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Genetic Variability and Quantitative Traits Inheritance in Different Origins of Sesame (*Sesamum indicum* L.) Genotypes

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Abstract

Evaluation of phenotypic variability, heritability, and genetic advancement in germplasm collections is important for both plant breeders and germplasm curators to optimize the use of the variability available. A total of 300 sesame germplasm collected from diverse ecologies of Ethiopia and germplasm introduced from different African and Asian countries, including 16 released varieties, were planted at the Gondar Agriculture Research Center, Metema, and Tach/ Armacho trial sites using alpha lattice design in the 2017/18 and 2018/19 cropping seasons.

Analysis of variance revealed significant differences among germplasm for the twenty-two characters studied except for the number of secondary branches, petiole length at the middle leaf, mean capsule width, and mean capsule thickness. This indicated the existence of much genetic variation among germplasm for most characters studied. High heritability combined with high genetic advance was recorded for plant height, primary branch, petiole length of top leaf, days to flower initiation, days to 50% flowering, pod bearing zone, seed yield per plant, and bacterial blight reaction indicating that these characters are controlled by additive gene effect and thereby phenotypic selection of these characters would be effective for further breeding purpose. The results obtained in this study would facilitate the improvement of climate-friendly sesame varieties through breeding and conservation of sesame genetic resources.

Keywords: variability, heritability, genetic advance

Introduction

Sesame (*Sesamum indicum* L., 2n = 26), a member of the Pedaliaceae family, is one of the most ancient oil crops, having grown widely in both tropical and subtropical areas since time immemorial (Bedigian and Harlan, 1986; Ashri, 1998).

Sesame seeds are good sources of fat, protein, carbohydrates, fiber, and essential minerals. Seeds are chemically composed of 44–57% oil, 18–25% protein, and 13–14% carbohydrates (Borchani et al. 2010). Sesame also referred to as the "queen of oilseeds", is employed in sweets such as sesame bars and halva (dessert), and bakery products or milled to get high-grade edible oil (Dorothea Bedigian, 2004). Despite the nutritional and economic importance in different

parts of the world, little focus is given to sesame research at both the national and international levels (Bedigian and Harlan, 1986; Bhat et al. 1999; IPGRI and NBPGR, 2004; Bedigian, 2010).

In Ethiopia, sesame is among the most important oil crops both in terms of area coverage and total national annual production (CSA, 2019). It grows in almost all regions of the country with an altitude of less than 2000 m above sea level (Adefris et al. 2011) and is a well-established crop in Amhara, Tigray Oromia, and Benishangul-Gumz regions. In Ethiopia, sesame is grown mainly for export (more than 95%) and direct consumption (5%) (Kindie, 2007).

However, the national average productivity of sesame in Ethiopia is very low, at 0.68t ha^{-1} (CSA, 2019), compared to its potential yield of 20 t ha^{-1} (Mkamilo and Bedigian, 2007). This national productivity is also lower as compared to Egypt (1.29 t ha^{-1}), Nigeria (1.1 t ha^{-1}), Tanzania (1 t ha^{-1}), and China (1.4 t ha^{-1})(Sharaby and Butovchenko, 2019). The improved varieties released in the country have been reported to yields ranging from 0.3 to 1.3 t ha^{-1} under rainfed conditions, and 1 to 2.4 t ha^{-1} under irrigation on research stations (Gebremichael, 2017); and 0.4-1.3 t ha^{-1} on farmers' fields (MoANR, 2010-2017).

Low productivity has been attributed to a lack of varietal replacement, low-yielding varieties, significant yield loss during threshing, indeterminate growth, uneven ripening of capsules, and lack of improved varieties tolerant to biotic and abiotic stresses like diseases, pests, and drought (Ashri, 2007; Lakhanpaul et al. 2012). Sesame improvement is not given attention by the breeding (Ashri, 2007).

Plant germplasm of a particular crop collected from local sources provides greater genetic variability and can furnish useful traits to broaden the genetic base of crop species. The success in genetic improvement of the crop and the development of a species needs the availability and accessibility of genetic variability. Local germplasm contributes to the genetic variability of a crop species by introducing new genetic material. This expanded genetic pool is crucial for breeding programs as it provides more options for selecting traits that can improve yield, quality, and resilience (Frankel and Bennett, 1970)

Despite the huge amount of both locally collected and introduced germplasm held in the Ethiopian gene bank and breeders' stock available at federal and regional research centers, the genetic variability studies are limited to a limited number of genotypes (Gebremichael and Parzies 2011; Abate and Mekbib, 2015) and the environmental sensitivity of sesame crop was reported by different researchers (Narayanan and Reddy, 1982).

Therefore, the objective of this study was to assess the genetic variability for yield and yield-related traits of sesame.

Materials and Methods

Plant materials

A total of 300 genotypes comprising 225 local Ethiopian collections including 16 released varieties and 75 exotic collections received from the Biodiversity Conservation Institute (IBC) of Ethiopia and different federal and regional research centers of Ethiopia were used in this study. The collections were mainly from Ethiopia, Africa, and Asia. These materials were planted at the Metema trial site in the 2017/18 cropping season and they were repeated in the 2018/19 cropping season at the Metema and T/Armacho trial sites. Metema (120 39'N, 360 17' E) is located at 760 meters above sea level and receives 1030.2 mm of rainfall annually. Its soil is a vertisol T/Armacho (13088'N, 370 43'E) located at 1022 meters above sea level, and receives 970.88 mm of rainfall annually. Its soil is a vertisol (Figure 1).

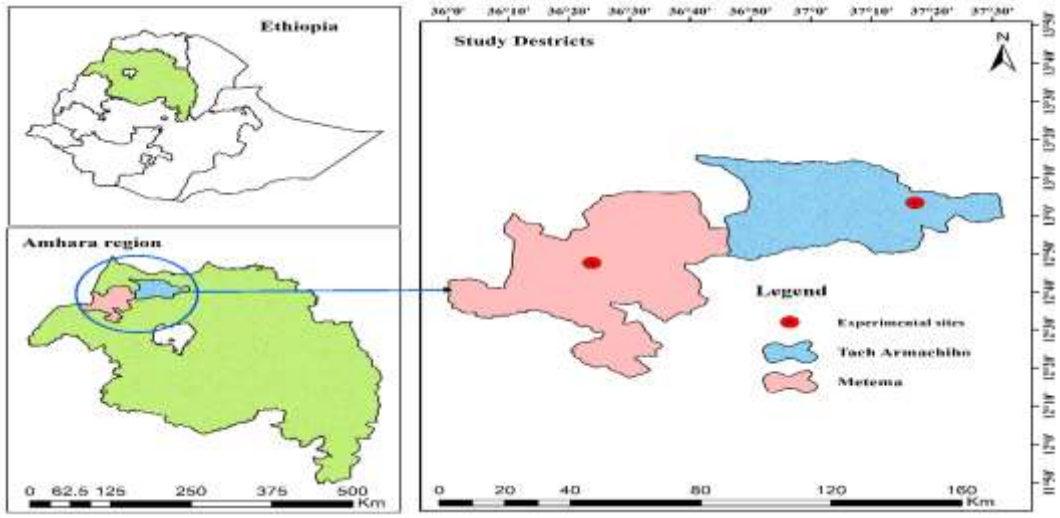

Figure 1. Map of the experimental sites

The experiment was conducted using an alpha lattice design and consisted of two rows 4 m long with a spacing of 40 cm between rows and 10 cm between plants. Experienced workers took part in the planting and fertilizer applications manually, and thinning and hand weeding were carried out as needed. Other pre- and post-planting management practices including fertilizer were applied as recommended for each location.

All quantitative data were listed and recorded according to the sesame descriptors list (IPGRI and NBPGR, 2004). All traits were measured by tagging five randomly selected plants in each plot. The early flowering date of each genotype was recorded daily as the number of days from sowing to the observation of the first flower in 50% of the individuals. Flower and leaf-related traits were observed

and measured during the full-bloom stage. The yield-related traits were measured in the laboratory after harvesting the sesame grain. The grain yield was initially measured per plot and later converted to metric tonnes per hectare. The seed was poured out of the capsules and counted.

Data analysis

Analysis of variance (ANOVA)

Data obtained from the different environments were analyzed separately and then combined analysis was done after the error homogeneity test using SAS computer software (SAS, 2002). Mean separation was done using the LS means package of SAS for traits that show significant differences at $p < 0.01$ and $P \leq 0.001$ levels.

Estimation of phenotypic and genotypic variances

Components of variance were calculated as suggested by Burton and Devane (1953) and Wricke and Weber (1986) as follows:

Environnemental variance ($\sigma^2 e$) = MSE/r.

Genotypic variance ($\sigma^2 g$) = $\underline{\text{MSG - MSgl}}$

Phenotypic variance ($\sigma^2 p$) =$\sigma^2 g+\sigma^2 gl/1+\sigma^2 e/r/$

Where, MSE=error mean square, MSG=genotype mean square, MSgl = mean square of genotype by location interaction, σ2gl is genotype by location interactions, r = number of replications, and l = number of locations.

Estimation of genotypic and phenotypic coefficients of variability

Genotypic and phenotypic coefficients of variability were computed according to Burton and Devane (1953).

Genotypic coefficient of variability $(GCV) = \frac{\sqrt{\sigma^2 g}}{x} \times 100$

Phenotypic coefficient of variability $(PCV) = \frac{\sqrt{\sigma^2 p}}{x} \times 100$

Environmental coefficient of variability $(ECV) = \frac{\sqrt{\sigma^2 e}}{x} \times 100$

Where, $\sigma^2 g$=Genotypic variance, $\sigma^2 p$ = Phenotypic variance, $\sigma^2 e$=Environmental variance, = General mean of character.

The PCV and GCV values were ranked as low (0-10%), medium (10-20%), and high (>20%).

Estimation of heritability and genetic advance

Broad sense heritability (h^2) was estimated based on the ratio of genotypic variance to the phenotypic variance and was expressed in percentage (Falconer and Mackay, 1996).

$$\mathbf{h^2\ \%= \frac{Vg}{Vp} x\ 100}$$

Where h^2 =heritability in a broad sense; Vg=Genotypic variance; Vp = Phenotypic variance. Heritability values are categorized as low (0-30%), moderate (30-60%), and high (60% and above) (Robinson, Comstock and Harvey, 1949).

The genetic advance was calculated according to Robinson et al (1949) as follows:

Genetic advance (GA) =k. σp.h^2

Where: k=selection intensity at 5% (k=2.06); σp=Phenotypic standard deviation;

h^2=Heritability in a broad sense.

Genetic advance as a percent of the Mean was calculated as:

$$\mathbf{GAM = \frac{GA}{\bar{\chi}} x\ 100}$$

Where: GAM =Genetic advance as percent of the mean; $\bar{\chi}$ = General mean of the character

Results and Discussion

Analysis of variances for yield and yield components of sesame germplasm

The analysis of variance revealed statistically significant differences at 0.01% and 0.001% probability levels among three hundred sesame germplasm for yield and yield component characters (Table 1) except for number of secondary branches, petiole length at middle leaf, mean capsule width, and mean capsule thickness**.** This indicates considerable genetic variation among germplasm in most characters studied. The present study's findings agree with Saha et al (2012) and Aye et al (2018) . The mean values and ranges of all quantitative characters revealed a large genetic diversity. Accessions with a wide range of agronomic characters can be used to find the best genotypes for different environments.

Table 1. Analysis of variance for quantitative characters of sesame genotypes

Character	Min	Max	Mean	Range	F Value
PTH	47.36	181.32	131.32	133.96	2.56***

PBR	0.12	6.50	3.23	6.38	2.16***
SBR	0	2.2	0.32	2.2	1
LBL	5.51	13.72	10.26	8.21	1.34**
WBL	2.51	9.52	6.71	7.01	1.54***
LML	5.49	12.68	9.53	7.19	1.84***
WML	2.00	6.44	3.83	4.44	1.42***
LTL	3.67	7.25	5.29	3.58	1.36***
WTL	0.46	7.25	0.83	6.79	1.31**
PLBL	2.84	8.44	5.84	5.6	1.46***
PLML	0.95	4.67	2.67	3.72	1.04
PLTL	0.24	1.44	0.54	1.2	1.89***
DFI	30	72	47.34	42	1.37***
DF	35	82	51.69	47	1.35**
NCPP	7.14	57.06	33.97	49.92	2.29***
CAPL	2.01	3.81	2.86	1.8	2.47***
CW	0.55	1.01	0.72	0.46	1.15
CT	0.33	0.74	0.51	0.41	1.06
SPC	48.44	82.40	68.43	33.96	1.4***
TSW	1.66	3.33	2.32	1.67	2.32***
DM	79	128	99.81	49	1.73***
PBZ	20.56	83.46	46.66	62.9	2.67***
YLD	34.10	1239	544.48	1204.9	3.95***
BBL	8.64	69.10	22.22	60.46	1.54***

PTH= plant height; PBR= primary branch; LBL= length of basal leaf; WBL=width of basal leaf ; LML= length of middle leaf; WML= width of middle leaf ; LTL=length of top leaf ; WTL= width of top leaf; PLBL= petiole length of basal leaf; PLTL= petiole length of top leaf ; DFI= days to flower initiation; DF= days to 50% flowering ; COL= corolla length; LLL=length of longest lip; NCPP = Number of capsules per plant; CAPL= capsule length; SPC= seeds per capsule; TSW= 1000 seed weight; DM= days to maturity; PBZ= Pod bearing zone; YLD= yield; BBL= bacterial blight reaction.
** Significant at P ≤ 0.01; *** Significant at P ≤ 0.001

Coefficients of variation, heritability, and genetic advance for quantitative traits in sesame germplasm

The mean performance, phenotypic variance, genotypic variance, phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV), heritability estimates, and predicted genetic advance over the mean for all the characters are presented in Table 2**.** The phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV) for all characters. This indicates that the environment had an important role in the expression of these characters. Similar findings were reported by Abate et al (2015), Gidey et al (2013), and Sabiel et al (2015).

The number of primary branches per plant, petiole length of top leaf, seed yield per hectare, and bacterial blight showed high PCV and GCV estimates while the width of the top leaf and number of capsules per plant showed high PCV and moderate GCV, indicating the scope for selection to improve these characters in the breeding program. The high PCV and GCV values for the number of primary and secondary branches per plant, the number of capsules per plant, and seed yield per hectare are substantiated by the findings of Aye et al., (2018), Shadakshari et al (1995), Alegbejo et al. (2003), Solanki and Gupta (2003), and Sumathi and Muralidharan (2010). Anitha (2000) also reported a high coefficient of variation for the number of capsules per plant. Teklu et al (2014) reported a high coefficient

of variation for the number of capsules per plant and seed yield per hectare, and medium genotypic coefficients of variation (GCV) and high phenotypic coefficients of variation (PCV) for the number of primary branches per plant.

Plant height, days to flower initiation, days to 50% flowering, 1000 seed weight, and pod-bearing zone showed moderate PCV and GCV. Similarly, Moderate coefficient of variation for plant height and 1000 seed weight were reported by Aye et al., (2018). The width of basal and middle leaf, length of middle leaf, petiole length of basal leaf, and capsule length showed moderate PCV and low GCV. The other traits such as length of basal leaf, length of top leaf, corolla length, length of the longest lip, seeds per capsule and days to maturity recorded low PCV and GCV. A low coefficient of variation for days to maturity was reported by several authors (Shadakshari et al 1995; Krishnaiah et al 2002; Sudhakar et al 2007; Aye et al. 2018). Estimate of PCV and GCV values gives only the extent of variability existing in traits; but, when combined with estimates of heritability and genetic advance, it would give a better idea about the possible gains of selection in the breeding program.

Heritability and Genetic Advance

The heritability in broad sense values ranged from 4.01 (corolla length) to 96.22 (days to 50% flowering). High heritability estimates were observed for plant height, primary branch, petiole length of top leaf, days to flower initiation, days to 50% flowering, capsule length, 1000 seed weight, days to maturity, pod bearing zone, seed yield and bacterial blight reaction (Table 2). High Heritability for days to 50% flowering (>80%), and plant height (90.04%) were reported by Desawi et al. (2014).

The heritability estimate recorded for traits such as length of top leaf, number of capsules per plant, capsule width, capsule thickness, and seeds per capsule was moderate, while the estimate recorded for length of basal leaf, width of basal leaf, length of middle leaf, width of middle and top leaf, petiole length of basal leaf, corolla length and length of the longest lip was low**.** The moderate to high heritability of a trait indicates that it is least affected by environmental influences, thereby allowing for the direct selection of the trait for improvement.

Genetic advance as a percent of the mean (GA) is a more reliable index for understanding the effectiveness of selection in improving traits because the estimates are derived by the involvement of heritability, phenotypic standard deviation, and intensity of selection. Thus, genetic advance along with heritability provides a clear picture regarding the effectiveness of selection for improving the plant characters. Estimates of heritability and genetic advancement are more important for selection than estimates of heritability alone. The range of genetic advance as a percent of the mean ranged from 1.5% for the length of the longest lip to 70.06% for bacterial blight.

High heritability combined with high genetic advance (as a percent of mean) was observed for plant height, primary branch, petiole length of top leaf, days to flower initiation, days to 50% flowering, pod bearing zone, seed yield per plant, and bacterial blight reaction. This indicates the lesser influence of environment in the expression of these characters and the prevalence of additive gene action in their inheritance, suggesting that direct phenotypic selection may be effective. The number of primary branches per plant, number of capsules per plant, and seed yield per plant were reported to have high heritability along with high genetic advance (Aye et al. 2018; Furat and Uzun 2010; Krishnaiah et al 2002; Reddy et al 2001).

Table 2. Estimation of variance components

Traits	ENV	trt	ENV.trt	Error	σ2g	√ σ2g	σ2P	√ σ2p	σ2e	√ σ2e	GCV (%)	PCV (%)	H2b (%)	GA	GAM
PTH	238.30	408.80	40.30	159.40	408.80	20.22	448.80	21.18	159.40	12.63	15.40	16.13	91.09	39.75	30.27
PBR	0.39	0.47	0.14	0.96	0.47	0.69	0.68	0.82	0.96	0.98	21.29	25.55	69.41	1.18	36.53
SBR	0.17	0.01	0.16	0.26	0.01	0.10	0.11	0.33	0.26	0.51	31.18	102.00	9.34	0.06	19.63
LBL	10.98	0.11	1.12	2.55	0.11	0.33	0.90	0.95	2.55	1.60	3.20	9.27	11.94	0.23	2.28
WBL	2.24	0.19	0.79	2.15	0.19	0.44	0.81	0.90	2.15	1.47	6.51	13.44	23.49	0.44	6.51
LML	95.87	0.35	1.42	3.23	0.35	0.59	1.36	1.17	3.23	1.80	6.21	12.25	25.70	0.62	6.49
WML	0.71	0.12	0.18	2.19	0.12	0.35	0.55	0.74	2.19	1.48	9.16	19.33	22.44	0.34	8.93
LTL	-0.02	0.13	-0.01	0.69	0.13	0.36	0.24	0.49	0.69	0.83	6.88	9.34	54.27	0.55	10.44
WTL	0.01	0.01	0.02	0.17	0.01	0.11	0.05	0.22	0.17	0.42	12.81	26.10	24.10	0.11	12.96
PLBL	18.17	0.11	0.77	2.29	0.11	0.33	0.75	0.87	2.29	1.51	5.65	14.81	14.55	0.26	4.44
PLTL	0.01	0.02	0.01	0.05	0.02	0.13	0.03	0.16	0.05	0.22	23.91	30.57	61.19	0.21	38.53
DFI	2.17	30.43	3.34	2.92	30.43	5.52	32.03	5.66	2.92	1.71	11.65	11.96	95.01	11.08	23.40
DF	2.70	37.01	2.83	3.08	37.01	6.08	38.46	6.20	3.08	1.75	11.77	12.00	96.22	12.29	23.78
COL	354.04	0.02	0.49	1.90	0.02	0.14	0.50	0.71	1.90	1.38	1.00	5.00	4.01	0.06	0.41
LLL	121.24	0.04	0.28	1.44	0.04	0.19	0.37	0.61	1.44	1.20	2.30	7.19	10.23	0.13	1.51
NCPP	144.94	38.83	121.45	88.32	38.83	6.23	94.03	9.70	88.32	9.40	18.34	28.54	41.29	8.25	24.28
CAPL	0.00	0.08	0.02	0.06	0.08	0.28	0.10	0.31	0.06	0.24	9.84	10.84	82.49	0.53	18.42
CW	0.00	0.00	0.00	0.01	0.00	0.04	0.00	0.05	0.01	0.08	5.47	7.48	53.38	0.06	8.23
CT	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.04	0.00	0.07	5.18	7.53	47.35	0.04	7.35
SPC	5.30	15.32	8.49	46.60	15.32	3.91	25.92	5.09	46.60	6.83	5.72	7.44	59.11	6.20	9.06
TSW	0.02	0.06	0.05	0.04	0.06	0.25	0.09	0.29	0.04	0.21	10.89	12.67	73.90	0.45	19.29
DM	20.19	73.60	8.21	26.14	73.60	8.58	80.69	8.98	26.14	5.11	8.59	9.00	91.21	16.88	16.91
PBZ	-4027.72	55.74	30.48	66.41	55.74	7.47	76.97	8.77	66.41	8.15	16.00	18.80	72.42	13.09	28.05
YLD	8338.0	45747.0	45543.0	21234.0	45747.0	213.9	64467.0	253.9	21234.0	145.7	39.3	46.6	71.0	371.2	68.17
BBL	4.84	60.70	0.24	22.32	60.70	7.79	64.50	8.03	22.32	4.72	35.06	36.14	94.11	15.57	70.06

PTH= plant height; PBR= primary branch; LBL= length of basal leaf; WBL=width of basal leaf ; LML= length of middle leaf; WML= width of middle leaf ; LTL=length of top leaf ; WTL= width of top leaf; PLBL= petiole length of basal leaf; PLTL= petiole length of top leaf ; DFI= days to flower initiation; DF= days to 50% flowering ; COL= corolla length; LLL=length of longest lip; NCPP = Number of capsules per plant; CAPL= capsule length; SPC= seeds per capsule; TSW= 1000 seed weight; DM= days to maturity; PBZ= Pod bearing zone; YLD= yield; BBL= bacterial blight reaction.

Conclusion and Recommendation

This study highlights a significant variability in yield and yield-related components among sesame germplasm, with certain traits such as plant height, primary branch, petiole length top leaf, days to flower initiation, days to 50% flowering, pod bearing zone, seed yield per plant, and bacterial blight resistance demonstrating high heritability and genetic advance. This suggests that progeny selection will be a promising approach for enhancing these traits. Additionally, capsule length, 1000 seed weight, and days to maturity exhibited high heritability but with moderate genetic advance, indicating that these traits may benefit from heterotic breeding strategies. The findings of this study contribute to a deeper understanding of sesame populations across various ecological regions, providing a foundation for breeding climate-resilient varieties. To maximize the benefits of these results, it is recommended to implement targeted breeding programs, alongside in situ and ex situ conservation efforts for sesame genetic resources. Additionally, the application of molecular markers is suggested to validate the findings and facilitate more precise breeding strategies.

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