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Assessment of Genetic Variability, Genetic Advance, Correlation and Path Analysis for Morphological Traits in Sesame Genotypes

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ABSTRACT

Sixty four sesame genotypes were evaluated in 8×8 simple lattice design at Dansha, in Western Tigray, in 2013/14. The objectives of the study were to estimate the extent of genetic variability and association between yield and related traits. Analysis of variance revealed that there was highly significant ($p<0.01$) difference among the sixty four genotypes for all the fourteen characters studied. Number of capsule per plant and seed yield per ha recorded high Genotypic Coefficients of Variation (GCV) and Phenotypic Coefficients of Variation (PCV). The highest heritability value was for days to 50% flowering. Traits like, number of capsule per plant and seed yield per ha had high Phenotypic Coefficients of Variation (PCV), Genotypic Coefficients of Variation (GCV), moderately high heritability (h^2) and genetic advance as a percentage of mean (GAM). This indicates that these characters can be improved through selection than heritability estimates alone. Number of primary branches per plant showed positive significant phenotypic and genotypic correlation with grain yield. Genotypically, path coefficient analysis based on grain yield as a dependent variable revealed that plant height and number of primary branches per plant exerted positive direct effect on seed yield. These characters had also positive and significant correlation with seed yield and this indicates true relationship between these traits and see yield. Therefore, emphasis should be given for these characters of sesame improvement program in future.

Key words: Genetic variability, heritability, correlation, path coefficient, *Sesamum indicum*

INTRODUCTION

Sesame (*Sesamum indicum* L.) is probably the most ancient oilseed known and used by man (Weiss, 1983). The cultivated sesame belongs to order Tubiflorae, family Pedaliaceae. About 36 species have been described in to the genus *Sesamum* but only *Sesamum indicum* has been recognized as a cultivated species (Alemawu *et al*., 1998). Even though the origin of sesame is still in debate (Mehra, 1967; Mahajan *et al*., 2007), Ethiopia considered as the origin of cultivated sesame. Bedigian (1981) argues that, owing to the wide genetic diversity in East Africa (Ethiopia), it is reasonable to assume that this subcontinent is the primary center of origin and India would then be thought of as a secondary center for sesame. Sesame seed, also known as sesamum, gingelly, benniseed, sim-sim and til is an important annual oilseed crop. It has been cultivated for centuries, particularly in Asia and Africa, for its high content of edible oil and protein (Johnson *et al*., 1979; Weiss, 1983). Ethiopia ranks sixth in the world in sesame production (181376 mt) (FAO, 2010) but its yield is quite low (757 kg ha^{-1}) (CSA, 2013) as compared to the crop genetic potential which is 200 kg ha^{-1} under research (Wijnands *et al*., 2009). For any

crop improvement program, nature and magnitude of genetic variability is essential. Findings depending on the nature and magnitude of genetic variability have of vital value for planning efficient breeding program to improve the yield potential of genotypes. Information on the association of plant characters with seed yield is of great important to breeder in selecting desirable genotypes.

Spandana *et al.* (2011) reported high PCV and GCV values for number of primary branches and seed yield per ha. Similarly, Gidey *et al.* (2012) reported high PCV and GCV values for height to first capsule, number of primary branches, number of seeds per capsule and seed yield per ha, for days to 50% flowering and capsule filling period. Siva *et al.* (2013) reported high GCV values for number of primary branch per plant.

According to Gidey *et al.* (2012), high heritability values for days to 50% flowering, height to first capsule and number of capsule per plant at Humera and days to 50% flowering, height to first capsule and plant height at Dansha was reported. Similar result was reported by Siva *et al.* (2013) as high heritability values for number of capsule per plant.

Menzir (2008) reported that number of capsules per plant and number of primary branches per plant contributed significant positive correlation with seed. Akbar *et al.* (2011) reported that number of capsules per plant contributed significant positive correlation with seed yield. According to Menzir (2008), number of capsule per plant, 1000 seed weight and oil content which had positive direct effect on seed yield. Days to 50% flowering, capsule filling period, plant height and capsule length had showed negative direct effect on seed yield. Contrast result was reported by Gidey *et al.* (2012) for days to maturity, height to first capsule and oil content which had negative direct effect on seed yield. The objective of the present study was to assess genetic variability for yield and related traits and to estimate the extent of correlation between pairs of characters at phenotypic and genotypic levels and thereby compare the direct and indirect effects of the characters on yield.

MATERIALS AND METHODS

Experimental sites: The experiment was conducted at Kebabo site Tasegese wereda of the Western low land part of Tigray Region, Ethiopia during 2013 cropping season. The location receives low annual rain full. Moreover, poor distribution of the rain fall coupled with high temperature. It is located at geographical coordinates at 25°12'18" N latitude and 15°10 23" 'E longitude. The mean annual temperature is 28°C and it has vertisol soil type. Average annual rain fall varies from 850-1400 mm (HAM, 2013).

Experimental materials: A total of sixty four different sesame germplasm accessions, that include one local check and two standard checks, were the testing materials of the study. The germplasm accessions represent the northern collections and that are maintained at Institute of Biodiversity Conservation. The details of the germplasm accessions are given in Table 1.

Experimental design: The trial was laid out using 8×8 simple lattice design. Each germplasm accessions will be planted in a plot size of 6.4 m^2 (4 rows, 4 m row length, 40 cm between rows and 10 cm between plants within row and spacing of 1,1.5 m between plots and blocks, respectively) (Gidey *et al.*, 2012).

Data collection: Data was collected either on plot basis or from randomly taken 10 plants on days to 5 0% flowering, days to maturity, capsule filling period, plant height (cm), height to first capsule (cm), length of capsule bearing zone (cm), number of capsules per plant,

Table 1: Sesame accessions used in the study

Accession	Location	Region	Accession	Location	Region
Endelemikiram sel-2	Metema	Amara	NN-0143	Shewa Robit	Amara
Bounja filwuha sel-2	Metema	Amara	NN-0145	Shewa Robit	Amara
Bounja sel-2	Metema	Amara	NN-0144	Shewa Robit	Amara
Gojam azene yohanis sel-1	Metema	Amara	NN-0128	Shewa Robit	Amara
Bounja maksegnit	Metema	Amara	NN-0136 sel-2	Shewa Robit	Amara
Bounja gobate sel-3	Metema	Amara	NN-0088	Shewa Robit	Amara
Gojam azene yohanis sel-6	Metema	Amara	NN-0084	Shewa Robit	Amara
Bounja filwuha sel-6	Metema	Amara	Acc-#031	Humera	Tigray
Gobyo (83)	Metema	Amara	Acc-22-12	Humera	Tigray
Gojam azene yohanis sel-2	Metema	Amara	Acc-031 sel-1	Humera	Tigray
Bounja maksegnit sel-5	Metema	Amara	Acc-202-516	Humera	Tigray
Bounja fiyel kolet sel-4	Metema	Amara	Acc-#032	Humera	Tigray
Gobyo 82-3	Metema	Amara	Acc-111-323	Humera	Tigray
Gobyo 82-2	Metema	Amara	Acc-00053	Humera	Tigray
Bounja fiyel kolet	Metema	Amara	Acc-No-024	Humera	Tigray
7B	Gonder	Amara	Acc-202-950	Wello	Amara
G-01	Gonder	Amara	Acc-111-524-1	Gojam	Amara
Abuna	Humera	Tigray	Acc-#226	Wello	Amara
Un known alamata sel-3	Wello	Amara	Acc-202-327	Wello	Amara
G-02	Gonder	Amara	Acc-020	Wello	Amara
NN-0097	Shewa Robit	Amara	Acc-044	Gojam	Amara
NN-0089	Shewa Robit	Amara	Acc-203-104	Gojam	Amara
Acc-111-866	Humera	Tigray	Acc-210-989 sel-1	Humera	Tigray
Acc-00026	Humera	Tigray	Acc-051-02 sel-2	Humera	Tigray
Acc-111-840	Humera	Tigray	Acc-No- 026	Humera	Tigray
Acc-00048	Humera	Tigray	Acc-038-sel-2	Metema	Amara
Acc-08	Humera	Tigray	Acc-200-495	Humera	Tigray
Acc-203-103	Humera	Tigray	Acc-202-307	Metema	Amara
Acc-016 sel-1	Humera	Tigray	Acc-208-950	Humera	Tigray
Acc-051-02 sel-5	Humera	Tigray	Setit-1	Cultivars	
Acc-00029	Humera	Tigray	Humera-1	Cultivars	
Acc-036	Humera	Tigray	Hirhir	Cultivars	

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number of primary branches per plant, internodes length (cm), capsule length (cm), number of seeds per capsule, 1000 seed weight (g), Oil Content (OC) (%) and seed yield per hectare (kg).

Data analysis

Analysis of variance (ANOVA): The data collected for each quantitative trait was subjected to analysis of variance (ANOVA) for simple lattice design. Analysis of variance was done using Proc lattice and Proc GLM procedures of SAS version 9.2 (SAS, 2008). Efficiency of the lattice design relative RCBD was checked and in most of the response variables, the lattice was found to be more efficient than that of the RCBD. After testing the ANOVA assumptions. Treatment means were tested for significance (LSD) at 1% probability levels (SAS, 2008).

Estimation of variance components: The phenotypic and genotypic coefficients of variation were estimated according to the method suggested by Burton and de Vane (1953) as follows:

$$\text{Environmental variance } (\sigma^2 e) = Ms_e$$

$$\text{Phenotypic variance } (\sigma^2 p) = (\sigma^2 g + \sigma^2 e)$$

$$\text{Genotypic variance } (\sigma^2 g) = \frac{Mse - Mst}{r}$$

Where:
Mse = Mean square error
Mst = Mean square treatment
r = Replication

$$\text{Phenotypic coefficients of variation (PCV)} = \frac{\sqrt{\sigma^2 px}}{x} \times 100$$

$$\text{Genotypic coefficients of variation (GCV)} = \frac{\sqrt{\sigma^2 gx}}{x} \times 100$$

Where:
$\sigma^2 p$ = Phenotypic variance
$\sigma^2 g$ = Genotypic variance
x = Grand mean of a character

Estimation of heritability in broad sense: Broad sense heritability (h^2) expressed as the percentage of the ratio of the genotypic variance (g) to the phenotypic variance (p) and was estimated on genotype mean basis as described by Allard (1960) as:

$$h^2 B = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where:
$h^2 B$ = Heritability in broad sense
$\sigma^2 p$ = Phenotypic variance
$\sigma^2 g$ = Genotypic variance

Estimation of genetic advance: Genetic Advance (GA) and percentage of the mean (GAM) assuming selection of superior 5% of the genotypes was estimated in accordance with the methods illustrated by Johnson *et al.* (1955) as:

$$GA = \frac{K \times \sqrt{\sigma^2 p} \times \sigma^2 g}{\sigma^2 p}$$

Where:
GA = Expected genetic advance
k = Standardized selection differential at 5% selection intensity (K = 2.063)
$\sigma^2 p$ = Phenotypic variance
$\sigma^2 g$ = Genotypic variance

The genetic advance as percentage of mean (GAM) was computed as:

$$GAM(\%) = \frac{GA}{x} \times 100$$

Where:
GAM = Genetic advance as percentage of mean
GA = Expected genetic advance
x = Grand mean of a character

Estimation of correlation coefficients: Phenotypic and genotypic correlation coefficients were estimated using the standard procedure suggested by Miller *et al.* (1958) as from corresponding variance and covariance components as:

$$r_p = \frac{pcov\ x.y}{\sqrt{\delta^2 px.\delta^2 py}}$$

$$r_g = \frac{pcov\ x.y}{\sqrt{\delta^2 gx.\delta^2 gy}}$$

where, r_p is phenotypic correlation coefficient, r_g is genotypic correlation coefficient between characters x and y, Pcov xy is phenotypic covariance and Gcov xy is genotypic covariance between characters x and y.

Path coefficient analysis: Path coefficient analysis was conducted as suggested 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 equation:

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

where, r_{ij} is mutual association between the independent trait (i) and dependent trait (j) as measured by the correlation coefficient, p_{ij} is component of direct effects of the independent trait (i) on the dependent variable (j) and $r_{ik}p_{kj}$ is assumption of components of indirect effect of a given independent trait via all other independent traits.

The residual effect (h) was calculated using the formula (Dewey and Lu, 1959) as:

$$U = \sqrt{1 - R^2}$$

Where:
$R^2 = \Sigma r_{ij} p_{ij}$

Path coefficient was calculated by using GENRES statistical package (GENRES, 1994).

RESULTS AND DISCUSSION

In the present study, highly significant difference among sesame genotypes ($p<0.001$) was observed for all traits studied. These findings indicate the presence of large variation among the tested sesame genotypes. Similarly, Arameshwarappa *et al.* (2009) reported significant differences

mong 151 sesame accessions for days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of capsules per plant, capsule length, number of seeds per capsule, oil content and seed yield per plant. Menzir (2008) also reported highly significant differences among 64 sesame accessions for days to 50% flowering, days to maturity, capsule filling period, plant height (cm), number of branches per plant, number of capsules per plant, seed yield (kg ha^{-1}), seed yield per plot (g), 1000 seed weight and oil content. Further, Spandana *et al.* (2011) reported significant differences among 60 sesame accessions for plant height, number of primary branches per plant, number of capsules per plant, inter node length, number of seeds per capsule, 1000 seed weight and seed yield per plant. Moreover, Gidey *et al.* (2012) reported highly significant differences among 81 sesame accessions for days to 50% flowering, days to maturity, capsule filling period, plant height, number of capsules per plant, number of primary branches per plant, number of capsules per plant, capsule length, number of seeds per capsule,1000 seed weight, oil content and seed yield per hectare.

Variance components and coefficients of variation: Estimates of phenotypic (σ^2p), genotypic (σ^2g) and environmental (σ^2e) variances and Phenotypic Coefficients of Variation (PCV) and Genotypic Coefficients of Variation (GCV) are given in Table 2. The genotypic coefficients of variation ranged from 2.78 for oil content to 27.54 for number of capsule per plant. Similarly, phenotypic coefficients of variation ranged from 2.00 for days to maturity to 30.83 for number of capsule per plant. In this study, the GCV values were lower than that of PCV, indicating that the environment had an important role in the expression of these characters. Generally, quantitative characters are highly influenced by the environment.

According to Deshmukh *et al.* (1986), PCV and GCV values greater than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10 and 20% to be medium. Based on this argument, number of capsule per plant and seed yield per hectare recorded high Genotypic Coefficients of Variation (GCV) and Phenotypic Coefficients of Variation (PCV) but number of primary branch per plant had medium genotypic coefficients of variation (GCV) and high Phenotypic Coefficients of Variation (PCV). It indicates that selection may be effective based on these characters with high and medium Phenotypic Coefficients of Variation (PCV) and Genotypic Coefficients of Variation (GCV) values and their phenotypic expression would be a good indication of genetic potential.

Similar finding was reported by Sumathi and Muralidharan (2010) for seed yield per hectare. Arameshwarappa *et al.* (2009) reported similar result considering number of capsules per plant, number of primary branches per plant and number of seeds per capsule showed high PCV and GCV. Low coefficient of variation for number of seeds per capsule was reported by Thangavel *et al.* (2000) which is opposite to the present study. Sudhakar *et al.* (2007) and Shadakshari *et al.* (1995) reported low phenotypic and genotypic co-efficient of variation for the characters days to 50% flowering, days to maturity and oil content. Spandana *et al.* (2011) reported high PCV and GCV values for number of capsule per plant and seed yield per ha. Similarly, Gidey *et al.* (2012) found high PCV and GCV values for seed yield per ha. Siva *et al.* (2013) obtained high GCV values for number of capsule per plant.

Heritability and genetic advance: A heritability estimate for characters under study is given in Table 2. Heritability values are helpful in predicting the expected progress to be achieved

Table 2: Estimates of range, mean, Standard Error (SE), phenotypic (σ^2p), genotypic (σ^2g) and environmental (σ^2e) components of variances, phenotypic (PCV) and genotypic (GCV) coefficient of variability, broad sense heritability (H^2), expected genetic advance (GA) and genetic advance as percentage of the mean (GA%) for 64 characters of sesame genotypes

Characters	Range	Mean±SE	σ^2g	σ^2e	σ^2p	GCV (%)	PCV (%)	H^2 (%)	GA	GAM
Days to 50% flowering	35-54	41.0±1.375	7.74	0.97	8.22	6.79	6.99	94.16	5.57	13.59
Days to maturity	83-95	89.0±1.652	2.03	2.34	3.20	3.25	2.00	63.44	2.34	2.63
Capsule filling period	40-56	47.0±1.950	36.50	4.03	5.67	4.06	5.06	64.33	3.16	6.72
Plant height (cm)	54.2-163.9	127.7±14.665	98.10	188.16	192.18	7.76	10.86	51.05	14.59	11.43
Height to first capsule (cm)	26.0-108.2	73.7±8.783	117.37	84.65	159.69	14.69	17.15	73.49	17.15	23.27
Length of capsule bearing zone (cm)	25.6-85.5	54.0±9.692	16.72	80.06	56.75	7.57	13.95	29.46	4.58	8.48
No. of capsules per plant	10.0-90.0	29.3±6.177	65.10	33.01	18.61	27.54	30.83	79.77	14.87	50.75
No. of primary branches per plant	1.0-4.0	2.6±0.530	0.24	0.021	0.035	18.84	22.75	68.57	0.84	32.31
Inter node length (cm)	2.5-9.4	5.3±0.949	0.37	0.52	0.63	11.48	14.98	58.73	0.96	18.11
Capsule length (cm)	1.5-3.3	2.3±0.200	0.04	0.03	0.06	8.69	10.65	66.67	0.34	14.78
No. of seeds per capsule	27.0-74.0	55.4±7.496	22.32	47.5	46.07	8.53	12.25	48.45	6.78	12.22
1000 seed weight (g)	1.3-4.1	2.7±0.347	0.15	0.09	0.19	11.71	16.14	78.95	0.71	26.29
Oil content (%)	38.6-55.5	50.5±2.260	1.32	4.73	3.68	2.78	3.79	35.87	1.42	2.81
Seed yield (kg ha^{-1})	134.64-1214.0	742.54±663.724	26403.65	20545.00	36676.15	21.88	25.79	71.99	284.43	38.31

through the process of selection. Genetic coefficient of variation along with heritability estimate provides a reliable estimate of the amount of genetic advance to be expected through phenotypic selection (Wright, 1921).

Heritability ranged from 29.46% for length of capsule bearing zone to 94.16% for days to 50% flowering. According to Singh (2001), heritability values greater than 80% are very high, values from 60-79% are moderately high, values from 40-59% are medium and values less than 40% are low. Accordingly, heritability estimate was very high (>80%) for days to 50% flowering (94.16%). Similarly, Gidey *et al.* (2012) reported high heritability values for days to 50% flowering and similar result was reported by Siva *et al.* (2013). Very high heritability indicates selection will be effective.

Johnson *et al.* (1955) classified genetic advance as percentage of mean (GAM); values from 0-10% are low, 10-20% are moderate and 20% and above are high. Based on this delineation, the range for GAM was from 2.63% for days to maturity to 50.75% for number of capsule per plant. High GAM were recorded for number of primary branches per plant (32.31%), height to first capsule (23.27%), seed yield per ha (38.31%), number of capsule (50.75%) and 1000 seed weight (26.29%) and medium for days to 50% flowering (13.59%), plant height (11.43%), inter node length (18.11%), capsule length (14.78%) and number of seeds per capsule (12.22%). The lowest genetic advance as percentage of mean were for days to maturity (2.63%), capsule filling period (6.72%), length of capsule bearing zone (8.48%) and oil content (2.18%). Similarly, Gidey *et al.* (2012) reported low genetic advance as a percent of mean values for days to maturity.

Traits like, number of capsule per plant and seed yield per ha had high Phenotypic Coefficients of Variation (PCV), Genotypic Coefficients of Variation (GCV), moderately high heritability and high genetic advance as a percent of mean which are very important for selection than heritability estimates alone.

According to Siva *et al.* (2013), moderately high heritability coupled with high genetic advance was observed for number of capsules per plant indicating that these characters are controlled by additive gene action and phenotypic selection for these characters will be effective. Similarly, high heritability and high genetic advance for yield trait have been reported by Mahajan *et al.* (2007).

Association among characters: The phenotypic and genotypic correlations of seed yield with other characters are indicated in Table 3. Seed yield is the result of many characters which are interdependent. Breeders always look for genetic variation among traits to select desirable types. Some of these characters are highly associated among themselves and with seed yield. The analysis of the relationship among these characters and their association with seed yield is essential to establish selection criteria (Singh, 1990).

Seed yield showed non-significant phenotypic association with all studied traits. Similar result was reported by Trehan *et al.* (1975) where, oil content had non-significant positive genotypic correlation with seed yield. Similarly, Gidey *et al.* (2012) reported non-significant positive phenotypic and genotypic correlations oil content with seed yield.

Seed yield had positive and significant genotypic correlation with days to 50% flowering ($r = 0.553$), plant height ($r = 0.366$), length of capsule bearing zone ($r = 0.701$), number of capsule ($r = 0.511$), number of primary branches per plant ($r = 0.298$) and number of seeds per capsule ($r = 0.404$). This indicating that accessions providing higher percentage of days to 50% flowering, plant height, length of capsule bearing zone, number of capsule, number of primary branches and

Table 3: Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients (rg) at Dansha (2013/14)

Parameters	DF	DTM	CFP	pH	HFC	LCBZ	NC	NB	IL	CL	NSPP	TSW	OC	SYH
DF	1	0.776**	-0.901**	0.497**	0.684**	-0.395**	0.182	0.512**	-0.099	-0.239	-0.025	-0.624**	-0.565**	0.553**
DTM	0.429**	1	-0.400**	0.393**	0.322*	-0.175	0.028	0.242	-0.333**	-0.418**	-0.097	-0.390**	-0.558**	-0.325**
CFP	-0.725**	0.243	1	-0.279*	-0.544**	0.647**	-0.112	-0.436**	0.024	0.031	0.082	0.570**	0.597**	-0.082
PH	0.301*	0.107	-0.222	1	0.844**	0.512**	0.277*	0.443**	0.416**	-0.454**	0.039	-0.356**	-0.158	0.366**
HFC	0.473**	0.325**	-0.287*	0.636**	1	-0.126	-0.107	0.338**	0.294*	-0.586**	0.275*	-0.443**	-0.614**	-0.621**
LCBZ	-0.145*	-0.271*	0.021	0.455**	-0.099	1	0.602**	0.029	0.231	0.231	-0.152	0.086	0.910**	0.701**
NC	0.133	-0.073	-0.147	0.287*	-0.040	0.424**	1	0.517**	0.09	0.271*	0.121	-0.170	0.172	0.511**
NB	0.318*	0.024	-0.309*	0.432**	0.363**	0.180	0.532**	1	0.292*	-0.175	0.068	-0.23	-0.095	0.298*
IL	-0.026	-0.018	0.017	0.192	0.134	0.153	0.059	0.204	1	-0.001	-0.399**	0.230	0.339**	-0.726**
CL	-0.180	-0.313*	-0.013	-0.187	-0.258*	0.026	0.198	-0.053	-0.156	1	0.219	0.061	0.405**	-0.247*
NSPC	-0.013	-0.162	-0.077	0.250*	0.196	0.176	0.095	0.141	0.152	0.033	1	-0.321*	0.658**	0.404**
TSW	-0.437**	-0.330**	0.212	-0.097	-0.255*	0.224	0.045	-0.024	0.170	0.097	-0.005	1	0.142	0.16
OC	-0.305*	-0.312*	0.210	-0.006	-0.235	0.240	0.133	-0.017	-0.073	0.273*	0.237	0.160	1	0.224
SYH	-0.006	-0.104	-0.050	0.122	-0.022	0.186	0.178	0.243	0.057	-0.181	0.174	0.162	0.086	1

*,**Significance at 0.05 and 0.01 probability levels, respectively, DF: Days to 50% flowering, DTM: Days to maturity, CFP: Capsule filling period, PH: Plant height (cm), HFC: Height to first capsule, LCBZ: Length of capsule bearing zone, NC: No. of capsules per plant, NB: No. of primary branches per plant, IL: Inter node length, CL: Capsule length, NSPC: No. of seeds per capsule, TSW: 1000 seed weight (g), OC: Oil content, SYH: Seed yield (kg ha^{-1})

number of seeds per capsule are high yielders. Similarly, Menzir (2008) reported that number of capsules per plant manifested significant positive correlation with seed yield. Similar result was reported by Siva *et al.* (2013). Similar result were report by EARO (2002) for number of capsules per plant displayed significant positive correlation with seed. Akbar *et al.* (2011) reported that number of capsules per plant showed significant positive correlation with seed yield. Similar finding was reported for number of primary branches/plant by Sakila *et al.* (2000) and for number of capsule per plant by Kathiresan and Gnanamurthy (2000) which contributed significant and positive correlation with seed yield. Similarly, Tamina and Dasgupta (2003) reported that number of primary branches/plant had significant and positive correlation with seed yield at genotypic level. Bhuvan and Sharma (2004) reported that seed yield was positive and significantly correlated with number of primary branches per plant at genotypic.

The phenotypic correlation revealed that number of branches per plant exhibited a positive and significant phenotypic correlation with plant height, height to first capsule, number of capsule and 50% flowering and it had positive and significant genotypic correlation with inter node length and positive non significant with number of seeds per capsule. This indicates that late flowering genotypes had higher number of branches than early flowering. Number of capsules per plant had a positive and significant phenotypic correlation with length of capsule bearing zone and positive and significant with plant height and positive and non significant with days to 50% flowering and it had positive and highly significant genotypic correlation with number of primary branches per plant and positive and significant with capsule length and positive and non significant with inter node length. This indicates that long capsule bearing zone genotypes had higher number of capsules per plant. Capsule length had a positive and significant phenotypic correlation with length of capsule bearing zone and number of capsule per plant and it had positive and highly significant genotypic correlation with oil content and seed yield per ha. Oil content had a positive and significant phenotypic correlation with capsule length and positive and non-significant with capsule filling period, length of capsule bearing zone, number of capsule, number of seeds per capsule and 1000 seed weight and negative and significant phenotypic correlation with days to 50% flowering, days to maturity and negative and non significant phenotypic correlation with plant height, height to first capsule, number of primary branches, inter node length and it had positive and non significant genotypic correlation with oil content. Generally, positive and significant association of pairs of characters at phenotypic and genotypic level justified the possibility of correlated response to selection.

Path coefficient analysis: The genotypic direct and indirect effect of different characters on seed yield per hectare is presented in Table 4. Plant height had the highest positive direct effect on grain yield followed by number of primary branch per plant. These characters had also positive and significant correlation with seed yield. This suggests the correlation revealed the true relationship and direct selection through these characters will be effective. This means that a slight increase in one of these above traits may directly contribute to seed yield increase. The 1000 seed weight and oil content had also positive direct effect on seed yield but their association with the same trait was non significant.

Similar result was reported by Menzir (2008) for 1000 seed weight and oil content which had positive direct effect on seed yield. Capsule length showed negative direct effect on seed yield.

Table 4: Estimates of direct (bold diagonal) and indirect effect (off diagonal) at genotypic level for different characters on grain yield of in 64 sesame genotypes

Parameters	DF	DTM	CFP	pH	HFC	LCBZ	NC	NB	IL	CL	NSPC	TSW	OC	r_g
DF	0.467	-0.610	0.290	0.53	0.293	-0.036	-0.31	0.77	0.212	0.018	0.003	-0.704	-0.370	0.553**
DTM	0.139	-0.075	0.129	0.21	-0.976	-0.016	-0.047	0.364	0.711	0.031	0.011	-0.441	-0.365	-0.325**
CFP	-0.323	0.831	-0.322	-0.861	0.028	0.06	0.19	-0.657	-0.051	-0.002	-0.010	0.644	0.391	-0.082
PH	0.729	-0.815	0.09	2.081	-0.597	0.047	-0.472	0.667	-0.887	0.033	-0.005	-0.402	-0.103	0.366**
HFC	0.003	-0.071	0.375	0.602	-0.891	-0.012	0.182	0.509	-0.427	0.043	-0.032	-0.50	-0.402	-0.621**
LCBZ	-0.579	0.364	-0.208	0.578	0.239	0.092	-0.025	0.043	-0.494	-0.019	0.018	0.097	0.595	0.701**
NC	0.267	-0.057	0.036	0.853	0.202	0.055	-1.705	0.779	0.194	-0.02	-0.014	-0.192	0.113	0.511**
NB	0.751	-0.501	0.14	0.365	-0.639	0.203	-0.882	1.506	-0.623	0.313	-0.008	-0.265	-0.062	0.298*
IL	-0.146	0.692	-0.008	0.281	-0.556	0.021	0.155	0.44	-2.133	0.00	0.047	0.259	0.222	-0.726**
CL	-0.35	0.867	-0.01	-0.398	0.108	0.024	-0.462	-0.263	0.003	-0.074	-0.026	0.069	0.265	-0.247*
NSPC	-0.037	0.201	-0.027	0.119	-0.521	-0.014	-0.206	0.103	0.852	-0.016	-0.118	-0.362	0.43	0.404**
TSW	-0.915	0.81	-0.184	-0.098	0.838	0.008	0.29	-0.354	-0.49	-0.005	0.038	0.129	0.093	0.16
OC	-0.629	0.257	-0.192	-0.486	0.26	0.084	-0.293	-0.143	-0.733	-0.038	-0.078	0.76	1.455	0.224

*,**Significance at 0.05 and 0.01 probability levels, respectively, Residual effect: 0.349, DF: Days to 50% flowering, DTM: Days to maturity, CFP: Capsule filling period, pH: Plant height (cm), HFC: Height to first capsule, LCBZ: Length of capsule bearing zone, NC: No. of capsules per plant, NB: No. of primary branches per plant, IL: Inter node length, CL: Capsule length, NSPC: No. of seeds per capsule, TSW: 1000 seed weight (g), OC: Oil content, rg: Genotypic correlation with seed yield (kg ha^{-1})

Contrasting result was reported by Gidey *et al.* (2012) for oil content which had positive direct effect on seed yield. However, capsule filling period and capsule length had negative direct effect on seed yield.

The residual (0.349) indicates that characters which are included in the genotypic path analysis explained 65.1% of the total variation in seed yield which indicates that there may be some more components that are contributing towards seed yield.

The result of genetic variability, character association and path coefficient analysis confirmed that the characters plant height and number of primary branch per plant were important. Therefore, these characters could be used for the development of high yielding varieties through selection.

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