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Correlation, Path coefficient and Principal Component Analysis of Some Indigenous and Exotic Sesame (sesamum indicum L.) Genotypes in Ethiopia

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The productivity of sesame in Ethiopia is below the world avergae mainly lack of high yielding improved variety. Understanding of association and chief contributors of characters becomes essential. Therefore, this study was conducted to assess the association and pricinpal characters among yield and 19 yield components. Hundered sesame genotypes were evaluated in 10x10 triple lattice design at Werer from 2017 to 2018. The combined analysis of variance revealed that genotypes differed significantly. Seed yield showed positive and significant correlation with length of capsule bearing zone, length of first capsule, capsule length, capsule per main axis, number of capsule per plan, harvest index and oil content. Path coefficient analysis revealed capsule per main axis, capsule per plant and harvest index had positive direct effect on yield. Principal component analysis showed that seven principal components have accounted 78.67% of the total variation. The present study showed that to increase sesame seed yield, the genotypes should possess more number of capsules per main axis, capsule per plant and high harvest index.This study suggested these characters are important yield contributing traits and selection based on these characters would be most effective in line with molecular markers assisted breeding should be considered in the future.

Key Words*: Oil crop, Sesame, Character, Correlation, Path coefficient and Principal Component.*

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INTRODUCTION

Sesame (*Sesamum indicum* L.) belongs to the genus *Sesamum* in the *Pedaliaceae* family (Ashri, 1998). It has two alternative centers of origin; Ethiopia and India (Bedigian 2015). There are about 36 species of sesame; the most cultivated one is S*esamum indicum (*Kobayashi, 1990*).* The cultivated species of sesame is diploid species with chromosome number of 2n=2x=26 (Morinaga *et al*., 1929). It is the most important oil crop successfully grown in tropical and sub-tropical climates (Daniel and Parzies, 2011; and Weiss, 1983). It is an excellent sources of vegetable oil and is designated as "queen of oil seeds" containing high oil content (44-58%) with 83-90% unsaturated fatty acids, (18-25%) proteins and (11-13%) carbohydrate. The oil has primary demand in the food industry because of its excellent cooking quality, flavor and stability. It is also a good source of lignans such as sesamin, sesamol and sesamolin with remarkable oxidation resistance and thereby a long shelf life (Nupur *et al*., 2010).

Globally, sesame is cultivated in more than 78 counties across all comfortable continents covering a total area of about 11.3 million hectares with a worldwide production of about 6.9 million metric tons. The world largest volume of sesame production is concentrated in India, Myanmar, Tanzania, Nigeria, Burkina Faso, China and Ethiopia; and contributing 51% of the world total sesame production. Similarly, sesame was grown by 29 countries in Africa on a total land of 6.8 million hectare with a total production of 3.4 million ton (FAOSTAT, 2017). The average productivity in Ethiopia is very low (0.793 $tonha^{-1}$) compared to the world average 2.0 $tonha^{-1}$. It is constrained by many factors like: indeterminate flowering nature, shattering of capsules at maturity, biotic and abiotic stresses (Geremew *et al.,* 2012).

Association studies are helpful in determining the components of complex characters. The practical value of selecting for a given character as a means of improving another depends on the extent to which improvement in major characters is assisted by selection for the indicators. Characters should be highly heritable, innately positive association physiologically related in a positive manner (Sidwell *et al*., 1967). Falconer (1989) and Rangaswamy (1995) suggested significant correlation coefficients among various characters may occur from pleotropic effects of genes or from linkage effects.

Path-coefficient analysis: Choice for yield should take into account all the significantly correlated characters in the positive direction. However, correlation coefficient does not give a complete picture of the relative direct and indirect influence of each component on seed yield is possible through the path coefficient analysis (Woldemariam, 1985). To improve grain yield via selection of its components path coefficient analysis is a convenient tool for thoughtful seed yield formation and provides valuable extra information about the characters (Garcia *et al*., 2003).

Principal component analysis (PCA) is one of the multivariate statistical procedures which is a powerful tool for examining and summarizing fundamental trends in complex data structures (Legendre and Legendre, 1998). PCA reflects the importance of the major contributor to the total variation at each alignment for differentiation (Sharma, 1998). The PCA generates three important products, the eigenvalues, eigenvectors and scores, the dominant modes representing the most important characteristics from the original data. According to Chahal and Gosal (2002) characters with largest absolute values closer to unity within the first principal component influence the clustering more than those with lower absolute values closer to zero.

Future production of sesame in Ethiopia is very promising due to its economic value and export potential. Eventhough there is a huge genetic potential of the crop as center of diversity; yield of sesame is very low. In order to initiate appropriate breeding procedure for crop improvement and developing genotypes with high productivity, information on association between yield and yield related characters is a pre requisite (Kumar *et al*., 2010). To increase sesame production and productivity in Ethiopia research efforts are aimed at supplying farmers with improved varieties. Under Ethiopian sesame improvement project, large numbers of sesame genotypes were introduced by FAO (Food and Agricultural Organization). Little is known about characters in these sesame genotypes. Hence, the present study was conducted with objectives of assessing correlation, path coefficient and principal component analysis of some genotypes among yield and yield related characters.

MATERIALS AND METHODS

Experimental Site: A field experiment was carried out at Werer Agricultural Research Center (WARC), Eastern part of Ethiopia about 280 km from Addis Ababa. The altitude of Werer is 740 meter above sea level.

Genetic Materials: Hundred sesame genotypes were randomly taken and considered in this study. The genetic material consists of one standard (Adi) and local check, 71 genotypes collected from major sesame growing regions of Ethiopia and 27 introduced genotypes from FAO presented in Appendix Table.1.

Experimental Design and Trial Management: The experiment was conducted from 2017 to 2018 in two cropping seasons and laid out in 10x10 triple lattice design with three replications. Each plot was 4m long, and 1.2m wide, which consisted of 3 rows with a spacing of 40cm between rows and 0.4m between plots. Sowing was done by hand drilling. Thinning was carried out after 21 days, and plant to plant distance was kept at 10cm.

Data Collected: Data were collected for each experimental unit by using IPGRI descriptor (IPGRI, 2004): days to flower initiation, days to 50% flowering, capsule filling period, days to maturity, 1000 seed weight (g), biomass yield per hectare (ton), harvest index (%), seed yield per hectare ($kgha^{-1}$), plant height (cm), length of capsule bearing zone (cm), length of first capsule (cm), capsule length (cm), capsule width (cm), capsule thickness (cm), number of primary branches per plant, number of capsules per main axis, number of capsules per plant, number of seed per capsule, oil content (%) and estimating the level of shattering resistance(%).

Data Analysis: All the data were subjected to analysis using SAS software 9.3 (SAS, 2014)
The combined analysis of variance (ANOVA) over two seasons was carried out using the model: $\mathrm{Pijks} = \mu + \mathrm{gi} + \mathrm{bk(j)(s)} + \mathrm{rj(s)} + \mathrm{Ss} + \mathrm{(gs)is} + \mathrm{eijks}$

Where, P_{ijks} = phenotypic value of i^{th} genotype under j^{th} replication at s^{th} season and k^{th} incomplete block within replication j and season s; μ= grand mean; g_i = the effect of i^{th} genotype; $b_{k(j)(s)}$ = the effect of incomplete blocks within replication j and season s; $r_{j(s)}$ = the effect of replication *j* within season s; S_s= the effect of season; $(gs)_{is}$ = the interaction effects between genotype and season; and e_{ijks} = the residual error.

Estimation of correlation coefficients: The correlation coefficients among all possible characters combinations at phenotypic (rp) and genotypic (rg) levels were estimated according to Miller *et al.* (1958) as follows:-
Phenotypic

$$\mathbf{covariance}\left(\boldsymbol{\sigma p_{xy}}\right) = \boldsymbol{\sigma g_{xy}} + \frac{\boldsymbol{\sigma_{e\,xy}}}{\mathbf{r}}$$

$$\text{Genotypic covariance } (\sigma g_{xy}) = \frac{\mathrm{MSPg - MSPe}}{\mathrm{r}},$$

Where, MSPe = mean square of cross product for error, MSPg = mean square of cross products for genotypes, σ^exy environmental covariance between x and y, and r = number of replications.
Phenotypic correlation (rp), the observable correlation between two variables, which includes both genotype and environmental components between two variables was estimated using the formula suggested by Johnson *et al.*(1955) and Singh and Chaudhury (1996) as follows:-

Phenotypic correlation coefficient **(**$\mathrm{rpxy}) = (\mathrm{pcovx.y})/(\sqrt{\sigma}^2\mathrm{px}.\sigma^2\mathrm{py})$,
Genotypic correlation coefficient$(\mathrm{rgxy}) = (\mathrm{gcovx.y})/(\sqrt{\sigma}^2\mathrm{gx}.\sigma^2\mathrm{gy})$
Where: rp_{xy} and rg_{xy} are phenotypic and genotypic correlation coefficients, respectively; pcov x.y and gcov x.y are phenotypic and genotypic covariance between variables x and y, respectively; σ^2px and σ^2gx are phenotypic and genotypic variances for variable x; and σ^2py and σ^2gy are phenotypic and genotypic variances for the variable y.

Path Coefficients Analysis: Path coefficient analysis was conducted as recommended by Wright (1921) and operated out by Dewey and Lu, (1959) using the phenotypic as well as genotypic correlation coefficients to governed the direct and indirect effects of yield components based on the following relationship: $\mathbf{rij} = \mathbf{Pij} + \mathbf{\Sigma rikpkj}$;
Where: rij=mutual association between the independent character (i) and dependent character (j) as measured by the correlation coefficient, Pij=component of the direct effects of the independent character (i) on the dependent variable (j) as measured by the path coefficient, Σrikpkj = Summation of components of indirect effect of a given independent character (i) on the given dependent character (j) by all other independent characters (k). Whereas, the contribution of the remaining unknown characters measured residual effect estimated as follows: Residual effect =$\sqrt{1-R^2}$;
Where:-R^2 = $\Sigma p_{ij}r_{ij}$, R^2 is the residual factor, P_{ij} is the direct effect of yield by i^{th} characters, and r_{ij} is the correlation of yield with the i^{th} characters.

Principal Component Analysis: Principal components (PCs) with Eigen value greater than 1.0 had been used as criteria to determine the number of PCs as suggested by Kaiser (1960). The general formula to compute the scores on the first component extracted in a principal component analysis is: **- $PC_1=b_{11}(X_1) +b_{12}+\ldots b_{1p}\ (X_p)$**
Where: PC1=the subject's score on principal component1 (the first component extracted); b1p=the regression coefficient (or weight) for observed variable p, as used in creating principal component1; Xp =the subject's score on observed variable p.

RESULT AND DISCUSSION

Combined analysis of variance across seasons for the different characters is presented in Table 1. Analysis of variance declare significance mean square due to genotype showed significant differences (P<0.01) for all the characters, indicating that presence of genotypic difference among the tested sesame genotypes. This finding is in line with the result of Gadisa *et al.* (2015) reported highly significant differences in 64 sesame populations for days to 50% flowering, days to maturity, plant height, capsule filling period, number of primary branches, number of branches per plant, number of capsules per plant, biological yield, seed yield, harvest index and thousand seed weight. The mean squares due to genotype x season interaction effects were highly significant (P<0.01) for all traits except capsule width and number of capsule per main axis. It indicates differential response of variety across testing environment.

Table 1. Mean squares of combined analysis of variance for 20 characters of 100 sesame genotypes evaluated in 2017 and 2018

Characters	MSG	MSGxseason	MS.Season	MS. error	CV(%)
DFI	20.104**	4.224**	337.500**	2.643	4.301
DF	51.060**	6.883**	4113.402**	2.711	3.826
$DCFP	25.156**	10.261**	165.375**	2.453	3.135
DM	309.912**	67.793**	20265.282**	26.059	4.855
PLH	1414.643**	486.548**	23826.602**	64.438	7.148
$LCBZ	58.412**	9.514**	3710.107**	3.099	3.609
LFC	0.089**	0.041**	0.002	0.027	6.716
CL	0.116**	0.041**	0.002	0.024	6.243
CW	0.007**	0.004	0.402**	0.003	7.206
CTK	0.004**	0.002**	0.002	0.001	6.928
#PBPP	0.074**	0.046**	0.954**	0.024	8.199
$CPMA	22.505**	3.830	1117.935**	3.243	6.680
$CPP	121.981**	24.303**	2009.340**	5.827	5.623
$SPC	31.235**	11.610**	58.907**	6.522	5.191
ISR	26.743**	1.824**	29.748**	0.548	16.434
BY	2.271**	1.202**	11.946**	0.253	9.801
$HI	39.622**	4.237**	581.544**	2.254	6.650
TSW	0.541**	0.086**	0.173**	0.031	5.198
OL	19.071**	4.675**	9.627*	2.102	2.876
YLD	227063.000**	30710.500**	188219.050**	9243.730	9.862

MS=mean square, G=genotypes, CV = coefficient of variation, *= ($p< 0.05$),**= ($p < 0.01$), DFI =days to flower initation, DF=days to 50% flowering, DCFP=days to capsule filing period, DM=days to physiologically maturity, PLH=plant height(cm), LCBZ=length of capsule filing zone(cm), LFC=length of first capsule(cm), CL=capsule length(cm), CW=capsule width (cm), CTK=capsule thickness (cm), PBPP=primary branch per plant, CPMA=capsule per main axis, CPP=capsule per plant, SPC=seed per capsule, ISR=percent of shattering resistance (%),BY=biomass yield per hectare (ton), HI=harvest index (%), TSW=1000 seed weight (g), OL=oil content (%) and YLD=yield $kgha^{-1}$; $=arcsine transformed data and, # = square root transformed data.

Correlation Coefficient Analysis

Phenotypic correlation coefficient of seed yield with other characters: Phenotypic(rp) correlation estimates between the various characters are presented above diagonal in Table 2. Seed yield showed positive and significant phenotypic association with length of capsule bearing zone, length of first capsule, capsule length, number of capsule per main axis, number of capsule per plant, harvest index, 1000 seed weight and oil content. This signifies that the improvement of one character will simultaneously improve the other. Fazal et al. (2011) reported that number of capsules per plant had significant positive correlation with seed yield. Furthermore, Prithvras et al. (2015) reported that seed yield had positively and significantly associated with number of

Table 2. Phenotypic (**above diagonal**) and genotypic (**below diagonal)** correlation coefficient for studied quantitative traits studied

Traits	DFI	DF	MD	LCBZ	LFC	CL	CPMA	CPP	ISR	BY	HI	TSW	OL	YLD
DFI	1	0.80**	0.62**	0.01	-0.15	-0.16	-0.19	-0.11	0.23**	0.35 **	-0.43**	-0.36**	-0.16	-0.24*
DF	0.87**	1	0.81**	0.07	-0.12	-0.12	-0.16**	-0.13	0.31**	0.49**	-0.58**	-0.41**	-0.12*	-0.28**
MD	0.75**	0.89**	1	0.18	-0.13	-0.11	-0.06	-0.06	0.29**	0.19	-0.27**	0.05	-0.08	-0.25**
LCBZ	0.03	0.09	0.19	1	0.32**	0.35*	0.59**	0.41**	-0.11	0.44**	-0.54**	-0.24**	-0.13	0.27**
LFC	-0.2	-0.15	-0.15	0.36**	1	0.77**	0.41**	0.24**	-0.19	0.53**	-0.42**	-0.22**	0.09	0.24*
CL	-0.2	-0.14	-0.14	0.36**	0.88**	1	0.43**	0.18	-0.20**	0.27*	0.06	0.04	0.35**	0.23*
CPMA	-0.17	-0.15	-0.09	0.63**	0.45**	0.44**	1	0.72**	-0.22**	0.01	0.09	-0.01	0.35**	0.49**
CPP	-0.11	-0.13	-0.06	0.42**	0.23*	0.15	0.77**	1	0.11	-0.01	0.11	0.03	0.34**	0.49**
ISR	0.26**	0.33**	0.32**	-0.12	-0.25*	-0.24*	-0.28**	-0.23*	1	0.01	0.03	0.20*	-0.12*	-0.22**
BY	0.44**	0.56**	0.52**	0.31**	0.04	-0.01	0.12	0.13	0.15	1	0.03	0.05	0.10	-0.15*
HI	-0.49**	-0.62**	-0.63**	0.05	0.06	0.08	0.28**	0.31**	-0.23*	-0.37**	1	0.07	-0.06	0.57**
TSW	-0.39**	-0.43**	-0.33**	-0.01	-0.06	0.01	-0.1	-0.12	0.01	-0.28**	0.58**	1	0.37**	0.21*
OL	-0.15	-0.12	-0.16	0.36**	0.41**	0.37**	0.41**	0.24*	-0.35**	0.13	0.18	-0.09	1	0.23*
YLD	-0.24*	-0.28**	-0.28**	0.25*	0.26**	0.24*	0.51**	0.50**	-0.24*	-0.18	0.60**	0.19	0.22*	1

*=Significant at p≤0.05,**highly significant at p≤0.01,DFI=days to flower initation, DF=days to 50% flowering, DM=days to physiologically mature, LCBZ=length of capsule filing zone(cm), LFC=length of first capsule(cm),CL=capsule length(cm),CPMA=capsule per main axis, CPP=capsule per plant, ISR=percent of shattering resistance(%),BY=biomass yield per hectare(ton),HI=harvest index(%),TSW=1000seed weight(g),OL=oil content(%) and YLD=yield kgha^{-1}

capsule per main stem, number of capsule per plant, capsule length, 1000 seed weight and oil content. On the other hand, seed yield showed negative and significant phenotypic correlation with date of flower initiation, date of 50 % flowering, date of maturity and percent of shattering resistance; which implies separate improvement among traits.

Genotypic correlation coefficient of seed yiel d with other characters: Genotypic (rg) correlation estimates between the various characters are presented below diagonal in Table 2. Seed yield showed positive and significant genotypic association with length of capsule bearing zone, length of first capsule, capsule length, numbers of capsule per main axis, number of capsule per plant, harvest index and oil content, indicating the existence of pleiotropic as one of the genetic causes for correlation. The positive and significant correlation between seed yield characters signified that the improvement of one trait will simultaneously improve the other. This finding is similar with the result of Prithvras *et al.* (2015) who reported that seed yield had positive and significant relationship with number of capsule per main stem, number of capsule per plant, capsule length and oil content at genotypic level. On the other hand, seed yield showed negative and significant genotypic correlation with date of flower initiation, date of 50% flowering, date of maturity and percent of

Table 3. Phenotypic path coefficient analysis indicating the direct (**diagonal**) and indirect (off diagonal) effect of the characters

YLD	DFF	DF	MD	LCBZ	LFC	CL	CPMA	CPP	ISR	BY	HI	TSW	OL	rp
DFI	**-0.076**	0.170	-0.017	0.000	-0.011	0.000	-0.031	-0.024	-0.009	-0.037	-0.209	0.001	0.002	-0.24*
DF	-0.061	**0.213**	-0.022	0.003	-0.009	0.000	-0.027	-0.028	-0.012	-0.052	-0.284	0.001	0.001	-0.28**
MD	-0.047	0.171	**-0.027**	0.008	-0.009	0.000	-0.010	-0.012	-0.011	-0.047	-0.266	0.000	0.001	-0.25**
LCBZ	-0.001	0.015	-0.005	**0.047**	0.023	-0.001	0.098	0.089	0.004	-0.028	0.028	0.000	-0.004	0.27**
LFC	0.011	-0.025	0.003	0.015	**0.073**	-0.002	0.068	0.051	0.007	-0.001	0.046	0.000	-0.003	0.24*
CL	0.012	-0.026	0.003	0.016	0.056	**-0.003**	0.071	0.039	0.007	0.001	0.052	0.000	-0.003	0.23*
CPMA	0.014	-0.034	0.002	0.028	0.030	-0.001	**0.166**	0.155	0.009	-0.011	0.135	0.000	-0.004	0.49**
CPP	0.008	-0.027	0.001	0.019	0.017	0.000	0.119	**0.216**	0.008	-0.012	0.144	0.000	-0.002	0.49**
ISR	-0.017	0.065	-0.008	-0.005	-0.014	0.001	-0.040	-0.047	**-0.038**	-0.015	-0.104	0.000	0.003	-0.22*
BY	-0.026	0.104	-0.012	0.012	0.001	0.000	0.017	0.025	-0.005	**-0.106**	-0.155	0.000	-0.001	-0.15*
HI	0.032	-0.123	0.015	0.003	0.007	0.000	0.046	0.064	0.008	0.034	**0.491**	-0.001	-0.002	0.57**
TSW	0.027	-0.087	0.007	0.002	-0.001	0.000	-0.006	-0.018	0.000	0.023	0.268	**-0.001**	0.000	0.21*
OL	0.012	-0.025	0.003	0.016	0.025	-0.001	0.062	0.049	0.011	-0.011	0.095	0.000	**-0.010**	0.23*

Residual=0.717, *=significant at $p \leq 0.05$, ** highly significant at $p \leq 0.01$, DFI=days to flower initation, DF=days to 50 % flowering, DM=days to physiologically mature, LCBZ=length of capsule filing zone(cm), LFC=length of first capsule(cm), CL=capsule length (cm), CPMA=capsule per main axis, CPP=capsule per plant, ISR=% inverted shattering resistance (%),BY=biomass yield per hectare (ton), HI=harvest index (%), TSW=1000 seed weight (g), OL=oil content (%), YLD=yield $kgha^{-1}$ and rp = phenotypic correlation value

shattering resistance.

This indicates that the improvements of one character leads to decrease the other, as a result independent improvement of the character must be followed.

Path Coefficient Analysis

Phenotypic path coefficient analysis: Characters that showed significant correlation with yield ($kgha^{-1}$) were advanced to path coefficient analysis at phenotypic levels. Phenotypic path coefficient analysis between yield and yield related characters is presented in Table 3.

Harvest index had the highest direct (0.49) on seed yield with positive and highly significant association (0.57**). The magnitude of the direct effect was almost equivalent to that of phenotypic correlation coefficient. This justifies that the correlation explains the true association and direct selection through harvest index would be effective in improving seed yield of sesame.

Biomass yield had negative direct effect on seed yield with negative and significant association. The indirect effects through other characters were negligible. Therefore, the phenotypic correlation with seed yield was largely due to the direct effects.

Table 4. Genotypic Path coefficient analysis indicating the direct (**diagonal**) and indirect (off diagonal) effect of the characters

YLD	DFI	DF	MD	LCBZ	LFC	CL	CPMA	CPP	ISR	HI	OL	rg
DFI	**-0.090**	0.237	-0.016	-0.001	-0.029	0.004	-0.037	-0.018	-0.014	-0.289	0.009	-0.24*
DF	-0.078	**0.272**	-0.019	-0.003	-0.022	0.003	-0.033	-0.022	-0.018	-0.368	0.007	-0.28**
MD	-0.067	0.242	**-0.022**	-0.006	-0.022	0.003	-0.019	-0.010	-0.018	-0.371	0.009	-0.28**
LCBZ	-0.003	0.024	-0.004	**-0.030**	0.053	-0.008	0.138	0.068	0.006	0.027	-0.021	0.25*
LFC	0.018	-0.041	0.003	-0.011	**0.148**	-0.019	0.098	0.037	0.014	0.036	-0.024	0.26**
CL	0.018	-0.038	0.003	-0.011	0.130	-**0.022**	0.095	0.025	0.013	0.047	-0.022	0.24*
CPMA	0.015	-0.041	0.002	-0.019	0.066	-0.009	**0.218**	0.125	0.015	0.163	-0.024	0.51**
CPP	0.010	-0.037	0.001	-0.012	0.034	-0.003	0.168	**0.162**	0.013	0.181	-0.014	0.50**
ISR	-0.024	0.089	-0.007	0.003	-0.037	0.005	-0.061	-0.038	**-0.055**	-0.137	0.020	-0.24*
HI	0.044	-0.169	0.014	-0.001	0.009	-0.002	0.060	0.049	0.013	**0.593**	-0.010	0.60**
OL	0.014	-0.031	0.003	-0.011	0.061	-0.008	0.089	0.039	0.019	0.104	**-0.058**	0.22*

Residual=0.688, *= significant at $p \leq 0.05$, ** highly significant at $p \leq 0.01$, DFI=days to flower initation, DF= days to 50 % flowering, DM=days to physiologically mature, LCBZ=length of capsule filing zone (cm), LFC=length of first capsule (cm), CL=capsule length (cm), CPMA=capsule per main axis, CPP=capsule per plant, ISR=percent of inverted shattering resistance (%), HI=harvest index(%), OL=oil content (%),YLD=yield $kgha^{-1}$ and rg = genotypic correlation value

Capsule per plant and capsule per main axis had positive direct effects. The phenotypic correlations they had with seed yield were significant and positive. Their indirect effect via other traits was mostly positive and negligible. Hence, their positive correlation with seed yield was mainly due to their direct effect. Days to 50% flowering positive direct effects; however, the phenotypic correlation of days to 50% flowering was negative and significant; while the indirect effect of via other characters negligible. The path analysis revealed the residual value of 0.717 which means the characters in the path analysis expressed the variability in seed yield by 28.3%.

Genotypic path coefficient analysis: Characters that showed significant correlation with yield ($kgha^{-1}$) were advanced to path coefficient analysis at genotypic level. Genotypic path coefficient analysis between yield and yield related characters are given in Table 4.

Harvest index had a positive direct effect (0.59) on seed yield which was almost equivalent to the correlation coefficient (0.60**).This suggests the true relationship and direct selection through this character will be effective.

Capsule per main axis, capsule per plant and length of first capsule had positive direct effects. The genotypic correlations they had with seed yield were significant and positive. Their indirect effects via other characters were mostly positive and negligible. Hence, their positive correlation with seed yield was mainly due to their direct effect. This finding is similar with Mohammed *et al.* (2015) who reported that number of capsules per plant had maximum positive direct effect on

Table 5. Eigen vector and Eigen value of the first seven principal components (PCs) for 20 characters of 100 sesame genotypes

Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Date of flower initiation	**0.881**	0.044	-0.268	-0.022	0.091	-0.075	-0.168
Date of 50% flowering	**0.553**	0.073	**0.589**	0.211	-0.252	-0.113	0.098
Date of capsule filing period	**0.940**	0.038	0.102	0.109	-0.073	-0.098	-0.056
Maturity date	**0.817**	**0.348**	0.018	0.120	-0.098	-0.007	-0.174
Plant height(cm)	0.272	**0.751**	0.299	0.041	-0.116	0.043	-0.202
Length of capsule b/ng zone(cm)	-0.278	**0.785**	-0.008	-0.018	**-0.326**	0.081	0.106
Lengthof1stcapsule(cm)	-0.206	**0.789**	0.068	-0.148	-0.272	0.006	0.216
Capsule length(cm)	**0.418**	-0.035	**0.599**	0.202	**0.310**	0.073	0.288
Capsule width(cm)	**0.341**	**0.430**	**0.554**	0.036	**0.412**	0.019	-0.054
Capsule thickness(cm)	-0.032	-0.164	-0.232	**0.672**	-0.040	**0.368**	**-0.314**
Primary branch per plant	-0.211	**0.773**	-0.112	**0.312**	0.101	-0.268	0.021
Capsule per main axis	**-0.348**	**0.455**	-0.275	**0.606**	0.150	-0.152	0.020
Capsule per plant	0.032	0.271	**-0.339**	-0.037	-0.021	**0.630**	0.461
Number of seed per capsule	**0.428**	-0.254	0.047	0.218	**-0.563**	0.170	0.178
% of Inverted Shattering resistance	**0.529**	**0.370**	**-0.318**	0.037	0.100	0.354	-0.152
Biomass yield per hectare(ton)	**-0.819**	-0.083	0.128	0.253	0.198	0.125	-0.143
Harvest index (%)	-0.285	-0.298	**0.604**	0.294	0.034	**0.408**	-0.064
100seedweight(g)	-0.162	**0.593**	0.063	**-0.423**	**0.375**	0.262	-0.103
Oil content (%)	**-0.591**	0.268	-0.034	0.185	-0.238	-0.141	-0.229
Yield(kgha^{-1})	0.258	-0.036	**-0.332**	**0.401**	**0.313**	-0.226	**0.530**
Eigen value:-	5.460	3.746	2.252	1.629	1.262	1.153	1.019
% of total variance	26.000	17.840	10.730	7.760	6.010	5.490	4.850
% of Cumulative variance	26.000	43.840	54.560	62.320	68.330	73.820	**78.670**

seed yield followed by harvest index. The genotypic path coefficient analysis exhibited the residual value of 0.688, indicating that the characters in the path analysis expressed the variability in seed yield by 31.20%, the remaining 68.8% of the contribution of other characters are not considered in the path analysis and environmental factor.

Principal Component Analysis:

The first seven principal components with Eigen values greater than one accounted for 78.67% of the total variation in Table 5 above. The first principal component (PC1) accounted for 26.00 % of the variability and the other major attributing characters include date of flower initiation, date of 50% flowering, date of capsule filling period, maturity date, capsule length, capsule width, capsule per main axis, seed per capsule, shattering resistance, biomass yield per hectare and oil content. Likewise, 17.84% of the total variability among genotypes accounted for the second principal component analysis originated maturity date, plant height, length of capsule bearing zone, length of first capsule, capsule width, primary branch per plant, capsule per main axis, shattering resistance and 1000 seed weight. Similarly, the third principal component (PC3) which accounted for 10.73% of the total variability among genotypes was attributed to discriminatory traits like date of 50% flowering, capsule length, capsule width, capsule per plant, shattering resistance, harvest index and seed yield.

The fourth principal component (PC4) accounted for 7.76% of the total variation for capsule thickness, primary branch; capsule per main axis, 1000 seed weight and seed yield were the main contributing characters. The fifth principal component (PC5) accounted for 6.01% of the variability among genotypes and contributed by length of capsule bearing zone, capsule length, capsule width, seed per capsule, 1000 seed weight and seed yield; the sixth principal component (PC6) explained 5.49% of the total variability with capsule thickness, capsule per plant, percentage of shattering resistance and harvest index were the main contributor to PC6. In the same way, seventh principal components (PC7) mainly originated from capsule thickness, number of capsule per plant and seed yield accounted for 4.85%. Principal component analysis indicated the existence of variation in the studied genotypes. This suggests opportunities for genetic improvement through selection directly from the accessions and/or selection of diverse parents for hybridization program and conservation of genotypes for future utilization. Fazal *et al*. (2011) stated that the four principal components (PCs) described about 63.63% of the total variation among 105 accessions of sesame.

SUMMARY AND CONCLUSION

The progress of crop improvement program depends on the choice of material, association existing and information of quantitative characters with yield and among themselves. One hundred sesame genotypes were evaluated with the objective of assessing associations and chief contributors of characters. Seed yield had positive and significant phenotypic and genotypic associations with length of capsule bearing zone, length of first capsule, capsule length, number of capsule per main axis, number of capsule per plant, harvest index and oil content. By selecting for these characters, there is a possibility to increase seed yield of sesame. Harvest index, capsule per plant and capsule per main axis had the highest positive direct effect on seed yield. Principal component analysis of the characters showed that the first seven principal components with Eigen values greater than one accounted for 78.67% of the total variation, indicating that there is genetic variation in the studied genotypes. Harvest index, capsule per plant and capsule per main axis as they showed positive correlation coefficient and maximum positive direct effect on seed yield. These will be useful characters for direct selection to increase seed yield in sesame.

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Appendix Table .1. Description of genetic materials

No	Name of genotypes	Origin	Seed source	No	Name of genotypes	Origin	Seed source
1	Acc- 00019	ET	WARC	51	EW - 020 (1)-sel-2	ET	WARC
2	Acc- 00065	ET	WARC	52	G - 03 – 1	ET	WARC
3	Acc - 024 - sel- 1	ET	WARC	53	Hihir Baker sel- 1	ET	WARC
4	Acc - 024 sel- 3	ET	WARC	54	Hirhir Adi Gosh sel-4	ET	WARC
5	Acc- 044-sel-1	ET	WARC	55	Hirhir humera sel- 6	ET	WARC
6	Acc - 111 - 848 – 1	ET	WARC	56	Hirhir Kebebew early sel-1	ET	WARC
7	Acc - 202 – 363	ET	WARC	57	K-74 X C_{22} (71-2)-3	ET	WARC
8	Acc - 202 - 374 – 2	ET	WARC	58	M - 80 # 402 – 2	ET	WARC
9	Acc - 203 – 187	ET	WARC	59	NN – 0021	ET	WARC
10	Acc - 205 – 180	ET	WARC	60	NN - 0029 (2)	ET	WARC
11	Acc - 205 – 344	ET	WARC	61	NN - 0036 – 1	ET	WARC
12	Acc - 205 - 374 – 1	ET	WARC	62	NN – 0052	ET	WARC
13	Acc - 205 - 374 – 2	ET	WARC	63	NN – 0054	ET	WARC
14	Acc - 211 – 015	ET	WARC	64	NN - 0068 - 2	ET	WARC
15	Acc - BG – 001	ET	WARC	65	NN - 0108 – 2	ET	WARC
16	Acc - BG - 001(3)	ET	WARC	66	NN - 0129-2	ET	WARC
17	Acc - BG – 003	ET	WARC	67	NN - 0183 – 3	ET	WARC
18	Acc - BG – 009	ET	WARC	68	NN - 088 – 2	ET	WARC
19	Acc - EW – 006	ET	WARC	69	Tejahir-2Late ginwuha-sel-1	ET	WARC
20	Acc - EW - 009(5)	ET	WARC	70	Tejareb-2 Late gindwuha	ET	WARC
21	Acc - EW - 011(1)	ET	WARC	71	W – 118	ET	WARC
22	Acc - EW - 012 (7)	ET	WARC	72	Acc - 203 - 336 – 2	FAO	WARC
23	Acc - EW - 017(6)	ET	WARC	73	Acc - 203 - 336 - 4	FAO	WARC
24	Acc - EW - 025(1)	ET	WARC	74	Acc - 203 – 612	FAO	WARC

Table.1. (*Continue*)

No	Name of genotypes	Origin	Seed source	No	Name of genotypes	Origin	Seed source
25	Acc - GA - 005(1)	ET	WARC	75	Acc - 203 - 623-sel-1	FAO	WARC
26	Acc - No – 024	ET	WARC	76	Acc - 203 – 630	FAO	WARC
27	Acc - No – 044	ET	WARC	77	Acc - 210 - 986 – 1	FAO	WARC
28	Acc - No – 045	ET	WARC	78	Acc - 210 - 991 – 4	FAO	WARC
29	Acc - No – 049	ET	WARC	79	BAR – 0004	FAO	WARC
30	Acc - No – 05	ET	WARC	80	BAR – 002	FAO	WARC
31	Acc - No 04 + 06 + 07	ET	WARC	81	Bering bowng	FAO	WARC
32	Acc - NS - 007(2)	ET	WARC	82	China FAO (ACC-68-542)	FAO	WARC
33	Acc - WW - 001 (4)	ET	WARC	83	Clusu - Acc- 2	FAO	WARC
34	Acc - WW - 001(6)	ET	WARC	84	HB - 22 - FAM (1- 4)	FAO	WARC
35	Acc - WW - 003(4)	ET	WARC	85	HB - 38 FAM - 2 BAR Grey	FAO	WARC
36	Acc # 033	ET	WARC	86	HB - 49 FAM - 2 – 2	FAO	WARC
37	Acc -111- 524 – 1	ET	WARC	87	JAPAN-651	FAO	WARC
38	Acc -111- 821	ET	WARC	88	SPS - SIK - # 811	FAO	WARC
39	AW – 001	ET	WARC	89	SSBS - (9 - 2) -3	FAO	WARC
40	AW – 007	ET	WARC	90	Tmax	FAO	WARC
41	BACKO-MW-42	ET	WARC	91	Unknown - sel- 3	FAO	WARC
42	Banja Gobate sel- 4	ET	WARC	92	Unknown Nguara sel-9	FAO	WARC
43	BCS - 001 (1)	ET	WARC	93	Unkown Kaja sel- 4	FAO	WARC
44	BCS – 033	ET	WARC	94	USR - 82 # 171 NS	FAO	WARC
45	Bounja – filwuha sel- 2	ET	WARC	95	Venezuela – 1	FAO	WARC
46	Bounja – filwuha sel- 6	ET	WARC	96	Win black (Tall) – 2	FAO	WARC
47	Bounja – filwuha sel- 8	ET	WARC	97	X - 30/40 # 403	FAO	WARC
48	Bounja - fiyel kolet sel- 4	ET	WARC	98	Ying White – 2	FAO	WARC
49	EW - 017(1)	ET	WARC	99	Local check	Check	WARC
50	EW - 017(5) x NS - 001 # 48	ET	WARC	100	Adi	Check	WARC

WARC=Werer Agricultural Research center, ET=Ethiopia collection; FAO=Food and Agricultural Organization

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