DOI: http://dx.doi.org/10.4314/star.v3i4.1
ISSN: 2226-7522(Print) and 2305-3372 (Online)
Science, Technology and Arts Research Journal
Sci. Technol. Arts Res. J., Oct-Dec 2014, 3(4): 01-09
Journal Homepage: http://www.starjournal.org/

Original Research

Correlation and Divergence Analysis for Phenotypic Traits in Sesame (*Sesamum indicum* L.) Genotypes

Gadisa Hika[1], Negash Geleta[2*] and Zerihun Jaleta[2]

[1]Arjo Preparatory school, P.O. Box: 10, Arjo, East Wollega, Ethiopia

[2]Department of Plant Sciences, College of Agriculture and Natural Resources, Wollega University, P.O. Box: 395, Nekemte, Ethiopia

Abstract

A study was conducted to determine the magnitude of associations of traits and genetic divergence among the 64 sesame genotypes. The genotypes were arranged in 8 x 8 simple lattice design and grown in Arjo district, Western Ethiopia during 2013 cropping season. Data were recorded for 12 phenotypic traits and analyzed using SAS software version 9.20 (2002, USA). The results showed that seed yield had positive and significant genotypic and phenotypic correlations with all traits, indicating they are important yield components and can be used for yield improvement in sesame breeding program except for PH and BY. Further analysis by path coefficient method indicated that at genotypic level DM, CFP and HI exerted high positive direct effects on seed yield and strong and positive correlation with seed yield. Similarly, at phenotypic level positive and high direct effects were exerted by CFP, NPB and HI on seed yield and these traits had also strong positive associations with SY. Genetic distance analysis showed that the 64 sesame genotypes were grouped in to 4 clusters and maximum inter cluster square distance (D^2) was recorded between cluster I and II followed by cluster I and III. Hence crossing involving cluster I with II and cluster I and III may exhibit high heterotic values and could give transgressive segregants. The principal component analysis revealed that four principal components explained about 66% of the total variation existed among the genotypes. The dominant seed color observed was brown followed by white in the genotypes. The study generally indicated that there was significance genetic variability or divergence among the genotypes. Thus, there is enormous opportunity to use the existing genotypes for direct selection as well as using distant parents for crossing purposes to improve specific traits.

Article Information

Article History:

Received : 19-10-2014

Revised : 21-12-2014

Accepted : 27-12-2014

Keywords:

Correlation

Divergence analysis

Genotypes

Path analysis

Sesame

***Corresponding Author:**

Negash Geleta

E-mail:

ayananegash@yahoo.com

INTRODUCTION

Sesame (*Sesamum indicum* L.) is a diploid species with 2x = 2n = 26 chromosomes. It is a self pollinated crop, belongs to the *Pedaliaceae* family, containing 60 species organized into 16 genera (Ashri 1998; Zhang *et al*., 2013). The genus Sesamum comprises of 36 species (Kobayashi, 1981). *Sesamum indicum* L. is the most commonly cultivated species (Nayar and Mehra, 1970). It is the oldest oilseed crop known to man and is now grown in many parts of the world (Bedigian and Harlan, 1986); and it is currently grown in more than 50 countries in the world. India ranks first in production and one third of the world production and nearly 30% of the sesame acreage in the world is from India. Sesame is a small farmers' crop in the developing countries and it is grown in the small plots (Gulhan *et al*., 2004).

Sesame is adapted in tropical to the temperate zones from about 40° N to 40° S latitude. It grows best on the areas between an altitude of 500 and 800 masl and it can grow even up to 1250 masl on well drained soils of moderate fertility. It is an annual occasionally perennial crop. It needs a growing period of 70 to 150 days; usually 100 to 120 days. The optimum pH for growth ranges from 5.4 to 6.7. Good drainage is crucial, as sesame is very susceptible to short periods of water logging. It is intolerant of very acidic or saline soils. The optimum temperature for growth varies with cultivar in the range 27 to 35 °C. Periods of high temperature above 40°C during flowering reduce number of capsule and seed development. It requires from 600 to 1000 mm amount of water (Nath *et al*., 2000).

Sesame seed is used for confectionery purpose and an important source of edible oil and is also widely used as a spice. The seed contains 50 to 60% oil which has excellent stability due to the presence of natural antioxidants such as sesamolin, sesamin and sesamol (Brar and Ahuja, 1979).The fatty acid composition of sesame oil varies considerably among the different cultivars worldwide (Yermanos *et al*., 1972). In addition, it is used as pharmaceutical and skin care products and as a synergist for insecticides (Salunkhe and Desai, 1986).

Generally 100 % of the world production area is found in developing countries with largest area in India, Myanmar, China, Nigeria, and Uganda (FAO, 1995). Total world production of sesame in 2005 was in 9.35 million hectare with 3.7 million metric tons, 70% of which was produced in Asia and 26 % in Africa (FAO, 2005). Sesame is a valuable crop for Ethiopia both for local uses and export market. Ethiopia is the 7th major sesame producing country in the world and has an export share of 5.1%. There are around 21 countries that are major importers of sesame from Ethiopia. In 1999, Ethiopia exported about 30,000 tons of sesame worth 28 million USD. The total area under sesame in Ethiopia is estimated at 384,682.79 hectare and production is about 327,740.922 tones and productivity is about 0.852 ton/ha (CSA, 2011).

The average productivity of sesame is low as compared to other oilseeds due to the lack of high yielding cultivars, resistant to major insect pests and diseases and shattering problem. Since sesame has been treated as less input intensive crop, the role of breeding improved varieties has been considered as promising approach (Ashri, 1988). But there is a potential harvest reported elsewhere, as of 3.6 t/ha in Nigeria (Uzo and Ojiake, 1981). Like other crops, productivity and associated increase in production of sesame could be achieved through development of improved varieties which have less shattering problem with better cultural practices. Selection of germplasms for desirable traits needs thorough studies about the manner of traits interrelationships and divergence among the populations. Selection is an integral part of breeding program by which genotypes with high productivity in a given environment are selected. However, selection for high yield is made difficult by the complex nature of this trait (Singh and Singh, 1973; Sastri, 1974); it is highly influenced by environment, which reduces the progress to be achieved through direct selection. In such cases, indirect selection techniques are more promising to improve the economic trait. This selection criterion takes into account the information on interrelationship among agronomic characters, their relationship with grain yield as well as their direct influence on grain yield (Dewey and Lu, 1959). In addition, knowledge on the extent and pattern of genetic divergence present in a population is absolutely essential for further improvement of the crop. Hence the objectives of the study were to estimate the magnitude of interrelationships among yield and yield related traits of sesame genotypes; and to estimate the extent of genetic divergence among sesame accessions.

MATERIALS AND METHODS

Experimental Site

The experiment was carried out at Jima Arjo district, Eastern Wollega Zone of Oromia Regional State, Western Ethiopia during 2013 cropping season. Jima Arjo district is 378 km to the west of Addis Ababa and 48 km away from the Nekemte town. The area is located at an altitudinal ranges from 1200-1816 masl. The area receives an average annual rainfall that ranges from 824-2616 mm. The average annual temperature ranges from 18-26^{0}C (Source: Jima Arjo Agricultural Office).

Experimental Materials and Design

The experimental material consisted of 64 sesame genotypes that were collected from the Institute of Biodiversity Conservation (IBC) (Table 1). The trial was laid out in 8x 8 simple lattice design. Seeds of each genotype was sown in rows by hand on a separate plot size of 6.4m^2 (4 rows x 4m row length x 40cm between rows and 10cm between plants with in rows). Other cultural practices were followed as recommended for the area and no fertilizer was applied.

Data Collection

Data were collected for days to 50% flowering, days to 90 % maturity, capsule filling period, plant height, number of branches per plant, number of primary branches per plant, number of capsules per plant, thousand seed weight, biomass yield, seed yield, harvest index, and seed color.

Data Analysis

Correlation Analysis

Estimation of the phenotypic and genotypic correlation coefficients were computed following the procedures suggested by Miller *et al*. (1958) and adopted by Dabholkar (1992) from corresponding variance and covariance components. The significance of phenotypic correlation coefficients was tested by the formula of Singh and Chaudhary (1985); whereas the significance of genotypic correlation coefficient is tested using the formula described by Robertson (1959).

Path Coefficient Analysis

In path coefficient analysis, direct and indirect effects of the independent characters on dependent character (seed yield) was estimated following the procedures of Dewey and Lu (1959).

Genetic Divergence Analysis

Genetic divergence analysis was computed based on multivariate analysis using Mahalanobis's D^2 statistic (Mahalanobis, 1936) using SAS Software program (SAS, 2002, Version 9.0, USA). Squared distance (D^2) for pairs of genotypes was computed using the following formula: $D^2ij = (Xi- Xj)/ S^{-1} (Xi – Xj)$; Where, D^2ij = the square distance between any two genotypes i and j, Xi and Xj = the vectors for the values for genotypes ith and jth, and S^{-1} = the inverse of pooled variance covariance matrix. Based on the squared distances (D^2) values, clustering of genotypes was done using Tocher's method as described by Singh and Chaudhary (1999).

Principal Component Analysis

Principal component analysis (PCA) was used to find out the characters, which accounted more to the total variation. The data were standardized to mean zero and variance of one before computing principal component analysis. Principal components based on correlation matrix were calculated using SAS software.

RESULTS

Correlations among Agronomic Traits

Estimates of phenotypic and genotypic correlation coefficients between each pair of characters are presented in Table 2. The magnitudes of genotypic correlation coefficients for most of the characters were higher than their corresponding phenotypic correlation coefficients, except in few cases, which indicate the presence of inherent or genetic association among various characters. Seed yield showed positive and significant correlations with DF, DM, PB, BPP, CPP, TSW and HI at both genotypic and phenotypic levels and

Table 1: List of sesame genotypes used for the study

No	Accession Code	Region	Zone	District	Altitude
1	9242	Oromiya	Misrak Harerge	Goro Gutu	1620
2	202286	Amhara	Semen Shewa	Kewet	1490
3	202287	Amhara	Oromiya	Artuma Fursina Jile	1730
4	202288	Amhara	Oromiya	Artuma Fursina Jile	1770
5	202289	Amhara	Oromiya	Artuma Fursina Jile	1770
6	202306	Amhara	Oromiya	ChefeGolanaDewerah	1510
7	202308	Amhara	Oromiya	Chefe Golana ewerah	1455
8	202309	Amhara	Oromiya	ChefeGolanaDewerah	1440
9	202312	Amhara	Oromiya	Chefe olana Dewerah	1393
10	202313	Amhara	Oromiya	Chefe olana Dewerah	1390
11	202315	Amhara	Oromiya	Chefe olana Dewerah	1445
12	202317	Amhara	Oromiya	Chefe Golana ewerah	1355
13	202318	Amhara	Debub Wello	Kalu	1525
14	202320	Amhara	Oromiya	Bati	1505
15	202323	Amhara	Oromiya	Bati	1585
16	202327	Amhara	Oromiya	Bati	1470
17	202329	Amhara	Oromiya	Bati	1420
18	202330	Amhara	Debub Wello	Werebabu	1430
19	202332	Amhara	Debub Wello	Werebabu	1690
20	202335	Amhara	Debub Wello	Werebabu	1360
21	202339	Amhara	Debub Wello	Tehuledere	1645
22	202343	Amhara	Semen Wello	Habru	1580
23	202345	Amhara	Semen Wello	Habru	1565
24	202353	Amhara	Semen Wello	Guba Lafto	1640
25	202356	Amhara	Semen Wello	Guba Lafto	1770
26	202360	Amhara	Semen Wello	Guba Lafto	1675
27	202364	Amhara	Semen Wello	Guba Lafto	1520
28	202370	Amhara	Semen Wello	Kobo	1590
29	202373	Amhara	Semen Wello	Kobo	1790
30	202374	Amhara	Semen Shewa	Efratana Gidim	1395
31	202511	Amhara	Semen Shewa	Not Available	1475
32	203099	SNNP	Gurage	Goro	1240
33	203104	Oromiya	Jimma	Sokoru	1400
34	211921	Amhara	Misrak Gojam	Dejen	1600
35	212632	Amhara	Debub Wello	Ambasel	1460
36	212633	Amhara	Debub Wello	Ambasel	1540
37	212994	SNNP	Bench Maji	Dirashe Special	1270
38	212995	SNNP	Semen Omo	Gofa Zuria	1290
39	214254	Amhara	Semen Gondar	Addi Arkay	1630
40	215816	Oromiya	Misrak Wellega	Diga Leka	1435
41	216896	Oromiya	Arssi	Merti	1570
42	228816	Oromiya	Misrak Harerge	Babile	1500
43	235405	Tigray	Debubawi	Rayaazebo	1650
44	241291	Amhara	Debub Wello	Kalu	1500
45	241992	Amhara	Debub Wello	Kalu	1660
46	241293	Amhara	Debub Wello	Kalu	1550
47	241294	Amhara	Oromiya	Bati	1380
48	241295	Amhara	Oromiya	Bati	1380
49	241296	Amhara	Oromiya	Bati	1350
50	241297	Amhara	Oromiya	Bati	1280
51	241298	Amhara	Oromiya	Bati	1280
52	241299	Amhara	Oromiya	Bati	1750
53	241300	Amhara	Oromiya	Bati	1500
54	241301	Amhara	Oromiya	Chefe olana Dewerah	1600
55	241302	Amhara	Oromiya	Chefe olana Dewerah	1450
56	241303	Amhara	Oromiya	Artuma Fursina Jile	1800
57	241304	Amhara	Oromiya	Artuma Fursina Jile	1750
58	241305	Tigray	Mirabawi	Tahtay Adiyabo	1200
59	241314	Amhara	Semen Gondar	Addi Arkay	1460
60	241320	Amhara	Semen Gondar	Lay Armacho	1300
61	241328	Amhara	Semen Gondar	Sanja	1230
62	241329	Amhara	Semen Gondar	Alefa	1400
63	241347	Amhara	Semen Gondar	Belesa	1700
64	241348	Amhara	Semen Gondar	Belesa	1700

significant and positive correlation with CFP at genotypic level. Therefore, from the correlation analysis it can be confirmed that DF, DM, CFP, PB, BPP, CPP, TSW and HI were found to be important yield related traits. Most phenologic and vegetative characters showed positive and significant correlations among themselves. Similarly, yield components also showed in most cases positive and significant correlations among each other at genotypic

and phenotypic levels. Number of branches per plant exhibited positive and significant genotypic and phenotypic correlations with DF, DM, PB, TSW; and HI at both genotypic and phenotypic levels; and it had significant and positive correlation with CFP, and PH, at genotypic level.

Number of capsule per plant had positive and significant genotypic and phenotypic correlations with CFP, PH, PB and TSW; and it had positive and significant correlation with days to 50 % flowering, at genotypic level only. Biomass yield had positive and significant genotypic and phenotypic correlations with days to 50 % flowering, days to 90 % maturity, and plant height while it had negative and significant correlation with harvest index. These indicate that these traits can be improved simultaneously through selection except for harvest index. Thousand seed weight had significant and positive genotypic and phenotypic correlations with capsule filling period, plant height and number of branches per plant, number of primary branches per plant; and it had positive and significant correlations with harvest index at genotypic level only. Generally, positive and significant association of pairs of characters at phenotypic and genotypic level justified the possibility of correlated response to selection.

Table 2: Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients among seed yield and other traits

Traits	DF	DTM	CFP	PH	PB	BPP	CPP	TSW	BY	SY	HI
DF		0.847**	0.456**	0.691**	0.825**	0.866**	0.404**	0.116	0.569**	0.753**	0.702**
DM	0.77**		0.043	0.307*	0.678**	0.598**	0.077	0.119	0.913**	0.878**	0.576**
CFP	0.306*	0.005		0.868**	0.297	0.465**	0.905**	0.354*	0.145	0.429**	0.079
PH	0.582**	0.167	0.867**		0.391*	0.457**	0.861**	0.925**	0.832**	0.075	0.383*
PB	0.742**	0.533**	0.148	0.239		0.931**	0.482**	0.689**	0.059	0.482**	0.937**
BPP	0.868**	0.5**	0.341*	0.291	0.931**		0.364*	0.583**	0.043	0.503**	0.865**
CPP	0.229	0.013	0.826**	0.817**	0.351*	0.218		0.974**	0.223	0.639**	0.385*
TSW	0.026	0.028	0.196	0.895**	0.576**	0.453**	0.963**		0.149	0.515**	0.432**
BY	0.412**	0.873**	0.059	0.809**	0.012	0.007	0.095	0.046		0.041	-0.755**
SY	0.654**	0.824**	0.268	0.011	0.473**	0.485**	0.509**	0.352*	0.005		0.399*
HI	0.576**	0.424**	0.024	0.209	0.91**	0.789**	0.233	0.28	-0.766**	0.385*	

*, ** = Significant at 5% and 1% probability level, respectively. DF = Days to 50% flowering, DM = Days to maturity, CFP = Capsule filling period, PH=Plant height (cm), PB= Number of primary barnches per plant, BPP = Number of branches per plant, CPP = Number of Capsules per plant, SY = Seed yield (kg/h), BY = Biomass yield (kg/h), SW = 1000 seed weight (g).

Path Coefficient Analysis

In the present study, based on their correlation coefficients, 10 independent variables that have direct relationship with seed yield were included in the path analysis. The phenotypic and genotypic correlations were partitioned in to direct and indirect effects using seed yield as a dependent variable separately. The genotypic direct and indirect effects of different characters on seed yield are presented in Table 3. Positive and high direct effect was exerted by DM, CFP, BPB, and HI on seed yield while negative and high direct effect was exerted by DF, NPB and CPP. The high significant correlation coefficient between seed yield and DF was due to its high indirect effects through DM and CFP on seed yield. The high positive correlation coefficient between seed yield and CPP was due the large indirect effects of CFP and HI. Similarly, DM, CFP and HI had high positive direct effects on seed yield and also they have strong correlation with seed yield indicating the most important yield components at genotypic level. The residual effect 8.74% indicates that characters which are included in the genotypic path analysis explained 91.26 % of the total variation in seed yield.

Positive and high direct effects on seed yield were observed at phenotypic level by CFP, PH, NPB, BY and HI while negative and high direct effect on seed yield were observed by DF, DM BPP, CPP, and TSW (Table 4). The positive and significant correlation coefficients of DF and DM with SY were due to the positive indirect effects of CFP, PH, NPB, BY and HI through DF on SY. Similarly, CFP, NPB, and HI had strong positive correlation as well positive direct effects on SY indicating they are more importantly related to SY at phenotypic level. The residual effect determines unaccounted variability of the dependent factor (seed yield). It's magnitude 3.4 % indicated that the characters included in the path analysis explained 96.6% of the phenotypic variation in seed yield.

Table 3: Estimates of direct (diagonal) & indirect (off diagonal) effects for different traits on seed yield at genotypic level

Traits	DF	DM	CFP	PH	NPB	BPP	CPP	TSW	BM	HI	rg
DF	**-5.71**	4.359	1.664	-0.019	-0.484	0.14	-0.299	-0.05	-0.148	1.301	0.753**
DM	-4.84	**5.15**	0.16	-0.01	-0.4	0.1	-0.06	-0.05	-0.24	1.07	0.878**
CFP	-2.6	0.22	**3.65**	-0.02	-0.17	0.08	-0.67	-0.15	-0.04	0.15	0.429**
PH	-3.95	1.58	3.17	**-0.03**	-0.23	0.07	-0.64	-0.4	-0.22	0.71	0.075
NPB	-4.711	3.489	1.084	-0.011	**-0.587**	0.151	-0.357	-0.296	-0.015	1.735	0.482**
BPP	-4.94	3.08	1.7	-0.01	-0.55	**0.16**	-0.27	-0.25	-0.01	1.6	0.503
CPP	-2.31	0.4	3.3	-0.02	-0.28	0.06	**-0.74**	-0.42	-0.06	0.71	0.639**
TSW	-0.662	0.612	1.292	-0.026	-0.404	0.094	-0.722	**-0.43**	-0.039	0.799	0.515**
BM	-3.25	4.7	0.53	-0.02	-0.03	0.01	-0.17	-0.06	**-0.26**	-1.4	0.041
HI	-4.01	2.96	0.29	-0.01	-0.55	0.14	-0.29	-0.19	0.2	**1.85**	0.399*

Residual = 0.0874;

DF = Days to 50% flowering, DM = Days to 95 % maturity, PH=plant height, CFP=Days to capsule filling period, PB= Number of primary branches per plant, BPP = Number of branches per Plant, CPP= number of capsules per plant, BY=Biomass yield per ha, SW= thousand seed weight, rp = phenotypic correlation with seed yield.

Table 4: Estimates of direct (bold diagonal) and indirect (off diagonal) effects of different traits on seed yield at phenotypic level

Traits	DF	DM	CFP	PH	NPB	BPP	CPP	TSW	BY	HI	rp
DF	**-16.43**	-5.219	3.938	6.698	28.125	-18.056	-4.145	-0.221	3.288	2.672	**0.654****
DM	-12.65	**-6.78**	0.06	1.92	20.2	-10.4	-0.24	-0.24	6.97	1.97	**0.820****
CFP	-5.03	-0.03	**12.87**	9.98	5.61	-7.09	-14.95	-1.67	0.47	0.11	**0.268**
PH	-9.56	-1.132	11.158	**11.51**	9.059	-6.053	-14.789	-7.607	6.456	0.97	**0.011**
NPB	-12.19	-3.61	1.9	2.75	**37.9**	-19.36	-6.35	-4.9	0.1	4.23	**0.470****
BPP	-14.26	-3.39	4.39	3.35	35.27	**-20.8**	-3.95	-3.85	0.06	3.66	**0.490****
CPP	-3.762	-0.088	10.631	9.403	13.305	-4.535	**-18.1**	-8.185	0.758	1.084	**0.509****
TSW	-0.43	-0.19	2.52	10.3	21.83	-9.42	-17.43	**-8.5**	0.37	1.3	**0.352***
BY	-6.77	-5.92	0.76	9.31	0.45	-0.15	-1.72	-0.39	**7.98**	-3.56	0.005
HI	-9.45	-2.87	0.31	2.4	34.49	-16.41	-4.22	-2.38	-6.12	**4.64**	0.385*

Residual =0.034

DF = Days to 50% flowering, DM = Days to maturity, PH=plant height, PB=Number of primary branch per plant, PB= Number of primary branches per plant, BPP = Number of branches per plant, CPP= number of capsules per plant, BY=Biomass yield per plots= thousand seed weight, rg = genotypic correlation with seed yield.

Genetic Divergence Analysis

Description of germplasm collection for agronomical useful characters is important prerequisite for effective and efficient utilization of germplasm collection in breeding program. Significant differences among varieties for all or majority of the characters would justify further calculation of D^2 (Sharma, 1998). The D^2 values based on the pooled mean of genotypes resulted in classifying the 64 genotypes in to four distinct clusters (Figure 1). Cluster II were the largest clusters (45.31%) containing 29 genotypes followed by Cluster I (26.56%) which had 17 genotypes, then Cluster III that had 15 (23.44%) genotypes and finally cluster IV (4.68%) with 3 genotypes which had outstanding performance than any other genotypes in other clusters.

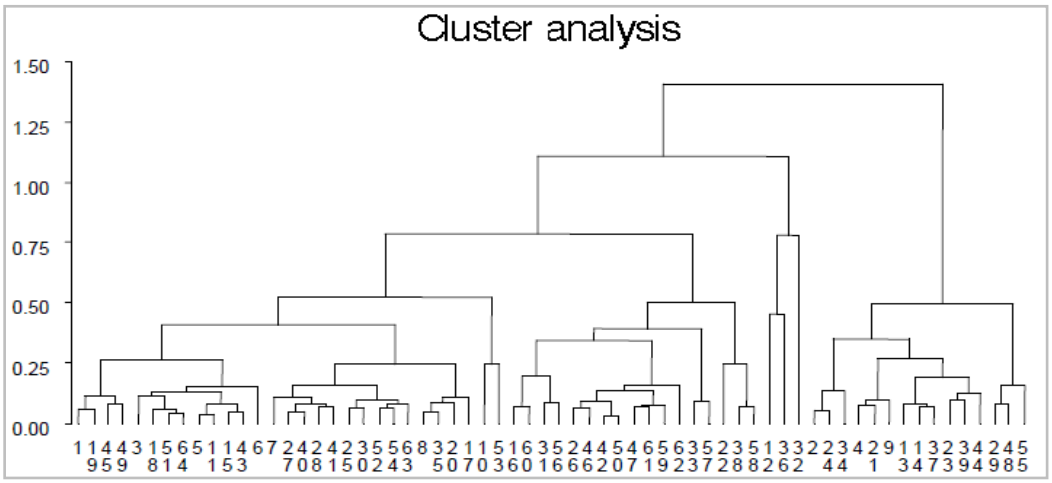

Figure 1: Dendrogram of 64 genotypes of sesame based on evaluation for 12 characters

Cluster Mean Analysis

The mean value of the 11 quantitative characters in each cluster is presented in Table 5. Cluster I consisted of fifteen genotypes having the characteristic of late flowering, late maturing, longer period of days to fill the capsule, lowest biomass and higher harvest index. Cluster II consisted of 3 genotypes. This cluster could be characterized by longer PH, higher NPB, BPP, TSW, BY, SY and HI. Cluster III consisted of 17 genotypes characterized by longer CFP, CPP, lowest for BY and HI. Cluster IV had 29 genotypes which are characterized by the following features: Highest in PH, lowest in SY and HI.

Table 5: Mean values of 11 morphological characters of the four clusters for sesame genotypes

Traits	CI*	CII	CIII	CIV
Days to 5% flowering	60.6	59.5	60.05	60.52
Days to 95 % maturity	135.17	133.5	134.3	131.16
Capsule filling period	45.43	46.67	48.09	46.03
Plant height, cm	102.93	105.3	103.2	105.66
Number of primary branches per plant	2.7	7.3	2.41	2.21
Number of branches per plant	2.9	7.5	3.12	2.91
Number of capsules per plant	87.57	90.67	92.8	90.62
Hundred seed weight, g	2.24	2.88	2.49	2.38
Biological yield (g/plot)	626.2	1087.67	1200.56	967.57
Seed yield (kg/ ha)	473.79	801.361	462.729	467.723
Harvest index	0.24	0.237	0.136	0.17

*CI-cluster 1; CII- Cluster 2; C-III Cluster 3 and CIV- Cluster 4

Estimation of Intra and Inter-Cluster Square Distances

The average intra- and inter-cluster D^2 values are presented in Table 6. Maximum average intra cluster D^2 was obtained in cluster III followed by cluster I. The lowest D^2 was recorded in cluster II, which shows the presence of less genetic variability or diversity within this cluster.

Table 6: Average intra (bold) and inter cluster (off diagonal) D^2 values among four clusters in sesame genotypes

Clusters	CI	CII	CIII	CIV
CI	**3.04**	141.63**	50.15**	42.50**
CII		**2.33**	34.75**	38.36**
CIII			**3.19**	9.02
CIV				**2.65**

x^2 = 22.36, and 27.69 at 5% and 1% probability level respectively

The x^2- test for the four clusters indicated that there was a statistically significant difference between pairs of clusters except cluster III with IV. The highest average inter-cluster D^2 value was recorded between cluster I and cluster II followed by cluster I and cluster III and cluster I and cluster IV which had shown these clusters were genetically more divergent from each other than any other clusters.

Minimum inter-cluster distance was observed between cluster III and cluster IV indicating that genotypes in these clusters were not genetically diverse or there was little genetic diversity between these clusters. This signifies that, crossing of genotypes from these two clusters might not give higher hetrotic value in F1 and narrow range of variability in the segregating F2 population. Maximum genetic recombination is expected from the hybridization of the parents selected from divergent cluster groups. Therefore, maximum recombination and segregation of the progenies is expected from crosses involving parents selected from cluster II and IV followed by I and cluster III; however the breeder must specify his/her objectives in order to make best use of the characters where the characters are divergent.

Principal Component Analysis

The principal component analysis (Table 7) revealed that four principal components PC1, PC2, PC3, and PC4 with eigen values 3.36, 2.94, 1.68,and 1.28, respectively, have accounted for 66% of the total variation. The first two principal components PC1 and PC2 with values of 24 % and 21 %, respectively, contributed more to the total variation. Therefore, in this study, differentiation of the genotypes into different cluster was because of a cumulative effect of a number of characters rather than the contribution of specific few characters. Agronomic characters having relatively higher value in the first principal component (PC1) were number of branch per plant, seed and biomass yield, harvest index and thousand seed weight had more contribution to the total diversity and they were responsible for the differentiation of the genotypes. Characters like capsule filling period, thousand seed weight and biomass yield per plot had contributed a lot for principal component (PC2); number of branches per plant , days to maturity and capsule filling period had contributed in the third principal component (PC3); days to 50 % flowering, days to maturity, harvest index ,number of capsule filling period, seed yield and number of capsules per plant in the fourth principal component (PC4); were the major contributors to each principal components (PC).

Table 7: Eigenvectors and eigen values of the first four principal components (PCs) for different characters of sesame genotypes

Traits	PC1	PC2	PC3	PC4
Days to 50% flowering	-0.014	-0.021	0.104	0.154
Days to maturity	0.034	0.037	0.327	0.624
Capsule filling period	-0.027	0.193	0.119	0.220
Plant height (cm)	0.083	-0.058	-0.505	0.097
Number of primary branches per plant	0.397	0.168	0.344	-0.190
Number of branches per plant	0.348	0.163	0.419	-0.124
Number of capsules per plant	-0.028	0.112	-0.012	0.643
Thousand Seed weight (g)	0.307	0.251	-0.187	-0.085
Biomass yield per plot (g/plot)	0.055	0.544	-0.188	-0.005
Harvest Index	0.244	-0.483	0.007	0.128
Seed yield (kg/ ha)	0.490	0.044	-0.220	0.119
Eigen value	3.36	2.94	1.68	1.28
Difference	0.414	1.26	0.408	0.08
Percent of total variance	24	21	12	9
Cumulative percent of total variance	24	45	57	66

DF = Days to 50% flowering, DM = Days to 95 % maturity, CFP = Capsule filling period, PH = Plant height (cm), BPP = Number of branches per plant, PB=Number of primary branch per plant, CPP = Number of capsules per plant, SY = seed yield (kg/ha, BYp=Biomass yield per plot(g/plot), HI= Harvest index ,SW = 1000 seed weight (g).

Quality Characteristics of Sesame Genotypes

Seed color is one of the most important quality traits of sesame for its commercial value. There are different color of sesame seed i.e. white, black, brown, red, and grey and others. Five types of colors had been identified in the studied genotypes namely white, black and brown, grey and red with varying frequencies (Figure 2).

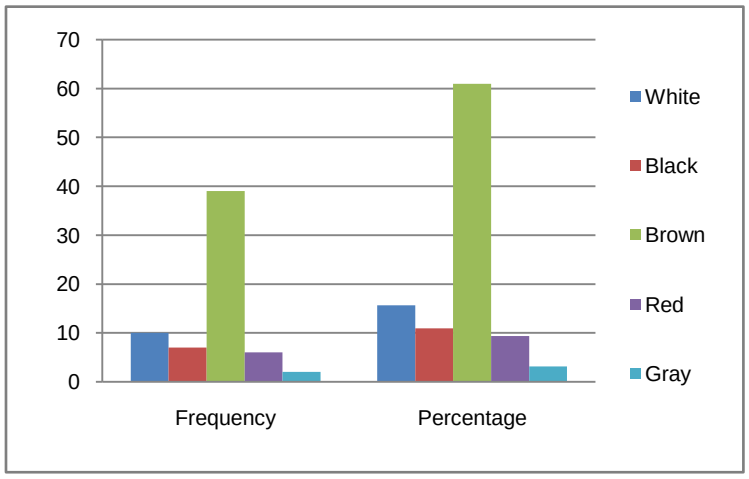

Figure 2: Frequency of seed colors among the 64 genotypes of sesame

DISCUSSION

Seed yield is the result of many yield contributing characters which are interdependent among themselves including seed yield. The analysis of the relationship among these characters and their associations with seed yield is essential to establish selection criteria (Singh *et al*., 1990). In the present study the magnitudes of genotypic correlation coefficients for most of the characters were higher than their corresponding phenotypic correlation coefficients, which indicate the presence of inherent or genetic association among various characters. Characters including DF, DM, CFP, PB, BPP, CPP, TSW and HI were found to be strongly associated with seed yield. Number of capsule per plant had positive and significant genotypic and phenotypic correlations with CFP, PH, PB and TSW; and it had positive and significant correlation with days to 50 % flowering, at genotypic level only. Therefore, any improvement of these characters would result in a substantial increment in seed yield. These results are corroborated with the finding of Yirgalem *et al*. (2013), who reported that HI was strongly associated with seed yield both at genotypic and phenotypic levels. Similarly, others reported (Sakila *et al.,* 2000; Kathiresan and Gnanamurthy, 2000) that number of capsules per plant, days to 50 % flowering and plant height were positively correlated with seed yield. This means number of capsules increases as the plant height and number of branches per plant increases. Similar results were reported by Reddy and Ramachandraiah (1990), i.e. number of capsules per plant was positively correlated with number of branches per plant, plant height and days to 50 % flowering. Biomass yield had positive and significant genotypic and phenotypic correlations with days to 50 % flowering, days to 90 % maturity, and plant height while it had negative and significant correlation with harvest index. Higher biomass yield can be obtained as the results of longer vegetative periods. Thousand seed weight had significant and positive genotypic and phenotypic correlations with capsule filling period, plant height and number of branches per plant, number of primary branches per plant; and it had positive and significant correlations with harvest index at genotypic level only. Generally, positive and significant association of pairs of characters at phenotypic and genotypic level justified the possibility of simultaneous improvement of traits through different breeding strategies.

When more characters are involved in correlation study, it becomes difficult to ascertain the characters which really contribute to yield. The path coefficient analysis under such situations helps to determine the direct contribution of these characters and their indirect contributions via other characters. In the present study, positive and high direct effect was exerted on seed yield by DM, CFP, BPB, and HI while negative and high direct effect was exerted by DF, NPB and CPP at genotypic level. The high significant correlation coefficient between seed yield and DF was due to its high indirect effects through DM and CFP on seed yield. The high positive correlation coefficient between seed yield and CPP was due the large indirect effects of CFP and HI. Characters including DM, CFP and HI had high positive direct effects on seed yield and also they had strong correlations with seed yield indicating the most important yield related traits at genotypic level. Positive and high direct effects on seed yield were exerted by CFP, PH, NPB, BY and HI at phenotypic level while negative and high direct effect on seed yield were exerted by DF, DM BPP, CPP, and TSW. The positive and significant correlation coefficients of DF and DM with SY were due to their positive indirect effects through CFP, PH, NPB, BY and HI. The present findings are in agreement with the results of (Yingzhong and Yishou, 2002; Yirgalem *et al*., 2013) in which days to 50% flowering had negative direct effect while capsule filling period exerted positive direct effect on seed yield. Both CFP, NPB, and HI had strong positive associations as well positive direct effects on SY indicating they are more related than other traits to SY at phenotypic level.

Cluster analysis showed that the 64 sesame genotypes were grouped in to four classes. Cluster I genotypes showed the characteristic of late flowering, late maturity, took longer period to fill the capsules and low harvest index. Cluster II genotypes showed characteristics of longer PH, higer NBP, BPP, TSW, highest SY and BY, and HI. Cluster III genotypes showed characteristics of longer period to fill the capsules, least BY and HI. Cluster IV had 29 genotypes characterized by highest in PH, and lowest in SY and HI.

Maximum average intra cluster D^2 was obtained in cluster III followed by cluster I. The lowest D^2 was recorded in cluster II, which shows the presence of less

genetic variability or diversity within this cluster. The highest average inter-cluster D^2 value was recorded between cluster I and cluster II followed by cluster I and cluster III indicating these pairs of clusters were genetically more divergent from each other than other clusters. According to Ghaderi *et al.* (1984) increasing parental distance implies a great number of contrasting alleles at the desired loci, and then to the extent that these loci recombine in the F2 and F3 generations following a cross of distantly related parents, the greater will be the opportunities for the effective selection for yield factors. Maximum genetic recombination is expected from the hybridization of the parents selected from distant groups. Therefore, maximum recombination and segregation of the progenies is expected from crosses involving parents selected from cluster I and II followed by I and cluster III; however the breeder must specify his/her objectives in order to make best use of the characters where the characters are divergent.

Principal component analysis (PCA) is one of the multivariate statistical techniques which is a powerful tool for investigating and summarizing underlying trends in complex data structures (Legendre and Legendre, 1998). Principal component analysis reflects the importance of factors majorly contributing to the total variation at each axis for differentiation (Sharma, 1998). The principal component analysis revealed that four principal components PC1, PC2, PC3, and PC4 have accounted for 66% of the total variation. According to Chahal and Gosal (2002), characters with largest absolute values closer to unity with in the first principal component influence the clustering more than those with lower absolute values closer to zero. Therefore, in this study, differentiation of the genotypes into different cluster was because of a cumulative effect of a number of characters rather than the contribution of specific few characters. Agronomic characters having relatively higher value in the first principal component (PC1) were number of branch per plant, seed yield, biomass yield, harvest index and thousand kernel weight and they were responsible for the differentiation of the four clusters. Characters like capsule filling period, thousand seed weight and biomass yield per plot had contributed a lot for principal component (PC2). Seed color is one of the most important quality traits of sesame for its commercial value. There are different color of sesame seed i.e. white, black, brown, red, and grey and others. Five types of colors had been identified in the studied genotypes namely white, black and brown, grey and red with varying frequencies; and brown seed color is the dominant one in the genotypes.

CONCLUSION

Seed yield had positive and significant genotypic and phenotypic correlations with all traits except with PH and BY. Therefore, they are important yield related characters and can be used for yield improvement in sesame breeding program. Positive and high direct effects were exerted by DM, CFP, BPB, and HI on seed yield while negative and high direct effects were exerted by DF, NPB and CPP. Characters including DM, CFP and HI had high positive direct effects and strong correlation with seed yield indicating that they are most important yield related traits at genotypic level. Positive and high direct effects on seed yield were observed at phenotypic level by CFP, PH, NPB, BY and HI while negative and high direct effects on seed yield were observed by DF, DM BPP, CPP, and TSW. Traits including CFP, NPB, and HI had strong positive correlations as well positive direct effects on SY indicating they are more related to SY at phenotypic level.

Genetic distance analysis is very important for hybridization program to get better yield and best recombinant parents. The maximum inter cluster square distance (D^2) was recorded between cluster I and II followed by cluster I and III. Hence crossing involving parents from cluster I with II and cluster I and III may exhibit high hetrotic values in F1 generation and could give transgressive segregants in proceeding generations. The principal component analysis revealed that four principal components (PC1, PC2, PC3, and PC4) explained or accounted for about 66% of the total variation existed among the genotypes. The dominant seed color observed was brown followed by white in the genotypes. The advantage and relation of color types and association with seed yield and fatty acid components can be investigated in the future in another experiment. This study generally indicated that there was significance genetic variability or divergence among the genotypes. Thus, there is enormous opportunity to go for direct selection as well as crossing of distant parents to improve specific traits in subsequent selections of the sesame genotypes.

ACKNOWLEDGEMENTS

The authors are grateful to the Institute of Biodiversity Conservation of Ethiopia (IBC/E) for providing the necessary materials.

REFERENCES

Ashri, A. (1988). Sesame breeding: Objectives and approaches, Pp. 157-164. *In*: Omran, A. (Ed.), Oil Crops: Sunflower, Linseed and Sesame. International Development Research Center (IDRC), Ottawa, Canada.

Bedigian D., Harlan, J. R. (1986). Evidence for the cultivation of sesame in the ancient world. *Economic Botany* 40:137-154.

Brar, G.S., Ahuja, K.L. (1979). Sesame: its culture, genetics, breeding and biochemistry. PP. 245-313. *In*: Malik, C.P. (Ed.), Annual Review of Plant Science, Kalyani publishers, New Delhi.

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

Chahal, G.S., Gosal, S.S. (2002). Principles and Procedures of Plant Breeding: Biotechnology and Conventional Approaches. Narosa Publishing House, New Delhi, 604 Pp.

CSA (Central Statistical Authority) (2011). Central Agricultural Census Commission, Ethiopian Agricultural Sample Enumeration.

Dabholkar, A. R. (1992). Elements of Biometrical Genetics. Concept publishing Company. New Dehli, 431Pp.

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

FAO Production Year Book (1995). Food and Agriculture Organization of the United Nations, Rome, vol. 49, p. 113.

FAO Production Year Book (2005). Food and Agriculture Organization of the United Nations-Rome, Vol. 40, p. 116.

Ghaderi, A., Adams, M.W., Nassib, A.M. (1984). Relationship between genetic distance and heterosis for yield and

morphological traits in dry edible bean and faba bean. *Crop Science* 24:37-42.

Ercan, A.G., Taskin, M., Turgut, K. (2004). Analysis of genetic diversity in Turkish sesame (*Sesamum indicum* L.) populations using RAPD markers. *Genetic Resources and Crop Evolution* 51: 599–607.

Kathiresan, G., Gnanmurthy, P. (2000). Studies on seed yield-contributing characters in sesame. *Sesame Safflower Newsletter* 15: 39-42.

Kobayashi, T. (1981). The wild and cultivated species in the genus *Sesamum*. Sesame: Status and improvement. Proceedings of Expert Consultation, Rome, Italy, 8-12 December, 1980. FAO Plant Production and Protection Paper 29, pp 157-163.

Legendre, P., Legendre, L. (1998). Numerical Ecology, 2nd edtion, Amsterdam, Elsevier, 853Pp.

Mahalanobis, P.C. (1936).The generalized distance in statistics. *Proceeding of Indian National Institute of Science* 2: 49-55.

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

Nath, R, Chakraborty, P.K., Chakraborty, A. (2000). Effect of microclimatic parameters at different Sowing dates on capsule production of sesame (*Sesamum indicum* L.) in a tropical humid region. *Journal of Agronomy and Crop Science* 184: 247–252.

Nayar, N.M, Mehra K.L. 1970. Sesame: Its uses: botany, cytogenetics, and origin. *Economic Botany* 24: 20-31.

Reddy, C.D.R., Ramachandraiah, D. (1990). Character association and path analysis in sesamum parents and their F1 hybrids. *Orissa Journal of Agricultural Res*earch 3: 37-44.

Robertson, A. (1959). The sampling variance of generic correlation coefficient. *Biometrics* 15: 469-485.

Sakila, M., Ibrahim, S.M., Kalamani, A., Backiyarani, S. (2000). Correlation studies in sesame (*Sesamum indicum* L.), Pp. 26-28. *In*: Fernández-Martínez, J. (Ed.), *Sesame and Safflower News Letter* No. 15, Institute of Sustainable Agriculture (IAS), CSIC, Apartado 4084, Córdoba, Spain.

Salunkhe, D.K., Desai, B.B. (1986). Post-Harvest biotechnology of oilseeds. CRC Press, Boca Raton, Florida, Pp. 105-117.

Sastri, A.B. (1974). Path analysis of yield components in Tobacco. *Indian Journal of Genetics* 34: 57-58.

SAS (Statistical Analysis System). (2002).Version 9.0, USA.

Singh, K.B., Geletu Bejiga, Malhorta, R.S. (1990). Association of some characters with seed yield in chick pea collection*. Euphytica* 49: 83-88

Singh, R.K., Chaudhary, B.D. (1977). Biometrical Methods in Quantitative Genetics Analysis, Kalyani publishers, New Delhi, 318 Pp.

Singh, T.P., Singh, K.B. (1973). Association of grain yield and its components in segregating populations of green gram. *Indian Journal of Genetics* 33:112-117.

Sharma, J.R. (1998). Statistical and Biometrical Techniques in Plant Breeding. New Age International Publisher, New Dehli, 432 Pp.

Uzo, J.O., Ojiake, G.V. (1981). Breeding and selection method for sesame on the basis of assessment of major Nigerian sesame strains, F1 hybrids and segregating generations. *In*: sesame-status and improvement. Proceedings of expert consultation. Rome.

Yermanos, D.M., Hemstreet, S., Saeeb, W., Huszar, C.K. (1972). Oil content and composition of the seed in the world collection of sesame introductions. *Journal of American Oil Chemistry Society* 49:20-23.

Yingzhong, Z., Yishou, W. (2002). Genotypic correlation and path coefficient analysis in sesame. *Sesame and Safflower News Letter* 17:40-45.

Yirgalem Tesfaye, Sintayehu Alamirewu, Geremew Terefe (2013). Assessment of genetic variability, genetic advance, correlation and path analysis for morphological traits in sesame genotypes. *International Journal of Plant Breeding and Genetics* 7: 21-34.

Zhang, H., Miao, H., Wang, L. Qu. L., Liu, H., Wang, Q., Yue, M. (2013). Genome sequencing of the important oilseed crop *Sesamum indicum* L. *Genome Biology* 14:1-9.