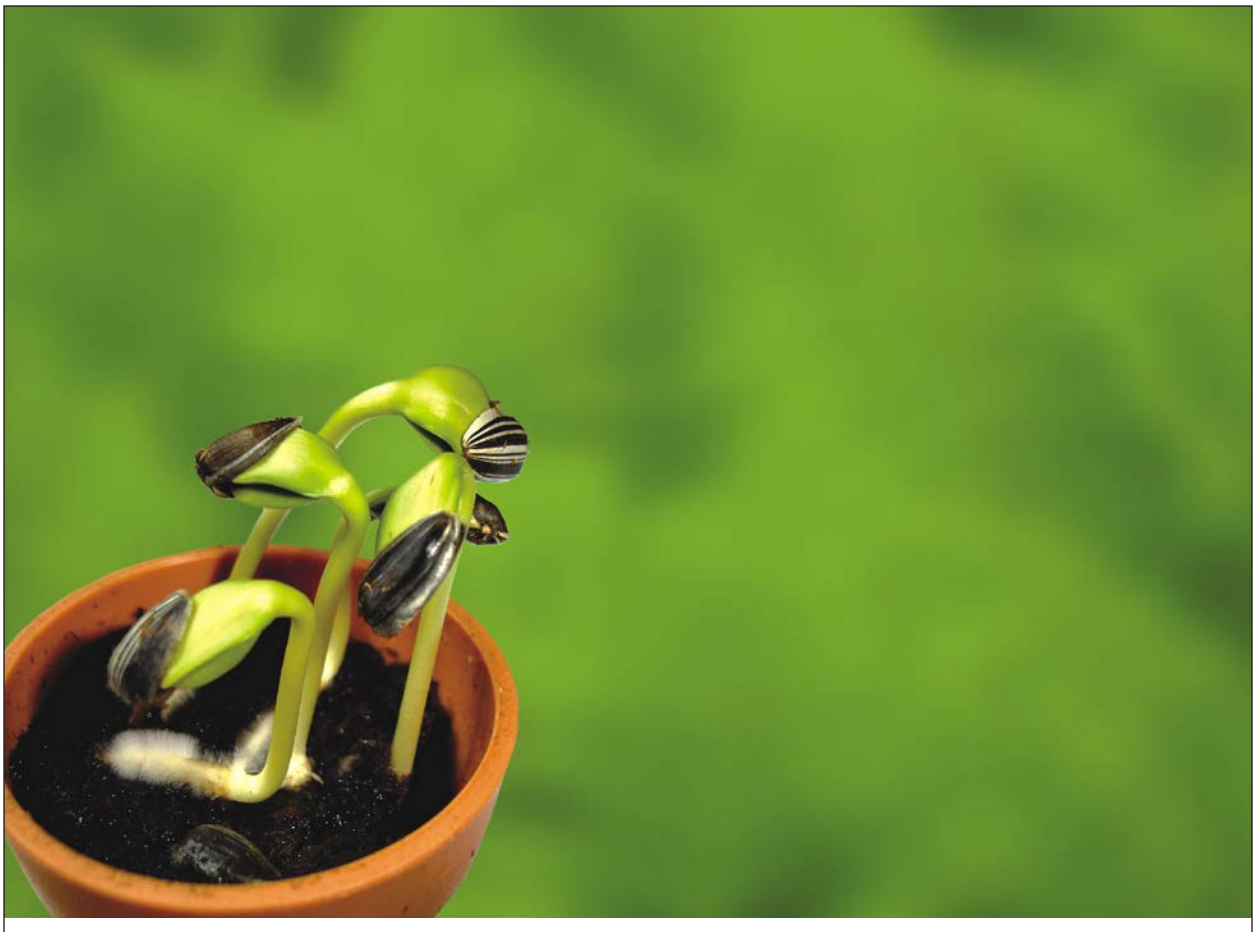

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Assessment of Genetic Variability, Genetic Advance, Correlation and Path Analysis for Morphological Traits in Sesame Genotypes

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ABSTRACT

Grain yield and oil content of sesame are usually low, depending on genetic variability and association of relevant characters with grain yield and oil content. Hence, the objectives of this research were estimating the genetic variability and association among characters. Eighty one sesame genotypes were tested in 9×9 simple lattice design at Kebabo Tsegede wereda Western Tigray, Ethiopia in 2010/11 cropping season. Analysis of variance revealed that there was highly significant ($p<0.01$) difference among the 81 genotypes for all the 15 characters studied. High genotypic and Phenotypic Coefficient of Variation (PCV) was recorded for harvest index, seed yield/ha, height to first capsule, biomass/ha, number of capsules/ha, number of primary branches/ha, number of seeds per capsule and plant height. Height to first capsule had the highest heritability value. High heritability coupled with high expected genetic advance as percent of mean was observed for number of primary branches per plant, height to first capsule and harvest index. This indicates that these characters can be improved through selection. Harvest index showed positive significant phenotypic and genotypic correlation with grain yield. Genotypically, path coefficient analysis based on grain yield as a dependent variable revealed that capsule filling period by days to 50% flowering and biological yield exerted positive direct effect on seed yield. Therefore, a greater emphasis should be laid on these characters in perspective of breeding programs.

Key words: Genetic variability, heritability, genetic advance, correlation, path coefficient sesame

INTRODUCTION

Sesame (*Sesamum indicum* L.) is a self pollinated diploid species with 2n = 26 chromosomes (Alemawu *et al*., 1998). It belongs to order Tubiflorae, family Pedalisceae. Only *Sesamum indicum* has been recognized as a cultivated species among the thirty six species of genus Sesamum (Alemawu *et al*., 1998). Sesame could have been distributed either eastward from Africa or westward along the ancient trade routes that are known to have existed (Bedigian, 2004). Sesame is among the oldest oil seed crops from which oil was extracted by the ancient Hindus and used for certain spiritual purposes (Weiss, 1983). According to Seegeler (1983) sesame was the first crop recorded in Babylon and Assyria before 2050 BC. Ethiopia ranks fifth in the world in sesame production (186772 t, 5.4% in production) (FAOSTAT, 2008) but its yield is quite low (780 kg ha^{-1}) (CSA, 2009) as compared to the crop genetic potential which is 2000 kg ha^{-1} under research

(Mkamilo and Bedigian, 2007). For any crop improvement programme nature and magnitude of genetic variability is essential. Findings depending on the nature and magnitude of genetic variabihty have of vital value for planning efficient breeding program to improve the yield potential of the genotypes. Information on the association of plant characters with seed yield is of great importance to breeder in selecting desirable genotypes.

Sudhakar (2003) revealed broad range of variability and high heritability concerning various traits studied in sesame genotypes. He also reported high genetic advance as per cent over mean for seed yield per plant, number of capsules per plant, number of primary branches, number of seeds per capsule and plant height. Likewise, wide range of variation for plant height, number of capsules per plant, number of seeds per capsule, 1000 seed weight, leaf area index, harvest index, seed yield per plant and oil yield per plant was reported by Babu *et al.* (2004). On the other hand, Narain *et al.* (2004) confirmed high genotypic coefficient of variation for seed yield per plant followed by harvest index, number of capsules per plant and primary branches per plant. Singh and Singh (2004) reported that number of capsules per plant and grain yield had high heritability along with high magnitude of genetic advance.

Uzun and Carigan (2001) revealed that number of capsules per plant was highly associated with grain yield. In addition to this he observed that path coefficient analysis on plant height had the greatest direct effect on seed yield. Similarly, Arulmozhi *et al.* (2001) reported significant and positive association of seed yield with number of branches and number of capsules per plant.

The present research was conducted to gather information on variability, character association and path co-efficient analysis in 81 germplasm collections of sesame for 15 characters.

MATERIALS AND METHODS

The experimental site: The experiment was conducted at Kebabo site Tsegede wereda of the western low land part of Tigray region, Ethiopia during 2011 cropping season. The location receives low annual rainfall. Moreover, poor distribution of the rainfall coupled with high temperature makes the area vulnerable to terminal moisture stress. It is located at geographical coordinates 25°12'16"N latitude and 15°10'23"E longitudes and at altitude of 948 m.a.s.l. The mean annual temperature is 28.7°C and it has vertisol soil type. Average annual rainfall varies from 850-1400 mm (HAM, 2010).

Experimental materials: Eighty one sesame accessions were used for this study. All of the accessions represent the national collections from different major sesame growing regions of Ethiopia and that were maintained at the Institute of Biodiversity Conservation of Ethiopia (IBC). The details of the accessions are given in Table 1.

Experimental design: The trial was laid out in 9×9 simple lattice designs. Each accession was planted in a plot size of 6.4 m^2 (4 rows of 4 m length, 40 cm between rows and 10 cm between plants within a row).

Data collected: Plot basis Quantitative data were measured from the central two rows of each plot and 10 randomly selected plants within rows were taken for the plant basis data, as described below:

Table 1: Sesame accessions used in the study

Accessions	Region	Locality	Accessions	Region	Locality
Acc 202 319	Oromiya	NA	Acc 111 502	Oromiya	Gonde Kore
Acc 227 882	Oromiya	Bebeka	Acc 227 902	Ben and Gumuz	Dabus
Acc 111 860	Oromiya	NA	Acc 111 809	Ben and Gumuz	Asosa
Acc 111 507	Oromiya	Fiche	Acc 227 916	Oromiya	Dimtu
Acc 111 811	Oromiya	NA	Acc 227 868	Oromiya	Anger Gutin
Acc 227 891	Oromiya	Cheleka	Acc 111 838	Oromiya	Dedesa
Acc 111 859	Oromiya	Cheleka	Acc 227 913	Oromiya	Dimtu
Acc 227 889	Amara	NA	Acc 202 513	Gambela	Gambela
Acc 227 863	Oromiya	Dedesa	Acc 202 300	Oromiya	Cheleleka
Acc 111 822	Amara	Gojam	Acc 227 885	Oromiya	Didesa
Acc 111 824	Amara	NA	Acc 227 919	Oromiya	Dimtu
Acc 227 905	Oromiya	Guba Koricha	Acc 111 850	Amara	Alimedo
Acc 227 914	Oromiya	NA	Acc 111 828	Amara	Kemisie
Acc 227 894	Gambela	Gambela	Acc 227 898	Amara	Kobo
Local*	Tigray	Humera	Acc 111 803	Amara	Dawey
Acc 227 918	Oromiya	Diga Lega	Acc 111 821	Amara	Dawey
Acc 227 896	Oromiya	Eastern-Welega	Acc 111 846	Amara	NA
Acc 111 858	Amara	NA	Acc 111 847	Amara	Kobo
Acc 111 866	Amara	Finote Selam	Acc 227 864	Oromiya	Fiche
Acc 227 886	Oromiya	NA	Acc 202 301	Amara	Kemisie
Acc 227 879	Oromiya	Dimtu	Acc 202 514	Ben and Gumuz	Asosa
Acc 111 848	Amara	S. East of Mota	Acc 111 518	Amara	Cherete Kemissie
Acc 227 915	Oromiya	NA	Acc 227 900	Oromiya	Cheleka
Acc 227 873	Amara	Kobo	Acc 111 826	Amara	Kobo
Acc 227 901	Amara	Finote Selam	Acc 111 854	Amara	Kobo
Acc 111 820	Amara	Mota	Acc 111 840	Amara	Finote Selam
Acc 227 887	Oromiya	Gutin	Acc 227 867	Oromiya	Godie
Acc 111 853	Oromiya	Fiche	Acc 227 872	Oromiya	Anger Gutin
Acc 111810	Amara	Gojam	Acc 227 893	Oromiya	Anger Gutin
Acc 227 907	Amara	Kemissie	Acc 111 816	Amara	Kemissie
Acc 111 806	Amara	Kemissie	Acc 227 897	Oromiya	NA
Acc 227 912	Amara	Kemissie	Acc 111 814	Amara	Dawey
Acc 227 880	Amara	Kemissie	Acc 227 858	Oromiya	Babile
Acc 227 910	Amara	Kemissie	Acc 227 924	Oromiya	NA
Acc 111 832	Amara	Kemissie	Acc 227 871	Oromiya	Anger Gutin
Acc 227 865	Amara	Kemissie	Acc 227 884	Oromiya	Godie
Acc 202 517	Amara	Kemissie	Acc 111 842	Amara	Dawey
Acc 227 876	Amara	Dewy	Acc 277 861	Oromiya	Didesa
Acc 227 911	Amara	Dewy	Acc 227 869	Oromiya	NA
Acc 111 865	Amara	Kobo	Acc 111 818	Amara	Kobo
Acc 227 917	Amara	Efeson			

Institute of biodiversity conservation and Research, Ethiopia, NA: Not identified

On plot basis:

- **Days to 50% flowering:** Number of days from emergence to a stage when 50% of the plants in a plot produced flowers
- **Days to maturity:** Number of days from emergence to a stage when 90% of the plants in a plot produced matured capsules

- **Capsule filling period:** Number of days from flowering to maturity
- **Biomass yield per hectare (kg):** Recorded by weighing the total above ground yield harvested from the two central rows of each experimental plot at the time of harvest and converted to biomass yield per hectare
- **Seed yield per hectare (kg):** Plot yield converted to per hectare yield
- **Thousand seed weight (g):** Weight in grams of 1000 seeds
- **Harvest index (%):** Ratio of seed yield to the above ground biomass yield
- **Oil content (%):** Oil content was determined by wide line Nuclear Magnetic Resonance (NMR). Seeds were bulked per each plot and oven dried at 130°C for 2 h and cooled for 30 min. Twenty two gram oven dried seed sample was used to analyze oil content using NMR (Newport analyzer) (Newport Pagnell, Bucks, UK). The NMR read oil content of the sample seed with reference to a standard of extracted sesame oil. The instrument provides three readings and average of the three readings was recorded for each sample

On plant basis:

- **Plant height (cm):** Height in centimeters from the soil level to the tip of the plant at maturity, mean of ten random plants
- **Number of primary branches per plant:** Total number of branches originated from the main stem of taken plants
- **Internodes length (cm):** Length in centimeters between two consecutive nodes at the middle part of the plant
- **Height to first capsule (cm):** Height from ground to first capsule
- **Number of capsules per plant:** Number of capsules recorded on a plant at harvest
- **Capsule length (cm):** Mean length of 5 capsules per plant
- **Seeds per capsule:** Mean number of seeds from 5 capsules of each plant

Data analysis

Analysis of variance (ANOVA): The data collected for each quantitative trait were 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 Institute, 2008) after testing the ANOVA assumptions. Homogeneity test for the error variance was done before computing the analysis of variance. Treatment means were tested for significance (LSD) at 5% and 1% probability levels.

Estimation of variance components: The phenotypic, genotypic and environmental variances and coefficient of variation were calculated according to the formula suggested by Singh and Chaudhury (1985) as follows:

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

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

where, MSG is mean square due to genotypes, MSE is mean square of error (Environmental variance) and r is number of replication:

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

Where, $\sigma^2 g$ is genotypic variance and $\sigma^2 e$ is environmental variance:

$$\text{Phenotypic coefficient of variantion (PVC)} = \sqrt{\frac{\sigma^2 p}{X}} \times 100$$

$$\text{Genotypic coefficient of variantion (GCV)} = \sqrt{\frac{\sigma^2 g}{X}} \times 100$$

Where:
$\sigma^2 p$ = Phenotypic variation
$\sigma^2 g$ = Genotypic variation and
X = Grand mean of the character studied

Estimation of heritability in broad sense: Broad sense heritability (h^2) expressed as the percentage of the ratio of the genotypic variance ($\sigma^2 g$) to the phenotypic variance ($\sigma^2 p$) as described by Allard (1960) as:

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

Estimation of genetic advance: The genetic advance expressed under selection in broad sense, assuming selection intensity of 5% 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
$\sigma^2 p$ = Phenotypic variation
$\sigma^2 g$ = Genotypic variation
k = The standardized selection differential at 5% selection intensity (K = 2.063):

$$GAM = \frac{GA}{\overline{X}} \times 100$$

Where:
GAM = Genetic advance as percent of mean
GA = Genetic advance under selection and
$\overline{X}$ = Mean of the population

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

$$\text{Phenotypic correlation coefficient } (r_p) = \frac{pCovxy}{\sqrt{\sigma^2 px \times \sigma^2 py}}$$

$$\text{Genotypic correlation coefficient } (r_g) = \frac{gCovxy}{\sqrt{\sigma^2 gx \times \sigma^2 gy}}$$

where, pCovxy and gCovxy 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, respectively.

The coefficients of correlation were tested using 'r' tabulated value at n-2 degrees of freedom, at 5 and 1% probability level, where n is the number of genotypes.

Path coefficient analysis: Seed yield per hectare was selected as resultant (dependant) variable and the test of traits as causal (independent) variables. Path coefficient analysis was estimated 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 relationship:

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

Where:

r_{ij} = Mutual association between the independent character (i) and dependent character (j) as measured by the genotypic correlation coefficients

P_{ij} = Components of direct effects of the independent character (i) on the dependant character (j) as measured by the genotypic path coefficients and

$\Sigma r_{ik} \times p_{kj}$ = Summation of components of indirect effect of a given independent character (i) on a given dependent character (j) via all other characters (k)

The contribution of the remaining unknown factor was measured as the residual factor (P_R), which was calculated as:

$$P_R = (I\sqrt{\Sigma r_{ij} p_{ij}})$$

The magnitude of PR indicates how best the causal factors account for the variability of the dependent factor (Singh and Chaudhary, 1999). That is, if P_R value is small (for instance, nearly zero), the dependent character considered (seed yield) is fully explained by the variability in the independent characters, where as higher P_R value indicates that some other factors which have not been considered, need to be included in the analysis to account fully the variation in the dependent character (seed yield).

RESULTS AND DISCUSSION

In the present study highly significant differences among sesame genotypes ($p<0.01$) were observed for all traits studied. These findings indicate the presence of large genetic variation among the tested sesame genotypes. Similarly, Arameshwarappa *et al.* (2009) recorded significant

Table 2: Estimates of ranges, 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), expected genetic advance (GA) and genetic advance as percent of the mean (GA % mean) for 15 characters of sesame genotypes

Characters	Range	Mean±SE	σ^2g	σ^2e	σ^2p	GCV (%)	PCV (%)	H^2 (%)	GA	GAM
Capsule length (cm)	1.8-3.62	2.54±0.0084	0.06	0.03	0.10	9.86	12.10	66.30	0.42	16.53
Plant height (cm)	65.3-154	107.45±0.4070	403.38	72.88	476.26	18.69	20.31	84.70	38.08	35.43
Height to first capsule (cm)	10.4-73.2	34.92±0.0817	292.68	3.05	295.73	48.98	49.24	98.90	35.06	98.40
Number of capsule plant^{-1}	14-102	47.41±0.3900	80.39	416.73	497.12	17.11	42.55	16.10	6.72	14.17
Days to maturity	82.0-113	95.52±0.0700	59.71	1.99	61.70	8.09	8.22	96.70	15.66	16.39
Capsule filling period (days)	17.0-80	44.65±0.1470	67.83	7.94	75.77	18.44	19.49	89.50	16.05	35.95
Harvest index	0.3-19.4	3.58±0.0110	5.70	2.11	7.80	69.15	80.95	72.90	4.37	121.70
Biomass/ha (kg)	9.7-598	193.5±0.45100	10855.23	12851.30	23706.50	50.21	74.21	45.70	135.49	70.00
Number of primary branches/plant	1.0-8.3	3.63±0.1100	1.80	0.05	1.85	36.89	37.43	97.10	2.72	74.90
Inter node length (cm)	2.8-6.8	4.12±0.0160	0.39	0.12	0.51	15.17	17.36	76.30	1.13	27.29
Number of seeds/capsule	25-87	51.39±0.2100	191.41	20.89	212.30	26.92	28.35	90.10	27.06	52.65
1000 seed weight (g)	2.0-3.8	2.80±0.0280	0.10	0.03	0.13	11.38	12.86	78.20	0.58	20.74
Days to 50% flowering	29.0-66.0	51.40±0.0470	76.67	0.90	77.57	17.03	17.13	98.80	17.93	34.88
Oil content (%)	34.6-55.4	49.46±0.0280	5.05	0.34	5.39	4.55	4.69	93.70	4.48	9.06
Seed yield/ha (kg ha^{-1})	162.0-1361	557.68±1.9900	106821.00	14831.30	121652.30	58.99	62.95	87.81	635.03	113.87

differences among 151 sesame genotypes for days to 50% flowering, days to maturity, plant height, number of primary branches/plant, number of capsules/plant, capsule length and number of seeds/capsule, oil content and seed yield/plant. Similarly, Sumathi and Muralidharan (2010) reported that thirty hybrids of eleven sesame genotypes and observations were recorded on days to 50% flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, capsule length, capsule breadth, number of seeds per plant, 100 seed weight, seed yield per plant and oil content and analysis of variance confirmed highly significant differences among genotypes for all the characters without capsule breadth indicating considerable amount of genetic variation in the experimental materials.

Variance components and coefficients of variation: Estimates of phenotypic (σ^2p), genotypic (σ^2g) and environmental (σ^2e) variances and phenotypic (PCV) and Genotypic Coefficients of Variation (GCV) are given in Table 2. The genetic coefficient of variation ranged from 4.55% for oil content to 69.15% for harvest index. At the same time the range for phenotypic coefficient of variation was from 4.69% for oil content to 80.95% for harvest index. 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 or agronomic traits are highly influenced by environment. Similarly, Sumathi and Muralidharan (2009) reported for both phenotypic and genotypic coefficient variations the highest was for number of primary branches/plant and the lowest was for oil content.

Phenotypic coefficient of variation and genotypic coefficient of variation 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 (Deshmukh *et al.*,1986). Based on this delineation, harvest index, seed yield/ha, height to first capsule, biomass/ha, number of primary branches/plant and number of seeds/capsule had high genotypic (GVC) and phenotypic (PCV) coefficients of variation. This finding indicates that selection may be effective based on these characters and their phenotypic expression would be a good indication of genetic potential. There is large scope for selection based on these characters and the diversity in genotypes provides huge potential for

future breeding program. The PCV and GCV values for days to 50% flowering, capsule filling period, internodes length and 1000 seed weight were medium. Days to maturity and oil content had low PCV and GCV values indicating the low scope of selection for improvement.

Similar finding was reported by Sumathi and Muralidharan (2010) for number of primary branches/plant and seed yield/ha. Arameshwarappa *et al.* (2009) reported similar results considering number of capsules/plant, number of primary branches/plant and number of seeds/capsule where high PCV and GCV values were recorded except for number of capsules/plant that had medium GCV. In the contrary, low coefficient of variation was reported by Saravanan *et al.* (2000) for number of seeds/capsule . Solanki and Gupta (2003) and Saravanan and Nadarajan (2003) recorded high coefficient of variation for number of capsules per plant and branches per plant. Furthermore, Vasline *et al.* (2000) reported high coefficient of variation for number of capsules per plant while, plant height showed moderate PCV and GCV and the remaining traits recorded low PCV and GCV. Sudhakar *et al.* (2007) and Shadakshari *et al.* (1995) reported low phenotypic and genotypic co-efficient of variation for the characters days to fifty per cent flowering, days to maturity and oil content. On the contrary, Thangavel *et al.* (2000) reported low co efficient of variation for number of seeds per capsule.

The difference between PCV and GCV was high for number of capsules/plant, biomass/ha, harvest index, capsule length, seed yield/ha and internodes length and low difference between PCV and GCV for days to 50% flowering, days to maturity and height to first capsule. High difference between PCV and GCV shows high influence of the environment on the characters whereas low difference shows low influence of the environment on the characters. Similar results were found by Arameshwarappa *et al.* (2009) for capsule length and seed yield.

Heritability and genetic advance: Heritability estimate for characters under study is given in Table 2. Heritability values are helpful in predicting the expected progress to be achieved 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 16.1% for number of capsules/plant to 98.9% for height to first capsule. According to Singh (2001), heritability values greater than 80% are very high, values from 60 to 79% are moderately high, values from 40 to 59% are medium and values less than 40% are low. Accordingly, characters, like plant height, height to first capsule, days to maturity, capsule filling period, number of primary branches/plant, number of seeds/capsule, days to 50% flowering, oil content and seed yield/ha had very high heritability. This indicates that selection will be the best step for selecting sesame genotypes having these traits with very high heritability. This is because there would be a close correspondence between the accessions and the phenotype due to the relative small contribution of the environment to the total variability. Similar results were reported by Sumathi and Muralidharan (2009, 2010) for days to maturity. Number of capsules/plant exhibited low heritability values, showing that the environmental effect constitutes a major portion of the total phenotypic variation (Moghaddam *et al.*, 1998).

The range for genetic advance as percent of mean was from 9.06% for oil content to 121.70% for harvest index (Table 2). Seed yield/ha (113.87%), height to first capsule (98.4%) and number of primary branches/plant (74.90%) had relatively high genetic advance as a percent mean. The lowest genetic advance as percent of mean was observed for number of capsules/plant (14.17%), days to maturity (16.39%) and capsule length (16.53). This low estimate of genetic advance as a

percent mean arises from low estimate of phenotypic variance and heritability. Selection based on those traits with a relatively high GAM will result in the improvement of the performance of the genotypes for the traits. A case in point is harvest index that had very high and moderately high heritability values.

The number of capsules/plant had low heritability and genetic advance on the contrary to the findings of Rajaravindran *et al.* (2000) and Paramasivam (1980). Oil content showed very high values of heritability and low genetic advance as percent of mean. These results are in conformity with the findings of Reddy *et al.* (2001) and Sudhakar *et al.* (2007).

According to Johnson *et al.* (1955), high heritability estimates along with the high genetic advance is usually more helpful in predicting gain under selection than heritability estimates alone. The present study showed that high heritability coupled with high expected genetic advance as percent of mean for number of primary branches/plant, height to first capsule and harvest index. These characters were controlled by additive gene effects and phenotypic selection for these characters would likely to be effective than other characters measured (Sumathi and Muralidharan, 2009). Similar result to the present finding was reported by Reddy *et al.* (2001) and Krishnaiah *et al.* (2002) for number of primary branches/plant.

Association among characters: Estimates of phenotypic and genotypic correlation coefficients between each pair of characters are presented in Table 3. The magnitudes of genotypic correlation coefficients for most of the characters were higher than their corresponding phenotypic correlation coefficients, except few cases, which indicate the masking effect of the environment in the total expression of the genotypes. Such results are in concurrence with the results of Ganesh and Sakila (1999).

The phenotypic and genotypic correlations of seed yield with other characters are indicated in Table 3. The range of phenotypic correlation was from -0.066 for number of seeds/capsule to 0.325 for harvest index. Seed yield showed positive and significant phenotypic association with harvest index but none significant association with the rest of characters. This shows that genotypes provided higher percentage of harvest index are high yielder. Similarly, Pawar *et al.* (2002) observed that seed yield exhibited positive significant correlation with harvest index. Similar results excepting number of primary branches/plant were reported by Sakila *et al.* (2000). Contrary to this study Kathiresan and Gnanamurthy (2000) reported that number of capsules/plant contributed significant positive correlation with seed yield. In opposite to the present study, Tamina and Dasgupta (2003) reported that number of branches per plant, plant height, number of capsules per plant, capsule length and number of seeds per capsule were significantly and positively correlated with seed yield at genotypic and phenotypic levels. Seed yield had low and none significant phenotypic and genotypic correlation with oil content in this study, indicating that simultaneous improvement of these traits is difficult. The present study is consistent with the results reported by Trehan *et al.* (1975), where oil content had none significant positive genotypic correlation with seed yield. Therefore, separate breeding program has to be formulated for yield and oil content improvement (Sumathi *et al.*, 2007).

The range of genotypic correlation of seed yield with other characters was from 0.011 (non significant) for thousand seeds weight to 0.404 ($p<0.01$) for harvest index (Table 3). Traits significantly correlated with seed yield may be important yield predictors in sesame breeding. Vanisri *et al.* (1994) obtained similar results in sesame. Ayiecho (1985) also reported that harvest index is an essential yield estimator and selection for harvest index led to a substantial grain yield

Table 3: Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients of fifteen sesame morphological traits

	CL	PH	HFP	NC	DTM	CFP	HI	BPH	NB	IL	NSPP	TSW	FPF	OC	SYH
CL	1	-0.268*	-0.388**	-0.417**	-0.316**	0.054	0.264*	-0.507**	-0.093	-0.254*	-0.369**	-0.108	-0.351**	0.105	0.089
PH	-0.221	1	0.883**	0.672**	0.432**	0.353**	-0.155	0.506**	0.551**	0.014	0.371**	0.338**	0.752**	-0.296*	0.155
HFP	-0.268*	0.808**	1	0.603**	0.506**	-0.253*	-0.191	0.49**	0.487**	0.107	0.402**	0.303**	0.724**	-0.243*	0.053
NC	-0.166	0.328**	0.252*	1	0.248*	-0.083	0.507**	0.381**	0.628**	0.098	0.445**	0.58**	0.355**	-0.428**	0.054
DTM	-0.263*	0.378**	0.495**	0.099	1	0.438**	-0.100	0.256*	0.329**	0.071	0.220	0.282*	0.509**	-0.143	0.123
CFP	0.017	0.348**	-0.241*	-0.027	0.439**	1	0.029	-0.291*	-0.103	0.061	-0.155	0.140	-0.544**	0.195	0.027
HI	0.187	-0.134	-0.161	0.164	-0.076	0.022	1	-0.367**	-0.138	0.148	-0.048	-0.037	-0.134	0.257*	0.404**
BPH	-0.307**	0.355**	0.334**	0.176	0.160	-0.164	-0.298*	1	0.388**	0.282*	0.377**	0.288*	0.522**	-0.165	0.216
NB	-0.091	0.515**	0.479**	0.274*	0.314**	-0.101	-0.113	0.256*	1	-0.113	0.113	0.141	0.429**	-0.042	0.15
IL	-0.167	-0.007	0.090	-0.064	0.056	0.045	0.097	0.181	-0.104	1	0.242*	-0.001	0.003	0.065	0.159
NSPP	-0.313**	0.322**	0.376**	0.142	0.215	-0.134	-0.037	0.253*	0.100	0.198	1	0.007	0.358**	-0.107	0.084
TSW	-0.023	0.267	0.267*	0.143	0.255*	0.139	-0.008	0.163	0.126	-0.014	-0.001	1	0.075	-0.052	0.011
FPF	-0.277*	0.692**	0.717**	0.129	0.499**	-0.523**	-0.112	0.343**	0.422**	0.006	0.334**	0.075	1	-0.329**	0.083
OC	0.075	-0.270*	-0.231	-0.151	-0.131	0.176	0.229	-0.106	-0.044	0.078	-0.088	-0.043	-0.318**	1	0.075
SYH	0.112	0.143	0.040	0.009	0.113	0.024	0.325**	0.132	0.139	0.148	-0.066	0.035	0.082	0.066	1

Simple linear correlation coefficients, r, at *5% and **1% levels for this table are 0.232 and 0.302, respectively, CL: Capsule length (cm), PH: Plant height (cm), HFP: Height to first capsule (cm), NC: Number of capsules/plant, DTM: Days to maturity, CFP: Capsule filling period, HI: Harvest index, BPH: Biomass/hectare (kg), NB: Number of primary branches/plant, IL: Internodes length (cm), NSPP: Number of seed/capsule, TSW: Thousand seed weight (g) and FPF: Days to 50% flowering, OC: Oil content (%), SYH: Seed yield/hectare (kg ha^{-1})

response in amaranths. On the contrary to this study, Bhuvan and Sharma (2004) observed that seed yield was significantly and positively correlated with number of capsules per plant, number of branches per plant, plant height and 1000-seed weight.

The phenotypic correlation revealed days to 50% flowering had positive and significant correlation with plant height, days to maturity and height to first capsule, number of seeds/capsule and number of primary branches as well as biomass yield. This shows the earliest flowering were the earliest maturing genotypes. This character exhibited negative and significant correlation with capsule filling period and oil content. Days to maturity had positive and highly significant association with plant height, height to first capsule, capsule filling period, number of primary branches, days to 50% flowering and positive significant correlation with 1000 seed weight. The correlation coefficient of this character with capsule length was negative and significant. Capsule filling period had positive and highly significant correlation with days to maturity and plant height. It had negative highly significant correlation with days to 50% flowering. Plant height had positive and highly significant correlation with height to first capsule, number of capsules/plant, days to maturity, capsule filling period, biomass yield, number of branches, number of seeds/capsule and days to 50% flowering. It had negative and non significant correlation with harvest index. Seeds/capsule showed positive and highly significant correlation with plant height, height to first capsule and days to 50% flowering. This indicates that late flowering accession had higher number of seeds/capsule than the early one. This character had negative and highly significant correlation with capsule length. Number of capsules/plant had positive and significant correlation with height to first capsule, biomass/plot, number of primary branches/plant and highly significant with plant height. This indicates the tallest plant had large number of capsules. Harvest index had negative and significant correlation with biomass/ha, but it was not correlated with any of the rest characters. Concerning oil content, it was negatively correlated with days to 50% flowering and plant height, while correlation with any other trait was not significant. This indicates the difficulty to select related traits in order to get high oil content (Table 3).

The genotypic correlation among other traits showed days to 50% flowering to have positive and highly significant correlations with plant height, height to first capsule, number of capsules/plant, days to maturity, biomass/ha, number of primary branches/plant and number of seeds/capsule. This suggests that dwarf plants were early in flowering. It had negative and highly significant correlation with capsule length, capsule filling period and oil content. This indicates early flowering plants had high oil content when compared to the late maturing plants. Days to maturity had positive and highly significant correlation with plant height, height to first capsule, capsule filling period, number of primary branches/plant and days to 50% flowering and significant correlation with number of capsules/plant, biological yield and 1000 seed weight. Only capsule length had negative and highly significant correlation with days to maturity. Harvest index had highly significant and positive correlation with number of capsules and also had positive and significant correlation with capsule length and oil content. This suggests selection of plants with large number of capsules is indirect selection of high harvest index. On the contrary it had negative and significant correlation with biological yield (Table 3).

Path coefficient analysis: The genotypic direct and indirect effect of different characters on seed yield/ha is presented in Table 4. Capsule filling period followed by days to 50% flowering, biomass/ha, 1000 seed weight and number of capsules/plant exerted positive prominent direct effect on seed yield. This indicates that a slight increase in one of the above traits may directly contribute to seed yield. Therefore, selecting genotypes having long capsule filling period, high biomass yield, days to 50% flowering and 1000 seeds weight could be used to improve seed yield in sesame genotypes as a result of their direct effect on yield.

Similar to this study, Bhuvan and Sharma (2004) observed that number of capsules per plant had a relatively high direct positive effect on seed yield per plant. The number of capsules per plant was significantly correlated with seed yield per plant having also maximum direct positive effect on it, as suggested by Narain *et al.* (2004). However, days to maturity, harvest index and oil content showed negative direct effect on seed yield. They only contributed to seed yield mainly via their highest and positive indirect effect with other characters. The oil content did not reveal prominent indirect effects via other traits on the seed yield/ha. Similar result, that oil content had negative direct effect on grain yield, was reported by Sumathi and Muralidharan (2010). Number of capsules/plant, height to first capsule, biomass/ha, number of primary branches/plant, number of seeds/capsule and plant height recorded a high positive indirect effect via days to 50% flowering on the seed yield/ha. Capsule length caused a high positive indirect effect via days to maturity on the seed yield/ha. Days to maturity revealed high positive indirect effect via capsule filling period and days to 50% flowering on seed yield/ha. Harvest index caused high and positive indirect effect via number of capsules/plant and days to maturity on seed yield/ha. Therefore, yield can be improved by selecting for number of capsules/plant, height to first capsule, biomass/ha, number of primary branches/plant, number of seeds/capsule, plant height, capsule length, days to maturity and harvest index as the result of their indirect effect on yield. The residual (0.1109) indicates that characters included in the genotypic path analysis explained 88.91% 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 harvest index, capsule filling period, days to 50% flowering and biological yield

Table 4: Estimates of direct (bold diagonal) and indirect effect (off diagonal) at genotypic level of 15 traits on grain yield in 81 sesame genotypes

	CL	PH	HFP	NC	DTM	CFP	HI	BPH	NB	IL	NSPP	TSW	FPF	OC	rg
CL	**0.079**	-0.061	-0.057	0.098	0.347	0.078	-0.076	0.174	-0.054	0.028	-0.06	-0.078	-0.321	-0.008	0.089
PH	0.021	**0.044**	0.022	-0.159	-0.475	-0.382	0.016	0.173	0.03	-0.001	0.011	0.09	0.742	0.023	0.155
HFP	0.027	0.039	**0.025**	-0.142	-0.556	-0.346	0.02	0.168	0.027	-0.11	0.012	0.08	0.791	0.018	0.053
NC	0.033	0.03	0.015	**0.236**	-0.379	-0.384	0.052	0.131	0.035	-0.303	0.013	0.154	0.39	0.031	0.054
DTM	0.025	0.019	0.013	-0.161	**-0.996**	0.475	0.01	0.088	0.018	-0.079	0.007	0.134	0.559	0.011	0.123
CFP	-0.004	-0.016	-0.006	0.02	-0.469	**0.997**	-0.003	-0.1	-0.006	-0.006	-0.005	0.037	-0.398	-0.014	0.027
HI	-0.021	-0.007	-0.005	0.32	0.31	0.235	**-0.102**	-0.13	-0.008	-0.014	-0.001	-0.01	-0.144	-0.019	0.404
BPH	0.04	0.047	0.012	-0.09	-0.281	-0.316	0.038	**0.343**	0.021	-0.026	0.011	0.076	0.329	0.012	0.216
NB	0.007	0.024	0.012	-0.151	-0.362	-0.111	0.014	0.133	**0.055**	0.011	0.003	0.038	0.471	0.006	0.15
IL	0.02	0.184	0.003	-0.023	-0.078	0.066	-0.015	0.096	-0.006	**-0.093**	0.007	0	0.003	-0.005	0.159
NSPP	0.057	0.044	0.038	-0.187	-0.341	-0.168	0.037	0.157	0.034	-0.023	**0.030**	0.004	0.393	0.008	0.084
TSW	0.009	0.015	0.008	-0.237	-0.392	0.151	0.004	0.099	0.003	0	0	**0.265**	0.082	0.004	0.011
FPF	0.028	0.134	0.018	-0.217	-0.559	-0.59	0.014	0.179	0.024	0	0.011	0.02	**0.995**	0.026	0.083
OC	-0.008	-0.013	-0.006	0.101	0.234	0.313	-0.026	-0.06	-0.002	-0.006	-0.003	-0.014	-0.361	**-0.074**	0.075

Residual Effect: 0.1109, CL: Capsule length (cm), PH: Plant height (cm), HFP: Height to first capsule (cm), NC: Number of capsules per plant, DTM: Days to maturity, CFP: Capsule filling period, HI: Harvest index, BPH: Biomass per hectare (kg), NB: Number of primary branches per plant, IL: Internodes length (cm), NSPP: Number of seed per capsule, TSW: Thousand seed weight (g) and FPF: Days to 50% flowering, OC: Oil content (%)

were important in respect of genetic variability, correlation and path coefficient analysis. The greater variability in these characters would give a prime scope for the development of high yielding through selection in the segregating generation.

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