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Research Article

Studies of Genetic Variability in Sesame (*Sesamum indicum* L.) Collections for Morpho-Agronomic Traits at Werer, Ethiopia

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Abstract

Knowledge of genetic variability is necessary to develop a suitable breeding method for crop improvement. Thus, further information on the existence of variability in sesame accessions is needed to set appropriate breeding strategies and improve sesame in terms of yield and desired quality traits. Based on this concern, this research was conducted to estimate the phenotypic and genotypic variability, heritability, and genetic advance among sesame accessions. A total of sixty-four sesame (*Sesamum indicum* L.) Accessions were evaluated in an 8*8 lattice design with two replications in 2021 at the Werer Agricultural Research Center. The results of the analysis of variance showed that, except for the 50% days to emergence and the number of seeds per pod, there were statistically significant differences between the accessions for all traits. A relatively high (>20%) phenotypic and genotypic coefficient of variation was estimated for the number of pods per plant, number of secondary branches per plant, seed yield, and biomass yield. High heritability coupled with high genetic advance as a percentage of the mean (GAM) was recorded for thousand seed weight, number of primary branches per plant, number of pods per plant, biomass yield, and seed yield. The information and genetic variability obtained in the present study could be used to plant appropriate breeding procedures and develop genotypes with high productivity in future sesame improvement programs.

Keywords

Accessions, Genetic Advance, Heritability, Sesame, Variability

1. Introduction

Sesame (*Sesamum indicum* L.) belongs to the Pedaliaceae family, and about 37 species have been described in the Genus Sesamum, but only *Sesamum indicum L.* has been recognized as a cultivated species [1]. It is normally a self-pollination species; the cultivated species of sesame is a diploid species with the chromosome number $2n = 2x = 26$ [2]. However, depending on the activity of pollinating agents, 2–48% of natural crossing may take place [3].

Sesame is a valuable export cash crop in Ethiopia. The Ethiopian Central Statistics Agency reported that the area under production of sesame is estimated to be 204,511.91 ha in 2021/2022 cropping seasons [4]. Also, total grain production and productivity were 137,807.1 tons and 674 kg ha1 in 2021/2022 cropping seasons [4]. Ethiopia was World's

fourth-largest exporter of sesame seeds, after Sudan, India, and the Republic of Tanzania, and Ethiopia is Africa's third largest exporter (107,719.21ton) after Sudan and the Republic of Tanzania [5].

As defined by Falconer *et al*. genetic variation is an individual difference that arises as a result of differences in genetic composition and the environment in which individuals reside [6]. Phenotypic variation, which would be the detectable variation in a character in a population, comprises both genetic variability and environmental components of variation [7].

Plant breeders are most concerned with genotypic variation, which is the component of variation caused by genotypic differences among individuals within a population [7]. Estimates of genotypic and phenotypic variance coefficients are used to examine the variability in a population [8]. To initiate an appropriate breeding procedure for crop improvement and develop genotypes with high productivity, information on genetic variability is a prerequisite [9]. Given the importance of generating information on genetic variability, heritability, and genetic advance as prerequisites for improv-

ing the crop, research to understand the existence of variability in genotypes is required to develop high-yielding sesame varieties. Therefore, the present research was undertaken to estimate the phenotypic and genotypic variability, heritability, and genetic advance in sesame accessions.

2. Materials and Methods

2.1. Description of Experimental Site and Experimental Materials

The experiment was conducted in 2021 at Werer Agricultural Research Center in the lowland of Ethiopia under irrigation conditions. The experimental materials consisted of sixty four sesame accessions obtained from the Ethiopian Biodiversity Institute were used in this study (table 1). The origin of those materials is Ethiopian country and which was collected from four regions (Benshungul Gumuz, Tigray, Oromia, and Amhara).

Table 1. Description of experimental materials used for the study.

S.№	Accessions	Genusname	Speciesname	Region	Zone	Woreda	Altitude
1	Acc.9015	*Sesamum*	*indicum*	Benishangul	Metekel	Guba	855
2	Acc.9017	*Sesamum*	*indicum*	Benishangul	Metekel	Guba	778
3	Acc.9019	*Sesamum*	*indicum*	Benishangul	Metekel	Guba	518
4	Acc.9026	*Sesamum*	*indicum*	Benishangul	Metekel	Guba	665
5	Acc.9027	*Sesamum*	*indicum*	Benishangul	Metekel	Guba	665
6	Acc.9028	*Sesamum*	*indicum*	Benishangul	Metekel	Guba	626
7	Acc.9690	*Sesamum*	*indicum*	Tigray	Mirabawi	KaftaHumera	933
8	Acc.9691	*Sesamum*	*indicum*	Tigray	Mirabawi	KaftaHumera	799
9	Acc.9692	*Sesamum*	*indicum*	Tigray	Mirabawi	KaftaHumera	652
10	Acc.9693	*Sesamum*	*indicum*	Tigray	Mirabawi	KaftaHumera	812
11	Acc.9694	*Sesamum*	*indicum*	Tigray	Mirabawi	Tsegede (Welkait)	773
12	Acc.9696	*Sesamum*	*indicum*	Tigray	Mirabawi	KaftaHumera	768
13	Acc.9697	*Sesamum*	*indicum*	Amhara	SemenGondar	LayArmacho	1081
14	Acc.17693	*Sesamum*	*indicum*	Oromiya	EastWollega	GitoGida	1346
15	Acc.17694	*Sesamum*	*indicum*	Oromiya	EastWollega	GitoGida	1352
16	Acc.17695	*Sesamum*	*indicum*	Oromiya	EastWollega	GitoGida	1346
17	Acc.17696	*Sesamum*	*indicum*	Oromiya	EastWollega	Diga	1345
18	Acc.17697	*Sesamum*	*indicum*	Oromiya	EastWollega	Diga	1360
19	Acc.17698	*Sesamum*	*indicum*	Oromiya	EastWollega	Sasiga	1385
20	Acc.17699	*Sesamum*	*indicum*	Oromiya	EastWollega	WayuTuqa	1755
21	Acc.17701	*Sesamum*	*indicum*	Oromiya	EastWollega	Ibantu	2055

S.№	Accessions	Genusname	Speciesname	Region	Zone	Woreda	Altitude
22	Acc.17702	*Sesamum*	*indicum*	Oromiya	EastWollega	GidaAyana	1361
23	Acc.17703	*Sesamum*	*indicum*	Oromiya	EastWollega	GidaAyana	1365
24	Acc.17704	*Sesamum*	*indicum*	Oromiya	KelemWollega	Anfilo	1517
25	Acc.17705	*Sesamum*	*indicum*	Oromiya	KelemWollega	HawaGelan	1346
26	Acc.17706	*Sesamum*	*indicum*	Oromiya	WestWollega	YamalagiWalal	1425
27	Acc.17707	*Sesamum*	*indicum*	Oromiya	KelemWollega	DaleWabera	1515
28	Acc.17708	*Sesamum*	*indicum*	Oromiya	WestWollega	Begi	1793
29	Acc.17709	*Sesamum*	*indicum*	Oromiya	EastWollega	GobuSeyo	1590
30	Acc.17710	*Sesamum*	*indicum*	Oromiya	EastWollega	WamaHagelo	1582
31	Acc.17711	*Sesamum*	*indicum*	Oromiya	EastWollega	LeqaDulcha	1869
32	Acc.28300	*Sesamum*	*indicum*	Amhara	SemenGondar	Kora	708
33	Acc.28301	*Sesamum*	*indicum*	Amhara	SemenGondar	Kora	721
34	Acc.28302	*Sesamum*	*indicum*	Amhara	SemenGondar	Kora	708
35	Acc.28303	*Sesamum*	*indicum*	Amhara	SemenGondar	Kora	602
36	Acc.28304	*Sesamum*	*indicum*	Amhara	SemenGondar	Metema	730
37	Acc.28305	*Sesamum*	*indicum*	Amhara	SemenGondar	Metema	729
38	Acc.28306	*Sesamum*	*indicum*	Amhara	SemenGondar	Metema	760
39	Acc.28307	*Sesamum*	*indicum*	Amhara	SemenGondar	Metema	793
40	Acc.28309	*Sesamum*	*indicum*	Amhara	SemenGondar	Metema	744
41	Acc.28311	*Sesamum*	*indicum*	Amhara	SemenGondar	Metema	864
42	Acc.28312	*Sesamum*	*indicum*	Amhara	SemenGondar	Metema	846
43	Acc.28313	*Sesamum*	*indicum*	Amhara	SemenGondar	Metema	693
44	Acc.28314	*Sesamum*	*indicum*	Amhara	SemenGondar	Metema	719
45	Acc.28316	*Sesamum*	*indicum*	Amhara	SemenGondar	Metema	872
46	Acc.28317	*Sesamum*	*indicum*	Amhara	SemenGondar	Metema	872
47	Acc.28318	*Sesamum*	*indicum*	Amhara	SemenGondar	Metema	744
48	Acc.28319	*Sesamum*	*indicum*	Amhara	SemenGondar	Metema	744
49	Acc.28320	*Sesamum*	*indicum*	Amhara	SemenGondar	Metema	744
50	Acc.28321	*Sesamum*	*indicum*	Amhara	SemenGondar	T/Armacho	983
51	Acc.28322	*Sesamum*	*indicum*	Amhara	SemenGondar	T/Armacheho	946
52	Acc.28323	*Sesamum*	*indicum*	Amhara	SemenGondar	T/Armacheho	877
53	Acc.28324	*Sesamum*	*indicum*	Amhara	SemenGondar	T/Akmacheho	900
54	Acc.28325	*Sesamum*	*indicum*	Amhara	SemenGondar	T.Armacheho	884
55	Acc.28326	*Sesamum*	*indicum*	Amhara	SemenGondar	T.Armacheho	1175
56	Acc.28327	*Sesamum*	*indicum*	Amhara	SemenGondar	T.Armacheho	957
57	Acc.28328	*Sesamum*	*indicum*	Amhara	SemenGondar	T.Armacheho	1010
58	Acc.28329	*Sesamum*	*indicum*	Amhara	SemenGondar	T.Armacheha	987
59	Acc.28330	*Sesamum*	*indicum*	Amhara	SemenGondar	T.Armacheho	956
60	Acc.202286	*Sesamum*	*indicum*	Amhara	SemenShewa	Kewet	1490

S.№	Accessions	Genusname	Speciesname	Region	Zone	Woreda	Altitude
61	Acc.241297	*Sesamum*	*indicum*	Amhara	Oromiya	Bati	1280
62	Acc.241326	*Sesamum*	*indicum*	Tigray	Mirabawi	KaftaHumera	650
63	Acc.241338	*Sesamum*	*indicum*	Amhara	SemenGondar	Quara	600
64	Acc.241344	*Sesamum*	*indicum*	Amhara	SemenGondar	Chilga	980

Source: Ethiopian Biodiversity Institute

2.2. Experimental Design and Field Management

The experiment was planted in 8*8 simple latticed designs. The spacing between plants and rows was 10cm and 40cm respectively, and 6 rows were used in each plot. After row preparation, seeds were drilled into the rows. After seedlings reached 15-20 cm, thinning was made to adjust the distances of 10cm between plants to retain the recommended plant stand per hectare. Regular crop management procedures were carried out, including weeding, thinning, watering, protecting the crop from higher animals, and securing it.

2.3. Data Collection

To avoid border effects, the data for all of the parameters considered were taken from the net plot area. Data were collected for the following parameters using IPGRI sesame descriptor [10] for Days to 50% emergency, Days to 50% flowering, Days to 75% maturity, Plant height, Length of pod bearing zone, Number of primary branches per plant, Secondary branches per plant, Number of pods per plant, Pod length, Pod width, Biomass yield per hectare, Seed yield, Thousand seed weight, Harvest index and Oil content.

2.4. Data Analysis

2.4.1. Analysis of Variance

The data were analyzed following procedures appropriate to the simple lattice design as described by [11]. 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 R, version 4.1.2 software.

2.4.2. Estimation of Variance Components

Genetic variance, phenotypic variance, and environmental variance were analyzed using the formula of [12] using R, version 4.1.2 software as follows; Environmental variance $(\delta^2 e) = MSe,$

$$Genotypicvariance\ (\delta^2 g)\ =\ (MSg - MSE)/r$$

$$Phenotypicvariance\ (\delta^2 p)\ =\ (\delta^2 g\ +\ \delta^2 e),$$

Where, Mse=Mean square error, r=replication,

Phenotypic coefficients of variation PCV=$(\frac{\sqrt{\delta p2}}{\bar{Y}})$*100

Genotypic coefficients of variation GCV=$(\frac{\sqrt{\delta g2}}{\bar{Y}})$*100

δp^2=phenotypic variance,
δg^2=genotypic variance,
$\bar{Y}$=grand mean of a character.
PCV and GCV values were classified as low (0-10%), moderate (10–20%), and high (>20%) [13].

2.4.3. Heritability, Genetic Advance and Genetic Advance as Percent of Mean

Heritability is expressed as the percentage of the ratio of the genotypic variance ($\delta 2g$) to the phenotypic variance ($\delta 2p$) and was estimated by the genotype mean basis as described by [14] using Version 4.1.2 software as follows:

$$H^2\ =\ \delta^2 g\ /\delta^2 p\ *\ 100$$

Where, H^2=Heritability in Broad sense,
$\delta^2 p$=phenotypic variance,
$\delta^2 g$=genotypic variance.
The heritability percentage was categorized as low (0-40%), moderate (40-60%), high (60-80%), very high (>80%) a suggested by [15].

Genetic advance as percent of mean (GAM) was calculated for each character using the formula given by [15]:

$$GA = H2 * K\delta p\ /\bar{Y}\ * 100$$

Where: H^2 is the heritability estimate, k is the selection differential (2.06) at 5% selection Intensity, σp is the phenotypic standard deviation and $\bar{Y}$ is mean of the trait.

Genetic advance as percent of mean was estimated as follows:

$$GAM=\frac{GA}{\bar{Y}}*100$$

Where, GAM=Genetic advance as percent of mean, GA=Genetic advance, $\bar{Y}$ = Population mean of the character being evaluate as low (0-10%); moderate (10-20%) and high (>20%).

3. Results and Discussion

3.1. Analysis of Variance

Analysis of variance (ANOVA) for 16 traits showed that the majority of the traits showed highly significant (P≤0.01) variation, and the length of the pod bearing zone and plant height were also significant at (P≤0.05). These traits included 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 (Table 2). This suggests that the examined sesame accessions exhibit genotypic variation. When it came to the number of seeds per pod and days to 50% emergence, accessions had shown non-significant variation.

Several researchers have observed the existence of significant variance among sesame genotypes, which is in agreement with the current findings. For instance, Gadisa *et al.*; Singh *et al*; Shammoro *et al.*; Pavani *et al.*; and Tesfaye *et al.* 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 to75% maturity among sixty four, sesame genotypes, seventy five sesame genotypes, one hundred genotypes, thirty sesame genotypes and three hundred genotypes, respectively [16-20]. Additionally, Gautam *et al.* [21] reported highly significant differences among tests for thousand seed weight, number of pods per plant, pod length, oil content, and plant height. Moreover, Sintayyo [22] reported highly significant differences among 64 genotypes for plant height, length of pod bearing zone, and pod length. Moreover, Shammoro *et al.* reported highly significant differences among one hundred genotypes for plant height, length of pod bearing zone, pod length, pod width, biomass yield, harvest index, and oil content [18]. Additionally, Singh *et al.* reported significant differences among 75 genotypes for number of secondary branches per plant [17].

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	Numberofseedpod^{-1}	111.079^{ns}	37.056^{ns}	33.44^{ns}	31.8565	8.99
12	1000seedweight (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

Note: **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. Estimates of Variance Components and Coefficient of Variation

The phenotypic coefficient of variation (PCV) estimations varied from 3.7 to 2.8 percent, where as the genotypic coefficient of variation (GCV) values ranged from 2.9 to 29.8 percent is presented in table 3. The number of pods per plant, secondary branches per plant, seed yield, and biomass yield

had high PCV. Similar results were reported by Iqbal *et al.* for seed yield and the number of pods per plant [23]; while, Kiruthika *et al.* reported high PCV for secondary branches per plant [24]. Medium PCV was recorded for harvest index, followed by primary branches per plant, length of pod bearing zone, thousand seed weight, and plant height. Desawi *et al.* and Kadvani *et al.* observed medium PCV for plant height and thousand seed weight, respectively [25, 26]. Sintayyo, also reported medium PCV for the Length of the pod-bearing zone[22]. The lowest PCV values were recorded for oil content, followed by pod width, days to 75% maturity, days to 50% flowering, and pod length. The lowest PCV values were recorded for oil content, followed by pod width, days to 75% maturity, days to 50% flowering, and pod length. Singh *et al.*; Kadvani *et al.*; and Mohan also reported low PCV for days to 50% flowering, pod length, and oil content, respectively [17, 26, 27]. Similarly Bamrotiya *et al.* and Sintayyo, reported low PCV for the width of pod and days to 75% maturity [28].

High GCV was recorded for the number of pods per plant, secondary branch per plant, seed yield, and biomass High GCV was recorded for the number of pods per plant, secondary branch per plant, seed yield, and biomass yield. In this case, selection should be effective because those traits exhibited high heritability, high GAM, and low ECV estimations. In agreement with the present result, Mohan observed high GCV values for seed yield and the number of pods per plant [27]. This indicates that the trait was less influenced by an environmental factor. Medium GCV was recorded by primary branch per plant, thousand seed weight, and harvest index. Similarly, Desawi *et al* and Kadvani *et al.* also reported similar results for primary branches per plant and thousand seed weights, respectively [25, 26]. The lowest GCV was recorded for plant height, pod length, length of pod bearing zone, days to 75% maturity, days to 50% flowering, pod width, and oil content. The lowest GCV was observed for length of pod bearing zone, pod length, pod width, number of seeds per pod, and oil content, in agreement with the finding of [18]. Lower GCV suggests that the traits are more susceptible to high environmental influences and that there is a low chance of improving this trait through selection. Yield. In this case, selection should be effective because those traits exhibited high heritability, high GAM, and low ECV estimations. In agreement with the present result, Mohan observed high GCV values for seed yield and the number of pods per plant [27]. This indicates that the trait was less influenced by an environmental factor. Medium GCV was recorded by primary branch per plant, thousand seed weight, and harvest index. Similarly, Desawi *et al* and Kadvani *et al.* also reported similar results for primary branches per plant and thousand seed weights, respectively [25, 26]. The lowest GCV was recorded for plant height, pod length, length of pod bearing zone, days to 75% maturity, days to 50% flowering, pod width, and oil content. The lowest GCV was observed for length of pod bearing zone, pod

length, pod width, number of seeds per pod, and oil content, in agreement with the finding of [18]. Lower GCV suggests that the traits are more susceptible to high environmental influences and that there is a low chance of improving this trait through selection.

High PCV and GCV (>20%) were recorded for the number of pods per plant, secondary branches per plant, seed yield, and biomass yield. Similar results were also reported for the number of pods per plant, secondary branch per plant, and seed yield by [21, 27]. Likewise Gadisa *et al.* reported similar results for biomass yield [16]. Medium PCV and GCV (10-20%) were recorded for thousand seed weight, primary branch per plant, length of pod bearing zone, and harvest index. Similar results to this finding were reported by Bamrotiya *et al* and Kadvani *et al.* for harvest index and thousand seed weight, respectively [28, 26]. For plant height and the length of the pod-bearing zone, medium PCV and low GCV were observed. Mohammed and Firew also reported similar results for plant height [30]. The lowest PCV and GCV (<10%) values were recorded for oil content, pod width, days to 75% maturity, days to 50% flowering, and pod length, indicating that improvement may not be reached by selection for these traits. Results for all traits included under low PCV and GCV in this study were reported similarly by studies of [18].

The values of PCV were slightly higher than the corresponding GCV and ECV values for all traits and the values of PCV were slightly far than the values of corresponding GCV for most of the traits, indicating some influence of the environment. This revealed that the traits, namely, secondary branches per plant, days to 50% flowering, plant height, number of pods per plant, and seed yield, were greatly influenced by the environment, and that selection based solely on phenotype may be ineffective for improving traits. Mohammed *et al* also reported similar results, and the authors mentioned that this type of result indicates the sensitivity of most of the traits to environmental modifications and the lower scope of improving them through selection [31]. However, the value of PCV was closest to the values of corresponding GCV for pod length and thousand seed weight. This suggests that a small contribution n of environmental variance to the phenotypic variance or the influence of the environment was minimal on the genotypic expression of these traits. In this case, a traits highly controlled by genetic factors and simple selection can be used for improvement.

3.3. Heritability and Expected Genetic Advance

3.3.1. Estimates of Heritability

Estimates of heritability values for traits under study were presented in table 3. The present study showed low to high heritability estimates for 14 traits. The estimate of heritability in a broad sense ranged from 31.5% for days to 50% flowering to 99.3% for pod length. High to very high heritability values were recorded for pod length, thousand seed weight, primary branch per plant, number of pods per plant,

biomass yield, seed yield, and days to 75% maturity. Saxena, and Bisen also reported similar result the number of pods per plant and seed yield [29]. In addition, Gautam *et al* and Gupta *et al*., reported similar results for thousand seed weight, primary branch per plant, number of pods per plant, and days to 75% maturity [21, 32]. Shammoro *et al*.; Saxena and Bisen also reported similar results for seed yield and pod length, respectively [18, 29]. High heritability estimates indicated that the characters had a high capacity for transmission to succeeding generations and were least affected by environmental factors [24]. Therefore, traits with high heritability estimates could be amenable to selection since the traits are less influenced by environmental factors and can be easily expressed in the selected genotypes.

Medium heritability (40-60%) was recorded for harvest index, oil content secondary branches per plant, plant height, pod width, length of pod bearing zone, and days to 50% flowering. Medium heritability estimates for days to 50% flowering and pod width were also reported similarly by [18] and [21]. Moderate broad sense heritability indicates the possibility of using these traits in sesame improvement programs, but the expressions could be influenced by the environment.

3.3.2. Estimates of Expected Genetic Advance

The genetic advance (GA) and genetic advance as the percentage of the mean (GAM) at 5% selection intensity a represented below in Table 3. The estimated value of expected genetic advance expressed as the percentage of mean ranged from (4.6%) for the oil content to (55.99%) for the number of pods per plant. Traits were revealed as the lowest to highest genetic advance as a percentage of the mean. The highest genetic advance as the percentage of the mean (GAM) was recorded for the number of pods per plant, seed yield, biomass yield, secondary branch per plant, thousand seed weight, primary branch per plant, and harvest index. According to Gadisa *et al*. the highest genetic advance as the percentage of the mean (GAM) was recorded for biomass yield, primary branch per plant, seed yield, and harvest index [16]. As Begum *et al*. reported, the number of pods per plant and

thousand seed weights had the highest genetic advance as a percentage of the mean (GAM) [33].

Moderate genetic advance as the percentage of the mean (GAM) >10% was recorded for pod length, plant height, length of pod bearing zone, and days to 75% maturity. Moderate genetic advance as the percentage of the mean (GAM) for plant height, length of pod bearing zone, and days to 75% maturity were similarly reported by [18]. A similar result was also reported by Kadvani *et al*. for pod length and plant height [26]. Low genetic advance as the percentage of the mean (GAM) was recorded for pod width, days to 50% flowering, and oil content. In line with this result, Desawi *et al*. also reported similar results for days to 50% flowering [25]. Although Pavani *et al*. and Bamrotiya *et al* reported similar results for pod width and oil content [19, 28], respectively. The low estimates for genetic advance as a percent of the mean arise from the low estimate of phenotypic variance and heritability and vice-versa. This indicates the characters are governed by non-additive gene action and direct selection for these traits is ineffective.

High heritability coupled with high genetic advance as the percentage of the mean (GAM) was recorded for thousand seed weight, primary branch per plant, number of pods per plant, biomass yield, harvest index, and seed yield. Similar findings for seed yield and biomass were reported by [16], as well as for thousand seed weights, primary branch per plant, and the number of pods per plant by [30]. This indicates that selection is a more effective method for these traits in sesame improvement. Medium heritability coupled with medium genetic advance as the percentage of the mean (GAM) was recorded for plant height and length of the pod-bearing zone. According to Kadvani *et al*. the results for plant height were similar [26]. Medium heritability coupled with low genetic advance as the percentage of the mean (GAM) was recorded for oil content and pod width. Similar results were reported for pod width by [18]. This indicates that this trait is controlled by non-additive gene action, and selection is in effective for improvement, while hybrid development is a more successful method.

Table 3. Estimates of variability components of 14 traits for 64 sesame accessions.

SN	Trait	Range	Mean	δ^2e	δ^2g	δ^2p	ECV (%)	GCV (%)	PCV (%)	H^2 (%)	GA	GAM (%)
1	DF	51-74	60.62	19.40	8.89	28.29	7.3	4.9	8.8	31.5	3.44	5.67
2	DM	103-140	113.60	15.04	48.12	63.16	3.4	6.1	7.0	76.2	12.47	10.98
3	PH	83.7-137.4	110.87	149.52	113.72	263.24	11.0	9.6	14.6	43.2	14.44	13.02
4	LPBZ	39.35-69.1	52.28	40.20	26.80	67.0	12.1	9.9	15.7	40.0	6.75	12.91
5	PBP	2.3-3.4	2.80	0.015	0.165	0.18	4.4	14.5	15.0	91.7	0.80	29.0
6	SBP	0.2-0.4	0.28	0.003	0.004	0.007	19.7	22.9	30.1	57.8	0.10	35.71
7	NPP	20.4-75.1	45.58	37.90	184.96	222.9	13.5	29.8	32.8	83.0	25.52	55.99

SN	Trait	Range	Mean	$\delta^2 e$	$\delta^2 g$	$\delta^2 p$	ECV (%)	GCV (%)	PCV (%)	H^2 (%)	GA	GAM (%)
8	CL	2.17–3.35	2.76	0.001	0.072	0.073	0.8	9.7	9.8	99.3	0.552	20.0
9	CW	0.63-0.8	0.72	0.0011	0.0012	0.0023	4.5	4.8	6.7	52.2	0.05	6.94
10	TSW	2.285-3.75	2.93	0.007	0.18	0.187	2.8	14.3	14.6	96.2	0.85	28.87
11	BM	2479-5698	3926.67	152730	735888	888618	10.0	21.9	21.0	82.8	1608.03	40.95
12	SY	418-1318	830.33	11311.7	42929	54240.7	12.8	25.0	28.1	79.2	379.71	45.70
13	HI	15.5-30.5	21.12	3.65	7.93	11.58	9.0	13.3	16.1	68.5	4.80	22.72
14	OC	45.3-53.7	49.30	1.32	1.996	3.32	2.3	2.9	3.7	60.2	2.26	4.58

$\sigma^2 g$=Genotypic variance, $\sigma^2 p$=Phenotypic variance, $\sigma^2 e$=environmental variance, ECV= Environmental coefficient of variation GCV=genotypic coefficient of variation, PCV=phenotypic coefficient of variation, H^2=heritability in broad sense, GA=Genetic Advance, GAM=genetic advance as percent of mean 5% selection intensity; DF=Days to 50% flowering, DM=Days to 75% maturity, PH=Plant height (cm), LPBZ=Number of pod bearing zone (cm), PBP=Primary branch per plant; SBP=Secondary branch per plant, NPP=Number of pod per plant, PL=Pod length; PW=Pod width's=Thousand seed weight(g), BM=Biomass, SY=Seed yield per hectare, HI=Harvest index, OC=Oil content.

4. Conclusion

From this study, it can be concluded that 1) adequate genetic variability among 64 tested accessions for seed yield and related traits was identified. 2) The PCV and GCV levels of the characters evaluated in this study were low, moderate, and high. 3) The following promising traits viz. thousand seed weight, number of primary branches per plant, number of pods per plant, biomass yield, and seed yield were identified to respond positively to selection because of their better high broad-sense heritability coupled with relatively high genetic advance.

Abbreviations

CSA: Central Statistical Authority of Ethiopia
FAOSTAT: Food and Agriculture Organization of the United Nations

Acknowledgments

Conflicts of Interest

The authors declare no conflicts of interests.

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