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Original Research Article||

Correlation and path coefficient analysis for yield and its related traits in sesame (*Sesamum indicum* L.) genotypes

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Abstract

Forty-nine sesame genotypes were evaluated in simple lattice design at Bako and Uke during 2018 cropping season. The objective of the study was to estimate the extent of associations between yield and its related traits. The combined analysis showed highly significant differences among the genotypes for all studied traits. Both phenotypic and genotypic correlation coefficient analyses showed positive and significant association of seed yield with plant height, branches per plant, capsule per plant, biomass yield and harvest index. On the other hand, the association of bacterial blight with grain yield was negative and highly significant at both phenotypic and genotypic levels. Biomass yield, harvest index and capsule per plant had high and positive direct effect on grain yield. The result of the study showed that biomass yield, harvest index and capsule per plant were important yield related traits that should be considered for sesame seed yield improvement.

Key words: Breeding, character association, genotypic correlation, phenotypic correlation, seed yield

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INTRODUCTION

Sesame (*Sesamum indicum L.*) is a diploid with 2n = 26 chromosomes (Morinaga *et al.*, 1929), which belongs to the family of *Pedaliaceae*. Two alternative centers viz., East Africa (Ethiopia) or Asia (Indian Subcontinent or further east or central Asia) have been proposed for its origin. Domestication of sesame is believed to have happened about 5000 years ago as per evidences found in archaeological excavations in Harappa (Fuller, 2003). Sesame has been given less attention by the farmers because of poor yield due to non-availability of varieties suitable and adaptable to the diverse agro-climatic conditions (Ashri, 2007). In Ethiopia, the national average seed yield of sesame is 691 kg ha^{-1} (CSA, 2018), which is quite low in contrast with yield potential of the crop up to 2000 kg ha^{-1} under experimental stations (Mkamilo and Bedigian, 2007). For these reasons, sesame production and extension in Ethiopia is quite limited, particularly because of its low yield. To overcome problems of the low productivity of sesame, there must be a sound procedure for selection of high yielding varieties adapted to the local environments (Tadele, 2005).

Seed yield in sesame like other field crops is a multi-facet character and direct selection or this trait may often be misleading. The components that determine the yield are best indices for selection. Therefore, knowledge of relationship between important yield traits and seed yield may help the researchers to identify suitable donors for a potential and successful breeding program (Kumaresan and Nadrajan, 2002). Correlation analysis provides information about the degree of relationship between plant characters. The knowledge of their coefficients provides a measure of genetic association between traits in order to identify the important ones to be considered in breeding programs.

Yield is a complex quantitative character controlled by many genes interacting with the environment and is the product of many factors called yield components. Selection of parents based on yield alone is often misleading. Hence, the knowledge about relationship between yield and its contributing characters is needed for an efficient selection strategy for the plant breeders to evolve an economic variety. According to Gnanasekaran *et al*. (2008) correlation studies provide reliable information on nature, extent and direction of selection. Yirga (2017) and Singh *et al*. (2018) reported significant association of seed yield with traits such as plant height, branches and capsules per plant. The result may differ from trait to trait depending on the germplasm sources. The information on the planting material under this study is missing. Hence, the present study was initiated to determine the associations between seed yield and related traits in sesame.

MATERIALS AND METHODS

Description of the study area

The experiment was conducted at two locations viz. Bako Agricultural Research Center (BARC) and Uke (sub site of BARC) during the 2018 cropping season. BARC is located in Oromia Regional State at 250 kilometers West of Addis Ababa at altitude of 1650 meter above sea level. BARC has a warm, humid climate with mean minimum and maximum temperatures of 13.97ºC and 29.80ºC, respectively. Annual rain falls and relative humidity of BARC is 1161.7 mm and 49.81%, respectively (BARC Agro metrology data, 2018). Uke is located in East Wollega zone Oromia regional state, Guto Gida district that is about 365 kilometers away from Addis Ababa to the west. The area is located at altitude of 1383 meters above sea level and it is an area with high temperature and rain fall conditions. The geographical location of Uke is 14º 06' N latitude and 38º 31'E longitude.

Experimental materials

The experimental materials consisted of 46 genotypes and three checks (Waliin, Chalasa & Obsa) (Table 1). 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 (F_7) through selfing using F_2- derived pedigree breeding method at Bako Agricultural Research Center. The original parent materials were collections from Western Ethiopia and included: EW002, EW003, BG006, EW023 (2), EW006, EW003 (1), EW019, EW010 (1), Obsa, Dicho and Wama. These eleven parent materials were crossed in 11 x 11 diallel mating design, including reciprocals in the 2011 cropping season.

Table 1. 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 on 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 on 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 planting, the plants were thinned to maintain the spacing between plants of 10 cm. Fertilizer was applied at the rate of 100 kg ha^{-1} of NPS at planting time whereas, 100 kg ha^{-1} of Urea was applied two times in split at planting time and four weeks after planting.

Data collection

All plant-based data (plant height (cm), number of branches per plant, number of capsules per plant and bacterial blight (%)) and plot-based data (days to 50% flowering, days to maturity, 1000 seed weight (g), biomass yield per hectare (kg ha^{-1}), seed yield (kg ha^{-1}), harvest index and oil content (%)) were collected from the two central rows for both plant and plot-based data. The data were collected according to the International Plant Genetic Resources Institute (IPGRI, 2004) descriptor for sesame.

Data analysis

The efficiency of simple lattice design over RCBD was checked and in most of the response variables simple lattice design was found to be more efficient than RCBD. Thus, ANOVA was computed based on simple lattice design. The quantitative data for each location was subjected to analysis of variance (ANOVA) and done using Proc lattice and Proc GLM procedures of SAS version 9.3 (SAS, 2012). Before computing the combined analysis, homogeneity test for the error variance of 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, justifying the suitability of combined analysis.

Estimation of correlation coefficients

Phenotypic and genotypic correlation coefficients were computed using the CANDISC procedure of SAS software (SAS, 2012). Correlation coefficients were estimated from the components of variance and covariance based on the method described by Singh and Chaudhary (1999).

Path coefficient analysis

Path coefficient analysis was conducted as suggested by Wright (1921) and worked out by Dewey and Lu (1959) using the phenotypic as well as genotypic correlation coefficients to determine the direct and indirect effects of yield components on seed yield based on the following relationship.

$$r_{ij} = P_{ij} + \sum r_{ik} \times P_{kj}$$

Where: r_{ij} = mutual association between the independent character (i) and dependent character, grain yield (j) as measured by the correlation coefficients; P_{ij} = components of direct effects of the independent character (i) as measured by the path coefficients; and $\Sigma r_{ik}\ p_{kj}$ = summation of components of indirect effect of a given independent character (i) on a given dependent character (j) via all other independent characters

The contribution of the remaining unknown factor will be measured as the residual factor (PR), which is calculated as shown below, with the magnitude of PR indicating how best the causal factors account for the variability of the dependent factor (Singh & Chaudhary, 1999).

$$PR = \sqrt{(1 - \sum r_{ij} \times P_{ij}\ )}$$

RESULTS AND DISCUSSION

Analysis of variance (ANOVA)

The analysis of variances 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 (kg ha^{-1}), seed yield (kg ha^{-1}), harvest index (%), thousand seed weight (g), oil content (%) and severity of bacterial blight (%) indicating that the presence of considerable variations among the genetic materials (Table 2). Supportive results were reported by Mohammed *et al.* (2015), Iqbal *et al.* (2018) and Singh *et al.* (2018) reported significant difference for days to flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, thousand seed weight (g), seed yield and oil content.

Table 2. Analysis of variance for seed yield and seed related traits over two locations

Traits	MSl (Df =1)	MSr(l) Df=1	MSb(r) Df=12)	MSg (Df =48)	MSgl (Df = 48)	MSe (Df = 84)	CV (%)	R^2
Days to flowering	861.84**	3.19	3.99	27.22**	11.05**	2.15	2.34	0.94
Days to maturity	4585.22**	2.47	1.75	12.97**	5.36**	1.49	1.08	0.98
Plant height(cm)	38.88ns	3.42	24.59	133.82**	71.81**	28.57	4.59	0.82
No. of branch/plant	22.22**	0.06	1.13	4.63**	1.78**	0.46	10.79	0.90
No. of capsule/plant	12542.40**	432.94	300.84	833.32**	288.06**	147.41	12.73	0.86
Biomass yield/ha(kg)	3259905.05**	15788.82	316724.80	1040847.35**	313201.83^{ns}	237629.93	14.09	0.80
Seed yield/ha (kg)	400989.23**	81052.76	60298.10	218667.70**	60193.05**	33417.32	17.22	0.85
Harvest index	4.69^{ns}	35.52	15.69	60.31**	34.54^{*}	19.34	14.38	0.76
1000 seed weight (g)	12.13**	0.06	0.29	2.62**	0.88^{ns}	0.65	12.55	0.79
Oil content (%)	80.00**	0.06	0.19	2.27**	0.90**	0.18	0.77	0.94
Bacterial blight %	412.53**	1.25	5.53	47.36**	16.87**	5.29	12.09	0.90

*Key: *, ** and ns indicate significant (p<0.01), highly significant (p<0.05) and non-significant, respectively; MSl = mean square of location,* MSr (l) = mean square of replication into location, MSb (r) = mean square of block into replication, *MSg = 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 *= coefficient of determination*

Phenotypic and genotypic correlations

Estimates of phenotypic and genotypic correlation coefficients of 49 sesame genotypes between each pair of traits were presented in Table 3. The magnitudes of genotypic correlation coefficients for most of the traits were higher than their corresponding phenotypic correlation coefficients (Table 3). 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. Shekhawat *et al.* (2013); Soundharya *et al.* (2017) 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 showed positive and highly significant phenotypic associations with plant height (r = 0.301), number of branches per plant (r = 0.523**), number of capsules per plant (r = 0.677**), biomass yield (r = 0.784**), harvest index (r = 0.676**) and thousand seed weight (r = 0.192**). These showed that improvement of these traits would result in a substantial increment on seed yield of sesame. Haruna *et al.* (2012) report that significant and positive correlations for some traits viz. plant height, number of branches per plant, number of capsules per plant, harvest index and seed yield in sesame, suggesting the interdependency between these characters as important yield determinants.

According to Fazal *et al*. (2015) seed yields were positive and significantly correlated at phenotypic level for plant height, branches per plant, capsules per plant and thousand seed weight. Desawi *et al.* (2017) also observed that seed yield showed positive and highly significant phenotypic association with number of capsule and number of branches per plant. Seed yield had negative and significant association with bacterial blight severity (r = -0.454).

Days to 50% flowering revealed a positive and highly significant phenotypic correlation with days to maturity, oil content and bacterial blight severity. This showed that early flowering genotypes matured early; maximize oil content and increases disease severity. Days to maturity exhibited positive and highly significant phenotypic correlation with oil content, significant with plant height, and bacterial blight severity. Plant height showed a positive and highly significant phenotypic correlation with the number of branches per plant, number of capsules per plant and biomass per hectare as well as negative and significant phenotypic correlation with bacterial blight severity. Number of branches per plant showed positive and highly significant phenotypic correlation with the number of capsules per plant, biomass yield per hectare and harvest index and negative and highly significant with bacterial blight severity. This indicated that more branching genotypes accommodated more capsule per plant, high biomass yield and harvest index which significantly maximize the seed yield. Supportive result was also reported by Akram *et al.* (2016).

Number of capsules per plant showed positive and highly significant phenotypic correlation with biomass yield per hectare and harvest index and significant phenotypic correlation with thousand seed weight. Harvest index shows positive significant and negative highly significant phenotypic correlation with thousand seed weight and bacterial blight severity, respectively. Biomass yield per hectare showed negative and highly significant phenotypic and genotypic correlation with bacterial blight severity. Thousand seed weight showed negative and significant phenotypic and genotypic correlations with bacterial blight severity. Similar result was reported by Fazal *et al.* (2015) and Tesfaye (2015). Additionally, Soundharya *et al.* (2017) reported that days to 50% flowering had significant positive association with days to maturity, which in turn had significant positive association with plant height.

Table 3. Genotypic (above) and phenotypic (below) diagonal correlation coefficients of yield and yield related traits of 49 sesame genotypes evaluated at Bako and Uke, 2018 cropping season

Traits	DF	DM	PH	BPP	CPP	BY	HI	SW	OC	SI	SY
DF		0.369**	0.142	0.278	0.036	0.033	-0.058	0.029	0.431**	0.041	-0.010
DM	0.605**		0.398**	0.168	0.078	0.226	-0.098	-0.211	-0.002	-0.388**	0.107
PH	0.085	0.181*		0.455**	0.384**	0.406**	0.050	-0.122	-0.051	-0.204	0.315**
BPP	0.114	-0.159*	0.342**		0.780**	0.634**	0.404**	0.091	0.130	-0.218	0.669**
CPP	-0.093	-0.287**	0.350**	0.716**		0.712**	0.518**	0.176	-0.016	-0.309*	0.794**
BY	0.001	-0.057	0.340**	0.481**	0.570**		0.268	0.132	0.035	-0.530**	0.855**
HI	-0.035	-0.031	0.081**	0.268**	0.404**	0.088		0.221	0.097	-0.269	0.721**
SW	-0.137	-0.235**	-0.080	0.087	0.181*	0.139	0.154*		0.072	-0.170	0.206
OC	0.546**	0.503**	-0.038	-0.056	-0.220**	-0.076	-0.005	-0.114		-0.127	0.099
SI	0.184*	0.165*	-0.177**	-0.268**	-0.331**	-0.430**	-0.224**	-0.158*	0.107		-0.525**
SY	-0.024	-0.062	0.301**	0.523**	0.677**	0.784**	0.676**	0.192**	-0.042	-0.454**	

*Key: *, ** indicates significant ($p<0.05$) and ($p<0.01$) probability levels, respectively; DF = days to 50% flowering, DM = days to 90% maturity, PH = plant height, BPP = number of branches per plant, CPP = number of capsules per plant, BY = biomass yield per hectare (kg ha^{-1}), SY = seed yield per hectare (kgha^{-1}), HI = harvest index, SW = thousand seed weight (g), OC = oil content (%) and SI = bacterial blight severity*

Genotypic correlations

Days to maturity showed positive and highly significant genotypic correlation with days to flowering. Plant height showed a positive and highly significant genotypic correlation with the number of branches per plant, number of capsules per plant and biomass yield. Number of branches per plant showed positive and highly significant genotypic correlation with the number of capsules per plant, biomass yield per hectare and harvest index. Number of capsules per plant showed positive and highly significant genotypic correlation with biomass yield per hectare and harvest index (Table 3).

Seed yield had positive and highly significant genotypic correlation with plant height (r = 0.315**), number of branches per plant (r = 0.669**), number of capsules per plant (r = 0.794**), biomass yield per hectare (r = 0.855**) and harvest index (r = 0.720**) (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. Similar results were reported by Pawar *et al.* (2002), Fazal *et al.* (2015) and Mohammed *et al.* (2015). Positive significant correlation of the number of capsules per plant with seed yield had been reported by Azeez and Morakinyo (2011) and Saha *et al.* (2012).

Seed yield had a negative and highly significant genotypic correlation with bacterial blight severity (r = -0.5253) (Table 3). This indicated that there is a possibility for simultaneous selection of cultivars based on seed yield and tolerance/resistance traits to bacterial blight. Days to maturity, thousand seed weight and oil content showed positive and non-significant genotypic correlation with seed yield per hectare. Hence simultaneous improvement of oil content and seed yield doesn’t affect each other. Similar results were reported by Chowdhury *et al.* (2010), Desawi *et al.* (2017), Yirga (2017) and Singh *et al.*, (2018), where oil content had non-significant positive genotypic correlation with seed yield.

Generally, traits such as height, branches per plant, capsules per plant, biomass yield and harvest index were important in 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. Shabana *et al.* (2015) reported that the genotypic correlation coefficients were slightly higher than the phenotypic correlation coefficients in sesame, indicated the masking effect of the environment that did not mask the expression of the genotypes.

Saxena *et al.* (2016) reported positive correlation of characters days to 50% flowering, days to maturity, number of branches, number of capsules per plant, 1000-seed weight, oil content and harvest index with seed yield whereas plant height negatively correlated with seed yield. Similar trend was report by Kathiresan and Gnanamurthy (2002), where the number of capsules per plant contributed to significant positive correlation with seed yield. Similar to the present study, Ahadu (2012) reported that number of capsules per plant and number of branches per plant contributed significant positive correlation with seed yield. Fazal *et al.* (2011) reported that the number of capsules per plant exhibited significant positive correlation with seed yield. These showed that genotypes were providing higher number of capsule and branches are high yielders.

Bacterial blight severity showed negative and significant correlated genotypically with days to maturity, number of capsules per plant and biomass yield (Table 3). The result showed that effective selection for superior genotypes is possible by considering the traits viz. plant height, branches per plant, capsules per plant, biomass yield per hectare and harvest index. However, oil content showed insignificant genotypic correlation with all tested traits except days to flowering. Mohammed and Firew (2015) reported that oil content showed insignificant negative genotypic correlation with most of the yield components indicating that selection for high oil content would not bring change to seed yield of the plant.

Soundharya *et al.* (2017) reported that days to 50% flowering had significant positive association with days to maturity. Begum *et al.* (2017) reported that days to 50% flowering has significant positive association with days to maturity, which in turn has significant positive association with plant height. Number of branches per plant has significant positive association with number of capsules per plant. Generally, the study showed that most of the studied traits had positive and highly significant correlations with seed yield and to each other. This positive and significant associations among traits were due to the effect of genes that can be the result of strong coupling linkage between their genes or the result of pleiotropic genes that could control the traits within the same direction (Kearsey and Pooni, 1996).

So far again, from the study some traits were negative and significantly correlated as well as positive and negative non-significantly correlated among each other. Such associations may arise from different factors of gene action (additive or non-additive) and the other factors such as pleiotropy (Welsh, 2008). The negative correlation of traits might be because of different genes or pleiotropic gene that have dominance on the trait different directions (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.

Phenotypic path analysis

The phenotypic direct and indirect effect of different characters on seed yield is presented in Table 4. Biomass yield (0.717) had the highest positive phenotypic direct effect on seed yield followed by harvest index (0.603) and capsules per plant (0.027). These traits also had significant and positive phenotypic correlation with grain yield, showing that maximizing one of the above traits may directly contribute to yield of sesame. This implied that true relationship is mainly due to the additive gene effect and thus direct selection for seed yield through these traits will be effective. Yet, traits with negative indirect effect through biomass yield, harvest index and capsules per plant need to be managed during selection because the inclusion of these traits might have negative effect on yield of sesame. Similar results were reported by Mohammed *et al.* (2015), Gadisa *et al.* (2015) and Iqbal *et al.* (2016).

Plant height, branches per plant and thousand seed weight had negative direct effect on seed yield and positive correlation with seed yield, showing a positive correlation of these traits with seed yield were due to their considerable positive indirect effect via biomass yield, harvest index, capsules per plant, thousand seed weight and the severity of bacterial blight. The residual effect determines unaccounted variability of the dependent factor (seed yield). It′s magnitude 0.118 indicated that the traits included in the path analysis explained 88.2% of the variation in seed yield (Table 4). Supportive result was reported by Gnanasekaran *et al*. (2008) for plant height, branches per plant, capsules per plant and thousand seed weight. Mohammed *et al*. (2015) also reported similar result for branches per plant and thousand seed weight (g).

Genotypic path analysis

The genotypic direct and indirect effect of different traits on seed yield is presented in Table 5. The result of genotypic path analysis also revealed that biomass yield (0.689) had maximum positive direct effect on seed yield followed by harvest index (0.516) and capsules per plant (0.040). These traits also had significant and positive association with seed yield at genotypic level. Therefore, these traits can be considered as the principal traits while working towards seed yield improvement.

Negative direct effect was also observed for bacterial blight severity (-0.012) on seed yield and the trait had negative and significant association with seed yield. Similar results were reported by Muhammad *et al.* (2010) and Goudappagoudra *et al.* (2011) for the number of capsules per plant for biomass yield and harvest index. Plant height and branches per plant had negative and direct genotypic effect on seed yield with positive correlation. The positive correlation of these traits with seed yield were due to their considerable positive indirect effect via biomass yield, harvest index, capsules per plant and severity of the bacterial blight (Table 5).

Singh and Chaudhary (1985) explained that if direct effect value is almost equal to correlation coefficient, the direct selection for that particular trait will be effective. If correlation is positive but direct effect is negative or negligible, the character may be selected indirectly based on high indirect effects. Based on the above results, traits such as biomass yield, harvest index, capsule per plant and severity of bacterial blight will be used as direct selection with plant height and branches per plant used as indirect selection in sesame yield improvement programs.

Table 4. Estimates of direct (bold diagonal) and indirect (off diagonal) phenotypic effects of the traits on seed yield among 49 sesame genotypes evaluated at Bako and Uke in 2018 cropping season

Traits	PH	BPP	CPP	BY	HI	SW	SI	rp
PH	**-0.002**	-0.001	0.009	0.244	0.049	0.001	0.001	0.301**
BPP	-0.001	**-0.003**	0.019	0.345	0.161	-0.001	0.001	0.523**
CPP	-0.001	-0.002	**0.027**	0.409	0.244	-0.001	0.001	0.677**
BY	-0.001	-0.001	0.015	**0.717**	0.053	-0.001	0.002	0.784**
HI	0.000	-0.001	0.011	0.063	**0.603**	-0.001	0.001	0.676**
SW	0.000	0.000	0.005	0.100	0.093	**-0.006**	0.001	0.192**
SI	0.000	0.001	-0.009	-0.308	-0.135	0.001	**-0.004**	-0.454**

*Residual= 0.118; Key: ** indicates significant ($p<0.01$) probability level, respectively; PH = plant height (cm), BPP = number of branches per plant, CPP= number of capsules per plant, BY = biomass yield per hectare (kg ha^{-1}), HI = harvest index, SW= thousand seed weight (g), SI = bacterial blight severity (%) and r_p = phenotypic correlation coefficients (against seed yield)*

Therefore, selecting genotypes having high biomass yield, harvest index and capsules per plant and low bacterial blight severity could be used to improve seed yield of sesame genotypes as a result of their direct effect and plant height and branches per plant due to their indirect effect on yield. The residual (0.0905) indicates that traits which are included in the genotypic path analysis explained 91.95% of the total variations in seed yield (Table 5). Similar trends were reported in literatures (Mohammed and Firew, 2015; Saxena and Desawi et al., 2017).

Table 5. Estimates of direct (bold diagonal cells) and indirect (off diagonal) genotypic effects of the traits on seed yield among 49 sesame genotypes evaluated at Bako and Uke in the 2018 cropping season

Traits	PH	BPP	CPP	BY	HI	SI	r_g
PH	**-0.005**	-0.004	0.015	0.280	0.026	0.002	0.315*
BPP	-0.002	**-0.008**	0.031	0.437	0.209	0.003	0.669**
CPP	-0.002	-0.006	**0.040**	0.491	0.267	0.004	0.794**
BY	-0.002	-0.005	0.028	**0.689**	0.138	0.006	0.855**
HI	0.000	-0.003	0.021	0.185	**0.516**	0.003	0.721**
SI	0.001	0.002	-0.012	-0.365	-0.139	**-0.012**	-0.525**

*Residual= 0.0905, Key: *, ** indicates significant at 0.05 and 0.01 probability level, respectively. PH = Plant height (cm), BPP = Number of branches per plant, CPP= number of capsules per plant, BY=Biomass yield per hectare (kgha^{-1}), HI = Harvest index, SW= thousand seed weight (gm), SI = Bacterial blight severity (%) and r_g = genotypic correlation coefficients (against seed yield)*

CONCLUSIONS AND RECOMMENDATIONS

Yield related traits such as plant height, branches per plant, capsules per plant, biomass yield and harvest index showed positive and highly significant phenotypic and genotypic associations with seed yield. The result of path analysis showed that biomass yield, harvest index and capsules per plant had positive and high phenotypic and genotypic direct effect on seed yield, implying the suitability of these traits as parameters while working for sesame seed yield improvement.

CONFLICT OF INTEREST

The authors declare that there is no conflict of interest regarding the publication of this article.

REFERENCES

Ahadu M., 2012. Phenotypic variability, divergence analysis and heritability of characters in sesame (Sesamum indicum L.) genotypes. Nature and Science, 10(10):117-126. [Scholar Google]

Akram, S., Hussain, B. N., Al Bari, M. A., Burritt, D. J. and Hossain, M. A., 2016. Genetic variability and association analysis of soybean (Glycine max (l.) Merrill) for yield and yield attributing traits. Plant Gene and Trait, 7(13):1-1. [Scholar Google]

Ashri, A., 2007. Sesame (Sesamum indicum L.) In: Genetic Ressources, Chromosome Engineering and Crop Improvement, Singh, RJ (Ed.). Vol. 4. Oilseed crops. [Scholar Google]

Azeez, M. A. and Morakinyo, J. A., 2011. Path analysis of the relationships between single plant seed yield and some morphological traits in sesame (Genera Sesamum and Ceratotheca). Int. J. Plant Breed. Genet, 5:358-368. [Scholar Google]

Begum, T., Iqbal, A. and Dasgupta, T., 2017. Genetic variability and divergence among genotypes of sesame (Sesamum indicum L.). Bangladesh journal of botany, 46(3):955-962. [Scholar Google]

CSA (Central Statistical Agency). 2018. Agricultural Sample Survey for the 2017/2018 crop season .Volume I. Report on Area and Production of Major crops for Private Peasant Holdings (Meher Season). Statistical Bulletin 278. FDRE/CSA, Addis Ababa, Ethiopia.

Desawi H. T, Sentayehu A. K, and Daniel E. G, 2017. Assessment of genetic variability, genetic advance, correlation and path analysis for morphological traits in sesame genotypes. Asian Journal of Agricultural Research, 4(2): 34-44. [Scholar Google]

Dewey, D. R. and Lu, K., 1959. A Correlation and Path-Coefficient Analysis of Components of Crested Wheatgrass Seed Production

1. Agronomy journal, 51(9):515-518. [Scholar Google]

Fazal, A., Mustafa, H. S. B., Hasan, E. U., Anwar, M., Tahir, M. H. N. and Sadaqat, H. A., 2015. Interrelationship and path coefficient analysis among yield and yield related traits in sesame (Sesamum indicum L.). Nature and Science, 13(5):27-32. [Scholar Google]

Fuller, D. Q., 2003. Further evidence on the prehistory of sesame. Asian Agri-History, 7(2):127-137. [Scholar Google]

Gadisa, H., Negash, G. and Zerihun, J., 2015. Correlation and divergence analysis for phenotypic traits in sesame (Sesamum indicum L.) genotypes. Science, Technology and Arts Research Journal, 3(4):01-09. [Scholar Google]

Gnanasekaran, M., Jebaraj, S. and Muthuramu, S., 2008. Correlation and path co-efficient analysis in sesame (Sesamum indicum L.). Plant archives, 8(1):167-169. [Scholar Google]

Gomez, K. A., Gomez, K. A. and Gomez, A. A., 1984. Statistical procedures for agricultural research. John Wiley & Sons. [Scholar Google]

Goudappagoudra, R., Lokesha, R. and Ranganatha, A. R. G., 2011. Research Note Trait association and path coefficient analysis for yield and yield attributing traits in sesame (Sesamum indicum L.). Electronic Journal of Plant Breeding, 2(3):448-452. [Scholar Google]

Hartley, H. O., 1950. The maximum F-ratio as a short-cut test for heterogeneity of variance. Biometrical, 37(3/4):308-312. [Scholar Google]

Haruna, I. M., Aliyu, L., Olufajo, O. O. and Odion, E. C., 2012. Contributions of some growth characters to seed yield of sesame (Sesamum indicum L.). ISABB Journal of Food and Agricultural Sciences, 2(1):9-14. [Scholar Google]

IPGRI, N., 2004. Descriptors for sesame (Sesamum spp.). International Plant Genetic Resources Institute, Rome, Italy, National Bureau of Plant Genetic Resources, New Delhi, India. [Scholar Google]

Iqbal, A., Akhtar, R., Begum, T. and Dasgupta, T., 2016. Genetic estimates and diversity study in Sesame (Sesamum indicum L.). IOSR Journal of Agriculture and Veterinary Science, 9(8):01-05. [Scholar Google]

Iqbal, A., Bhattacharyya, U., Akhtar, R. and Dasgupta, T., 2018. Genetic diversity computation in sesame genotypes using morphological traits and genic SSR markers. Indian Journal of Genetics and Plant Breeding (The), 78(3):348-356. [Scholar Google]

Kathiresan, G. and P.Gnanamurthy, 2002. Studies on seed yield contributing characters in sesame. Sesame and Safflower News Letter 15:25-30. [Scholar Google]

Kearsey, M. J. and Pooni, H. S., 1996. The genetical analysis of quantitative traits. (Chapman and Hall: New York).275p. [Scholar Google]

Kumaresan D, Nadrajan N (2002). Association of yield with some biometrical and physiology characters over different environments in sesame (Sesamum indicum L.). Sesame and Safflower Newsletter 17: 13-16. [Scholar Google]

Mkamilo, G. S. and Bedigian, D., 2007. Sesamum indicum L. Vegetable Oils. Plant Resources of Tropical Africa, 14:153-158. [Scholar Google]

Mohammed A. and Firew M., 2015. Study on genetic divergence in low-altitude sesame (Sesamum indicum L.) germplasm of Ethiopia based on agro morphological traits. Journal of Advanced Studies in Agricultural, Biological and Environmental Sciences, 2(3):78-90. [Scholar Google]

Mohammed A., Firew M., Amsalu, A. and Mandefro, N., 2015. Genetic variability and association of traits in mid-altitude sesame (Sesamum indicum L.) germplasm of Ethiopia. American Journal of Experimental Agriculture, 9(3):1-14. [Scholar Google]

Morinaga, T., Fukushima, E., Kano, T., Maruyama, Y. and Yamasaki, Y., 1929. Chromosome numbers of cultivated plants II. Shokubutsugaku Zasshi, 43(515):589-594. [Scholar Google]

Pawar, K. N., Chetti, M. B. and Jahagirdar, S., 2002. Association between seed yield and yield attributing characters in sesamum (Sesamum indicum L.). Agricultural Science Digest, 22(1):18-20. [Scholar Google]

Saha, S., Begum, T. and Dasgupta, T., 2012. Analysis of genotypic diversity in sesame based on morphological and agronomic traits. In Conference on international research on food Security, natural resource management and rural development organised by Georg-August Universität Göttingen and University of Kassel-Witzenhausen, Germany during Sept. [Scholar Google]

SAS, 2012. Statistical analysis System. Version 9.3., SAS Institute Inc. Cary, NC., USA.

Saxena, K. and Bisen, R., 2016. Genetic variability, correlation and path analysis studies for yield and yield component traits in sesamum (Sesamum indicum L.). International Journal of Agriculture Sciences, 8(61):3487-3489. [Scholar Google]

Shabana, R., El-Mohsen, A. A., El-Haleem, A. A. and Saber, A. A., 2015. Validity of conventional and restricted selection indices in selecting promising lines of sesame. J. of Agri-Food and Applied Sci, 3(4):68-84. [Scholar Google]

Shekhawat, R. S., Meena, S. K. and Singh, B., 2013. Genetic divergence analysis in sesame. Indian Research Journal Genetics & Biotechnology, 5(2):105-110. [Scholar Google]

Singh, A., Bisen, R. and Tiwari, A., 2018. Genetic Variability and Character Association in Sesame (Sesamum indicum L.) Genotypes. International Journal of Current Microbiology and Applied Sciences 7(11): 2407 – 2415. [Scholar Google]

Singh R. K. and Chaudhary B. D., 1999. Biometrical Methods in Quantitative Genetics Analysis, Kalyani publishers, New Delhi.73p. [Scholar Google]

Singh, R. K., 1985. Biometrical methods in Quantitative Genetic Analysis. Kalyani Pub. Ludhiana. New Delhi, pp 318. [Scholar Google]

Soundharya, B., Hemalatha, V., Rani, T. S. and Edukondalu, B., 2017. Trait association and path coefficient analysis for yield and yield attributing traits in sesame (Sesamum indicum L.). Environment and Ecology, 35(4E):3617-3620.

Tadele A., 2005. Sesame (Sesamum indicum L.) Research in Ethiopia: A review of past work and potential and future prospects. Werer Agricultural Research Center. EIAR, Addis Ababa, Ethiopia. [Scholar Google]

Tesfaye W. M., 2015. "Broad sense heritability estimation, interrelationship and path coefficient analysis of yield and yield traits in Ethiopian mustard (Brassica carinata A. Braun) genotypes." Journal of Gene and Environmental Resources Conservation3 (1): 38-47. [Scholar Google]

Welsh, J. R., 2008. Fundamentals plant genetics and breeding. John Willey and Sons, Inc., New York. 290. [Scholar Google]

Wright, S., 1921. Correlations and causations. Journal of Agricultural Research 20:557- 587.

Yirga B. K., 2017.Correlation and cluster analysis of white seeded sesame (Sesamum indicum L.) genotypes oil yield in northern Ethiopia. African Journal of Agricultural Research.12 (12): 970-978. [Scholar Google]