Phenotypic variability, divergence analysis and heritability of characters in sesame (*Sesamum indicum L.*) genotypes.

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ABSTRACT: Sixty four sesame genotypes were tested using an 8x8 simple lattice design at Metema, North Gondar, Ethiopia, in main cropping season. The objectives of the study were to estimate the phenotypic variability and genetic diversity and how much heritable the observed variation is in each character among the genotypes. Analysis of variance revealed that there was highly significant difference among the 64 genotypes for all the characters studied (p<0.01). High phenotypic coefficient of variation (PCV) was recorded for number of branches per plant, number of capsules per plant, biomass yield per hectare, seed yield per hectare. High heritability value was observed for days to maturity followed by thousand seed weight and oil content. Moderate heritability coupled with high genetic advance as percent of mean was observed for number of branches per plant and plant height. Cluster analysis revealed that the 64 genotypes were grouped in 9 distinct clusters. Grouping of the genotypes in to 9 clusters was due to the cumulative effect of the traits like days to 50% flowering, days to maturity, seed and biomass yield and number of capsules per plant and others. The presence of clear phenotypic and genotypic differences in the characters under consideration between or among clusters gives us a possibility or opportunity to bring about improvement through hybridization of genotypes between these clusters and subsequent selection can be made from the segregant generations. Principal component analysis showed that the first four principal components explained about 75.59% of the total variation of characteristics of the different Ethiopian sesame local land races. Agronomic characteristics like seed yield per plot(gm/plot), biomass yield (kg/ ha)& gm/plot, capsule filling period and days to maturity had contributed a lot in the formation of the clusters since they are the most contributor for variation in the first principal component(PC1).

1. Introduction

Sesame (*Sesamum indicum* L.) is a diploid species with 2n= 26 chromosomes. It is a self pollinated crop, under the family of pedaliacea. It is one of the major often called the queen of oil crops. It is grown in tropical to the temperate zones from about 40° N latitude to 40° S latitude. It is 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 alone (Bedigian and Harlan, 1986). It is a small farmers' crop in the developing countries (Gulhan *et al.*, 2004). Its center of origin is thought to be in Africa, Ethiopia (Bedigian and Harlan, 1986).

Sesame grows best on the areas which have an altitude of 500 to 800 meter above sea level (masl) and it can grow even upto1250 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 (Nath *et al.*, 2000). The optimum pH it requires 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. Periods of high temperature above 40°C during flowering reduce capsule and seed development. It requires from 600 to 1000 mm amount of water (Nath *et al.*, 2000).

All of the world production area is found in developing countries with largest area in India, Maynmar, China, Nigeria, and Uganda (FAO, 1995). Total world production of sesame in 2005 was in 9.35 million hectare and 3.7 million metric tons, 70% of which was produced in Asia and 26 % in Africa (FAO, 2005).

Sesame seed is used for confectionery, as an important source of edible oil and as a spice. It is also used for pharmaceutical and skin care products and as a synergist for insecticides (Salunkhe and Desai, 1986). 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).

The average productivity of sesame is as low as compared to other oilseed crops due to the lack of high yielding cultivars, resistant to major insect pests 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). A potential high harvest, 3600 kg/ha was reported in Nigeria (Uzo and Ojiake, 1981).

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% (Increasing Productivity and Market Success (IPMS)-Ethiopia Farmers Project, unpublished, 2005). In 1999, Ethiopia exported about 30,000 tons of sesame worth $28 million. The total area under sesame in Ethiopia is estimated at 65,000 hectare and production is about 49,000 tons and productivity is about 479kg/ha (IPMS-Ethiopia Farmers Project, unpublished, 2005). One of the major factors for such low national productivity is the use of unimproved cultivars. Like other crops, productivity and associated increase in production of sesame could be achieved through development of improved varieties which have less shattering problem and by using better cultural practices.

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 trait in Sesame. Yield per unit area is the end product of components of several yield contributing characters (Singh and Singh, 1973; Sastri, 1974). The polygenic inheritance of yield components makes selection more difficult. Moreover, these complex traits are highly influenced by environment, which reduces the progress to be achieved through direct selection. In such cases, there is another option to hasten the genetic improvement which is known as indirect selection for yield. So the phenotypic and genotypic variability study play of sesame crop characteristics was quite important for the improvement of the crop.

Knowledge on the extent and pattern of genetic and phenotypic variability present in a population and heritability of characters is absolutely essential for further improvement of the crop. Besides, knowledge of the naturally occurring diversity in a population helps to identify diverse groups of genotypes that can be useful for the breeding program. Little information is generated in sesame genetic diversity and phenotypic variability of Ethiopian land race collections. Therefore, this experiment was initiated with the following objectives:

1. To assess the nature and magnitude of phenotypic variability and genetic diversity for different traits.
2. To estimate the heritability of different sesame characteristics in the given environment
3. To identify traits that influence the sesame genotypes or land races in cluster or diversity formation

2.   MATERIALS AND METHODS
2.1 Experimental Site Description

The experiment was conducted at Gondar Agricultural Research Center main station which is located at Metema, Ethioipia. Metema is located about 900 km northwest of Addis Ababa in the northern part of the country and about 180 km west of Gondar town. The site is located at 12°N latitude and 36°E longitude. The altitude of Metema ranges from as low as 550 to 1608 meter above sea level. The mean annual temperature is 28°C. The minimum annual temperature is 24°C and the maximum annual temperature is 32°C. Nearly all of the land in the Metema district is the lowland. According to the available digital data, the mean annual rainfall for the area ranges from about 850 to around 1100 millimeter. The main rainy months extend from June until the end of September in metema district.

2.2 Experimental Materials

The experimental material consisted of 64 genotypes or local collections from different regions which are the major growing regions of Ethiopia. The accessions were obtained from Ethiopian Institute of Biodiversity Conservation & Werer Agricultural Research Center.

2.3 Experimental Design

The trial was laid out using an 8x 8 simple lattice design. Each genotype was planted in a plot size of 6.4m^2 (4 rows, 4m row length, 40cm between rows and 10cm between plants with in row). Other cultural practices were followed as recommended for the area. No fertilizer was applied.

2.4 Data Collection

The following data were collected from the central two rows both per plot and per plant basis.

1. Days to 50% flowering: number of days from planting to a stage when 50% of the plants in a plot produced flower.
2. Days to maturity: number of days from planting to a stage when 90% of the plants in a plot produced matured capsules.
3. Capsule filling period: period in days from flowering to maturity.
4. 1000 Seed weight: weight in grams of 1000 seeds.
5. Biomass yield per plot: weight in grams recorded by weighing the total above ground biomass harvested from the two central rows from each experimental plot at the time of harvest.
6. Seed yield per plot: seed yield obtained from each experimental plot from the central two rows.
7. Biomass yield per hectare: weight in grams recorded by weighing the total above ground biomass harvested from the two central rows

from each experimental plot at the time of harvest and converted to get biomass yield per hectare.

8. Seed yield per hectare: Seed yield obtained from each experimental plot and converted to get seed yield per hectare.
9. Harvest index: ratio of dry seed yield to the above ground biomass yield.

The data for the following characters were recorded from ten randomly taken plants on each experimental plot and the average was considered per plant and plot basis.

1. Plant height: height in centimeters from the ground level to the tip of the plant at maturity.
2. Number of branches per plant: number of branches on each of the ten randomly taken plants.
3. Number of capsules per plant: mean number of capsules obtained from ten randomly taken plants at harvest after maturity.
4. Oil content: determined from samples taken from each plot by Gas-Chromatography method.

2.5 DATA ANALYSIS
Analysis of variance (ANOVA)
Analysis of variance (ANOVA) was conducted using Statistical Analysis System (SAS) computer software program following SAS statement for simple lattice design (SAS, 2001).

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 ($\sigma^2 e$) = MS_e

Genotypic variance ($\sigma^2 g$) = $\left[\dfrac{MS_g - MS_e}{r} \right]$

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

Phenotypic coefficient of variation (PCV) = $\dfrac{\sigma_p}{\bar{x}}$ x 100

Genotypic coefficient of variation (GCV) = $\dfrac{\sigma_g}{\bar{x}}$ x 100

Where, $\bar{x}$ = 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 ($\sigma^2 g$) to the phenotypic variance ($\sigma^2 p$) and was estimated on genotype mean basis as described by Allard (1960) as:

$$h^2 = \left[\frac{\sigma^2_g}{\sigma^2_p} \right] x100$$

Estimation of genetic advance
Genetic advance in absolute unit (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 :

$$GA = K \sigma_p h^2$$

$$GAM = (GA/ \bar{x}) \text{ x } 100$$

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

Genetic Divergence Analysis
Description of genotype collection for agronomically useful characters is an important prerequisite for effective and efficient utilization of germplasm collection in breeding program. Divergence analysis is a technique used to categorize genotypes that are similar into one group and others into different groups. D-square statistics (D^2) developed by Mahalanobis (1936), has been used to classify the divergent genotypes into different groups. Squared distance (D^2) for each pair of genotype combinations was computed using the following formula:

$$D^2_{ij} = (X_i - X_j) S^{-1} (X_i - X_j)$$

Where, D^2_{ij} = the square distance between any two genotypes i and j,

X_i and X_j = the vectors for the values for genotype i[th] and j[th] genotypes, and

S^{-1} = the inverse of pooled variance covariance matrix.

Principal component analysis
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 the largest contributor to the total variation at each axis for differentiation (Sharma, 1998).

3. RESULTS
3.1 Analysis of Variance (ANOVA)
The result of the analysis of variance showed that there was highly significant difference among the characteristics of genotypes (p<0.01) indicating the presence of adequate variability among the local land races which can be exploited through selection.

There was high phenotypic coefficient of variation in the characters number of branches per plant and number of capsules per plant which is 20.35 % and 21.90% respectively The 64 genotypes studied showed wide range of variability for most of the characters. Days to 50% flowering ranged from 43.0 to 68. Days to

maturity ranged from 77 to 97days. The number of days to fill the capsule ranged from 21.5 to 43.0(Table 1)

Plant height varied from 65.87 cm to 167.88 cm with a mean height of 116.60 cm. Number of branches per plant ranged from 1.70 to 5.12 with a mean of 2.78. Number of capsules per plant varied from 7.73 to 33.04 with a mean of 18.82. Biomass yield ranged from 1555.87 kg/ha to 3707.47kg/ha with a mean of yield of 2320.73 kg/ha. The range of seed yield per plot was 100.79 g/plot to 259.28 g/plot with mean value of 165.10 g/plot and biomass yield per plot ranged from 506.29 g/plot to1185 g/plot with mean value of 742.63 g/plot. The range of harvest index ranged from 0.177 to 0.304 with a mean value of 0.223.Thousand seed weight ranged from 2.04 to 2.76g with a mean value of 2.31g and there was a wide variation for the oil content it ranged from 48.78 to 56.19 with a mean value of 54.46%.

Seed yield per hectare ranged from 314.97 kg/ha to 810.26 kg/ha which showed wide variation with a mean value of 515 kg/ha. The maximum yield was obtained from Acc- EW -001 followed by Acc-EW -009 (3) and Acc- EW -023 (3). The high yielding genotype Acc-EW-001 had a yield advantage of 45.6 % and 48.3%, respectively compared with that of the standard checks (Adi and Tate). Similarly it had a yield advantage of 50% as compared with the local check (Table 1).

3.2 Estimates of variance components

The phenotypic coefficient of variation values of genotypes was high for some characteristics like oil content (2.41%) followed by days to maturity (5.58%) and thousand seed weight(5.93%). For the rest characters the phenotypic coefficient of variation was ranged from 10% to 25%. Genotypic coefficient of variability (GCV) values were low for oil content (1.97%) followed by thousand seed weight (5.04%) and days to maturity (5.34%) (Table 1).

3.3 Estimation of broad-sense heritability and genetic advance

In this study estimate of heritability in broad sense ranged from 29.19 % for seed yield per hectare to 91.79 % for days to maturity (Table 1). According to Singh (2001), if heritability of a character is very high, say 80% or more, selection for such characters could be fairly easy. 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. But, for characters with low heritability, say 40% or less, selection may be considerably difficult or virtually impractical due to the masking effect of the environment. Considering this benchmark, heritability estimate was high (>80%) for days to maturity only (91.79%). It was low for number of capsules per plant, seed yield and biomass yield per hectare, seed yield and biomass yield per plot. It was moderate (40-80%) for the remaining quantitative characters in this study.

Estimates of GA for seed yield was 84.95 kg/ha indicating that whenever selecting the best 5% high yielding genotypes as parents, mean seed yield of progenies could be improved by 84.95 kg/ha for the first cycle, that is, mean genotypic value of the new population for seed yield will be improved from 515.95 kg/ha to 600.9 kg/ha. In the same way, it will be 2817.62 kg/ha for biomass yield (Table 1).

Genetic advance as percent of mean (GAM) at 5% selection intensity was high for number of branches per plant (36.66%) followed by number of capsules per plant (25.05%) and biomass yield per hectare (21.38); it was minimum for oil content (3.32%), thousand seed weight (8.76%), and days to maturity (10.56%) (Table 1).

Table 1. Estimates of range, mean, genetic components of variance, heritability and genetic advance of sesame genotypes evaluated.

Traits	Range	Mean	SE	$\sigma^2 p$	$\sigma^2 g$	$\sigma^2 e$	PCV (%)	GCV%	h^2 (%)	GA	GA (%)
DF	43-68	55.65	4.39	41.85	22.56	19.29	11.62	8.53	53.90	7.19	12.93
DM	77-97	92.75	1.48	26.77	24.58	2.19	5.58	5.34	91.79	9.80	10.56
CFP	21.5-43	37.12	4.59	37.42	16.33	21.08	16.48	10.89	43.64	5.51	14.84
PH	65.87-167.88	116.60	16.94	543.53	256.66	286.87	19.99	13.74	47.22	22.71	19.48
BPP	1.7-5.12	2.78	0.63	0.85	0.45	0.392	33.10	24.25	53.69	1.02	36.66
CPP	7.73-33.04	18.82	4.73	36.16	13.74	22.42	31.95	19.70	38.00	4.71	25.05
SY	314.97-810.26	515.95	118.69	19896.23	5808.64	14087.591	27.34	14.77	29.19	84.95	16.47
BY	1555.87-3703.47	2320.73	503.43	407127.57	153684.20	253443.33	27.50	19.00	37.75	496.89	21.38
SYp	100.79-259.28	165.10	37.98	2037.38	594.79	1442.59	27.34	14.77	29.21	27.18	16.47
BYp	506.29-1185.10	742.63	161.09	41689.78	15737.27	25952.52	27.50	19.00	37.75	159.01	21.38
HI	0.1770-0.3040	0.223	0.02	0.000817	0.000453	0.000364	12.82	9.54	55.45	0.03	14.66
SW	2.04-2.76	2.311	0.07	0.02	0.01	0.00532	5.93	5.02	71.64	0.20	8.76
OC	48.78-56.19	54.46	0.75	1.72	1.15	0.5703	2.41	1.97	66.80	1.81	3.32

DF = Days to 50% flowering, DM = Days to maturity, CFP = Capsule filling period, PH = Plant height (cm) BPP = Number of branches per plant, CPP = Number Capsules per plant, , SY = Seed yield (kg/ha), BY = Biomass yield (kg/ha), SYp= Seed yield per plot(g), BYp= Biomass yield per plot(g) HI=Harvest index, SW = 1000 Seed weight (g), OC=Oil content, ,SE= standard error of the mean, phenotypic (σ^2p), genotypic (σ^2g) and environmental (σ^2e) components of variances, phenotypic (PCV) and genotypic (GCV) coefficient of variability, broad sense heritability (h^2), expected genetic advance (GA) and genetic advance as percent of the mean (GA%).

3.4 Genetic Divergence Analysis

Significant differences among varieties for all or majority of the characters would justify further calculation of D^2 (Sharma, 1998). In the present study, analysis of variance (ANOVA) revealed the presence of significance difference among the tested genotypes for all the characters studied (Appendix 2) justifying the need to estimate squared distance values for the genotypes.

Estimation of squared distance (D^2) and clustering of genotypes

The D^2 values based on the pooled mean of genotypes resulted in classifying the 64 genotypes in to nine distinct clusters (Table 4 & 6). This indicated that the presence of wide diversity or variability among the genotypes. Clusters III and IV were the largest clusters containing 34, (53.12%) of genotypes together. Cluster I and II (23.43%) had 7 and 8 genotypes respectively, Clusters VI and VII had 10 genotypes together (15.65%) 5 genotypes each and Cluster V and VIII constituted 4 genotypes (6.25%) with 2 genotypes each, Cluster IX had 1 genotype (1.56%), this cluster had outstanding performance than any other genotypes tested in this study.

Cluster mean analysis

The genotypes were classified in Nine clusters each clusters has a distinct feature and characteristics from other genotypes or accessessions in the characteristics under considerations(table 2).

Table 2. Distribution of genotypes in to nine clusters based on D^2 analysis for sesame genotypes.

Cluster	Total number of genotypes	Pedigree name
Cluster I	7	Acc- EW -007(2),Acc-WW-001(3), Acc- EW -009(6), Acc-BG-002,Acc-BG-001, Acc-BG-010, Acc-NS-008
Cluster II	8	Acc- EW -011(5), Acc- EW -009(1), Acc- EW -0013(4), Acc- EW -023(3), Acc-WW-001(1), Acc-WW-002(2), Acc-BG-019(1), Acc-GA-002(3)
Cluster III	13	Acc- EW -006 ,Acc-BG-007, Acc-BG-001(3), Acc-BG-002(3), Acc-BG-003(2), Acc-GA-002(2), Acc-GA-005(1), Acc-GA-003(3), Acc-NS-005, Acc-NS-010, Acc-NS-003(1), Acc-NS-007(2), Tejareb(local), 003(1)
Cluster IV	21	Acc-EW-018, Acc- EW -017(6), Acc- EW -012(7), Acc-WW-001(4), Acc-WW-003(3), Acc-WW-001(7), Acc-WW-002(4), Acc-WW-001(5), Acc-BG-008, Acc-BG-012(3), Acc-BG-006, Acc-BG-004, Acc-BG-009, Acc-BG-013, Acc-GA-009(2), Acc-GA-001(1), Acc-GA-003(2), Acc-NS-006, Acc-NS-002, Adi, Tate
Cluster V	2	Acc- EW -08(2), Acc-WW-003(2)
Cluster VI	5	Acc- EW -017(6), Acc- EW -012(3), Acc-WW-001(6), Acc-WW-002(1), Acc-WW-003(4)
Cluster VII	5	Acc- EW -017(5), Acc-BG-012(2), Acc-GA-004(2), Acc-GA-001(3), Acc-GA-004(2)
Cluster VIII	2	Acc- EW -009(3), Acc-BG-003
Cluster IX	1	Acc- EW-001

The mean value of the 13 quantitative characters in each cluster was presented in Table 5. Cluster I consisted of 7 genotypes having the characteristic of late flowering (58.6), less number of days to fill the capsule (36.7), relatively high number of branches per plant (2.91), relatively high oil content (54.78) next to cluster VI and VIII and low harvest index (0.21).

Cluster II consisted of 8 genotypes. This cluster could be characterized by high number of branches per plant (3.13), relatively high seed (675.36 kg) and biomass yield (3101.67 kg) kg per ha, high seed yield per plot (216.11 g/plot) and high amount of biomass yield per plot(992.53 g/plot), it had the shortest plant structure (110.16 cm).

Cluster III consisted of 13 genotypes including the local check were characterized by the following features: the shortest time to fill the capsule (33.12), the earliest maturing types (87.92 days), lowest oil content (53.84%) and lowest number of capsules per plant (16.48(Table 2 & 3).).

Twenty one genotypes including the two released varieties and standard checks (Adi and Tate) made cluster IV. The cluster could be characterized as early flowering (54.10) and had intermediate characteristics in other agronomic traits (Table 2 & 3)..

Cluster V consisted of two genotypes characterized by high number of days to fill the capsule (41), least number of branches per plant (2.20), low harvest index (0.21), lowest thousand seed weight (2.21) than the other clusters. Cluster VI consisted 5 genotypes with a characteristic feature of late maturing (95.6 days), low number of capsules per plant (17) except cluster III, relatively high thousand seed weight (2.33 g), the highest oil content (55.01%)(Table 2 & 3)..

Five genotypes made Cluster VII. This cluster had features of late flowering (57.40), short time for capsule filling period (33.90 days), short time for capsule filling period (33.90), lowest in seed yield (360.19kg/ha) and lowest biomass yield (1594.51 kg/ha) and lowest in seed yield per plot (115.20g/plot) and biomass yield per plot (510.26g/plot) . Cluster VIII had only two genotypes. This cluster could be characterized by late flowering (57.40) and late maturing (96.00), highest number of branches per plant (3.14), high number of capsules per plant (22.62) next to cluster IX, high yielder in seed yield and biomass which was 688.37kg/ha and 3333.60kg/ha respectively and seed yield (220.28g/plot) and biomass yield (1066.75g/plot) which was next to cluster IX again, lowest in harvest index (0.20) (Table 2 & 3).

Cluster IX had one genotype which was outstanding type by its performance in most of the traits or agronomic characters, the cluster characterized by the following essential features, late maturing (96) and highest number of days to fill capsule (42), the highest in seed and biomass yield per hectare which was 810.26 and 3703.47 kg/ha, highest in seed yield per plot (259.50 g/plot) and biomass yield per plot (1185.10g/plot),highest number of capsules per plant (23.46) and highest number in thousand seed weight (2.37g) (Table 2 & 3).

Table 3. Mean value of 13 quantitative characters of the nine clusters for sesame genotypes.

Traits	Clusters								
	I	II	III	IV	V	VI	VII	VIII	IX
DF	58.60	54.50	56.30	54.10	54.00	56.80	57.40	57.50	54.00
DM	94.64	93.56	87.92	92.93	95.00	95.60	91.30	96.00	96.00
CFP	36.07	39.06	33.12	38.86	41.00	38.80	33.90	38.50	42.00
PH	118.89	110.16	123.73	111.66	112.64	116.70	129.71	111.02	116.74
BPP	2.91	3.13	2.99	2.55	2.20	2.60	2.95	3.14	3.12
CPP	19.45	21.56	16.48	18.62	19.55	17.00	19.67	22.62	23.46
SY	497.45	675.36	434.66	496.17	605.87	573.22	360.19	688.37	810.26
BY	2360.74	3101.67	1892.75	2154.47	2856.81	2656.38	1594.51	3333.60	3703.47
SYp	159.18	216.11	139.08	158.77	193.88	183.43	115.26	220.28	259.50
BYp	755.43	992.53	605.68	689.42	914.17	850.03	510.24	1066.75	1185.10
HI	0.21	0.22	0.23	0.23	0.21	0.21	0.22	0.204	0.21
SW	2.29	2.33	2.33	2.30	2.21	2.33	2.31	2.28	2.37
OC	54.78	54.69	53.84	54.51	54.24	55.01	54.62	54.83	54.01

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

Estimation of intra and inter cluster square distances (D^2)

The average intra and inter cluster D^2 values are presented here under. Maximum average intra cluster D^2 was obtained in cluster IX (D^2=8.31) followed by cluster V and cluster VIII (D^2=6.93). The lowest D^2 was recorded in cluster IV (D^2=2.22), which shows the presence of less genetic variability or diversity within this cluster ((Table 4).

The χ^2- test for the nine clusters indicated that there was a statistically significant difference in all characters except cluster I with IV (13.83), III with IV (20.52) and II with VIII (21.62). The highest average inter cluster D^2 was recorded between cluster VII and cluster IX (D^2=1160.00) followed by cluster III and cluster IX (D^2=850.53) and cluster VII and cluster VIII (D^2= 776.89) which had shown these clusters were genetically more divergent from each other than any other clusters (Table 4).

Table 4. Average intra (bold) and inter cluster (off diagonal) D^2 values among nine clusters in sesame genotypes.

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	**4.42**	150.70	57.37	13.83	70.49	29.00	153.90	253.70	489.45
II		**4.15**	372.65	234.25	30.59	63.90	586.66	21.62	109.54
III			**3.18**	20.52	233.59	150.05	32.30	530.27	850.53
IV				**2.22**	127.43	69.07	87.19	363.01	634.79
V					**6.93**	18.70	401.40	73.77	210.67
VI						**5.09**	290.65	133.18	307.29
VII							**5.09**	776.89	1160.00
VIII								**6.93**	53.25
IX									**8.31**

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

3.5 Principal component analysis

The principal component analysis (Table 5) revealed that four principal components PC1, PC2, PC3 and PC4 with eigenvalues 5.33, 2.49, 2.24 and 1.27, respectively, have accounted for 75.59% of the total variation. The first two principal components PC1 and PC2 with values of 35.55 % and 16.61 %, respectively, contributed more to the total variation.

Agronomic characters having relatively higher value in the first principal component 1 (PC1) were seed and biomass yield per plot and hectare respectively, capsule filling period, days to maturity, seed yield per hectare and number of capsules per plant had more contribution to the total diversity and they were responsible for the differentiation of the nine clusters. Characters like days to flowering and maturity, plant height and thousand seed weight had contributed a lot for principal component 2(PC2); number of branches per plant ,biomass yield per hectare and per plot, capsule filling period and oil content had contributed in the third principal component 3 (PC3); harvest index and branches per plant, seed yield per plot and per ha and number of capsules per plant in the fourth principal component 4 (PC4) were the major contributors to each principal components (PC) (Table 5).

Table 5. Eigenvectors and eigenvalues of the first four principal components (PCs) for characters of sesame genotypes.

Character	Eigenvectors			
	PC1	PC2	PC3	PC4
Days to 50% flowering	-0.040	0.588	0.136	0.032
Days to maturity	0.272	0.386	-0.140	-0.024
Capsule filling period	0.304	-0.254	-0.321	-0.082
Plant height (cm)	-0.224	0.284	0.290	-0.125
Number of branches per plant	-0.114	0.261	0.393	0.304
Number of capsules per plant	0.244	0.249	-0.191	-0.212
Seed yield (kg/ ha)	0.377	-0.088	0.234	0.240
Biomass yield (kg/ ha)	0.356	-0.068	0.351	-0.094
Seed yield per plot(gm/plot)	0.377	-0.088	0.234	0.240
Biomass yield per plot(gm/plot)	0.356	-0.068	0.351	-0.094
Harvest Index	0.015	-0.038	-0.251	0.748
Thousand Seed weight (gm)	-0.104	-0.330	0.209	-0.173
Oil Content (%)	0.201	0.239	-0.315	0.058
Eigenvalue	5.33	2.49	2.24	1.27
Difference	2.84	0.24	0.97	0.27
Percent of total variance explained	35.55	16.61	14.97	8.47
Cumulative percent of total variance explained	35.55	52.15	67.12	75.59

4. Discussion

Mean square values of all morphological attributes showed highly significant differences (p<0.01) in all the traits which is in agreement with the finding of Sarwar and Haq (2006).

Generally low PCV values were observed for days to 50% flowering, days to maturity, harvest index, thousand seed weight and oil content; medium for capsule filling period, plant height, number of capsules per plant, biomass yield per hectare, seed yield per plot, biomass yield per plot; high for number of branches per plant. Similar results were reported by Thangavel *et al* (2000) in which most of the characters i.e. plant height, number of capsules per plant, number of branches per plant, seed yield per hectare, seed per plant and number of seeds per capsule showed medium PCV and GCV values. The high GCV value of characters suggest that the possibility of improving these trait through selection**.**

The difference between PCV and GCV values was high for capsule filling period, plant height, and number of branches per plant, number of capsules per plant, seed yield per hectare, seed yield per plot and biomass yield per plot; which indicated how much the environment influenced these characters. However, this difference was low for days to 50% flowering days to maturity, thousand seed weight and oil content; suggesting minimal influence of environment on the expression of the characters so that it is easy to improve these characters/traits in our improvement program.

Generally characters or agronomic traits are highly influenced by the environment. In this study, characters were reacting in different way & magnitudes. The magnitude of response which was measured by the phenotypic coefficient of variation was quite different. 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, the number of branches per plant, number of capsules per plant, seed yield per hectare, biomass yield per hectare, seed yield per plot and biomass yield per plot had high coefficient of variation (PCV) values. The PCV values for days to 50% flowering, capsule filling period, plant height and harvest index were medium. Days to maturity, thousand seed weight and oil content had low PCV values. Phenotypic coefficient variation was generally higher than GCV values in all characters in this study.

The magnitudes of heritability for most of the quantitative characters were moderate, which may be attributed due to uniform environmental conditions during the conduct of the experiment. Dabholkar (1992) explained that whenever values are stated for heritability of a character, it refers to a particular population under particular environmental conditions.

Genetic advance under selection (GA) refers to improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at a given selection intensity (Singh, 2001).

This study showed medium heritability and low genetic advance as percent of mean for plant height which was inconsistent with high heritability and a high genetic advance as reported by Govidarasu *et al*. (1990). The number of capsules per plant showed low heritability and genetic advance which was inconsistence with the reports by Rajaravindran *et al*. (2000) and Paramasivam (1980) i.e. high heritability and genetic advance for the number of capsules per plant, plant height and oil content showed very high values of heritability and moderate genetic advance as percent of mean. Emphasis should be placed on those characters which had high heritability and genetic advance for formulating reliable selection indices for the development of high yielding sesame genotypes.

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. This study showed that moderate heritability coupled with high expected genetic advance as percent of mean for number of branches per plant and plant height alone. Therefore, these characters could be improved more easily than other characters measured. Most of the characters in these genotypes showed moderate heritability and very minimum/low genetic advance as percent of the mean, which makes the improvement program of important traits or characters of sesame is difficult.

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 F_2 and F_3 generation following a cross of distantly related parents, the greater will be the opportunities for the effective selection for yield factors. Minimum inter cluster distance was observed between cluster I and cluster IV (D^2=13.83) 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 IX and cluster VIII and V, followed by cluster

VI and VII, however the breeder must specify his 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 the largest contributor to the total variation at each axis for differentiation (Sharma, 1998). 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 as indicated in table 5, differentiation of the genotypes into different clusters was because of a cumulative effect of a number of characters rather than the contribution of specific few characters ($\pm$ 0.015-0.748). In this experiment sesame characteristics like seed yield per plot(gm/plot), biomass yield (kg/ ha)& gm/plot, capsule filling period and days to maturity had contributed a lot in the formation of the clusters and they were the characteristics which has a big influence in making clusters.

5. CONCLUSION

This study generally indicated that there was significance phenotypic & genetic variability or divergence among the genotypes. Thus, there is enormous opportunity in the improvement program of the sesame through direct selection & crossing/hybridization involving distant clusters can be done to produce viable and a potential segregant population for the subsequent breeding work and making potential variability.

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