Genetic Variability and quantitative traits inheritance in Sesame (*Sesamum indicum* L.) Genotypes

[1]Feyera Takele*, [2]Dagnachew Lule and [3]Sentayehu Alemerew
[1]*Bako Agricultural Research Center, P.O. Box 3, Bako, West Shoa, Oromia*
[2] *Oromia Agricultural Research Institute, P.O. Box 81265, Addis Ababa, Ethiopia*
[3]*Jimma University, P.O. Box 307, Jimma, Ethiopia*
Corresponding address: feyeratak143@gmail.com

Abstract

Growing of low yielding and poor quality genotypes is among the major constraints of sesame production in Ethiopia. Field experiment was conducted to assess the extent of genetic variation and traits inheritance in sesame genotypes. A total of forty nine sesame genotypes were evaluated using simple lattice design at Bako and Uke during 2018 cropping season. The combined analysis of variance showed highly significant differences (P<0.01) among the genotypes for all quantitative traits. Branches per plant, capsule per plant, biomass yield, harvest index, thousand seed weight and bacterial blight severity showed medium Phenotypic and Genotypic Coefficient of Variations. Seed yield, biomass yield, capsule per plant, bacterial blight severity and branches per plant showed moderately high heritability with high genetic advance as percent of mean. Thousand seed weight showed high heritability with moderate genetic advance as percent of mean. Harvest index showed medium heritability and genetic advance percent mean. Whereas, all the remaining traits showed medium heritability with low genetic advance as percent mean. Generally, this study depicted the presence of significant genetic variation among tested sesame genotypes and the possibility to get genetic progresses in the succeeding breeding generations.

Keywords: Genetic advance, Heritability, Sesame (*Sesamum indicum* L.), Variability

Introduction

Sesame (*Sesamum indicum* L.) is an annual plant of the *Pedaliaceae* family with diploid chromosomes (2n = 26) and considered as the oldest oilseed crop cultivated by man (Kafiriti and Deckers, 2001). It is a self-pollinated crop containing 60 species organized into 16 genera (Zhang *et al.*, 2013). It is commonly known with various names such as til (Hindi), huma (Chinese), sesame (French), goma (Japanese), gergelim (Portuguese) and ajonjoli (Spanish) (Anilakumar *et al.*, 2010). Sesame originated in East Africa and India (Nayar and Mehra, 1970; Bedigian, 2003). It has been grown in the Near East and Africa for over 5,000 years for cooking and medicinal needs (Ekta *et al.*, 2014) but, recently it has been introduced into some American countries; viz., Mexico, Central America, South

America and U.S.A (Lalpantluangi and Shah, 2018).

In Ethiopia, the national average seed yield of sesame is 691 kg ha^{-1} (CSA, 2018), which is quite low when compared to the yield potential of the crop (up to 2000 kg ha^{-1}) when grown at experimental stations (Mkamilo and Bedigian, 2007). An estimation of genetic variability is essential for understanding the genetic nature of yield and its components. Knowledge of heritability is essential for selection-based improvement, as it indicates the extent of transmissibility of a character into future generations (Sabesan *et al*., 2009). Heritability can judge whether observed variability is heritable or non-heritable. Genetic advance measures the difference between the mean genotypic values of selected population and the original population from which these were selected.

Gadisa *et al.* (2015); Mohammed *et al.* *(*2015) and Desawi *et al.* (2017) reported the presence of genetic variability among sesame genotypes for days to flowering, days to maturity, plant height (cm), branches per plant, capsule per plant, biomass yield, seed yield, thousand seed weight (g), harvest index and oil contents traits.

Increasing yield is always a major aim in any plant breeding experiment. However, yield is the end product of action and interaction of vital activities of a plant throughout the life cycle and is controlled by numerous factors shaped by genetics and environment. Therefore, assessing factors responsible for increasing yield is crucial issue. Improvement in plant breeding depends on variability, because superior genotypes cannot be selected from homogenous populations; but homogeneity is desirable in the final product of the crop variety. Hence, the present study was initiated to estimate variability, heritability and genetic advance in sesame genotypes.

Materials and Methods

Description of the study areas

The experiment was conducted at two locations; viz., Bako Agricultural Research Center (BARC) and Uke research subsite during the 2018 cropping season. BARC is located in East Wollega zone of Oromia Regional State at 250 kilometers West of Addis Ababa. BARC has a warm, humid climate with mean minimum and mean maximum temperatures of 13.97 ^{o}C and 29.80 ^{o}C, respectively. Relative humidity of BARC is 49.81% (BARC Agro metrology data, 2018).

Uke is located in East Wollega zone of Oromia Regional State, Guto Gida district at about 365 km away from Addis Ababa to the west and 34 km away from Nekemte town. The area is located at altitude of 1383 m.a.s.l. and it is an area with high temperature and abundant rainfall amount. Major crops produced in the area include: maize, sorghum, soybean, sesame and

groundnut. Some of the important agro-climatic and ecological descriptions for both study areas are shown in Table 1.

Table 1. Description of the study area.

Site	Rain fall(mm)	Longitude (E)	Latitude (N)	Altitude (m.a.s.l.)	Soil type	Soil PH
Bako	1161.7	037° 09' E	09°06'N	1590	Sandy-clay	4.9- 5.1
Uke	NI	036° 31'E	09°22'N	1383	Sandy-loam	NA

NI = Not Available

Experimental materials

The experimental materials consisted of 46 genotypes (pure lines) and three checks (Waliin, Chalasa & Obsa) (Table 2). These genotypes are progenies of the intra-specific cross of 11 morphologically diverse sesame genotypes through continuous maintenance of progenies up to the seventh filial generation (F7) through selfing using F2-derived pedigree breeding method at Bako Agricultural Research Center (Table 2). The original parent materials were collections from Western Ethiopia such as: EW002, EW003, BG006, EW023 (2), EW006, EW003 (1), EW019, EW010 (1), Obsa, Dicho and Wama. These eleven parent materials were crossed in a 11 x 11 diallel mating design, including reciprocals in the 2011 cropping season.

Table 2. List of sesame genotypes used for the study.

No.	Pedigree	No.	Pedigree
1.	EW002 X Obsa-1-1	26.	BG006 x EW023(2)-10-2-1
2.	EW002 X Obsa-16-1	27.	BG006 x EW010(1)-11-1-1
3.	EW002 X Obsa-22-1	28.	EW023(2) x Obsa-9-1-1
4.	Obsa x Dicho-19-1	29.	Obsa x BG006-2-2-1
5.	Obsa x Dicho-19-3	30.	Wama x Dicho-6-1-1
6.	Obsa x Dicho-27-1	31.	Obsa x EW023(2)-5-2-1
7.	EW002 x Dicho-1-1	32.	EW003(1) x EW002-4-1-1
8.	EW002 x Dicho-5-3	33.	Obsa x BG006-2-4-1
9.	EW002 x Dicho-12-1	34.	EW003 (1) x EW019-4-1-1
10.	EW002 x Dicho-17-2	35.	EW019 x Obsa-16-2-1
11.	EW002 x EW006-3-1	36.	EW003(1) x Obsa-2-1-1
12.	Dicho x EW006-9-1	37.	EW019 x Obsa-16-1-1
13.	Dicho x EW006-1-14-1	38.	Dicho x Wama-10-1-1
14.	BG006 x EW023(2)-11-2-1	39.	EW002 x EW019-1-2-1
15.	EW003 (1) x EW019-3-1-1	40.	EW019 x Dicho-8-2-1
16.	EW006 x EW003 (1)-4-1-1	41.	EW010(1) x EW003-1-1-1
17.	Dicho x EW006-2-1-1	42.	Obsa x EW019-6-3-1
18.	EW002 x BG006-4-1-1	43.	EW002 x Wama-6-1-1
19.	EW002 x BG006-7-2-1	44.	Dicho x Wama-11-1-1
20.	EW023(2) x EW006-11-1-1	45.	EW019 x Dicho-6-1-1
21.	EW002 x WAMA -2-1-1	46.	EW019 x Dicho-8-1-1
22.	Dicho x EW006-1-1-1	47.	Chalasa/EW023(2)(Parental check)
23.	EW006 x BG006-2-2-1	48.	Waliin (standard check)
24.	BG006 x EW010(1)-9-1-1	49.	Obsa (parental check)
25.	Obsa x EW023(2)-5-5-1		

Experimental design and trial managements

The trial was laid out using 7 x 7 simple lattice design. Each genotype was planted in 4 rows in plot size of 6.4 m^2 (4 m row length, 40 cm between rows and 10 cm between plants within row and spacing of 1 m between plots and 1.5 m between blocks). The seeds were drilled by hand in each row at the rate of five kg ha^{-1} and then covered by soil. The plant depth and soil compactions were kept at a minimum. Twenty days after sowing, the plants were thinned to maintain the spacing between plants of 10 cm. Fertilizer was applied at the rate of 100 kg ha^{-1} NPS at planting time. Whereas, 50 kg ha^{-1} Urea was applied two times; at planting time and four weeks after planting. Other cultural practices were kept constant for all experimental units.

Data collection

All data were collected from the two central rows for both plant-based and plot-based data. Plant height, number of branches per plant, number of capsules per plant and bacterial blight severity (%) were collected from 10 randomly selected plants, but days to 50% flowering, days to maturity, biomass yield per plot, seed yield per plot, thousand seed weight (g), harvest index (%) and oil content (%) were collected on plot bases. The data were collected according to the International Plant Genetic Resources Institute (IPGRI, 2004) descriptor for sesame.

Data analysis

The efficiency of a simple lattice design over RCBD was checked, and for most of the response variables, a simple lattice design was found to be more efficient than RCBD. Thus, ANOVA for quantitative analyses was computed based on a simple lattice design using Proc lattice and Proc GLM procedures of SAS version 9.3 (SAS, 2012). Homogeneity test for the error variance of the two locations was done using Hartley`s test (1950) and checked by using F-test (ratio of the largest mean square error to the smallest mean square error in the set) according to Gomez and Gomez, (1984) and they were homogeneous. Hence, a combined analysis was computed.

Estimation of genetic parameters

The phenotypic and genotypic coefficients of variation were estimated according to the method suggested by Burton and Devane (1953) as follows:

Genotypic variance (δ^2_g)

$\delta^2_g = \frac{MSg - MSgl}{rl}$, for over two locations;

Where, MS_g = mean square of genotype,

MSgl is the mean square due to genotype by environment interaction,
l = number of locations, and
r = number of replications

Genotype by environment interaction variance (δ^2_{gl})

$$\delta^2_{gl} = \frac{MSgl - MSe}{r}$$

Where, MSgl is the mean square due to genotype by environment interaction, and
MS_e = combined error mean square = (δ^2_e)

Phenotypic variance (δ^2_p)

$\delta^2_p = \delta^2_g + (\delta^2_{gl}/l) + (\delta^2_e/rl)$

Where, δ^2_g = genotypic variance, δ^2_{gl} = genotypic by environmental variance, δ^2_e = environmental variance, l = number of locations, and r = number of replications
Estimates of coefficient of variation were obtained as follows.

Phenotypic coefficients of variation (PCV)

$$PCV = \frac{\sqrt{\delta^2 p}}{\bar{X}} \times 100$$; where, PCV = phenotypic coefficient of variation, δ^2_p = phenotypic
Variance and $\bar{X}$= population mean for the trait considered

Genotypic coefficients of variation (GCV)

$$GCV = \frac{\sqrt{\delta^2 g}}{\bar{X}} \times 100$$; where, GCV = genotypic coefficient of variation,
δ^2_g = genotypic variance, $\bar{X}$= population mean for the trait considered

Environmental coefficients of variations (ECV)

$$ECV = \frac{\sqrt{\delta^2 e}}{\bar{X}} \times 100$$

Genotype by environment interaction coefficients of variation (GECV)

$$GECV = \frac{\sqrt{\delta^2 gl}}{\bar{X}} \times 100;$$

where, δ^2_{gl} = genotypic x environment variance
$\bar{X}$ = population mean for the trait considered

Estimation of heritability in broad sense

Broad sense heritability (H^2) expressed as the percentage of the ratio of the genotypic variance ($\sigma^2 g$) to the phenotypic variance ($\sigma^2 p$) and were estimated on genotype mean basis as described by Allard (1999):

$$H^2 = [\frac{\sigma^2 g}{\sigma^2 p}] * 100;$$

where, H^2 = broad sense heritability

δ^2_g = genotypic variance
δ^2_p = phenotypic variance

Estimation of genetic advance

Genetic advance in absolute unit (GA) and percent of the mean (GAM), assuming selection of superior 5% of the genotypes, were estimated in accordance with the methods illustrated by Johnson *et al*. (1955) as:

$$GA = k\,\sigma_p * H^2$$

$$GA \text{ (as \% of the mean)} = \left[\frac{GA}{\bar{X}}\right] \text{ X } 100;$$

where k = selection differential (k = 2.06 at 5% selection intensity)
σ_p = phenotypic standard deviation
H^2 = heritability (Broad sense)
$\bar{X}$ = Grand mean

Results and Discussion

Analysis of variance (ANOVA)

The pooled analysis of variance showed highly significant ($P < 0.01$) genotype effects across locations for days to 50% flowering, days to maturity, plant height (cm), branches per plant, capsules per plant, biomass yield per hectare (kg ha^{-1}), seed yield per hectare (kg ha^{-1}), harvest index (%), thousand seed weight (g), oil content (%) and severity of bacterial blight (%), indicating the presence of considerable variation among the study genotypes (Table 3). Similarly, the variances for genotype by environment interactions were also highly significant for all traits except for biomass yield per hectare, harvest index and thousand seed weight ((Table 3). Supportive results were reported by Mohammed *et al.* (2015), Iqbal *et al.* (2018) and Singh *et al.* (2018).

Table 3. Mean square of combined analysis of variance for 11 traits of 49 Sesame genotypes evaluated at Bako and Uke in 2018 cropping season

Traits	MSl (Df =1)	MSg (Df =48)	MSgl (Df = 48)	MSe (Df = 84)	CV (%)	R^2
Days to Flowering	861.84**	27.22**	11.05**	2.15	2.34	0.94
Days to maturity	4585.22**	12.97**	5.36**	1.49	1.08	0.98
Plant height	38.88^{ns}	133.82**	71.81**	28.57	4.59	0.82
No. of branch/plant	22.22**	4.63**	1.78**	0.46	10.79	0.90
No capsule/plant	12542.40**	833.32**	288.06**	147.41	12.73	0.86
Biomass yield/ha	3259905.05**	1040847.35**	313201.83^{ns}	237629.93	14.09	0.80
seed yield/ha	400989.23**	218667.70**	60193.05**	33417.32	17.22	0.85
Harvest index	4.69^{ns}	60.31**	34.54*	19.34	14.38	0.76
1000 Seed weight (g)	12.13**	2.62**	0.88^{ns}	0.65	12.55	0.79
Oil content (%)	80.00**	2.27**	0.90**	0.18	0.77	0.94
Bacterial blight %	412.53**	47.36**	16.87**	5.29	12.09	0.90

Key: ***, * and ns Indicate highly significance (P < 0.01), significant (P < 0.05) and not significance, respectively; MSl = Mean square of location, Mean square of genotype, MSgl = Mean square of genotype by location, MSe = Mean square of error, Df = degree freedom, CV= Coefficient of variation and* R^2 = R square

Mean and Range Values

Mean and range for the 11 traits of 49 sesame genotypes are shown in Table 4. Days to 50% flowering ranged from 57.5 to 69.75, with a mean of 62.59. Days to maturity ranged from 108.25 to 12, with a mean of 112.87. The wider variability for days to flowering and maturity provides an opportunity to develop improved varieties for environments with a variable rainfall season or crop growing season. Plant height varied from 103.33 cm to 130.63 cm, with a mean of 116.48 cm. Number of branches per plant ranged from 4.40 to 8.93 with a mean of 6.31. Number of capsules per plant varied from 65.70 to 134.23 with a mean of 95.38, biomass yield ranged from 2232.90 to 4741.10 kg ha^{-1} with a mean of 3458.99 kg ha^{-1}.

Seed yield per hectare ranged from 510.10 kg ha^{-1} to 1694.20 kg ha^{-1} with a mean yield of 1061.53 kg ha^{-1}, and harvest index ranged from 20.73% to 40.01% with a mean value of 30.58%. Thousand seed weight ranged from 5.09 g to 8.38 g with a mean value of 6.4 g and oil content ranged from 53.84 to 57.06 with a mean value of 55.52 and bacterial blight severity ranged from 11.33 to 26.00, with the mean of 19.03. This showed the wide range of variability for all tested traits of sesame genotypes used in the present study. Similar results were reported by Ahadu (2012), Begum and Dasgupta (2014), Mohammed *et al. (*2015), Desawi *et al.* (2014), Iqbal *et al.* (2016) and Begum *et al.* (2017).

Table 4. Estimation of mean, range and other genetic parameters of 49 sesame genotypes evaluated at Bako and Uke, 2018

Traits	Mean	Range		δ^2g	δ^2p	δ^2e	δ^2gl
		Minimum	Maximum				
Days to 50% Flowering	62.59	57.50	69.75	4.04	6.81	2.15	4.45
Days to 90% maturity	112.87	108.25	117.00	1.90	3.24	1.49	1.94
Plant height	116.48	103.33	130.63	15.50	33.46	28.58	21.62
No. of branch/plant	6.31	4.40	8.93	0.71	1.16	0.46	0.66
No capsule/plant	95.38	65.70	134.23	136.32	208.33	147.41	70.33
Biomass yield/ha	3458.99	2232.90	4741.10	181911	260212	237629.93	37785.95
seed yield/ha	1061.53	510.10	1694.20	39619	54667	33417.32	13387.87
Harvest index	30.58	20.73	40.01	6.44	15.08	19.34	7.60
1000 Seed weight (g)	6.40	5.09	8.38	0.43	0.66	0.65	0.12
Oil content (%)	55.52	53.84	57.08	0.34	0.57	0.18	0.36
Bacterial blight (%)	19.03	11.33	26.00	7.62	11.84	5.29	5.79

Key: δ^2g = genotypic variance, δ^2p= phenotypic variance, δ^2e= environmental variance, δ^2gl = genotypic by environmental interaction variance

Estimation of genetic parameters

Phenotypic variance (δ^2p), genotypic variance (δ^2g), environmental variance (δ^2e), genotype by environmental variance (δ^2gl) and their coefficients of variation were estimated and presented in Tables 4 and 5. According to Deshmukh *et al*. (1986), PCV and GCV values greater than 20% are regarded as high, while values less than 10% are considered to be low and values between 10% and 20% are medium. Phenotypic coefficients of variation (PCV) ranged from 22.03% for seed yield per hectare to 1.36% for oil content; and genotypic coefficients of variation (GCV) ranged from 18.75% for seed yield per hectare to 1.05% for oil content (Table 5). Therefore, seed yield in the present study showed relatively high PCV and medium GCV (Table 5). Medium PCV and GCV (10% up to 20%) were obtained for the number of branches per plant, number of capsules per plant, biomass yield per hectare, harvest index, thousand seed weight and bacterial blight severity. The medium to high PCV and GCV value indicated that the variation observed among genotypes for these traits were due to their genetic difference rather than environmental influences. This showed effectiveness of simple selection based on these traits and their phenotypic expression would be a good indication of genetic potential.

Close relationship between phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were found in most of the traits considered in the current study. PCV values were slightly greater than GCV, revealing minor influence of environment for their expression. Similar result was reported by Thangavel *et al.* (2000). Low values (<10%) of PCV and GCV were obtained for days to 50% flowering, days to maturity, plant height (cm) and oil

content (%). Lower PCV and GCV suggested that the traits are rendering to the effects of high environmental influences and lower opportunity exists for improvement of these traits through simple selection. This result was correspondent with that reported by Mohammed *et al.* (2015). Additionally, Sumathi and Murlidharan (2010), Ahadu (2012), and Gidey *et al.* (2013) also reported low GCV and PCV values for days to 50% flowering, days to maturity and oil content.

Saxena and Bisen (2016) also reported low phenotypic and genotypic coefficients of variation for days to 50 per cent flowering and harvest index. Genotype by environmental coefficients of variation (GECV) ranged from 12.85% for branches per plant to 1.08% for oil content. Relatively the highest GECV were recorded for branches per plant (12.85%), bacterial blight severity (12.65%) and seed yield per hectare (10.9%). Environmental coefficients of variation (ECV) and genotype by environmental coefficients of variation (GECV) were higher than genotypic coefficients of variation (GCV) for days to 50% flowering, days to maturity, plant height (cm), harvest index (%) and oil content (%).

This indicated that the phenotypic expression of these traits were highly influenced by environmental conditions rather than their genetic makeup; and hence improving these traits of interest would be effective based on a stability test that selection for such traits should be environmental-specific. However, numbers of branches per plant, number of capsules per plant, seed yield per hectare, biomass yield per hectare, thousand seed weight (g) and bacterial blight severity showed that higher genotypic coefficients of variation (GCV) than genotypic by environment coefficients of variation (GECV). However, the high GCV recorded alone is not sufficient for the determination of the extent of genetic advance to be expected by selection.

Table 5. Estimation of genetic parameters for major morphological traits of 49 sesame genotypes evaluated at Bako and Uke, 2018

Traits	GCV	PCV	ECV	GECV	H^2	GA	GAM (%)
Days to 50% flowering	3.21	4.17	2.34	3.37	59.41	3.19	5.09
Days to 90% maturity	1.22	1.60	1.08	1.23	58.69	2.17	1.93
Plant height (cm)	3.38	4.97	4.59	3.99	46.34	5.51	4.73
No. of branch/plant	13.37	17.04	10.79	12.86	61.54	1.36	21.57
No capsule/plant	12.24	15.13	12.73	8.79	65.43	19.42	20.36
Biomass yield/ha	12.33	14.75	14.09	5.62	69.91	733.20	21.20
seed yield/ha	18.75	22.03	17.22	10.90	72.47	348.39	32.82
Harvest index (%)	8.30	12.70	14.38	9.01	42.73	3.41	11.16
1000 Seed weight (g)	10.30	12.65	12.55	5.39	66.29	1.10	17.24
Oil content (%)	1.05	1.36	0.77	1.08	60.31	0.93	1.68
Bacterial blight (%)	14.51	18.09	12.09	12.65	64.38	4.55	23.94

Key: GCV = genotypic coefficients of variation, PCV = phenotypic coefficients of variation, ECV = environmental coefficients of variation, GECV = genotypic by environmental coefficients of variation, H^2 = heritability, GA = genetic advance and GAM (%) = genetic advance as percent of mean

Estimation of broad-sense heritability and genetic advance

Heritability estimates provide information on the extent to which a particular genetic character can be transmitted to successive generations. According to Singh (2001), heritability values less than 40% are considered as low; heritability values between 40 to 59% are medium, heritability values between 60 to 79% are moderately high and heritability values ≥ 80% are considered as very high. In this study, broad sense heritability ranged from 72.47% for seed yield per hectare to 42.73 % for harvest index (Table 5). Moderately high heritability values were obtained for seed yield (72.47%), biomass yield (69.91%), thousand seed weight (66.29 %), number of capsule per plant (65.43%), bacterial blight severity (64.38%), number of branches per plant (61.54%), oil content (60.31%) (Table 5). Such results indicated that the genetic makeup played a major role in the expression of these traits; and close correspondence between the genotypic and the phenotypic is due ultimately to less environmental influence on phenotypic expression of these traits, which is good for crop improvement through simple selection. Desawi *et al*. (2017) reported that moderately high heritability with high genetic advance mean for seed yield; and moderately high heritability with low genetic advance mean for oil content. Iqbal *et al.* (2016) and Begum *et al.* (2017) reported moderately high heritability for thousand seed weight and seed yield, respectively.

Medium heritability values were observed for days to 50% flowering (59.41%), days to maturity (58.69%), plant height (46.34%) and harvest index (42.73%) (Table 5). Narayanan and Murugan (2013) reported medium heritability for days to 50% flowering (57.30%) and plant height (58.06%). Genetic progress expected from selection increases with an increase in genotypic variance. High heritability coupled with high genotypic coefficient of variation of the traits indicated that the traits respond effectively to phenotypic selection; hence, traits which had moderately high heritability coupled with medium genotypic coefficients of variation in the present study can be improved by conventional breeding through selection breeding. In general, genotypic coefficients of variation along with heritability estimate provide a reliable estimate of the amount of genetic advance to be expected through phenotypic expression. Medium heritability coupled with low genotypic coefficient of variation in the present study for days to 50% flowering, days to maturity, plant height and oil content indicated limited success in achieving genetic gain in the next breeding phases, if used as it is. Thus, direct selection for these traits will not be effective.

Falconer and Mackay (1996) classified genetic advance as percent of mean (GAM) values as low from 0 to 10%, medium/intermediate from 10 to 20%, and high ≥ 20% values. Accordingly, GAM at 5% selection intensity was high for seed yield (32.82%), bacterial blight severity (23.94%), number of branches per plant (21.56%), biomass yield (21.2%) and number of capsules per plant (20.36%). Medium Genetic advance as percent of mean was obtained for thousand seed weight (17.24%) and harvest index (11.15%) (Table 5). The results indicated that these traits are governed by additive genes. Hence, simple selection based on those traits with high genetic advance as percent of mean will result in the improvement of the genotypes considered in this study. Gadisa *et al*. (2015) reported that high genetic advance as percent of mean was observed for number of branches per plant, number of capsules per plant, biomass yield, seed yield, harvest index, and thousand seed weight (g).

Low GAM was obtained for days to 50% flowering (5.092%), days to maturity (1.925%), plant height (4.731%), and oil content (1.68%) (Table 5). This showed that these traits are governed by non-additive genes, and thus simple selection, cannot be applied for the improvements of these traits. Generally, genetic advance as percent mean ranged from high (32.819%) for seed yield to low (1.681%) for oil content (%). The present study showed medium heritability and low genotypic coefficients of variation as well as low genetic advance as percent of mean for days to 50% flowering, days to maturity, and plant height. On the contrary, high heritability, medium genotypic coefficients of variation (GCV) and a high genetic advance for plant height was reported by Begum *et al*. (2017). Besides, Thirumala *et al*. (2014) reported high heritability with high genetic advance as percent of mean for days to 50% flowering.

Medium genotypic coefficients of variation (GCV), with moderately high heritability and high genetic advance as percent of mean, were observed from number of branches per plant, number of capsule per plant, biomass yield per hectare, seed yield per hectare and bacterial blight severity. This result indicated that the phenotypic expression of these traits could be governed by the genes acting additively; and thus the importance of these traits through selection is reliable for the development of high yielding sesame genotypes. According to Johnson *et al*. (1955), high heritability estimates along with the high genetic advance is usually more helpful in predicting gain under selection than heritability estimates alone.

The present study showed that moderately high heritability coupled with high genetic advance as percent of mean was recorded for number of branches per plant, number of capsules per plant, biomass yield, seed yield, and bacterial blight severity. Ismaila and Usman (2014) reported high

heritability coupled with high genetic advance for number of capsules per plant, number of branches per plant, and yield per hectare, which indicated the additive nature of inheritance. However, a contrary result was reported by Mohammed *et al.* (2015) where high estimates of heritability coupled with medium genetic advance as a percent mean for oil content; and low heritability coupled with low genetic advance as percent of mean for number of branches per plant, number of capsules per plant, harvest index, and thousand seed weight in sesame genotypes.

According to Desawi *et al*. (2017), moderately high heritability with high genetic advance as a percent of mean was recorded for seed yield per hectare, and moderately high heritability with low genetic advance was observed for oil content. Generally, the high value for heritability and genetic advance of the traits considered in the present study provide information for the existence of wider genetic diversity among sesame genotypes, and this offers high chances for improving several traits of the crop through simple selection. Moreover, most of the traits considered in the present study recorded medium GCV and medium to moderately high heritability, and also exhibited high genetic advance reflecting the importance of additive gene effects in their inheritance and their expression. Hence, improving such traits through selection could be efficient. Phunda and Narayanan (1993) reported that high values of genetic advance are indicative of additive gene action; whereas, low values are indicative of non-additive gene action.

Conclusions

The results of the study showed that there were high significant differences among tested genotypes for all traits indicating the presence of high variability for yield and other related traits in the studied genotypes, thereby indicating the possibility for further genetic analyses. Seed yield showed maximum PCV and moderate GCV. Moderately high heritability coupled with high genetic advance as percent of mean was recorded for number of branches per plant, number of capsules per plant, biomass yield, seed yield, and bacterial blight severity. This implied the possibility in achieving genetic gain in the next breeding phases. Generally, the present study showed existence of significant genetic variability among tested genotypes indicating the presence of a huge opportunity for further improvement through selection and other breeding approaches. Therefore, selection of promising genotypes could be possible to produce superior sesame varieties among the materials included in the present study.

Acknowledgements

This study was funded by Oromia Agricultural Research Institute Agricultural Growth Program (AGP-II). Bako Agricultural Research Center and team members of pulse and oil crops research are highly acknowledged for hosting the experiment and for assisted in field works, respectively.

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