Novelty Journals

ISSN 2394-966X

International Journal of Novel Research in Life Sciences
Vol. 4, Issue 2, pp: (34-44), Month: March – April 2017, Available at: www.noveltyjournals.com

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

[1]Desawi Hdru Teklu, [2]Sentayehu Alamerew Kebede, [3]Daniel Endale Gebremichael

[1]Ethiopian Agricultural Transformation Agency, P.O.Box 708, Addis Ababa, Ethiopia
[2]Jimma University P.O.Box 307, Jimma, Ethiopia
[3]Werer Agricultural Research Center, P.O.Box 2003, Addis Ababa, Ethiopia

Abstract: **Sixty four sesame accessions were evaluated in 8x8 simple lattice design at Humera in Western Tigray, in 2013/14. The objectives of the study were to estimate the genetic variability, association among characters, and to estimate genetic divergence among the accessions. Analysis of variance revealed that there was highly significant ($p<0.001$) difference among the sixty four accessions for all the fourteen characters studied. Number of capsule per plant and seed yield per hectare recorded high genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) but medium genotypic coefficients of variation (GCV) and high phenotypic coefficients of variation (PCV). The highest heritability value were for days to 50% flowering, plant height, height to first capsule and number of capsule per plant. Traits like, number of capsule per plan with high phenotypic coefficients of variation (PCV), genotypic coefficients of variation (GCV), heritability and genetic advance as a percent of mean. 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. Genotypic ally, path coefficient analysis based on grain yield as a dependent variable revealed that length of capsule bearing zone, number of primary branches per plant and 1000 seed weight exerted positive direct effect on seed yield. Thus, improvement through direct selection rather than a lengthy crossing program and hybridization involving crossing of the accessions from different clusters would produce viable and a potential segregant population.**

Keywords: **Genetic variability, Heritability, Genetic Advance, Genetic Advance as percentage of mean, Correlation, Path coefficient, sesamum indicum.**

1. 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 (Getinet *et al*. 1998). Even though the origin of sesame is still in debate, Mehra (1967) and Mahajan (2007) considered Ethiopia 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 Metric tons) (FAOSTAT, 2012) 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) was reported high PCV and GCV values for number of primary branches and seed yield per ha. Similarly, Yirgalem *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 Yirgalem *et al.* (2012) was a reported high heritability value 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. Similar result was reported by Siva *et al.* (2013) high heritability values for number of capsule per plant.

Ahadu (2008) reported that number of capsules per plant and number of primary branches per plant contributed significant positive correlation with seed yield and Fazal *et al.* (2011) reported that number of capsules per plant contributed significant positive correlation with seed yield.

Ahadu (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. In contrast result was reported by Yirgalem *et al*. (2012) days to maturity, height to first capsule and oil content which had negative direct effect on seed yield.

2. MATERIALS AND METHODS

The Experimental Sites: The experiment was conducted at Adebay site kafta Humera wereda of Western low lands 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 14^{o} 06' N latitude and 38^{o} 31'E longitude. The mean annual temperature is 33 ^{o}C and it has chromic vertisol soil type. Average annual rain fall varies from 400-650mm (EARO, 202).

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 Table1.

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

Data Collected: plot basis Quantitative data were measured from the central rows of each plot and 10 randomly selected plants with in rows were taken for the plant basis data, as described below.

Table 1: Sesame accessions used in the study

N0-	Accession	Location	Region	N0-	Accession	Location	Region
1	Endelemikiram sel-2	Metema	Amara	33	NN-0143	Shewa Robit	Amara
2	Bounja filwuha sel-2	Metema	Amara	34	NN-0145	Shewa Robit	Amara
3	Bounja sel-2	Metema	Amara	35	NN-0144	Shewa Robit	Amara
4	Gojam azene yohanis sel-1	Metema	Amara	36	NN-0128	Shewa Robit	Amara
5	Bounja maksegnit	Metema	Amara	37	NN-0136 sel-2	Shewa Robit	Amara
6	Bounja gobate sel-3	Metema	Amara	38	NN-0088	Shewa Robit	Amara
7	Gojam azene yohanis sel-6	Metema	Amara	39	NN-0084	Shewa Robit	Amara
8	Bounja filwuha sel-6	Metema	Amara	40	Acc-#031	Humera	Tigray
9	Gobyo (83)	Metema	Amara	41	Acc-22-12	Humera	Tigray
10	Gojam azene yohanis sel-2	Metema	Amara	42	Acc-031 sel-1	Humera	Tigray
11	Bounja maksegnit sel-5	Metema	Amara	43	Acc-202-516	Humera	Tigray

12	Bounja fiyel kolet sel-4	Metema	Amara	44	Acc-#032	Humera	Tigray
13	Gobyo 82-3	Metema	Amara	45	Acc-111-323	Humera	Tigray
14	Gobyo 82-2	Metema	Amara	46	Acc-00053	Humera	Tigray
15	Bounja fiyel kolet	Metema	Amara	47	Acc-No-024	Humera	Tigray
16	7B	Gonder	Amara	48	Acc-202-950	Wello	Amara
17	G-01	Gonder	Amara	49	Acc-111-524-1	Gojam	Amara
18	Abuna	Humera	Tigray	50	Acc-#226	Wello	Amara
19	Un known alamata sel-3	Wello	Amara	51	Acc-202-327	Wello	Amara
20	G-02	Gonder	Amara	52	Acc-020	Wello	Amara
21	NN-0097	Shewa Robit	Amara	53	Acc-044	Gojam	Amara
22	NN-0089	Shewa Robit	Amara	54	Acc-203-104	Gojam	Amara
23	Acc-111-866	Humera	Tigray	55	Acc-210-989 sel-1	Humera	Tigray
24	Acc-00026	Humera	Tigray	56	Acc-051-02 sel-2	Humera	Tigray
25	Acc-111-840	Humera	Tigray	57	Acc-No- 026	Humera	Tigray
26	Acc-00048	Humera	Tigray	58	Acc-038-sel-2	Metema	Amara
27	Acc-08	Humera	Tigray	59	Acc-200-495	Humera	Tigray
28	Acc-203-103	Humera	Tigray	60	Acc-202-307	Metema	Amara
29	Acc-016 sel-1	Humera	Tigray	61	Acc-208-950	Humera	Tigray
30	Acc-051-02 sel-5	Humera	Tigray	62	Setit-1	Cultivars	
31	Acc-00029	Humera	Tigray	63	Humera-1	Cultivars	
32	Acc-036	Humera	Tigray	64	Hirhir	Cultivars	

Source: Institute of biodiversity conservation and Research (IBC), Ethiopia

On plot basis:

1. Days to 50% flowering: number of days from emergence to a stage when 50% of the plants in a plot produced flower.

2. Days to maturity: number of days from p emergence to a stage when 90% of the plants in a plot produced matured capsules.

3. Capsule filling period: period in days from flowering to physiological maturity the plant two-third of the plant turns from green to yellow color.

4. 1000 Seed weight (g): weight in grams of 1000 seeds.

5. Seed yield per hectare (kg): seed yield was obtained from each experimental plot and was converted to get seed yield per hectare.

6. Oil content (%): Oil content was determined by wide line nuclear magnetic resonance (NMR). Seeds were bulked per each plot and oven dried at 130oC for 2 hrs and cooled for 30 minutes. 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:

1. Plant height (cm): height in centimeters from the ground level to the tip of the plant at maturity.

2. Height to first capsule (cm): Height from ground to first capsule.

3. Length of capsule bearing zone (cm): Height from first capsule to tip of the plant.

4. Number of primary branches per plant: number of branches originated from the main stem of on each of the ten randomly taken plants.

5. Number of capsules per plant: mean number of capsules will be obtained from ten randomly taken plants at harvest after maturity.

Novelty Journals

ISSN 2394-966X

International Journal of Novel Research in Life Sciences
Vol. 4, Issue 2, pp: (34-44), Month: March – April 2017, Available at: www.noveltyjournals.com

6. Capsule length (cm): length in centimeters of 5 capsules per plant from the ten randomly taken plants from the middle capsule.

7. Number of seeds per capsule: number of seeds per 5 capsules per plant from the ten randomly taken plants.

8. Inter node length (cm): length centimeters between two consecutive nodes at the middle part of the plant from the ten randomly taken plants.

3. 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). 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 5% and 1% probability levels. Homogeneity test for the error variance of two locations was done and they were heterogeneous. Hence, separate analysis was computed (SAS Institute, 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: -

Environmental variance (σ^2e) = MS_e

Phenotypic variance (σ^2p) =(σ^2g + σ^2e)

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

Where,

$Ms_{e=}$ Mean square error

$Ms_{t=}$ Mean square treatment

r= replication

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

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

Where,

σ^2p= phenotypic variance

σ^2g= 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 (σ^2g) to the phenotypic variance (σ^2p) and was estimated on genotype mean basis as described by Allard (1999) as:

$$h^2 B = \sigma^2 g / \sigma^2 p \text{ X } 100$$

Where,

Novelty Journals

ISSN 2394-966X

International Journal of Novel Research in Life Sciences
Vol. 4, Issue 2, pp: (34-44), Month: March – April 2017, Available at: www.noveltyjournals.com

h^2 B = Heritability in Broad sense

σ^2 p= phenotypic variance.

σ^2 g= genotypic variance.

Estimation of genetic advance: Genetic advance (GA) and percent 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 :

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

Where,

GA = expected genetic advance,

k = the standardized selection differential at 5% selection intensity (K = 2.063),

σ^2 p= phenotypic variance,

σ^2 g= genotypic variance.

The Genetic advance as % of mean (GAM) was computed as:

GAM = (GA/ x) x 100

Where,

GAM = genetic advance as percent 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:

$$r_p = \frac{pcovx.y}{\sqrt{\delta^2 px.\delta^2 py}} \qquad r_g = \frac{pcovx.y}{\sqrt{\delta^2 gx.\delta^2 gy}}$$

Where, r_p= phenotypic correlation coefficient and

r_g = genotypic correlation coefficient between characters x and y

Pcovxy = phenotypic covariance and

Gcovxy = 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 formula.

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

Where;-

r_{ij} = mutual association between the independent trait (i) and dependent trait (j) as measured by the correlation coefficient,

p_{ij} = component of direct effects of the independent trait (i) on the dependent variable (j); and $r_{ik}p_{kj}$ = 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 $R^2 = \Sigma rijpij$

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

Novelty Journals

ISSN 2394-966X

International Journal of Novel Research in Life Sciences
Vol. 4, Issue 2, pp: (34-44), Month: March – April 2017, Available at: www.noveltyjournals.com

4. RESULTS AND DISCUSSION

In the present study highly significant difference among sesame accessions ($p<0.001$) were observed for all traits studied. These findings indicate the presence of large variation among the tested sesame accessions. Similarly, Parameshwarappa *et al.* (2009) reported significant differences among 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. Ahadu (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 capsules per plant, seed yield (kg/ha), 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, Yirgalem *et al.* (2012) was 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.

Table 2: Estimates of range, mean, standard error (SE), phenotypic (σ2p), genotypic (σ2g) and environmental (σ2e) components of variances, phenotypic (PCV) and genotypic (GCV) coefficient of variability, broad sense heritability (H^2), expected genetic advance (GA) and genetic advance as percent of the mean (GA%) for 14 characters of sesame genotypes.

Characters	Range	Mean ± S.E Mean	$\sigma^2 g$	$\sigma^2 e$	$\sigma^2 p$	GCV (%)	PCV (%)	H^2(%)	GA	GAM
Days to 50% flowering	40-56	48±1.463	19.33	2.14	21.47	9.20	9.70	90.04	8.61	17.99
Days to maturity	80-100	92±1.480	7.32	2.190	9.51	2.94	3.35	76.97	4.89	5.31
Capsule filling period	31-51	44±1.902	6.74	3.62	10.36	5.85	7.26	65.07	4.32	9.72
Plant height (cm)	71.1-147.7	115.7±7.108	212.39	50.53	262.92	12.59	14.0	80.78	27.02	23.31
Height to first capsule (cm)	18.2-106.9	64.4±6.692	320.07	44.79	364.86	27.79	29.67	87.73	34.57	53.62
Length of capsule bearing zone (cm)	24-86.3	51.3± 6.005	87.92	36.06	123.98	18.37	21.82	70.92	16.29	31.87
Number Capsules per plant	11-76.5	36.3±3.413	148.41	11.65	160.06	33.59	34.88	92.72	24.17	66.63
Number of primary branches per plant	1.2-7.8	3.8±1.028	0.66	1.056	1.71	17.03	27.42	38.59	1.04	21.79
Inter node length (cm)	2.4-10.5	5.6±1.199	0.90	1.44	2.34	17.03	27.42	38.59	1.12	21.79
Capsule length (cm)	1.8-3.3	2.3±0.183	0.00	0.03	0.03	0.13	7.92	0.03	0.00	0.05
Number of seeds per capsule	27.3-79.2	55.8±5.763	54.09	33.22	87.30	13.24	16.82	61.95	11.94	21.46
1000 seed weight (g)	1.3-3.4	2.7±0.354	0.05	0.13	0.17	7.96	15.47	26.45	0.25	8.43
Oil content (%)	40-57.1	52.4± 1.250	4.25	1.56	5.82	3.94	4.60	73.13	3.63	6.93
Seed yield kg/ha	230.00-1290.00	846.70±156.73	48605.08	24563.81	73168.89	26.04	31.95	66.43	370.69	43.72

Variance components and coefficients of variation: Estimates of phenotypic (σ2p), genotypic (σ2g) and environmental (σ2e) 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 2.94 for days to maturity to 33.59 for number of capsule per plant. Similarly, phenotypic coefficients of variation ranged from 3.35 for days to maturity to 34.88 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 delineation, height to first capsule, 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 number of primary branches per plant and seed yield per hectare. Parameshwarappa *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) was reported high PCV and GCV values for number of primary branches and seed yield per ha. Similarly, Yirgalem *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.

Heritability and genetic advance: Heritability estimates for characters under study are 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 0.03% for capsule length to 92.72% for number of capsule per plant. 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 (90.04%), plant height (80.78%), height to first capsule (87.73%) and number of capsule per plant (92.72%). Similarly, Yirgalem *et al.* (2012) reported high heritability values for days to 50% flowering, height to first capsule and number of capsule per plant Similar result was reported by Siva *et.al.* (2013) high heritability values for number of capsule per plant. This indicates that very high indicates selection will be best approach. This is because there would be a close correspondence between the genotype and the phenotype due to the relative small contribution of the environment to the phenotype.

The range of genetic advance as a percent of mean ranged from 0.05% for capsule length to 66.6% for number of capsule. Within this range, height to first capsule (53.6), seed yield per hectare (43.7), length of capsule bearing zone (31.8) and plant height (23.3). And the Lowest estimate were observed below (23.3%) for days to 50% flowering, days to maturity, capsule filling period, number capsules per plant, number of primary branches per plant, inter node length, capsule length, number of seeds per capsule, 1000 seed weight and Oil content. This low genetic advance as percentage of 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.

Traits like, number of capsule per plant with high phenotypic coefficients of variation (PCV), genotypic coefficients of variation (GCV), heritability (h^2) and genetic advance as a percent of mean (GAM) and seed yield per hectare with high phenotypic coefficients of variation (PCV), genotypic coefficients of variation (GCV), moderately high heritability and genetic advance as a percent of mean very important for selection.

According to Siva *et al.* (2013) 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 economically important yield traits have been reported in sorghum by (Mahajan *et al*., 2011).

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 *et al*., 1990).

Seed yield showed positive and highly significant phenotypic association with length of capsule bearing zone (r=0.426), number of capsule (r=0.440) and number of primary branches (r=0.334). This shows that accessions providing higher percentage of length of capsule bearing zone, number of capsule and number of primary branches are high yielder. Similar result was report by Kathiresan and Gnanamurthy (2002) number of capsules per plant contributed significant positive correlation with seed yield. Similarly, Ahadu (2008) reported that number of capsules per plant and number of primary branches per plant contributed significant positive correlation with seed yield and Fazal *et al.* (2011) reported that number of capsules per plant contributed significant positive correlation with seed yield. Similarly, number of primary branches/plant was reported by sakila etal. (2000) and number of capsule/plant was reported by Kathiresan and Gnanamurthy (2000) contributed significant and positive correlation with seed yield.

Novelty Journals

ISSN 2394-966X

International Journal of Novel Research in Life Sciences
Vol. 4, Issue 2, pp: (34-44), Month: March – April 2017, Available at: www.noveltyjournals.com

Seed yield had positive and significant genotypic correlation with length of capsule bearing zone (r=0.49), number of primary branches per plant (r=0.353), capsule length (r=0.547) and 1000 seed weight (r=0.554) and number of seeds per capsule (r=0.275). Similarly, Tamina and Dasgupta (2003) reported that number of primary branches/plant contributed significant and positive correlation with seed yield at genotypic and phenotypic level. And Bhuvan and Sharma (2004) reported that Seed yield was positive and significant genotypic correlated with number of primary branches per plant and 1000 seed weight.

The phenotypic correlation revealed that number of branches/plant exhibited a positive and significant phenotypic correlation with days to 50% flowering and positive non significant with plant height to first capsule and length of capsule bearing zone. This indicates that late flowering genotypes had higher number of branches than early flowering. Number of capsules/plant had a positive and significant phenotypic correlation with length of capsule bearing zone and had positive non- significant with plant height and capsule filling period. This indicates that long capsule bearing zone genotypes had higher number of capsules/plant. Capsule length had a positive and significant phenotypic correlation with length of capsule bearing zone, number of capsule/plant and positive and non- significant with plant height, number of primary branches and inter node length. Oil content had a positive and significant phenotypic correlation with length of capsule bearing zone and positive and non-significant with capsule filling period, number of capsule per plant, inter node length, capsule length, number of seeds per capsule and 1000 seed weight and it had positive.

The genotypic correlation revealed that number of branches/plant exhibited positive and significant genotypic correlation with seed yield/ hectare and positive non- significant with inter node length, number of seeds per capsule and 1000 seed weight. This indicates that high branches/plant genotypes had higher seed yield/ hectare. Number of capsules/plant had positive and highly significant genotypic correlation with capsule length and number of seeds per capsule. Capsule length had positive and significant genotypic correlation with number of seeds per capsule, 1000 seed weight, seed yield per hectare and positive non-significant with oil content.

Table 3: Genotypic (above diagonal) and Phenotypic (below diagonal) correlation coefficients (rg) at Humera (2013/14).

	DF	DTM	CFP	PH	HFC	LCBZ	NC	NB	IL	CL	NSPP	TSW	OC	SYH
DF	1	0.819**	-0.815**	0.457**	0.641**	-0.427**	-0.178	0.513**	0.032*	-0.168	-0.171	-0.260*	-0.227	-0.156
DTM	0.718**	1	-0.335**	0.352**	0.220	-0.486**	-0.193	0.527**	0.038	-0.437**	-0.265*	-0.248	-0.264*	-0.440**
CFP	-0.736**	-0.064	1	-0.389**	-0.454**	0.220	0.108	-0.284*	0.014	-0.340**	-0.031	0.156	0.107	-0.088
PH	0.370**	0.265*	-0.268*	1	0.108	-0.049	0.115	0.131	0.018	-0.473**	0.07	-0.350**	-0.311*	-0.978**
HFC	0.568**	0.466**	-0.362**	0.762**	1	-0.623**	-0.308*	0.239	-0.193	-0.13	-0.089	-0.324*	-0.519**	0.031
LCBZ	-0.366**	-0.343**	0.201	0.072	-0.519**	1	0.713**	-0.236	0.357**	0.098	0.258*	0.097	0.539**	0.490**
NC	-0.140	-0.169	0.043	0.160	-0.265*	0.644**	1	0.249	0.059	0.349**	0.333**	-0.070	0.277*	-0.483**
NB	0.341**	0.282*	-0.211	0.213	0.175	0.034	0.266*	1	0.128	-0.45	0.052	0.187	0.079	0.353**
IL	0.035	0.039	-0.001	-0.073	-0.111	0.113	-0.010	-0.014	1	0.556**	0.202	-0.170	0.365**	-0.872**
CL	-0.082	-0.210	-0.085	0.085	-0.148	0.376**	0.373**	0.116	0.007	1	0.48**	0.544**	0.076	0.547**
NSPC	-0.115	-0.165	-0.021	0.125	-0.089	0.27	0.312*	0.115	-0.023	0.192	1	-0.425**	0.313*	0.275*
TSW	-0.137	-0.075	0.105	-0.101	-0.096	-0.030	-0.028	0.048	-0.010	-0.010	-0.157	1	0.110	0.554**
OC	-0.172	-0.169	0.091	-0.285*	-0.433**	0.315**	0.211	-0.031	0.183	0.183	0.154	0.120	1	0.211
SYH	-0.065	-0.166	-0.070	0.043	-0.202	0.426**	0.440**	0.334**	0.172	0.172	0.224	0.149	0.162	1

*and ** Indicates 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 = Number Capsules per plant, NB = Number of primary branches per plant, IL= Inter node length, CL= Capsule length, NSPC= Number of seeds per capsule, TSW = 1000 seed weight (g), OC=Oil content SYH= Seed yield (kg/ha).

Path coefficient analysis:

The genotypic direct and indirect effect of different characters on seed yield/hectare is presented in Table 4. Length of capsule bearing zone, had the highest positive direct effect on grain yield followed by 1000 seed weight, number of primary branch per plant, days to maturity, number of capsule/plant, height to first capsule, number of seeds per capsule and inter node length. 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. Therefore selecting genotypes having high length of capsule bearing zone, 1000 seed weight and number of primary branches/plant capsule and inter node length. This suggests the correlation revealed the true relationship a could be used to improve seed yield in sesame varieties as a result of their direct effect on grain yield.

Similar result was reported by Ahadu (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. In contrast result was reported by Yirgalem *et al*. (2012) days to maturity, height to first capsule and oil content which had positive direct effect on seed yield. However, days to flowering, capsule filling period, plant height and capsule length had negative direct effect on seed yield.

Therefore selecting genotypes having high length of capsule bearing zone, 1000 seed weight and number of primary branches/plant capsule and inter node length. This suggests the correlation revealed the true relationship could be used to improve seed yield in sesame varieties as a result of their direct effect on grain yield. The residual (0.285) indicates that characters which are included in the genotypic path analysis explained 71.5% 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 length of capsule bearing zone,1000 seed weight and number of primary branches/plant 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.

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

	DF	DTM	CFP	PH	HFC	LCBZ	NC	NB	IL	CL	NSPP	TSW	OC	Rg
DF	**-0.481**	0.31	0.891	-0.976	0.923	-0.74	-0.058	0.173	0.004	0.011	-0.041	-0.159	-0.013	-0.156
DTM	-0.214	**0.279**	0.366	-0.752	0.778	-0.842	-0.063	0.178	0.005	0.055	-0.063	-0.152	-0.015	-0.440**
CFP	0.207	-0.127	**-1.093**	0.829	-0.362	0.381	0.035	-0.096	0.002	0.041	-0.007	0.096	0.006	-0.088
PH	-0.677	0.134	0.425	**-1.135**	0.445	-0.084	0.038	0.044	0.002	0.044	0.018	-0.214	-0.018	-0.978**
HFC	-0.949	0.525	0.49	-0.739	**0.3**	-0.08	-0.101	0.381	-0.026	0.478	-0.021	-0.198	-0.029	0.031
LCBZ	0.632	-0.184	-0.24	0.104	-0.868	**0.735**	0.232	-0.079	0.048	-0.042	0.062	0.059	0.031	0.490**
NC	0.264	.-0.07	-0.118	-0.246	-0.925	0.237	**0.326**	0.084	0.008	-0.095	0.079	-0.043	0.016	-0.483**
NB	-0.759	0.199	0.311	-0.28	0.718	-0.409	0.081	**0.337**	0.017	0.008	0.012	0.114	0.004	0.353**
IL	-0.048	0.014	-0.016	-0.039	-0.579	-0.409	0.081	0.043	**0.133**	-0.017	0.048	-0.104	0.021	-0.872**
CL	0.211	-0.033	0.579	0.087	-0.392	0.05	0.015	-0.525	0.446	**-1.005**	0.634	0.228	0.252	0.547**
NSPC	0.253	-0.1	0.033	-0.159	-0.266	0.447	0.109	0.018	0.027	-0.085	**0.239**	-0.259	0.018	0.275**
TSW	0.385	-0.094	-0.171	0.748	-0.972	0.168	-0.023	0.063	-0.023	-0.044	-0.101	**0.612**	0.006	0.554**
OC	0.337	-0.4	-0.217	0.664	-0.758	0.334	0.09	0.027	0.049	-0.113	0.075	0.067	**0.056**	0.211

Residual Effect= 0.285 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 = Number Capsules per plant, NB = Number of primary branches per plant, IL= Inter node length, CL= Capsule length, NSPC= Number of seeds per capsule, TSW = 1000 seed weight (g), OC=Oil content rg = genotypic correlation with Seed yield (kg/ha).

REFERENCES

[1] Ahadu Menzir, 2008. Genetic Variability and Association of Characters in Sesame (*Sesamum Indicum* L.) Genotypes. An MSc Thesis presented to school of graduate Studies of Haramaya University. 20-45p. unpublished.

[2] Allard, R.W., 1999. Principles of Plant Breeding, 2nd ed. John Wiley and Sons Inc., New York. Pp.254.

[3] Bedigian, D., 1981. Origin, diversity, exploration and collection of sesame (*Sesamum indicum* L.). *In* Sesame: Status and Improvement. *FAO Plant Production and Protection Paper* 29, Pages 164-169.

[4] Bhuvan, J and M.K. Sharma, 2003.Character association studies in sesame (*Sesamum indicum* L.) under rain fed condition. Adv. Plant Sci., 17: 313-316.

[5] Burton, G.W. and E.H. de Vane., 1953. Estimating heritability in Tall Fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal* 45: 481-487.

[6] CSA, 2013. Ethiopian agricultural sample enumeration: Report on the primary results of area, production and yield of temporary crops of private Peasant holdings in Meher Season, Addis Ababa, Ethiopia.

[7] Deshmukh, S.N., M.S. Basu and P.S. Reddy, 1986. Genetic variability, character association and path coefficient analysis of quantitative traits in Viginia bunch varieties of ground nut. *Indian Journal of Agricultural Science*, 56:515-518

[8] Dewey, D.R. and K.H.Lu, 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal* 51: 515-518.

[9] Ethiopian Agricultural Research Organization (EARO), 2002. An assessment of the agricultural production base, Technological Packages and innovations and intervention strategies for commercial farmers in the Kafta-Humera Woreda of Tigray Regional State. Addis Ababa, Ethiopia.

[10] FAOSTAT of the United Nations, 2012. "Production Crops: sesame seeds".

[11] Fazal, A., Ashiq R., Zabta. And Shah Jehan K., 2011. Genetic Divergence in Sesame (*Sesamum Indicum* L.) Landraces Based on Qualitative and Quantitative Traits. Department of Biotechnology, Quaid-i-Azam University, Islamabad, Pakistan. *Pak. J. Bot., 43(6):* 2737-2744.

[12] Getinet Alemawu, Geremew Terefe, Kasahun Zewdie, and Bulcha Weyassa, 1998. Lowland Oil Crops: a three-decade research experiences in Ethiopia. Res. Report no.31, institute of agricultural Research, Addis Ababa. pp.13-18.

[13] Johnson, H.W., H.F Robinson and R.E. Comstock, 1955. Estimates of genetic and environmental variability in soybeans. *Agronomy Journal* 47: 314-318.

[14] Johnson, L.A., T.M. Suleiman, and E.W. Lusas., 1979. Sesame protein: A review and prospectus *Journal of American Oil Chemistry Society* 56:463-468.

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

[16] Mahajan, R.K., Bisht, I.S., and Dhillon, B.S., 2007. Establishment of a core collection of world sesame(*Sesamum indicum* l.) germplasm accessions. *SABRAO Journal of Breedingand Genetics.* 39(1):53-64.

[17] Mehra, K.L., 1967. Sesame in India. In:*Oilseed Crops, Tropical Agriculture Series*, p.p.282- 340, (Weiss, E.A., ed.). Longman, London.

[18] Miller, P.A., C. Williams, H.F. Robinson and R.E. Comstock, 1958. Estimates of genotypic and Environmental variances and co-variances in upland cotton and their implications in selection. *Agronomy Journal* 50:126 – 131.

[19] Parameshwarappa, K.G., M.G.Palakshappa and P.M.Salimath, 2009.Studies on genetic variability and character association in germplasm collection of sesame (*Sesamum indicum* L.).*Karnataka J. Agric. Sci.*, 22(2):252-254.

[20] Pascal Institute Software solution, 1994. GENRES, a statistical package for genetic researchers. Version 7.01.

[21] Sakila, M., S.M. Ibrahim, A. Kalamani and S. Backiyarani, 2000. Correlation studies in sesame (*Sesamum indicum* L.). *Sesame and Safflower News Letter* 15: 30-34.

[22] SAS, 2008. Statistical Analysis System. Version 9.2, SAS Institute Inc., Cary, NC., USA.

[23] Singh, B.D., 1990. Plant breeding: principles and methods. Kalyani Publishers, New Delhi.

[24] Siva P, Y. V. N., Krishna M.S.R. and Venkateswarlu Y., 2013. Correlation, path analysis and genetic variability for economical characteristics in F2 and F3 generations of the cross AVT 3 × TC 25 in Sesame (*Sesamum indicum* L.). Journal *of Environmental and Applied Bioresearch Department of Agricultural Botany, College of Agriculture, Pune, Maharashtra, India -411 005*, Vol. 1 (2):14-18.

[25] Spandana, B., Anuradha, G., Sivaraj N and Sivarama K.,2011. Determination of Genetic Variation in Indian Sesame (*Sesamum indicum*) Genotypes for Agro-Morphological Traits. Institute of Biotechnology (IBT), Acharya N.G. Ranga Agricultural University (ANGRAU), Hyderabad-500030, India. *Journal of Research in Agricultural Science* Vol. 7, No. 2, Pages: 88-99.

[26] Sudhakar, N., O .Sridevi and P. M. Salimath, 2007. Variability and character association analysis in sesame, *Sesamum indicum* L. *J Oilseeds Res*. 24 (1) :56-58.

[27] Sumathi, P. and V. Muralidharan, 2010. Analysis of genetic variability, association and path analysis in the hybrids of sesame (*Sesamum indicum L.*).*Tropical Agric. Res. and Ext.* 13(3).

[28] Tamina, B. and T.Dasgupta, 2003. Character association in sesame (*Sesamum indicum* L.). *Indian Agricst.*, 47(3/4): 253-258

[29] Thangavel, P., K. Saravanan, P. Senthil-Kumar, Y. Anbuselvan and J. Ganesan, 2000. Variabilty,heritability and genetic advance in sesame *(Sesamum indicum* L.). *Sesame and Safflower News Letter* 15:50-55.

[30] Weiss, E.A., 1983. *Oilseed Crops, Tropical Agriculture Series*. P.282-340. Longman, London.

[31] Wijnands, J.H.M., Biersteker, J. and Van Loo,E.N., 2009. Oilseeds business opportunities in Ethiopia. Public private partnership in oil seed.

[32] Yirgalem Tsehaye, Sintayehu Alamerew and Geremew Terefe, 2012. Extent and pattern of the genetic diversity for morpho-agronomic Traits in Ethiopian sesame landraces (*sesamum indicum* L.) *Asian Journal of Agricultural Research*, 6:118-128.