield per hectare. Group C comprised of genotypes UG1 and KSS. These accessions were characterized by early maturity, medium number of days to emergence, average plant height, maximum number of fruiting branches per plant, higher number of seeds per capsule and capsule per plant, high 1000-seed weight, high seed yield per plant and high seed yield per hectare. Group D possess genotypes KK4 and KL3 which are characterized by white seed color, sparse leaf hairiness, sparse capsule hairs, early flowering, early capsule initiation and early maturing, longer stem height, a higher number of fruiting branches per plant, relatively higher capsules per plant and medium capsule length.

The morphological descriptors used in the present study were able to distinguish the ten genotypes into distinct clusters of related genotypes. These results are in concord with the results of Saha *et al*. (2012) where sesame genotypes were clustered into different groups. Two genotypes revealed high morphological divergence (KK4 and KL3). This indicates that there was a wider genetic diversity among these genotypes which provides a broad genetic base for selection.

The UPGMA dendrogram grouped the genotypes into individual groups. The cluster analysis did not separate the germplasm lines based on their geographical distribution but due to their morphological differences. This shows evidence that geographical isolation is not the only factor causing genetic diversity in sesame. This may be due to the movement of sesame materials from one area to another in collection sites. Our results are in agreement with previous results of Bandila *et al.* (2011), Parameshwarappa *et al.* (2009), Akbar *et al*. (2011) and Gidey *et al*. (2012) in sesame. Moreover, the possible reason for grouping genotypes of different region in one cluster could be to allow for free exchange of germplasm among the breeders of different regions (Bhadru *et al.,* 2012). In a similar study, Surapaneni *et al*. (2014) did not observe any differentiation of sesame genotypes according to geographical origin.

**Principal Component analysis (PCA)**

**Table 3: PCA of 10 Sesame genotypes showing the contribution of both quantitative and qualitative traits to the total variation**

| Quantitative traits | | | | |
|---|---|---|---|---|
| Variables | PC1 | PC2 | PC3 | PC4 |
| 1000SW | 0.236 | -0.133 | 0.255 | 0.218 |
| 50%F | 0.207 | -0.388 | -0.474 | -0.359 |
| CD | 0.254 | 0.023 | -0.002 | -0.17 |
| CL | 0.277 | 0.065 | -0.248 | 0.331 |
| C/P | 0.444 | 0.011 | 0.13 | 0.073 |
| DCI | 0.183 | -0.127 | -0.315 | -0.256 |
| DFI | 0.194 | -0.136 | -0.264 | -0.215 |
| DM | -0.189 | 0.099 | -0.027 | 0.024 |
| DTE | -0.018 | 0.007 | 0.174 | -0.264 |
| NFB | 0.36 | 0.07 | 0.216 | -0.203 |
| PH | 0.184 | 0.443 | 0.351 | -0.54 |
| SH | 0.21 | 0.726 | -0.455 | 0.168 |
| SY/HA | 0.289 | -0.098 | 0.059 | 0.284 |
| SY/P | 0.347 | -0.124 | 0.197 | 0.235 |
| S/C | 0.211 | -0.171 | 0.115 | 0.018 |
| % variation | 50.92 | 21.87 | 15.06 | 5.99 |
| %Cumulative | 50.92 | 72.79 | 87.85 | 93.84 |

| Qualitative traits | | | | |
|---|---|---|---|---|
| Variables | PC1 | PC2 | PC3 | PC4 |
| CH | -0.043 | -0.566 | 0.524 | 0.13 |
| CC | 0.143 | -0.301 | -0.114 | 0.086 |
| FC | -0.042 | 0.415 | 0.268 | 0.82 |
| LA | 0.207 | -0.548 | -0.182 | 0.471 |
| LH | 0.182 | -0.265 | -0.214 | -0.069 |
| SC | -0.948 | -0.208 | -0.149 | 0.066 |
| SH | 0.02 | 0.049 | -0.735 | 0.268 |
| % Variation | 57.63 | 23.44 | 12.28 | 3.35 |
| % Cumulative | 57.63 | 81.07 | 93.35 | 96.7 |

A thousand seed weight (1000 SW), number of days to 50% flowering (50%F), capsule diameter (CD), capsule length (CL), number of seeds per capsule (S/C), number of capsule per plant (C/P), days to capsule initiation (DCI), days to flower initiation (DFI), days to maturity (DM), days to emergence (DTE), stem height (SH), number of fruiting branches (NB), plant height (PH), seed yield per plant (SY/P), seed yield per hectare (SY/HA). **S**tem Hairiness (SH), Seed Color (SC), Leaf Arrangement (LA), Capsule Hairiness (CH), Flower Color (FC), Leaf Hairiness (LH), No of carpels per capsule (C/C). PC=Principal component scores (1-4).

PCA in Table 3 above shows that the first four principal components were important. The four PCA factors were selected on the basis of the highest factor loadings. These components explained that qualitative traits accounted for 96.7% while quantitative traits accounted for 93.84% of the total variation. Based on the qualitative traits in Table below, PC1 accounted for 57.63% of the variation with the major contribution from leaf arrangement (0.207), leaf hairiness (0.182) and number of carpels per capsule (0.143). PC2 accounted for 23.44% of the variation with the major contribution from flower color (0.415) and stem hairiness (0.049). PC3 accounted for 12.28% with the major contribution from capsule hairiness (0.523) and flower color (0.268). PC4 accounted for 3.35% with the major contribution from flower color (0.82) and leaf arrangement (0.471). There was no variability among the genotypes in four traits. All the plants had one flower per leaf axil, indeterminate growth habit, branching and complete shattering of the capsule at ripening. These traits were not used to determine the relative contribution of genotypes to the total variation. On the basis of quantitative traits, PC1 accounted for 50.92% of the variation with the major contribution from the number of capsules per plant (0.444) and number of fruiting branches (0.359). PC2 accounted for 21.87% with the major contribution from stem height (0.725) and plant height (0.443). PC3 accounted for 15.06% with the major contribution from plant height (0.351) and 1000 seed weight (0.255). PC4 accounted for 5.99% with the major contribution from capsule length (0.331) and seed yield per hectare (0.284). The cumulative proportion of the variation reached 81.07% for qualitative traits and 72.79% for quantitative traits for the first two PC axes. The high degree of variation in PC1 and PC2 axes indicates a high degree of variation of these characters. PCA thus indicated that number of capsule/plant, number of fruiting branches/plant, seed yield/plant, stem length, plant height, leaf hairiness, leaf arrangement, flower color and number of carpels per capsule were among the most important characters which accounted for more than 70% of the phenotypic variation expressed in these sesame genotypes.

The cumulative proportion of the variation reached 81.07% for qualitative traits and 72.79% for quantitative traits for the first two PC axes. PC1 accounted for 57.63% and PC2 accounted for 23.44% for qualitative characters. For quantitative traits, PC1 accounted for 50.92% while PC2 accounted for 21.87% of the variation. The high degree of variation in PC1 and PC2 axes indicates a high degree of variation of these characters. Characters with high coefficients in the PC1 and PC2 should be considered as more important since these axes explain more than 70% of the total variation. PCA indicated that number of capsule/plant, number of fruiting branches/plant, seed yield/plant, stem length, plant height, leaf hairiness, leaf arrangement, flower color and number of carpels per capsule were among the most important characters which accounted for more than 70 % of the phenotypic variation expressed in these sesame genotypes. These characters were therefore found to be most useful for distinguishing sesame genotypes. The results of this study were close to those from Manggoel *et al*., (2011) and Sulnathi *et al*., (2007). These authors found that plant height, number of pods per plant, number of branches per plant and flower color

contribute very much to the divergence between cowpea accessions. Solanki and Gupta, (2002) in their studies also observed that seed yield per plant, number of capsules per plant, plant height and 1000 seed weight are the important contributing factors. Similar results were also reported by Alake *et al*., (2010a) who studied PCA and identified height at maturity, number of capsule per plant, stem height and number of seeds per capsule as the characters that contributed significantly to variations found in thirteen sesame genotypes.

## CONCLUSION AND RECOMMENDATION

A high level of genetic diversity based on morphological characters was observed in our study. The diversity could mainly be attributed to diverse agro-climatic conditions which have been reported to induce variability in sesame. Clustering was not related with the geographical distribution instead, genotypes were mostly grouped due to their morphological differences. This enables the breeders to better understand the genetic structure of sesame genotypes. Moreover, prudent use of the results obtained in this study could facilitate the improvement of sesame through breeding and the in situ and ex situ conservation of sesame genetic resources in these regions.

## ACKNOWLEDGEMENT


- I thank Almighty God for bestowing me attitudes of bouncing back with full confidence whenever the time was difficult and His heavenly blessing which has enabled me to achieve this seemingly invincible task.
- An exceptional appreciation goes to NICHE for funding this study.


## REFERENCE


Abate, M., Mekbib, F., Ayana, A., and Nigussie, M (2015). Assessment of genetic diversity in Ethiopian sesame (*Sesamum indicum* L.) germplasm using ISSR markers. Biotechnology. Journal. 8, 1–13.

Abberton M, Batley J, Bentley A (2015). Global agriculture intensification during climate change: a role of genomics. Plant Biotechnology.

Abdel-Galil, A. M., and R. E. A. Abdel-Ghany (2014). Effect of groundnut – sesame intercropping and nitrogen fertilizer on yield, yield components and infection of root-rot and wilt diseases. International Journal Plant Soil Sciences 3 (6):623–43.

Adjebeng-Danquah, J., Manu-Aduening, J., Gracen, V. and Asante, I. K (2017). AMMI stability analysis and estimation of genetic parameters for growth and yield components in cassava in Savannah ecologies of Ghana. International journal of agronomy

Akbar F, Rabbani MA, Shinwari ZK and Khan SJ (2011). Genetic divergence in sesame (*Sesamum indicum* L.) landraces based on qualitative and quantitative traits. Pakistan Journal. Botany. 43: 2737-2744

Alake CO, Ayo-Vaughan MA and Ajani OO (2010a). Estimate of variability for yield and its characters in Nigerian sesame (*Sesamum indicum* L.) genotypes. Journal of Agricultural Science and Environment: 2277 – 2755

Alege GO, Akinyele BO, Osekita OS (2014). Phytochemical studies and genetic diversity in sesame (*Sesamum indicum* L.). In Proceeding of the world congress on engineering, London, UK (Vol. 1, p. 1).

Alemu, A., Petros, Y., and Tesfaye, K (2013). Genetic distance of sesame (*Sesamum indicum* L) cultivars and varieties from northwestern Ethiopia using inter simple sequence repeat markers. East African science journal. 7, 31–40.

Arriel NHC., Mauro AOD., CARBO Arriel EF., Trevisoli SHU., Costa MM., Bárbaro IM., Muniz FRS (2007). Genetic divergence in sesame based on morphological and agronomic traits. Crop Breeding and Applied Biotechnology journal. 7: 253-260

Bandila S, Ghanta A, Natarajan S and Subramoniam S (2011). Determination of genetic variation in Indian sesame *(Sesamum indicum*) genotypes for agro-morphological traits. Journal of Research in Agricultural Science 7: 88-99

Basu SK, Acharya SN, Bandara MS, Friebel D, Thomas JE (2009) Effects of genotype and environment on seed and forage yield in fenugreek (Trigonella foenum-graecum L.) grown in western Canada. Australian Journal of Crop Science 3: 305-314

Bedigian D (2010a) Characterization of sesame (*Sesamum indicum* L.) germplasm: a critique. Genetic Resource Crop Evolution 57: 641-647
Bedigian D. (2003). Evolution of sesame (Revisited): Domestication, diversity, and prospects. Genetic Resource and Crop Evolution 50: 779-787
Bhadru D, Tirumala Rao V, Chandra Mohan Y and Bharathi D (2012). Genetic variability and diversity studies in yield and its component traits in rice (Oryza sativa L.). SABRAO Journal of Breeding Genetics. 44: 129-137
Dar AA, Choudhury AR, Arumugam N (2014). A study on seed protein profile of Indian cultivars of *Sesamum indicum* L. International journal of biotechnology. 2:10–17.
Dossa K., Diouf D., Wang L., Wei X., Zhang Y., Niang M. (2017). The emerging oilseed crop *Sesamum indicum* enters the "Omics" era. Front. Plant Science. 8:1154
Dossa, K (2016). A physical map of important QTLs, functional markers and genes available for sesame breeding programs. Physiology. Molecular Biology. Plants. 22, 613–619.

Dossa, K., Wei, X., Zhang, Y., Fonceka, D., Yang, W., Diouf, D. (2016a). Analysis of genetic diversity and population structure of sesame accessions from Africa and Asia as major centers of its cultivation. Genes 7:14.
Eskandari, H., A. Hamid, and A. Alizadeh-Amraie. "Development and maturation of sesame (*Sesamum indicum. L*) Seeds under different water regimes." Seed Science and Technology 43.2 (2015): 269-272
FAOSTAT (2016). Food and agricultural organization of the United Nations. Statistics Division. Accessed 10th January 2018.
FAOSTAT (2016). Food and agricultural organization of the United Nations. Statistical Database. http://faostat3.fao.org
Frary A, Tekin P, Celik I, Furat S, Uzun B, Doganlar S (2015). Morphological and molecular diversity in Turkish sesame germplasm and core set selection. Crop Science. 55:702–711.
Geleta, Hika, G., N, and Z. Jaleta (2015). "Correlation and divergence analysis for phenotypic traits in sesame (*Sesamum indicum* L.) Genotypes." Science, Technology, and Arts Research Journal 3: 01-09.
Gidey YT, Kebede SA and Gashawbeza G (2012).Extent and pattern of genetic diversity for morpho-agronomic traits in Ethiopian sesame landraces (*Sesamum indicum* L.). Asian Journal of Agricultural Resource 6: 118-128
Grichar, W, P. A. Dotray and D. R. Langham (2012). Sesame (*Sesamum indicum* L.) growth and yield as influenced by pre-emergence herbicides. International Journal of Agronomy.
Iman T, Leila P., Mohammad RB Sadolla M., Mokhtar JJ and Ülo N (2011). Genetic variation among Iranian sesame (*Sesamum indicum* L.) accessions genotypes on the basis of morphological traits. Australian Journal of crop Science. 5 (11): 1396-1407.
IPGRI and NBPGR (2004). Descriptors for Sesame (Sesamum spp.). International Plant Genetic Resources Institute, Rome, Italy; and National Bureau of Plant Genetic Resources, New Delhi, India. ISBN 92-9043- 632-8.
Islam, F.; Gill, R.A.; Ali, B.; Farooq, M.A.; Xu, L.; Najeeb, U.; Zhou W (2016). Sesame. In Breeding Oilseed Crop for Sustainable Production: Opportunities and Constraints; Gupta, S.K., Ed.; Academic Press: Cambridge, MA, USA: pp. 135–147.
Jaetzold, R. Schimidt, H., Hornets, B., and Shisanya, C (2009). Farm Management Handbook of West Kenya, Nyanza province. (2nd ed., vol. 11/A2). Nairobi: ministry of agriculture and German agency for technical cooperation.
Kumar V, Sharma S (2011). A comparative potential of phenotypic, ISSR and SSR Markers for characterization of sesame (*Sesamum indicum* L.) varieties from India. Journal of Crop Science Biotechnology.14:163–171.
Manggoel, W. and M. I. Uguru (2011). Comparative study on the phenology and yield components of two photoperiodic groups of cowpea (*Vigna unguiculata* (L.) Walp.) In two cropping seasons: African Journal of Agricultural Resource. 6(23): 5232-5241
Munyua, B., A. Orr, and J. Okwadi (2013). Open Sesame: A Value Chain Analysis of Sesame Marketing in Northern Uganda. Discussion Paper Series, No. 6. International Crops Research Institute for the Semi-Arid Tropics (ICRISAT).
Nupur M., Bhat KV and Srivastava PS (2011). Variation in fatty acid composition in Indian germplasm of sesame. Journal of the American Oil Chemists' Society 87: 1263-1269.
Ogbonna PE, Ukaa SI (2012). Yield evaluation of 13 sesame (*Sesamum indicum* L.) Accessions in the derived savannah agro-ecology of south-eastern Nigeria. African journal of Agricultural Resource. 7 (43): 5772-5778
Onginjo, E.O., Ayiecho, P.O (2009). Genotypic variability in sesame mutant lines in Kenya. Africa Crop Science Journal. 17, 101–107.
Pandey, S. K., Das, A., Rai, P., and Dasgupta, T (2015). Morphological and genetic diversity assessment of sesame (*Sesamum indicum* L.) accessions differing in origin. Physiological Molecular Biology Plants 21, 519–529.

Park J., Suresh S., Raveendar S., Baek H., Kim C., Lee S (2015). Development and evaluation of core collection using qualitative and quantitative trait descriptor in sesame (*Sesamum indicum* L.) germplasm. Korean Journal of crop science. *60 75–84*

Pathak N., Bhaduri A., Bhat K. V., Rai A. K (2015). Tracking sesamin synthase gene expression through seed maturity in wild and cultivated sesame species. Plant biology 1039–1046.

Pathak, N., Rai, A. K., Kumari, R., and Bhat, K. V (2014). Value addition in sesame: a perspective on bioactive components for enhancing utility and profitability. 8, 147–155.

Pervaiz, Z.H., M.A. Rabbani, I. Khaliq, S.R. Pearce and S.A. Malik (2010). Genetic diversity associated with agronomic traits using microsatellite markers in Pakistani rice landraces. Journal of Biotechnology, 13: 1-12

Pham TD, Tri MB, Gun W, Tuyen CB, Arnulf MA, Carlsson S (2009) A study of genetic diversity of sesame (*Sesamum indicum* L.) in Vietnam and Cambodia estimated by RAPD markers. Genetic Resource Crop Evolution. 56:679–690.

Ram SG, Sundaravel pandian K, Kumar M, Vinod KK, Bapu JK, Raveendran TS (2006). Pollen–pistil interaction in the inter-specific crosses of *Sesamum* sp. Euphytica: 379–385.

Renuka G, Lokesha R, Ranganatha ARG (2011). Trait association and path coefficient analysis for yield and yield attributing traits in sesame (*Sesamum indicum* L.). Electronic Journal of Plant Breeding 2 (3): 448-452

Saha, S., Tamina, B. and Tapash, D (2012). Analysis of Genotypic Diversity in Sesame Based on Morphological and Agronomic Traits. International Research Conference.

Salah, B., Ahmed, M. and Abubakri, FA (2013). Variability of yield and some morphological traits in some sesame (*Sesamum indicum* L.) genotypes under rain-fed conditions. International Journal of agricultural science.

Seymus Furat1 & Bulent Uzun (2010).The use of agro morphological characters for the assessment of genetic diversity in sesame. Plant Omics Journal 3(3): 85-91.

Sharma, JR (2014). Statistical and Biometrical Techniques in Plant Breeding. New Age International (P) limited, publishers. New Delhi. pp. 432.

Solanki Z.S. and D. Gupta (2002). Genetic divergence for seed yield and other characters in sesame (*Sesamum indicum* L.). Journal of Oilseeds Research, 19:35-37

Sulnathi, G., L. Prasnthi and M. Reddy Sekhar (2007). Character contribution to diversity in cowpea. Legume Resource. 30: 70-72.

Surapaneni M, Yepuri V, Vemireddy RL, Ghanta A, Siddiq EA (2014) Development and characterization of microsatellite markers in Indian sesame *(Sesamum indicum* L.). Molecular Breeding 34(3):1185–1200).

Uncu AO, Gultekin V, Allmer J, Frary A, Doganlar S (2015). Genomic simple sequence repeat markers reveal patterns of genetic relatedness and diversity in sesame. Plant Genome.

Uzun, B. & Cagirgan, M.I (2009). Identification of molecular markers linked to determinate growth habit in sesame. Euphytical 166(3), 379-384.

Wang L., Han X., Zhang Y., Li D., Wei X., Ding X (2014/a). Deep resequencing reveals allelic variation in *Sesamum indicum*. BMC Plant Biology. 14:225.

Wei X., Liu K., Zhang Y., Feng Q., Wang L., Zhao Y., Li D., Zhao Q. Zhu (2015).Genetic discovery for oil production and quality in sesame. Natural Community.

Were BA, Onkware OA, Gudu S, Welander M, Carlsson AS (2006). Seed oil content and fatty acid composition in East African sesame (*Sesamum indicums* L.) accessions evaluated over 3 years. Field Crops Res. 97: 254–260.

Yogranjan, G.K. Satpute and S.P. Mishra, (2015). Genetic and genomic intervention to upsurge nutritive values of sesame (*Sesamum indicum* L.). Asian Journal of Science 1296-1303.

Yue W., Wei L., Zhang T., Li C., Miao H., Zhang H (2013). Genetic diversity and population structure of germplasm resources in sesame (*Sesamum indicum* L.) by SSR markers. Acta Agron. Sin. 38, 2286–2296.

Zerihun, J (2011)."GGE Biplot Analysis of Multi-environment Yield trials of Barley (Hordeium vulgare L.) Genotypes in South-eastern Ethiopia Highlands." International journal of plant breeding and genetics 5.1: 59-75

Zhang Y, Zhang X, Hua W, Wang L, Che Z (2010). Analysis of genetic diversity among indigenous landraces from sesame (*Sesamum indicum* L.) core collection in China as revealed by SRAP and SSR markers. Genes Genomics. 32:207–215