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Genetic Variability and Trait Association Study in Ethiopian Sesame (Sesamum indicum L.) Genotypes

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Abstract

Field experiment was conducted on 25 Sesame (Sesamum indicum L.) genotypes to estimate genetic variability and trait association of yield and yield related traits in 5x5 simple lattice design during 2019 main cropping season. The analysis of variance showed highly significant differences ($P<0.01$) among the genotypes for all quantitative traits except days to maturity and biomass yield per hectare which was non-significant. Days to flowering, plant height and capsule length showed low Phenotypic and Genotypic Coefficient of Variations and genetic advance percent mean. Branches per plant showed medium Phenotypic and Genotypic Coefficient of Variations, heritability and genetic advance percent mean. Capsule per plant, seed yield per plant and seed yield per hectare showed moderate Phenotypic and Genotypic Coefficient of Variations and high heritability with genetic advance percent mean. Biomass yield per plant and harvest index showed high Phenotypic and Genotypic Coefficient of Variations, heritability and genetic advance percent mean. Both phenotypic and genotypic correlation coefficient analyses showed positive and significant association of seed yield with seed yield per plant and harvest index. Generally, this study painted the presence of significant genetic variation among tested sesame genotypes and the possibility to get genetic progresses in the succeeding breeding generations.

Keywords: Correlation, genetic advance, GCV, heritability, PCV and sesame
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Introduction

Sesame (*Sesamum indicum* L.) is an important crop in tropical and sub-tropical areas (Ashri, 1998). It has been grown in the Near East and Africa for over 5,000 years for cooking and medicinal needs (Sharm *et al.,* 2014). Ethiopia is considered as the center of origin for sesame and the genetic diversity is high, serving as resources for further improving the crop (Daniel and Parzies, 2011). Generally, 65% of world sesame production is used for edible oil extraction and 35% for confectionary purpose. Ethiopia, sesame is used as cash crop, export commodity, raw materials for industries and as source of employment opportunity. Currently, it has become the primary export oil crop, playing an important role in the agricultural GDP of the country.

Worldwide, sesame is produced over an area of 12821752 hectare and annual production around 6549725 tons with average productivity of 0.52 tha^{-1}, whereas, in Africa, 8737270ha and 3998148 tons of annual production with average productivity of 0.46 tha^{-1} (FAOSTAT, 2019). In Ethiopia sesame is produced over 375120 ha with annual production of 262654 tones with average productivity of 0.7 tha^{-1} (FAOSTAT, 2019). The production and productivity of sesame is very low in contrast with yield potential of the crop up to 2000 $kgha^{-1}$ under experimental stations (Mkamilo and Bedigian, 2007). The success of any crop improvement program essentially depends on the nature and magnitude of genetic variability present in the crop (Parameshwarappa *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. Desawi *et al.* (2017), Mohanty *et al.* (2020) and Feyera *et al. (*2020) 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.

Correlation analysis is used to understand the relationships existing between yield and yield components. Seed yield of sesame is 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 (Siva *et al.,* 2013). A breeder who wants to recognize key traits that can be profitably utilized in order to achieve the desired level of seed yield improvement needs to know the degree and direction of this relationship between different attributes and seed yield. Hence, the present study was initiated with estimation of genetic variability and trait association of sesame genotypes.

Materials and methods

The experiment was conducted at Bako Agricultural Research Center during 2019 cropping season. BARC is located in 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^{0}C and 29.80^{0}C, respectively. Elevation of the area is 1650 m.a.s.l. and soil type is sandy-clay with 4.9-5.1 soil PH. Relative humidity and rain fall of BARC is 49.81% and 1161.7mm respectively (BARC Agro metrology data, 2018). Twenty five sesame genotypes including standard checks were evaluated at Bako during 2019 main cropping season. The planting materials were developed by Bako Agricultural Research Center. The parental materials were collected from western parts of the countries. The trial was conducted in simple lattice design. All necessary data were collected according to the International Plant Genetic Resources Institute (IPGRI, 2004) descriptor for sesame and analyzed by SAS 9.3 software.

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)

δ^2_g = Where, MS_g = mean square of genotype,
MSe = is mean square of error and
r = number of replications

Environmental variance (δ^2_e) = MSe

Phenotypic variance (δ^2_p)

$\delta^2_p = \delta^2_g + \delta^2_e$ Where, δ^2_g = genotypic variance, δ^2_e = environmental variance and r = number of replications

Estimates of coefficient of variation were obtained as follows.

Phenotypic coefficients of variation (PCV)

PCV = x 100 where, PCV = phenotypic coefficient of variation, δ^2_p = phenotypic Variance and = population mean for the trait considered

Genotypic coefficients of variation (GCV)

GCV = x 100 where, GCV = genotypic coefficient of variation,
δ^2_g = genotypic variance, = 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 (^{2}g) to the phenotypic variance (^{2}p) and were estimated on genotype mean basis as described by Allard (1999):

$H^2 =$ 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 * H^2
GA (as % of the mean) =X100

Where k=selection differential (k=2.06 at 5% selection intensity)
$_p$ = phenotypic standard deviation
H^2 =heritability (Broad sense)
= Grand mean

Phenotypic and genotypic correlation coefficients were computed using the CANDISC procedure of SAS software (SAS, 2012) from the components of variance and covariance based on the method described by Singh and Chaudhary (1996).

Result and discussion

The Analyses of Variance (ANOVA) showed highly significant ($P < 0.01$) among tested genotypes for days to 50% flowering, plant height (cm), stem height (cm), branches per plant, capsule length, capsules per plant, biomass yield per plant, seed yield per plant, seed yield per hectare (kgha^{-1}) and harvest index (%) except days to maturity and biomass yield per hectare which were no significant indicating that the presence of considerable variation in the genetic materials. Comparative results were reported by Singh *et al. (*2018), Patidar *et al.* (2020) and Saravanan *et al.* (2020).

Table 1. Analysis of variance for seed yield and yield related traits of 25 sesame genotypes

Traits	MSg (Df = 24)	MSe(Df = 16)	CV (%)	R^2	SE
Days to Flowering	1.32*	0.44	0.97	0.83	0.66
Days to Maturity	6.21 ^{ns}	6.74	2.09	0.78	2.60
Plant height	48.82*	18.25	4.51	0.88	4.27
Stem height	24.62*	8.37	13.14	0.87	2.89
Branches per plant	0.81**	0.23	9.26	0.88	0.48
Capsule length	0.02**	0.00	4.32	0.88	0.07
Capsule per plant	111.52**	10.01	7.08	0.96	3.16
Biomass yield per plant	821.79**	34.25	7.10	0.98	5.85
Biomass yield per hectare	54387.55^{ns}	91797.47	10.76	0.61	302.98
Seed yield per plant	15.72**	0.50	4.71	0.98	0.70
Seed yield per hectare	2927.28**	192.19	3.62	0.96	13.86
Harvest index	94.50**	2.90	8.57	0.99	1.70

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

Estimation of Genetic Parameters

Phenotypic and genotypic variance, their coefficients of variation, heritability and genetic advance of percent mean value were presented in Table 2. 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. Most of tested sesame traits showed medium to high GCV, PCV, heritability and genetic advance as percent mean which indicated high variability among evaluated once. Phenotypic coefficients of variation (PCV) ranged from 35.12% for harvest index to 1.37% for days to flowering and genotypic coefficients of variation (GCV) ranged from 34.06% for harvest index to 0.97% for days to maturity (Table 2).

Medium to high value of PCV and GCV (>20%) were obtained from harvest index, seed yield per plant seed yield per hectare, biomass yield, capsule per plant, branches per plant and stem height (Table 2). This value indicated the variation observed among genotypes for these traits were more of due to their genetic difference rather than environmental influences. It leads that simple selection may be effective based on these traits and their phenotypic expression would be a good indication of genetic potential as different genotypes can provide materials for a sound improvement program. Gadisa *et al.* (2015) and Patidar *et al.* (2020) reported relatively equivalent phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) values.

However, low values (<10%) of PCV and GCV were obtained for days to 50% flowering, plant height and capsule length. Lower PCV and GCV suggested that the traits are rendering to high environmental influences and hence lower opportunity exists for development of these traits through simple selection in the tested genotypes. Similar result was reported Mohammed *et al.* (2015), Saxena and Bisen (2016), Feyera *et al.* (2020) and shammoro *et al.* (2020).

Table 2. Estimation of genetic variance for 10 traits of 25 tested sesame genotypes

Traits	δ^2g	δ^2p	GCV	PCV	H^2	GA	GAM
Days to Flowering	0.44	0.88	0.97	1.37	49.98	0.97	1.41
Plant height	15.29	33.53	4.13	6.12	45.59	5.44	5.74
Stem height	8.12	16.50	12.95	18.45	49.25	4.12	18.72
Branches per plant	0.29	0.52	10.40	13.92	55.76	0.83	16.00
Capsule length	0.01	0.01	4.70	6.39	54.17	0.12	7.13
Capsule per plant	50.76	60.76	15.94	17.44	83.53	13.41	30.02
Biomass yield per plant	393.77	428.02	24.08	25.10	92.00	39.21	47.57
Seed yield per plant	7.61	8.11	18.44	19.03	93.87	5.51	36.81
Seed yield per hectare	1367.55	1559.73	9.66	10.32	87.68	71.33	18.63
Harvest index	45.80	48.70	34.06	35.12	94.05	13.52	68.05

Key: ^2g = genotypic variance, ^2p = phenotypic variance, 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

Estimating heritability used to provide information on the extent to which a particular genetic character can be transmitted to successive generations (Schmidt, 2020). From the result, heritability ranged from 94.05% for harvest index to 45.59 % for plant height (Table 2). According 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.

Based on this bench mark, very high heritability value was obtained for harvest index (94.05%), seed yield per hectare (87.68%), seed yield per plant (93.87%), biomass yield per plant (92%) and capsule per plant (83.53%) (Table 2). Such result indicated that the genetic makeup played a major role in the expression of these traits and close correspondence between the genotypic and the phenotypic ultimately due to less environmental influence on phenotypic expression of these traits which is good for crop improvement through simple selection. Desawi *et al*. (2017), Aye and Htwe (2019) and Feyera *et al.* (2020) were reported moderately to high heritability with high genetic advance as present of mean for seed yield.

Medium heritability values were observed for days to 50% flowering (49.98%), plant height (45.59%), stem height (49.25%), branches per plant (55.76%) and capsule length (54.17%) (Table 2). Narayanan and Murugan (2013) reported medium heritability for days to 50% flowering (57.30%). The magnitudes of heritability for all of the tested characters were medium to high, which may be attributed due to their genetic difference of the genotypes in the study. 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 present study can be improved by conventional breeding through selection breeding.

GAM values classified by Falconer and Mackay (1996) as low from 0 to 10%, medium from 10 to 20% and high ≥20% values. Accordingly, genetic advance as percent of mean (GAM) at 5% selection intensity was high for harvest index (68.05%), seed yield per plant (36.81%), biomass yield per plant (47.57%) and number of capsules per plant (30.02%). Medium Genetic advance as percent of mean were obtained for seed yield per hectare (18.63%), branches per plant (16%) and stem height (18.72%) (Table 2). The result indicated that these traits are governed by additive gene. 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 the study. Kiruthika *et al. (*2018) and Kumari *et al.* (2020) reported that high genetic advance as percent of mean were observed for number of branches per plant, number of capsule per plant, biomass yield, seed yield and harvest index.

Low genetic advance as percent of mean were obtained for days to 50% flowering (1.41%), plant height (5.74%) and capsule length (7.13%) (Table 2). This showed that these traits are governed by non-additive gene and thus simple selection cannot be applied for the improvements of these traits. Generally, genetic advance as percent mean ranged from high (68.05%) for harvest index to low for days to flowering (1.41%). From the result, low genotypic coefficients of variation, phenotypic coefficient of variation, low heritability as well as low genetic advance as percent of mean were recorded for days to flowering, plant height, stem height and capsule length. Hence, improvement of these traits through simple selection is difficult as the traits are governed by non-additive genes.

In the contrary, medium to high genotypic coefficients of variation (GCV), phenotypic coefficients of variations (PCV), heritability and genetic advance as percent mean were recorded for stem height, branches per plant, capsule per plant, biomass yield per plant, seed yield per plant, seed yield per hectare and harvest index. 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 are reliable for the development of high yielding sesame genotypes. Aye and Htwe (2019), Umamaheswari. *et al.* (2019) and Mohanty *et al.* (2020). 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.

Desawi *et al*. (2017) and Umamaheswari. *et al.* (2019) reported high heritability coupled with high genetic advance for number of capsules per plant and seed yield which indicated the additive nature of inheritance. However, contrary result was reported by Mohammed *et al.* (2015) where low heritability coupled with low genetic advance as percent of mean for number of capsules per plant and harvest index in tested sesame genotypes. In general, the medium to high value for GCV, heritability and genetic advance of the traits considered in present study provide information for the existence of wider genetic variability among sesame genotypes and this offers high chances for improving several traits of the crop through simple selection. 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.

Phenotypic and genotypic correlation coefficients

Phenotypic and genotypic correlation coefficients of 25 sesame genotypes among each pair of traits were presented in Table 3. The magnitudes of genotypic correlation coefficients for some of the traits were higher than their corresponding phenotypic correlation coefficients. This indicated that although there is strong inherent association between the various pairs of traits studied and the low phenotypic correlation would result from the masking and modifying effects of environment on the association of traits at gene level. Kehie *et al.* (2020), Patidar *et al.* (2020) and Singh *et al.* (2018) also reported that genotypic correlation coefficients were higher than the respective phenotypic correlation coefficients for most of the traits.

Phenotypic correlations

Seed yield per hectare showed positive and highly significant phenotypic association with seed yield per plant (r = 0.61) and harvest index (r = 0.47). Harvest index showed positive and highly significant phenotypic correlation with seed yield per plant (0.66) and stem height (0.32). Biomass yield per plant positive and highly significant phenotypic correlation with plant height (0.41), branches per plant (0.36) and capsule per plant (0.56). Capsule per plant positive and highly significant phenotypic correlation with plant height (0.68) and branches per plant (0.64). Branches per plant positive and highly significant phenotypic correlation with plant height (0.48) (Table 3). These showed that improvement of these traits would result in a substantial increment on seed yield of sesame. Lalpantluangi and Shah (2018) and Takele *et al. (*2021) report that significant and positive correlations for some traits in sesame, suggesting the interdependency between these characters as important yield determinants.

Days to 50% flowering revealed a negative and highly significant phenotypic correlation with plant height and branches per plant. This indicated that early flowering genotypes minimizes plant height and number branches per plant. Plant height revealed a negative and highly significant phenotypic correlation with harvest index which indicated that increasing plant height may reduce the harvest index of the plant. Harvest index showed negative and highly significant phenotypic correlation with plant height, branches per plant, number of capsule per plant and biomass yield per plant. This indicated that more plant height, branching, capsule per plant and biomass yield per plant of genotypes and accommodated less harvest index. Supportive result also reported by Akram *et al.* (2016) and Lalpantluangi and Shah (2018)

Table *3*. Genotypic (above) and phenotypic (below) diagonal correlation coefficients of yield and yield related traits of 25 tested sesame genotypes

Variable	DF	PH	SH	BPP	CL	CPP	BYP	SYP	HI	SYha
DF		-0.39	-0.08	-0.37	-0.31	-0.29	0.11	-0.18	-0.08	-0.13
PH	-0.40**		-0.11	0.62**	0.52**	0.74**	0.44*	-0.06	-0.44*	-0.12
SH	-0.08	-0.05		-0.45*	0.01	-0.42*	-0.42*	0.33	0.41*	0.03
BPP	-0.31*	0.48**	-0.44**		0.23	0.72**	0.40*	-0.32	-0.53**	-0.14
CL	-0.22	0.42**	-0.07	0.16		0.31	0.22	-0.09	-0.25	-0.05
CPP	-0.27	0.68**	-0.31*	0.64**	0.22		0.59**	-0.11	-0.58**	-0.04
BYP	0.06	0.41**	-0.31*	0.36*	0.20	0.56**		-0.21	-0.82**	-0.22
SYP	-0.19	-0.04	0.27	-0.29*	-0.08	-0.11	-0.20		0.67**	0.71**
HI	-0.08	-0.41**	0.32*	-0.47**	-0.24	-0.55**	-0.82**	0.66*		0.39**
SYha	-0.12	-0.08	0.00	-0.06	-0.10	0.00	-0.17	0.61**	0.47*	

*Key: *, ** indicates significant at 0.05 and 0.01 probability level, respectively; DF = Days to 50% flowering, DM = Days to 90% maturity, PH = Plant height, SH = stem height, BPP = number of branches per plant, CL = capsule length, CPP = number of capsule per plant, BYP = Biomass yield per plant, SYP = Seed yield per plant, HI = Harvest index, SYha = seed yield per hectare*

Genotypic correlations

Seed yield per hectare had positive and highly significant genotypic correlation with seed yield per plant (0.71) and harvest index (0.39). Seed yield per plant had positive and highly significant genotypic correlation with harvest index (0.67). Biomass yield per plant had positive and highly significant genotypic correlation with capsule per plant (0.59), branches per plant (0.4) and plant height (0.44). Although capsule per plant had positive and highly significant genotypic correlation with branches per plant (0.72) and plant height (0.74) (Table 3). Positive significant correlation due to effect of genes can be the result of the presence of strong coupling linkage between their genes or the traits may be the result of pleiotropic genes that control these traits in the same direction. Comparative results were reported by Khairnar *et al.* (2013), Fazal et al. (2015) and Mohammed *et al.* (2015).

Harvest index was negative and highly significant genotypic correlation with biomass yield per plant (0.82), capsule per plant (0.58), branches per plant (0.53) and plant height (0.44) (Table 3). This indicated that increasing one character may reduce the other characters leads lack of possibility for simultaneous selection of the traits. There are some traits which was not significantly correlated. Hence simultaneous improvement of those traits doesn't affect each other. Similar results were reported by Aristya and Taryono (2016) and Singh *et al.,* (2018) where oil content had non-significant positive genotypic correlation with seed yield.

Generally, traits such as seed yield per plant and harvest index were important for indirect selection of sesame for higher seed yield. Hence, seed yield can be increased to a substantial level through direct selection of plants bearing higher values/number of these traits. Khairnar *et al.* (2013) recognized that total Seed yield per plant is predicted to be the most important selection criterion for breeding in sesame. Shabana *et al.* (2015) reported that the genotypic correlation coefficients were slightly higher than the phenotypic correlation coefficients in sesame. This indicated the masking effect of the environment was limited and did not mask the expression of the genotypes. Saxena *and* Bisen (2016) reported positive correlation of harvest index with seed yield whereas plant height negatively correlated with seed yield.

In general, some traits were negative and significantly correlated as well as positive and negative non-significantly correlated among each other. Such association may arise from different factors of gene action (additive or non-additive) and the other factors such as pleiotropy (Welsh, 2008). Also negative correlation of traits might be because of different genes or pleiotropic gene that have dominance on the trait may control them in different direction (Kearsey and Pooni, 1996). Therefore, selection for traits based on its close association (positive and negative) with other traits is very useful for simultaneous improvement of all the associated traits. Simultaneous improvement of traits those negatively associated with each other could be difficult and independent selection should be carried out to improve such traits.

Conclusion

Estimations of genetic variability and traits associations provide valuable information for plant breeders to design further breeding strategy. The present study revealed that there were highly significant differences among tested genotypes for all traits except days to maturity and biomass yield per hectare indicating the presence of valuable variability for seed yield and related traits in the studied genotypes. Most of the tested traits showed medium to high PCV and GCV values heritability and genetic advance as percent mean. Both phenotypic and genotypic correlation coefficient analyses showed positive and significant association of seed yield with seed yield per plant and harvest index. In general, this study painted the presence of significant genetic variation among tested sesame genotypes and the possibility to get genetic progresses in the succeeding breeding generations. Thus, selection of promising genotypes could be possible to produce superior sesame varieties among the materials included in the present study.

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Conflict of interests

The authors have declared that no conflict of interest exists

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