Genetic Variability and Association of Traits in Mid-altitude Sesame (*Sesamum indicum L.*) Germplasm of Ethiopia

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Authors' contributions

This work was carried out in collaboration between all authors. Author MA designed the study and wrote the first draft of the manuscript. Authors FM and AA reviewed the experimental design and all drafts of the manuscript. Author MN managed the analyses of the study. Author MA managed the literature searches and correction of the manuscript. All authors read and approved the final manuscript.

Original Research Article

ABSTRACT

Aim: The study was carried out to assess the genetic variability and association of traits with respect to seed yield and its components in (mid-altitude) sesame germplasm of Ethiopia.
Study Design: A 9 x 9 Simple Lattice Design (SLD) with two replications was used.
Place and Duration of Study: Melkassa Agricultural Research Centre Ethiopia, during the July-December, 2011 main cropping seasons.
Methodology: The data recorded on 14 quantitative traits were analyzed for phenotypic and genotypic coefficient of variances, heritability and genetic advance, correlation coefficient, path

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coefficient analysis, principal component analysis and divergence analysis based on Mahalanobis statistics, using SAS 9.2. Statistical software to evaluate the pattern and extent of variation among 81 mid-altitude genotypes.

Results: Analysis of variance revealed significant difference among genotypes for all traits studied. Less than 50% heritability was noted in all traits studied. Moderate heritability coupled with moderate to high genetic advance was recorded for most of yield related traits, indicating that these traits are controlled by both additive and non-additive genes. Characters viz., number of capsules, biomass yield, harvest index and 1000 seed weight showed highly significant positive correlation with seed yield. Maximum positive direct effect on seed yield was exerted by number of capsules, biomass yield, days to maturity and harvest index, showing that these traits can be used for selection to improve the primary trait. Divergence analysis based on Mahalanobis statistics grouped the genotypes into seven different clusters. Genotypes were not grouped in relation to their geographical distribution. Maximum inter cluster distance was observed between cluster V and VII; hence, genotypes from these two clusters are suggested as parents for hybridization program to achieve promising recombinants.

Conclusion: The germplasm lines had sufficient level of genetic variability for seed yield and its components. Clustering was not associated with the geographical distribution instead genotypes were mainly grouped due to their morphological differences. Seed yield, biomass/plant, harvest index and number of capsules contributed highest towards genetic divergence. The use of these traits in sesame improvement program would increase yield.

1. INTRODUCTION

Sesame (*Sesamum indicum L.*) is an annual plant of the *Pedaliaceae* family considered to be the oldest of the oilseed crops cultivated by man. It has been grown in the Near East and Africa for over 5,000 years for cooking and medicinal needs [1]. Generally, 65% of world sesame production is used for edible oil extraction and 35% for confectionary purpose. The fatty acid composition is rather attractive, due to the high level of unsaturated fatty acids. Sesame seed is the single readily available source of protein high in sulfur containing amino acids [2]. It is economically the major cash crop for smallholder farmers and a valuable foreign exchange revenue item for different countries economy. After oil extraction, the remaining residues are used as a source of crude protein for cattle feed.

In Ethiopia, sesame is used as cash crop, export commodity, raw materials for industries and as source of employment opportunity. Currently, it has becomes the primary export oil crop, playing an important role in the agricultural GDP of the country. A sizable proportion of the population, therefore, generates income from oilseed farming, trade and processing [3]. However, sesame production and extension in Ethiopia is quite limited, particularly because of its low yield. One of the major problems facing sesame production in Ethiopia has been growing of inferior genotypes with low yield and poor quality [4]. To overcome these problems, there must be a sound procedure for selection of high yielding genotypes adapted to the local environment. Despite all these, no comprehensive work has been done so far in Ethiopia on genetic variability of the local sesame collections. This situation has limited the success of sesame breeding program in the country.

The success of any crop improvement program essentially depends on the nature and magnitude of genetic variability present in the crop [5]. Phenotypic selection of parents for hybrids based on their performance alone may not always be a reliable procedure since phenotypically superior genotypes may yield inferior hybrids or poor recombinants. Hence, it is essential to select parents on the basis of their genetic worth, i.e., heritability along with genetic advance are both important for selection. As with other field crops, seed yield of sesame are strongly associated with numerous interrelated traits. Knowledge on the nature of association of seed yield with its components has great importance to breeders in selecting desirable genotypes for yield improvement [6]. Correlation analysis is used to understand the relationships existing between yield and yield components. In this regard, Azeez and Morakinyo [7] reported that leaf nodes per plant, number of capsules per plant, capsules per main stem, seeds per capsule, 100-seed weight, and number of seeds per plant were positively correlated with seed yield of sesame. However, correlation alone does not provide the exact knowledge and contribution made by the yield

attributes. Path coefficient analysis has been suggested [8] to separate correlation coefficient into direct and indirect effects. In sesame, path analysis has used to identify traits that have significant effects on seed yield [8,9,10,11]. Therefore, this study was conducted to gather information on genetic variability and character association of mid-altitude sesame genotypes in Ethiopia.

2. MATERIALS AND METHODS

2.1 Description of Experimental Site

The experiment was conducted at Melkassa Agricultural Research Centre (MARC) during the 2011 cropping season (July-December). Melkassa is located along the Upper Awash 'valley' between 8º33' N and 39º17' E. The altitude of the centre is 1550 m.a.s.l. and the mean annual temperature ranges from 15.2 to 27.5ºC. The mean annual rain fall is 560 mm with Verti-cambisol soil type.

2.2 Experimental Materials and Design

The material for the study comprised 81 (mid-altitude) sesame genotypes (Table 1). The experiment was laid out in 9 x 9 simple lattice designs with two replications and each genotype was planted in a plot consisting of two rows of 2.5 m long at a distance of 40 cm between rows and 10 cm between plants. Post planting management has been carried out as recommended for sesame [12].

2.3 Data Collection

Data were collected from net plot size. Five plants in each plot were selected at random and the data were recorded on the following parameters: days to 50% flowering (DF), days to 75% maturity (DM), number of primary branch/plant (PBPL), number of capsules/plant (CPPL), number of seeds/capsule (SDPC), capsule length (CL), plant height (PH), biomass/plant (BMPL), harvest index/plant (HIPL), 1000 seed weight (TSW), seed yield/plant (SYPL), seed yield/plot (SYP) and oil content (OC).

2.4 Data Analysis

Analysis of variance and correlation were carried out for the data with SAS (9.2.) statistical software, to test for significant differences among the genotypes following the procedure described by [13]. The phenotypic and genotypic variances

and their coefficients of variation and heritability in broad sense for each character were estimated by the formula suggested by Singh and Chaudhary [14] as follows:

Genotypic variance (σ^2g) = $\dfrac{MSg - MSe}{r}$ and

Phenotypic variance (σ^2p) = $\sigma^2g + \sigma^2e$.

Where; MSg= mean square genotypes, MSe= mean square error, r = number of replications, σ^2e= error variance.

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) computed as:

GCV = ($\sigma g/\bar{\chi}$) x 100; and PCV = ($\sigma p/\bar{\chi}$) x 100.

Where; σg and σp = genotypic and phenotypic standard deviations respectively, $\bar{\chi}$ = grand mean.

Heritability in broad sense (H) and the genetic advance as percent of the mean (GAM) for all traits were computed using the formula adopted by Allard [15] as follows:

Heritability (H) = (σ^2g/σ^2p) x 100; and the expected genetic advance (GA) = (k * σp * H).

Genetic advance as % of the mean (GAM) = (GA/$\bar{\chi}$) x 100.

Where; k= selection differential at 5% selection intensity (k= 2.06) and $\bar{\chi}$ = grand mean.

Phenotypic and genotypic correlations between morphological traits were estimated using the method described by Miller et al. [16]. The path coefficient analysis was done as described by Dewey and Lu [17]. Seed yield per plant was used as dependent character in separate path analysis and the remaining traits were used as independent variables as required.

Divergence and cluster analysis was carried out based on the mean values of all morphological traits following Mahalanobis's (D^2) statistics [18], and a dendrogram generated based on the Un-weighted Pair Group Mean (UPGMA). Clustering of genotypes into groups was done using the average linkage method and the appropriate number of clusters was determined from the Pseudo F and Pseudo T values using SAS version 9.2. The average intra and inter cluster distances were computed based on the generalized squared distances.

Table 1. List of 81 mid-altitude sesame genotypes and collection regions used in the experiment

No.	Genotype	Region*	No.	Genotype	Region
1.	Am-NSh-1	Amhara North Shoa	42.	SNNP-2	SNNP*
2.	Oromia-1	Oromia	43.	SNNP-3	"
3.	Oromia-2	"	44.	SNNP-4	"
4.	Oromia-3	"	45.	Am-NG-2	Amara North Gonder
5.	Oromia-4	"	46.	Oromia-13	Oromia
6.	Am-NG-1	Amhara North Gonder	47.	Oromia-14	"
7.	Am-SW-1	Amara South Wollo	48.	Oromia-15	"
8.	Oromia-5	Oromia	49.	Am-NG-3	Amhara North Gonder
9.	Oromia-6	"	50.	Am-NG-4	"
10.	Oromia-7	"	51.	Am-NW-16	Amhara North Wollo
11.	Oromia-8	"	52.	Tigray-1	Tigray
12.	Am-SW-2	Amhara South Wollo	53.	Am-SW-9	Amhara South Wollo
13.	Am-SW-3	"	54.	Am-NG-5	Amhara North Gonder
14.	Am-SW-4	"	55.	Oromia-16	Oromia
15.	Am-SW-5	"	56.	Oromia-17	"
16.	Am-SW-6	"	57.	Oromia-18	"
17.	Am-NW-1	Amhara North Wollo	58.	Oromia-19	"
18.	Am-NW-2	"	59.	Tigray-2	Tigray
19.	Am-NW-3	"	60.	Tigray-3	"
20.	Am-NW-4	"	61.	Oromia-20	Oromia
21.	Am-NW-5	"	62.	Am-SW-10	Amhara South Wollo
22.	Am-NW-6	"	63.	Am-SW-11	"
23.	Am-NW-7	"	64.	Am-SW-12	"
24.	Am-NW-8	"	65.	Oromia-21	Oromia
25.	Am-NW-9	"	66.	Oromia-22	"
26.	Am-NW-10	"	67.	Oromia-23	"
27.	Am-NW-11	"	68.	Oromia-24	"
28.	Am-NW-12	"	69.	Oromia-25	"
29.	Am-NW-13	"	70.	Oromia-26	"
30.	Am-NSh-2	Amhara North Shoa	71.	Oromia-27	"
31.	Am-NW-14	Amhara North Wollo	72.	Am-NG-6	Amhara North Gonder
32.	SNNP-1	SNNP*	73.	Am-NG-7	"
33.	Oromia-9	Oromia	74.	Am-NG-8	"
34.	Oromia-10	"	75.	Am-NG-9	"
35.	Oromia-11	"	76.	Am-NG-10	"
36.	Oromia-12	"	77.	Tigray-4	Tigray
37.	Am-NSh-3	Amhara North Shoa	78.	Tigray-5	"
38.	Am-NSh-4	"	79.	T-85	Local check
39.	Am-SW-7	Amhara South Wollo	80.	E	"
40.	Am-SW-8	"	81.	Tate	"
41.	Am-NW-15	Amhara North Wollo			

* Region = geographic region, SNNP = Southern Nation and Nationality People

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance and Mean Performance of Genotypes

The analysis of variance revealed significant difference among the genotypes for all traits, indicating the presence of sufficient variability among the evaluated germplasm for the traits under consideration (Table 2). This result was in agreement with the previous findings reported by [19,20,21,22,23,24].

Based on the mean performance of 81 sesame genotypes for 14 traits (data not shown), the highest number of capsules per plant (112.5) was recorded for Am-NSh-2 whereas the lowest number (40.5) scored for Am-NW-5. The tallest genotype (146.5 cm) was Oromia-22 whereas the shortest (95.5 cm) was Am-NG-3. The maximum harvest index (83.85%) was for Oromia-22 whereas the minimum (52.45%) was for Oromia-9. The highest yielder genotype was Am-NW-13 (6.8 g/plant), the lowest yielder was Oromia-9 (1.45 g/plant) and the highest oil content (52.15%) was for Oromia-13 while the

lowest (43.35%) was for Am-SW-7. A high variation in plant height, and number of primary branches/plant was found among the studied genotypes.

3.2 Variability, Heritability and Genetic Advance

Variability estimates revealed considerable variations for all the studied traits (Table 3). The phenotypic variance (PV) was higher than the genotypic variance (GV) for all the traits. Similarly, phenotypic coefficient of variance (PCV) was higher than genotypic coefficient of variance (GCV) for most of the traits, indicating sensitivity of most of the traits to environmental modifications and the lower scope of improving them through selection. Higher PCV and GCV were recorded for number of primary branches/plant, seed yield/plant, biomass/plant and number of capsules/plant (Table 3). However, the differences between PCV and GCV for these traits were higher except for number of capsules/plant indicating the influence of environment on them. Similar results were reported by previous studies [5,25,26,27]. The higher GCV and a relatively lower difference between PCV and GCV for number of capsules suggested that this character was under the influence of genetic control. Hence, this charac-ter can be relied upon and simple selection can be practiced for further improve-ment. However, high GCV value alone is not sufficient for the determination of the extent of genetic advance to be expected by selection. Burton [28] suggested that GCV together with heritability estimates would give the best picture of the extent of the advance to be expected by selection.

Below 50 percent heritability values were computed in all traits studied (Table 3). The highest values of heritability were noted in harvest index (47.08%) followed by number of seeds/ capsule (42.9%) and oil content (41.52%). Estimates of genetic advance as percent of mean at 5% selection intensity ranged from (0.9%) for capsule length to (24.62%) for seed yield/plot.

Heritability estimates would be reliable if accompanied by a high estimated genetic advance [14]. In our study, moderate estimates of heritability coupled with moderate to high genetic advance over mean was recorded for seed yield, number of capsules, biomass yield, and 1000 seed weight. This indicates that genotypic variance for these traits are probably owing to both additive and non-additive type of gene effects. This result is inconsistence with Ahadu [29] who reported low heritability coupled with low genetic advance for number of capsules and seed yield/ plant, and moderate heritability with high genetic advance for number of branches and plant height. Yield and its components are controlled by many genes, complex in nature of inheritance and much influ-enced by environmental conditions. Therefore, direct selection for yield and its components will not be effective and consequently there is a need for methods other than simple selection to improve yield in sesame. Moderate heritability coupled with low genetic advance for days to flowering, days to maturity, plant height and oil content render them unsuitable for improvement Through conventional selection which confirms that high or moderate heritability alone does not signify an increased genetic advance [30]

Table 2. Mean squares from analysis of variance for 14 morphological traits of sesame genotypes

Trait	Rep (1)	Block (8)	Gen (72)	Error (72)	CV (%)	SE
Days to emergence	0.89	0.06	0.22*	0.18	7.02	0.42
Days to flowering	4.17	19.88	17.57*	7.87	2.76	2.03
Days to maturity	1.04	14.70	12.72*	5.83	1.57	1.91
No. of Pr. branches	3.56	4.17	8.53*	5.27	25.25	2.29
No. of capsules/plant	0.01	79.53	428.83*	184.03	13.74	10.55
No. of seeds/capsule	111.50	18.44	17.46*	6.98	6.50	2.08
Capsule length (cm)	0.04	0.10	0.08*	0.07	10.60	0.27
Plant height (cm)	1063.12	262.38	242.88**	115.17	8.78	10.73
Biomass/plant (g)	9.18	1.05	3.12**	1.51	19.67	1.17
Harvest index (%)	235.45	41.34	83.26**	29.96	6.29	4.77
1000 seed weight (g)	0.57	0.07	0.13*	0.06	11.29	0.21
Seed yield/plant (g)	9.98	1.05	3.13**	1.46	24.63	1.14
Seed yield/plot (g)	24545.89	2575.81	7846.69**	3651.85	24.65	57.06
Oil content (%)	0.83	11.71	8.11*	3.35	2.54	1.20

**, * Indicate significance at P < 0.01 and P < 0.05 levels; Figures in parenthesis refer to degrees of freedom; CV= Coefficient of variation, SE= Standard error

In case of high heritability combined with low genetic advance, the character is mainly under the control of non-additive types of genes (epistasis, dominance). Saravanan et al. [31] also emphasized that if a character is controlled by non-additive type of genes then selection for this trait should be postponed and performed safely in advanced/succeeding generations. This result was in conformity with the findings of Reddy et al. [32]. However, the result of this study in general was inconsistence to the previous findings in sesame [33,34,35], who reported very high heritability coupled with high genetic advance for seed yield and its component traits.

3.3 Correlation and Path Coefficient Analysis

Correlation coefficients of the various traits are presented in Table 4. Number of capsules/plant, biomass/plant, harvest index and 1000 seed weight exhibited highly significant (<0.001) and very high positive association with seed yield/ plant indicating that these traits are reliable yield components. Tomar et al. [36] and Pawar et al. [37] also found similar observations. Plant height and number of seeds/capsule showed highly significant but moderate positive correlation with seed yield/plant. Number of primary branch showed significant (<0.05) and low positive association with plant height, biomass/plant, harvest index, seed yield/plant. Hence, indirect selection in favor of these traits can improve seed yield in sesame. Similar results were reported for plant height, number of branches, number of capsules, days to 50% flowering, days to maturity and 1000 seed weight [38,39]. However, oil content showed negative and significant (<0.05) genotypic correlation with most yield components (Table 4). This indicates that indirect selection for high oil content would reduce seed yield/plant. Similar result was found by Daniya et al. [40]. On the contrary, insignificant positive correlation of oil content with seed yield was reported [41], who suggested that selection for oil content had no adverse effects on seed yield. Generally, the result showed the presence of highly significant positive correlation between seed yield and its component traits and this finding was in line with other previous studies [42,43,44], who reported significant and positive correlations between yield traits and final seed yield in sesame.

However, as the number of independent variables influencing a particular dependent variable increases, certain amount of interdependence is expected [45]. Thus, correlation may be insufficient to explain the associations in a manner that will enable one to decide on either a direct or an indirect selection strategy.

Path coefficient analysis provides more effective means of separating direct and indirect factors, permitting a critical examination of the specific forces acting to produce a given correlation and measuring the relative importance of the causal factors.

The results of path coefficient analysis (Table 5) revealed that number of capsules/plant (0.98) had maximum positive direct effect on seed yield/plant followed by biomass/plant (0.70), days to maturity (0.44) and harvest index (0.35). These traits also had strong and positive correlation with seed yield at both phenotypic and genotypic level except days to maturity (Table 3). Therefore, these traits can be considered as the principal traits while selecting for seed yield. In other words, selection indices may be formed by considering all these traits for improvement of seed yield. Similar results were reported in previous studies [9,10,46]. Number of seeds/capsule had highest indirect effect on seed yield through capsules/plant (0.93) followed by harvest index (0.72) and 1000 seed weight (0.67) through biomass/plant, primary branches/ plant (0.66) through capsules/plant, capsule length (0.60) and plant height (0.45) through biomass/plant; though these traits had direct negative effect to seed yield/plant. This finding strongly emphasized that seeds per capsule made the greatest indirect contribution to seed yield. This result agreed with some of the recent reports [40,46].

3.4 Genetic Divergence

Genetic divergence of 81 sesame genotypes was determined for seed yield and attributing traits. Clustering of genotypes based on the quantitative traits categorized the germplasm into seven clusters. The composition of clusters and values of inter and intra clusters distances are given in Tables 6 and 7, respectively. Clusters were heterogeneous within themselves and among each other based on major character relations. Cluster-III contained maximum genotypes (22) followed by Cluster-II (19), cluster-V (14), cluster-I (10), cluster-IV each (9), cluster-VI (5), and cluster-VII (2). The range of inter and intra cluster distance was 14.98 to

570.34 and 2.61 to 7.40, respectively (Table 7). The result revealed that the inter cluster distances were larger than the intra cluster distances for all cases, suggesting wider diversity among the germplasm of different groups. The maximum inter cluster distance was found between clusters V and VII, followed by clusters III and VII (447.71), clusters V and VI (315.34), and clusters II and VII (308.69). The minimum inter cluster distance was recorded between clusters II and IV followed by clusters I and IV (18.69), clusters II and III (23.08), and clusters I and VI (23.45). The highest intra cluster distance was observed for cluster VII (7.40). It indicates that the germplasm lines in this cluster were more diverged than any other cluster. This was also reflected in the scatter diagram. The germplasm lines belonging to the distant clusters could be used in hybridization programme for obtaining a wider range of variability. The result indicated that the germplasm lines studied had a considerable level of variability that could be exploited in future breeding programs. Hybridization between genetically diverse genotypes in sesame to generate promising breeding material has been suggested by Alarmelu and Ramanathan [47]. The greater genetic divergence found between clusters V and VII indicated that superior hybrids or recombinants can be realized by mating between the lines of these clusters in a definite fashion.

Cluster means of sesame germplasm for 14 traits (Table 8) revealed that cluster-V had the highest plant height, days to maturity, number of primary branches, number of capsules/plant, 1000 seed weight, harvest index, seed yield/plant and yield/plot. Cluster-III comprised early flowering and early maturing accessions with highest harvest index and seed yield/plant next to Cluster-V. Accessions of this group were also characterized by high number of branches/ plant, number of capsules/plant, number of seeds/ capsule and taller plant height, but with lowest oil content (%). These clusters can be preferred in selecting germplasm lines for respective traits as they had good means. In contrast, Cluster-VII was mainly characterized by lowest number of capsules/ plant, number of seeds/ capsule, biomass/ plant, harvest index, 1000 seed weight and lowest seed yield/plant with moderate branching habit, longer capsules and highest oil content (%). Cluster-VI possessed genotypes with high emergence dates and high percentage of oil content, but with lowest number of branches/plant, short plant stature, low capsules/plant, 1000 seed weight and seed yield/plant. Genotypes in Cluster-II were characterized by late flowering and late maturing plants, with average plant height, number of branches/plant, number of capsules/plant, 1000 seed weight, seed yield and oil content (%). Cluster-I and IV both consisted genotypes with average plant traits for most traits with low seed yield/plant. Thus, a crossing programme should be initiated among the genotypes belonging different clusters. The greater the distance between two clusters, the wider the genetic diversity among the parents to be included in hybridization program [48].

Table 3. Genotypic and phenotypic coefficient of variances, heritability and genetic advance as percent of the mean for 14 morphological traits in sesame genotypes

Trait	Mean	$\sigma^2 g$	$\sigma^2 p$	GCV	PCV	H (%)	GA (%)
Days to emergence	5.98	0.02	0.20	2.55	7.47	11.63	1.79
Days to flowering	69.63	4.85	12.72	3.16	5.12	38.10	4.02
Days to maturity	116.67	3.45	9.27	1.59	2.61	37.16	2.00
No. of Pr. branches	9.09	1.63	6.90	14.06	28.91	23.67	14.09
No. of capsules/plant	76.75	122.40	306.43	14.42	22.81	39.94	18.77
No. of seeds/capsule	31.97	5.24	12.22	7.16	10.93	42.90	9.66
Capsule length (cm)	2.57	0.00	0.08	2.17	10.82	4.03	0.90
Plant height (cm)	122.23	63.85	179.02	6.54	10.95	35.67	8.04
Biomass/plant (g)	5.95	0.81	2.32	15.09	25.57	34.81	18.34
Harvest Index (%)	75.82	26.65	56.61	6.81	9.92	47.08	9.62
1000 seed weight (g)	1.87	0.03	0.10	9.73	16.76	33.73	11.64
Seed yield/plant (g)	5.33	0.83	2.29	17.13	28.42	36.33	24.49
Seed yield/plot (g)	266.50	2097.42	5749.27	17.18	28.45	36.48	24.62
Oil content (%)	47.14	2.38	5.73	3.27	5.08	41.52	4.34

$\sigma^2 g$ = Genotypic variance, $\sigma^2 p$ = Phenotypic variance, GA (%) = Genetic advance as % of mean at 5% selection intensity, GCV & PCV = Genotypic and phenotypic coefficient of variances respectively, H = Broad sense heritability

Table 4. Genotypic correlation above diagonal and phenotypic correlation below diagonal among 14 traits in sesame genotypes

Trait	DE	DF	DM	PBPL	CPPL	SDCP	CL	PH	BMPL	HIPL	TSW	SYPL	SYP	OC
DE		0.02	-0.08	0.04	-0.06	0.11*	-0.05	-0.01	-0.03	-0.01	-0.04	-0.03	-0.06	-0.03
DF	0.09		0.69***	0.05	-0.02	-0.04	-0.13*	-0.03	-0.01	0.01	0.09	-0.01	-0.01	-0.05
DM	-0.03	0.70***		0.05	0.03	0.00	-0.09	0.02	0.02	0.03	0.04	0.02	0.02	-0.02
PBPL	0.14	0.06	0.10		0.35***	-0.04	0.01	0.25***	0.27***	0.21***	0.06	0.27***	0.27***	-0.04
CPPL	0.00	-0.02	0.04	0.42***		0.13*	0.15**	0.33***	0.79***	0.73***	0.11	0.79***	0.79***	0.01
SDCP	0.13	0.00	0.08	-0.01	0.24*		0.00	0.08	0.48***	0.53***	0.22***	0.48***	0.48***	-0.07
CL	0.05	-0.08	-0.09	0.04	0.22	0.03		0.00	0.13*	0.16**	-0.01	0.13*	0.13*	-0.04
PH	0.00	0.01	0.03	0.38**	0.46***	0.30*	0.00		0.28***	0.22***	0.03	0.28***	0.28***	0.00
BMPL	0.03	0.02	0.05	0.31*	0.83***	0.53***	0.21	0.43***		0.94***	0.60***	1.00***	1.00***	-0.11*
HIPL	0.02	0.05	0.05	0.25*	0.78***	0.57***	0.24	0.37**	0.96***		0.62***	0.94***	0.94***	-0.13*
TSW	0.01	0.17	0.06	0.07	0.21	0.24*	-0.01	0.06	0.65***	0.62***		0.60***	0.60***	-0.21*
SYPL	0.02	0.02	0.05	0.31*	0.83***	0.53***	0.21	0.43***	0.99***	0.96***	0.65***		1.00***	-0.11*
SYP	0.03	0.02	0.05	0.31*	0.83***	0.52***	0.22	0.42***	0.98***	0.96***	0.65***	1.00***		-0.11*
OC	0.03	-0.02	-0.01	0.06	0.16	-0.06	-0.02	0.03	-0.08	-0.12	-0.06	-0.08	-0.08	

***, **, * = Significant < 0.001, < 0.01 and < 0.05 respectively. DE= Days to emergence, DF = Days to flowering, DM= Days to maturity, PBPL= Number of primary branches per plant, CPPL= Number of capsules per plant, SDPC= Number of seeds per capsule, CL= capsules length, PH= Plant height, BMP= Biomass per plant, HIPL= Harvest index, TSW= 1000 seed weight, SYPL= Seed yield per plant, SYP= Seed yield per plot, and OC= Oil content

Table 5. Direct (diagonal) and indirect (off diagonal) effects of 11 traits on seed yield/ plant at phenotypic level in mid-altitude sesame genotypes

Trait	DF	DM	PBPL	CPPL	SDCP	CL	PH	BMPL	HIPL	TSW	OC	SYPL
DF	**-0.50**	0.37	0.01	0.00	-0.06	-0.07	0.03	0.02	0.01	0.00	0.00	-0.19
DM	-0.42	**0.44****	0.06	0.14	-0.08	0.01	0.03	0.08	0.09	0.01	0.01	0.37
PBPL	0.01	-0.08	**-0.33**	0.66	-0.12	-0.13	-0.18	0.46	0.41	-0.14	0.00	0.56
CPPL	0.00	0.04	-0.23	**0.98****	-0.42	-0.13	0.21	0.47	0.39	-0.35	0.01	0.97
SDCP	-0.21	0.22	-0.03	0.93	**-0.15**	0.02	0.04	0.22	0.19	-0.39	0.01	0.85
CL	0.60	-0.10	-0.18	-0.72	0.04	**-0.06**	0.06	0.29	0.23	-0.05	0.00	0.11
PH	0.01	0.00	-0.03	0.43	-0.17	0.02	**-0.01**	0.45	0.21	0.00	0.00	0.91
BMPL	0.02	0.02	0.04	0.31	-0.34	0.02	-0.11	**0.70****	0.33	-0.05	0.00	0.94
HIPL	0.01	0.01	0.02	0.33	-0.39	0.02	-0.02	0.72	**0.35****	-0.15	-0.01	0.89
TSW	0.00	0.00	0.02	-0.39	0.12	0.05	0.00	0.67	0.32	**-0.05**	0.01	0.75
OC	0.00	0.00	0.00	0.12	-0.03	0.02	0.00	-0.35	-0.03	-0.10	**0.01**	-0.36

** = High direct effect, DE= Days to emergence, DF = Days to flowering, DM= Days to maturity, PBPL= Number of primary branches, CPPL= Number of capsules, SDPC= Number of seeds per capsule, CL= capsules length, PH= Plant height, BMP= Biomass yield, HIPL= Harvest index, TSW= 1000 seed weight, SYPL= Seed yield per plant, SYP= Seed yield per plot and OC= Oil content

Table 6. Clustering of 81 sesame genotypes based on Mahalanobis (D^2) distance

Cluster	Name of genotypes	No. of genotypes
I	Am-SW-3, Oromia-11, Am-SW-4, Am-SW-5, Oromia-23, Oromia-21, Oromia-7, Tigray-1, Am-NSh4, Am-NW-6	10
II	Am-SW-6, Am-NW-4, Am-NW-10, Am-SW-7, Oromia-3, Oromia-14, Am-NW-11, Am-NW-12, Am-NW-16, Oromia-8, Oromia-27, Am-NG-4, Tigray-2, Am-NW-2, Oromia-26, Am-SW-12, Am-NG-10, Am-NG-6, Oromia-2	19
III	Am-SW-1, Oromia-17, SNNP-2, SNNP-3, SNNP-1, Am-NW-7, Am-NW-9, Oromia-20, Tigray-4, T-85, Am-NW-14, Am-NW-1, Am-NW-15, Tate, Am-SW-11, Am-NG-8, Oromia-19, Am-NG-2, Am-SW-9, Oromia-5, Tigray-3, Am-NSh1,	22
IV	Oromia-6, Oromia-24, Am-NW-3, Oromia-13, Oromia-4, Am-NG-5, Am-NG-7, Am-SW-2, Am-NG-3	9
V	Am-NSh3, Oromia-15, Oromia-12, Am-SW-10, Oromia-16, E, Am-NW-13, Oromia22, SNNP-4, Oromia25, Oromia-10, Oromia-1, Am-NSh2, Oromia-18	14
VI	Am-NW-8, Am-SW-8, Am-NG-1, Tigray-5, Am-NG-9	5
VII	Am-NW-5, Oromia-9	2

Table 7. Average intra- (bold face) and inter-cluster divergence D^2 value in sesame genotypes

Cluster	I	II	III	IV	V	VI	VII
I	**4.18**	43.03	114.20	18.69*	208.54	23.45	148.80
II		**2.90**	23.08	14.98*	76.32	106.81	308.69
III			**2.61***	60.60	24.85	206.57	447.71**
IV				**4.39**	137.19	59.86	233.97
V					**3.51**	315.34	570.34**
VI						**5.57**	74.81
VII							**7.40**

**, * = Maximum and minimum distance values, respectively

Table 8. Mean values of clusters for 14 traits in sesame genotypes

Trait	I	II	III	IV	V	VI	VII
Days to emergence	5.9	5.9	6.0	6.2	5.9	6.2	5.8
Days to flowering	73.7	74.2**	72.7	73.8	74.0	73.6	73
Days to maturity	121.8	122.3	120.7	121.8	122.6**	121	121
No. of Pr. branches	8.5	9.2	9.6	7.8	10.0 **	7.6	9.0
No. of capsules/plant	59.9	76.1	84.6	69.9	93.9**	55.2	45.5
No. of seeds/capsule	31.1	31.6	33.4**	31.8	33.2	29.0	24.5
Capsule length (cm)	2.5	2.6	2.6	2.6	2.6	2.6	2.7**
Plant height (cm)	119.7	118.7	126.3	117.1	130.4**	111.4	116.0
Biomass/plant (g)	4.5	5.8	6.7	5.1	7.7 **	3.9	2.8
Harvest index (%)	69.0	76.3	80.1	73.2	82.5**	63.9	53.4
1000 seed weight (g)	1.8	1.9	1.9	1.7	2.1**	1.6	1.4
Seed yield/plant (g)	3.2	4.5	5.5	3.8	6.4**	2.5	1.6
Seed yield/plot (g)	159.3	225.0	271.1	189.2	316.7	126.3	75.1
Oil content (%)	47.3	47.5	46.4	47.7	47.2	47.5	47.9**

** = Maximum mean values

The UPGMA dendrogram (Fig. 1) grouped the genotypes into individual groups The cluster analysis did not separate the germplasm lines based on their geographical distribution instead genotypes were mainly grouped due to their morphological differences; showing evidence that geographical isolation is not the only factor causing genetic diversity in sesame. Our results were in agreement with previous reports of [49,50,51,52,53]. This may be the movement of sesame materials from one area to another in collection sites. A few ecological conditions could also lead to gene flow between populations from diverse geographical origins [53].
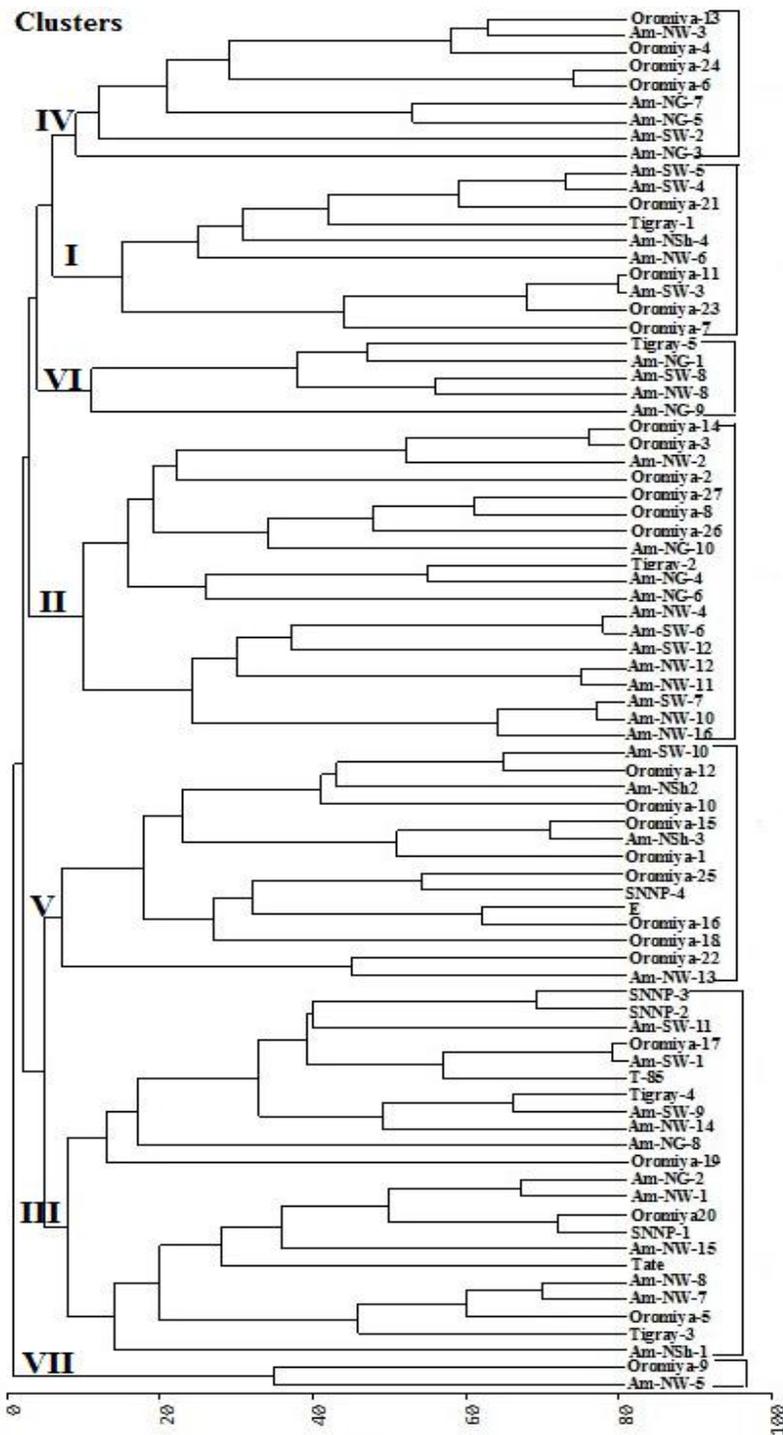
Fig. 1. Dendrogram generated based on mean values of quantitative traits depicting the clustering pattern of 81 mid-altitude sesame genotypes
See Table 1 for list of genotypes and their regions of collection

The number of times, each of the yield component character appeared first in rank and its respective percent of contribution towards genetic divergence was presented in Table 9.

Table 9. Contribution of different quantitative traits to diversity in sesame

No	Character	No. of times ranked first	Percent contribution
1.	Days to emergence	47	1.45
2.	Days to flowering	22	0.68*
3.	Days to maturity	44	1.36*
4.	No. of branches/ plant	74	2.30
5.	No. of capsules/plant	397	12.24**
6.	No. of seeds/capsule	187	5.78
7.	Capsule length (cm)	14	0.43*
8.	Plant height (cm)	151	4.68
9.	Biomass/plant (g)	529	16.33**
10.	Harvest index (%)	524	16.16**
11.	1000 seed weight (g)	154	4.76
12.	Seed yield/plant (g)	532	16.41**
13.	Seed yield/plot (g)	532	16.41**
14.	Oil content (%)	33	1.02*
	Sum	3240	100

*** = High contribution, * = Negligible contribution*

The result showed that seed yield/plant (16.41%) contributed highest towards genetic divergence followed by biomass/plant (16.33%), harvest index (16.16%), number of capsules (12.24 %), seeds/ capsule (5.78%) and 1000 seed wt. (4.76%). These results were in agreement with those given by Solanki and Gupta [54]; who reported that seed yield, number of capsules, plant height and 1000 seed weight are the important contributing attributes. On the other hand, Sudhakar et al. [25] reported that 1000 seed weight, number of capsules per plant, plant height, and capsule length recorded negligible contribution. In our study the least variation was recorded for capsule length, days to flowering and oil content, showing comparatively less contribution of these traits towards genetic divergence. In the contrary, Duhoon and Raghuwanshi [55] reported oil content and days to flowering to have maximum contribution to divergence.

4. CONCLUSION

The results of this study indicated that the germplasm lines had sufficient level of genetic variability for seed yield and its components that could be exploited in future breeding programs. Moderate heritability accompanied with moderate to high genetic advance were recorded for seed yield and its components which indicates both the additive and non-additive genes are acting in controlling the traits, whereas moderate heritability with low genetic advance for days to flowering, days to maturity, plant height and oil content indicate their dominant and epistatic nature of inheritance. Number of capsules/plant,

biomass/plant, days to maturity and harvest index showed maximum positive direct effect on seed yield. They can be considered as the principal traits while selecting for seed yield. Clustering was not associated with the geographical distribution instead genotypes were mainly grouped due to their morphological differences. Greater genetic divergence was found between clusters V and VII indicating that superior hybrids or recombinants can be realized by mating between the lines of these clusters in a definite fashion. Seed yield/plant, biomass/plant, harvest index and number of capsules/plant are the best traits contributing towards genetic divergence.

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COMPETING INTEREST

Authors have declared that no competing interests exist.

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