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**STUDY ON GENETIC DIVERGENCE IN LOW-ALTITUDE SESAME (*SESAMUM INDICUM* L.)
GERMPLASM OF ETHIOPIA BASED ON AGRO MORPHOLOGICAL TRAITS**

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ABSTRACT

Forty nine sesame genotypes collected from low-altitude areas of Ethiopia were evaluated at Werer Agricultural Research Centre, during the 2011/12 growing season for genetic variability and character association. Morphological data recorded on 14 quantitative traits were analyzed for analysis of variance, phenotypic and genotypic variability, heritability, genetic advance, genetic divergence based on Mahalanobis (D^2) statistics and principal component analysis. Analysis of variance revealed significant difference among the genotypes for each character except for primary branches. Higher genotypic variance was observed for seed yield and number of capsules/plant. Moderate heritability with moderate genetic advance was observed for most of the yield related traits, signifying that these attributes are governed by both additive and non-additive genes action. Based on D^2 values, the genotypes were grouped into seven clusters. The clustering pattern suggested that genotypes of the same origin were distributed into different clusters, indicating the absence of parallelism between clustering and geographic distributions. Maximum inter cluster distance was observed between clusters VI and VII while lowest distance was noticed between cluster I and III. Traits viz., harvest index, seed yield, biomass yield and plant height had highest contribution towards genetic divergence. There is high level of genetic variability in the studied germplasm with regard to seed yield and its component traits. The clustering pattern suggested the absence of relationship between geographic diversity and genetic diversity. Genotypes from distant clusters are suggested to be used as parents for hybridization program to achieve novel recombinants. The use of the selected traits in sesame improvement program would increase yield.

Keywords: Cluster distance; genetic divergence; principal component; sesame; yield related traits.

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INTRODUCTION

Sesame (*Sesamum indicum* L.) is a very ancient oilseed crop [1] and especially grows well and gives high yields in both tropical and temperate climates [2]. Sesame is cultivated on 7 million ha worldwide; India, Myanmar and China are the world's largest producers followed by the areas found in developing countries, Sudan, Ethiopia, Uganda, Nigeria, Tanzania, Pakistan and Paraguay [3]. It is a small farmers' crop in the developing countries [4], and its center of origin is thought to be in Africa, Ethiopia [5, 6, 7, 8 and 9]. It is often referred to "the queen of oil seeds" because of its high nutritive quality and quantity of oil ranging from 40 to 63% [10]. This oil is rich in antioxidants and has a significant amount of oleic and linoleic acids. Despite its long history and nutritional value, the crop has low yielding capacity compared to other oilseed crops, mainly due to its low harvest index, susceptibility to diseases, seed shattering and indeterminate growth habit [11].

Genetic diversity in crop plants is essential to sustain level of high productivity. Genetic variation survives for agronomically vital characters in sesame but its production is still very low in Ethiopia. Traditional sesame landraces as well as related wild species are an important source of genetic diversity for breeders and form the backbone of agricultural production. The characterization and conservation of sesame germplasm are essential for both safe guarding and the future use of existing genetic resources of sesame. Genetic diversity in sesame, based on morphological, biochemical, metabolic, and molecular markers, has been reported by many researchers worldwide (12, 13 and 14). However, the development of improved plant cultivars is restricted mainly due to narrow genetic pool which results into limited possibility to restructure the sesame crop. The knowledge of genetic diversity among landraces is of fundamental interest to plant breeders. It contributes to monitor the germplasm that will help in the selection and breeding of high yielding and good quality cultivars. However, in Ethiopia, to date, study on genetic diversity of sesame population is very limited. Hence, the lack of information on diversity of the local germplasm has been limiting the use of breeding materials in sesame improvement program of the country. Therefore, the present study was aimed to generate scientific knowledge on the genetic diversity of sesame genotypes collected from various lowland areas of Ethiopia and to choose sesame germplasm with diverse agronomic performances and yield potential.

MATERIALS AND METHODS

Description of experimental site

The experiment was conducted at Werer Agricultural Research Center (WARC) during the 2011/12 main crop season. WARC is located along the Middle Awash valley between 9° 60' N and 40° 9' E with altitude of 740 m.a.s.l. The mean annual temperature during the study season ranged from 19.5 to 32.5°C and the mean annual rain fall was 450 mm with Fluvisol and Vertisol soil type.

Experimental material and field layout

The material for the study comprised 49 low-altitude sesame genotypes (Table 1) received from the Ethiopian Biodiversity Institute (EBI). The experiment was laid out in 7 x 7 Simple Lattice Design with two replications where each genotype was planted in a plot consisting of two rows of 2.5 m long at a distance of 0.4 m between rows and 0.1 m between plants. All agronomical practices were carried out throughout the season as required.

Data collection

Data were collected from net plot size. Five plants in each plot were selected at random and the data were recorded on the following parameters: days to 50% flowering (DF), days to 75% maturity (DM), number of primary branch/plant (PBPL), number of capsules/plant (CPPL), number of seeds/capsule (SDPC), capsule length (CL), plant height (PH), biomass/plant (BMPL), harvest index/plant (HIPL), 1000 seed weight (TSW), seed yield/plant (SYPL), seed yield/plot (SYP) and oil content (OC). Oil content (%) was determined for each genotype from five gram of seeds using nuclear magnetic resonance spectroscopy (NMRS).

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Table 1. List of 49 sesame genotypes with areas (regions) of collection used in the study

No.	Genotypes	Region	Altitude	No.	Genotypes	Region	Altitude
1	Oromia-28	E. Wellega	1200	25	Tigray-14	Mirabawi	820
2	Gambella-1	Gambella	500	26	Tigray-15	"	710
3	Gambella-2	"	500	27	Am-NG-18	Amhara N. G	1110
4	SNNP-5	N.Omo	770	28	Tigray-16	Mirabawi	710
5	SNNP-6	Bench Maji	850	29	Tigray-17	"	710
6	Tigray-6	Mirabawi	600	30	Tigray-18	"	820
7	Tigray-7	"	650	31	Tigray-19	"	820
8	Tigray-8	"	650	32	Tigray-20	"	900
9	Oromia-29	Jimma	1200	33	Oromia-32	Jimma	1110
10	Oromia-30	"	1210	34	Oromia-33	"	1100
11	Tigray-9	Mirabawi	1090	35	Am-NG-19	Amhara N. G	600
12	Tigray-10	"	1140	36	Am-NG-20	"	600
13	Tigray-11	"	1130	37	Am-NG-21	"	650
14	Tigray-12	"	1200	38	Am-NG-22	"	650
15	Am-NG-13	Amhara N. G	900	39	Am-NG-23	"	700
16	Am-NG-14	"	900	40	Am-NG-24	"	650
17	Am-NG-15	"	980	41	Am-NG-25	"	780
18	Am-NG-16	"	830	42	Am-NG-26	"	760
19	Am-NG-17	"	810	43	Am-NG-27	"	750
20	SNNP-7	N. Omo	1050	44	Klf-74	Check variety	
21	SNNP-8	Gurage	1135	45	Abasena	"	
22	Gambella-3	Gambella	500	46	Serkamo	"	
23	Gambella-4	"	600	47	Adi	"	
24	Tigray-13	Mirabawi	700	48	Mehado-80	"	
				49	S	"	

Key: Amhara N. G = Amhara North Gonder, E. Wellega = East Wellega, N. Omo = North Omo, SNNP = Southern Nation and Nationality People.

Data analysis

Analysis of variance (ANOVA) was carried out for the data with SAS statistical software (9.2), to test for significant differences among the genotypes according to the standard statistical procedure described by Gomez and Gomez [15].

The phenotypic and genotypic coefficients of variation for each character were estimated by the formula suggested by Singh and Chaudary [16] as follows:

Genotypic coefficient of variation (GCV) = $(\sigma_g / \bar{x}) \times 100$ and phenotypic coefficient of variation (PCV) = $(\sigma_p / \bar{x}) \times 100$. Where; σ_g and σ_p = genotypic and phenotypic standard deviations, and \bar{x} = grand mean.

Heritability in broad sense (H) and genetic advance (GA) for all traits were computed using the formula adopted by Allard [17] as follows:

$H = (\sigma^2_g / \sigma^2_p) \times 100$ and $GA = (k * \sigma_p * H)$

Genetic advance as % of the mean (GA %) = $(GA / \bar{x}) \times 100$.

Where; k is selection differential at 5% selection intensity ($k = 2.06$) and \bar{x} = grand mean.

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Divergence and cluster analysis was carried out based on mean values of the studied traits following Mahalanobis's (D^2) statistics, and a dendrogram generated based on the Un-weighted Pair Group Mean (UPGMA). Clustering of genotypes was done using average linkage cluster analysis and the appropriate number of clusters was determined from the values of Pseudo-F and Pseudo-T statistics. Average intra and inter cluster distances were computed from the generalized squared distances using methods given by Singh and Chaudhary [18].

RESULTS AND DISCUSSION

Analysis of variance and mean performance of genotypes

The analysis of variance revealed significant difference among the genotypes for each character except for number of primary branches/plant, indicating the presence of considerable variability among the genotypes for the characters studied (Table 2). Previous studies [19 and 20] also reported the existence of enormous amount of genetic variability in the evaluation of 64 and 36 sesame accessions respectively, from Ethiopia, for several characters.

Mean performance of 49 sesame genotypes (data not shown) revealed high variation for the studied morphological traits. Generally, a high variation in seed yield/plant, days to flowering, plant height, number of capsules/plant, harvest index and oil content was found among the studied genotypes. The maximum mean performance for most yield components such as harvest index (84.55%), biomass/plant (8.7g), seed yield/plant (7.3g) and yield/plot (367g) was recorded for Am-NG-15. This genotype was found to be superior as compared to the check varieties, though it had the lowest oil content (38.15) of all genotypes. In the contrary, genotype Tigray-13 generally showed the lowest means for seed yield (3.15g) and its component traits viz., number of seed/capsule (30.05), biomass/plant (4.5g), harvest index (69.75%) and 1000 seed weight (1.25g); though it had highest mean oil content (53.7%). One of the important goals in sesame breeding is to improve varieties with high oil content and high seed yield. While the low yielding type Tigray-13 was the highest in oil content, the best high-yielding type Am-NG-15 was the lowest in oil content. Hence, it is important to combine high-yield potential with high oil content to create novel recombinant [21].

Table 2. Mean squares from analysis of variance for 14 morphological traits of 49 sesame genotypes

Trait	Rep (1)	Block (6)	Gen (42)	Error (42)	CV (%)	SE
Days to Emergence	0.37	0.30	0.46**	0.21	9.30	0.46
Days to Flowering	0.26	0.28	17.17**	0.37	0.88	0.61
Days to Maturity	0.01	55.44	195.87*	126.00	10.30	11.22
No. of Pr. Branches	13.30	1.39	4.09	3.61	34.64	2.02
No. of Capsules/plant	1116.62	347.30	376.42**	192.20	14.16	13.86
No. of Seeds/capsule	32.92	29.85	16.42*	12.49	11.70	4.05
Capsule Length (cm)	0.05	0.03	0.21**	0.10	11.34	0.31
Plant Height (cm)	9392.33	369.95	730.46*	498.57	17.86	22.33
Biomass/plant	0.85	0.60	1.52*	0.78	12.49	0.88
Harvest Index (%)	0.05	7.76	13.01**	5.33	2.86	2.31
1000 Seed weight (g)	0.02	0.06	0.11*	0.07	15.71	0.27
Seed Yield/plant (g)	0.61	0.61	1.49*	0.76	15.16	0.87
Seed Yield/plot (g)	1466.50	1571.97	3695.97*	1847.17	14.96	42.98
Oil Content (%)	0.36	1.17	32.34**	3.31	3.88	1.82

** , * significant at 0.01 and 0.05 probability level; figures in parenthesis refer to degrees of freedom. CV= coefficient of variation, Gen= genotypes, SE= standard error.

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Generally, 50% of the genotypes (24 of 49) expressed greater mean seed yield and mean number of capsules over the grand mean. Hence, there is an opportunity to find genotypes among the tested material that perform better than the existing varieties in moisture stressed areas and/or to use them as parents for hybridization program.

Phenotypic and genotypic variability

Variability estimates revealed considerable variations for all the studied traits (Table 3). The phenotypic coefficient of variance (PCV) was greater than the genotypic coefficient of variance (GCV) for all the traits. According to Deshmukh *et al.* [22] phenotypic and genotypic coefficients of variability 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, moderate PCV and low GCV values were observed for most of the yield related traits, indicating the low prevalence of additive gene action and the higher influence of environment in the expression of most of the traits.

Maximum value of PCV but low GCV was noted in number of primary branches/plant, while moderate PCV and GCV values were estimated for seed yield/plant and seed yield/plot. However most of the traits *viz.*, days to emergence, days to maturity, capsules/plant, seeds/ capsule, capsules length, plant height, and biomass/plant exhibited moderate PCV with low GCV values indicating that most of the traits are sensitive to changing environments. Similar result was reported by Thangavel *et al.* [23], where most of the traits *i.e.* number of branches/plant, number of capsules/plant, plant height, number of seeds per capsule and seed yield/plant showed medium PCV and low GCV values. Ahadu [19] also reported low PCV and GCV value for days to 50% flowering, days to maturity, harvest index, thousand seed weight and oil content. Gidey *et al.* [20] and Sumathi and Murlidharan [24] also reported more or less similar results in sesame.

Lower GCV suggested that the traits are rendered to high environmental influences and hence lower opportunity exists for improvement of these traits in the tested genotypes. However, the high or low GCV recorded alone is not sufficient for the determination of the extent of genetic advance to be expected by selection. Burton [26] suggested that GCV together with heritability estimates would give the best picture of the extent of the advance to be expected by selection.

Heritability and genetic advance

Low to high estimates of heritability, in the range between (6.02 – 95.77%) were observed for the studied traits (Table 3). The highest heritability was recorded for days to flowering followed by oil content (81.44%), whereas the lowest heritability was scored for number of primary branches/plant (6.02). Estimates of genetic advance as percent of mean at 5% selection intensity ranged from 3.07% for number of seeds/capsule to 15.13% for oil content. Generally, low to medium genetic advance as percent of the mean were observed for all traits considered. Johnson *et al.* [25] generally classified heritability estimates as low (0-30%), moderate (30-60%) and high (60% and above) and genetic advance (as % mean) as low (0-10%), moderate (10-20%) and high (20% and above). Based on this classification, high estimates of heritability coupled with moderate genetic advance for days to flowering and oil content; moderate heritability along with moderate genetic advance for capsules per plant, capsules length, biomass/plant, seed yield/plant and seed yield/plot were observed, signifying that these attributes were governed by both additive and non-additive type of genes and simple selection in favor of these traits may not be beneficial to improve seed yield. Seed yield is a complex trait, polygenic and highly influenced by environmental conditions, hence there is a need for methods other than simple selection to improve yield in sesame. This result was in accordance with Krishnaiah *et al.* [26]. Bhombe *et al.* [27], Bishwas *et al.* [28] and Khan *et al.* [29] also reported more or less similar results. On the other hand, moderate to low heritability coupled with low genetic advance for number of branches/plant, number of seeds/capsule, plant height, 1000 seed weight and harvest index exhibited render them unsuitable

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for improvement through conventional selection as non-additive type of genes operating in controlling these traits. These results are in the contrary with some of the previous findings [30, 31, 32] who observed high heritability and high genetic advance for number of branches, number of capsules, plant height, 1000 seed weight and seed yield in sesame.

High heritability indicates that a character is controlled by those genes which are less influenced by environment and vice versa. Johnson *et al.* [25], Panse [33] and Sarwar *et al.* [34] discussing the significance of additive type of gene action, pointed out that high values of genetic advance accompanied with high degree of heritability estimates offered a more effective criterion of direct selection due to its base on additive types of genes. They further stated that high heritability combined with low genetic advance may be mainly due to non-additive type of genes effect (dominant or epistasis).

Table 2. Genotypic and phenotypic coefficient of variances, heritability and genetic advance for 14 morphological traits in 49 sesame genotypes.

Trait	Mean	σ^2_g	σ^2_p	GCV	PCV	H (%)	GA (%)
Days to Emergence	4.94	0.12	0.33	7.09	11.69	36.73	8.85
Days to Flowering	68.93	8.40	8.77	4.20	4.30	95.77	8.48
Days to Maturity	108.97	34.94	160.94	5.42	11.64	21.71	5.21
No. of pr. Branches	5.84	0.24	3.85	8.37	33.61	6.20	4.29
No. of Capsules/plant	97.89	92.11	284.31	9.80	17.22	32.40	11.50
No. of Seeds/capsule	34.64	1.96	14.46	4.05	10.98	13.59	3.07
Capsule length (cm)	2.76	0.06	0.15	8.66	14.27	36.85	10.83
Plant Height (cm)	125.02	115.94	614.52	8.61	19.83	18.87	7.71
Biomass/plant	7.08	0.37	1.15	8.59	15.16	32.08	10.02
Harvest index (%)	80.75	3.84	9.17	2.43	3.75	41.87	3.24
1000 Seed weight (g)	1.73	0.02	0.09	7.91	17.59	20.20	7.32
Seed yield/plant (g)	5.75	0.36	1.12	10.50	18.44	32.41	12.31
Seed yield/plot (g)	287.34	924.40	2771.57	10.58	18.32	33.35	12.59
Oil content (%)	46.82	14.51	17.82	8.14	9.02	81.44	15.13

σ^2_g = genotypic variance, σ^2_p = phenotypic variance, GA (%) = genetic advance as % of mean at 5% selection intensity, GCV & PCV= genotypic and phenotypic coefficient of variances respectively.

Genetic divergence

On the basis of D^2 values the 49 germplasm lines were grouped into seven clusters (Table 4) with variable number of genotypes revealing the presence of considerable amount of genetic diversity in the material. The composition pattern showed that Cluster-II was the biggest cluster comprising 18 genotypes followed by Cluster-III (13), Cluster-I (8), and Cluster-IV (7) genotypes, while the rest three Clusters V, VI and VII were solitary clusters demonstrating the impact of selection pressure in increasing the genetic diversity. The pattern of group constellation proved that significant amount of variability existed. It is interesting to note that 49 genotypes representing differences in their origin were grouped in the same clusters. This is an indication for the absence of relationship between genetic diversity and geographic diversity. Similar results have been reported by Johnjoel *et al.* [35] and Parameshwarappa *et al.* [36].

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Vol.2.Issue.3.2015 (July-Sept.)**ISSN:2394-2606****Table 4. Clustering pattern of 49 genotypes of sesame based on Mahalanobis (D^2) distances**

Cluster	Genotypes	No. of genotypes
I	Klf, M-80, SNNP-5, Tigray-22, SNNP-8, Gambella-4, S, Abs	8
II	Am-NG-12, Am-NG-22, Am-NG-17, Am-NG-25, Am-NG-20, Am-NG-11, Am-NG-24, Gambella-2, SNNP-7, Tigray-7, Srk, Tigray-10, Tigray-12, Tigray-14, Tigray-15, Tigray-20, Tigray-21, Am-NG-23,	18
III	Oromia-28, Am-NG-13, Tigray-17, Am-NG-14, Am-NG-27, Am-NG-18, Adi, SNNP-6, Tigray-8, Tigray-9, Tigray-6, Tigray-18, Tigray-16,	13
IV	Am-NG-16, Am-NG-26, Tigray-11, Gambella-1, Am-NG-19, Am-NG-15, Am-NG-21	7
V	Tigray-19	1
VI	Gambella-3	1
VII	Tigray-13	1

There was a wide range of variation in the cluster mean values of most of the characters under study (Table 5). Cluster-VI had the highest mean for most of the characters such as days to flowering, days to maturity, number of Primary branches, plant height, number of capsules, harvest index and highest seed yield per plant, but the group exhibited lowest capsule length and low oil content (%). In contrast, genotypes in Cluster-VII were characterized mainly by lowest mean of number of capsules/plant, number of seeds/capsule, biomass/plant, harvest index, 1000 seed weight and seed yield/plant, but with the highest mean oil content (%). Crosses among diverse parents are likely to yield desirable combinations. While the low-yielding type (Cluster-VII) was the highest in oil content, the best high-yielding type (Cluster-VI) was the lowest. Therefore, a crossing program should be initiated between the genotypes belonging different clusters. The greater the distance between two cluster, the wider the genetic diversity among the parents to be included in hybridization program [36]. Cluster-V comprised genotypes with higher number of capsules/plant that had the largest capsule length, early in maturity, and medium plant height, but with lowest number of primary branches, 1000 seed weight and lowest oil content (%) than any other cluster. Genotypes in Cluster-IV were characterized by moderate branching habit and short plant stature with higher number of seeds/capsule, 1000 seed weight, harvest index and seed yield/plant, but with low oil content (%). Cluster-III was mainly characterized by lower seed yield/plant, short plant stature, high number of branches/plant, and moderate to high oil content (%). Genotypes in Cluster-I were characterized by shorter flowering dates, primary branches, tall plant height, moderate seed yield/plant, with high oil content (%). Most of the check varieties were grouped under this cluster. Cluster-II in general, possessed genotypes with average plant characteristics for the traits under consideration.

Table 5. Cluster means of 49 low-altitude sesame genotypes for 14 quantitative traits

Trait	I	II	III	IV	V	VI	VII
Days to Emergence	4.7*	4.8	5.1	5.0	5.5	5.5**	5.0
Days to Flowering	67.4*	69.3	68.6	69.6	69.0	72.5**	70.5
Days to Maturity	116.2	103.3	115.0	104.8	86.0*	120.5**	115.5
No. of Pr. Branches	6.8	5.2	6.2	6.0	4.65	8.5**	5.1*
No. of Capsules/plant	101.7	97.8	90.7	100.9	124.2	131.8**	81.9*
No. of Seeds/capsule	34.7	34.6	34.8	35.8**	34.4	32.0	30.0*

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Capsule Length (cm)	2.5	3.0	2.6	2.7	3.03**	2.4*	2.63
Plant Height (cm)	148.9	123.5	114.5*	115.2	127.7	166**	122.8
Biomass/plant (g)	7.1	7.3	6.2	8.3	6.8	8.7**	4.5*
Harvest Index (%)	80.6	81.6	78.7	83.7	80.2	83.9**	69.8*
1000 Seed weight (g)	1.7	1.8	1.6	2.0**	1.4	1.8	1.3*
Seed Yield/plant (g)	5.7	6.0	4.9	6.9	5.5	7.3**	3.2*
Seed Yield/plot (g)	284.5	299.5	245.8	345.6	274.2	365.8**	158.5*
Oil Content (%)	48.2	46.9	47.7	44.4	41.3	44.8	49.3**

** = highest mean, * = lowest mean

The dendrogram also clustered the genotypes into seven separate groups (Figure 1). The grouping pattern suggested that genotypes of the same origin were distributed into different clusters, indicating that there was no parallelism between clustering pattern and geographic distribution of germplasm. This might be due to difference in adoption, selection pressure and environmental conditions. Our results are in agreement with previous findings in sesame populations of different countries [35, 36, 37 and 38]. This could be the movement of sesame materials from one area to another in collection sites. A few ecological conditions could also lead to gene flow between populations from diverse geographical origins. Although sesame has been described as a self-pollinated plant, recent indication raises the option of natural out-crossing in it [39, 40].

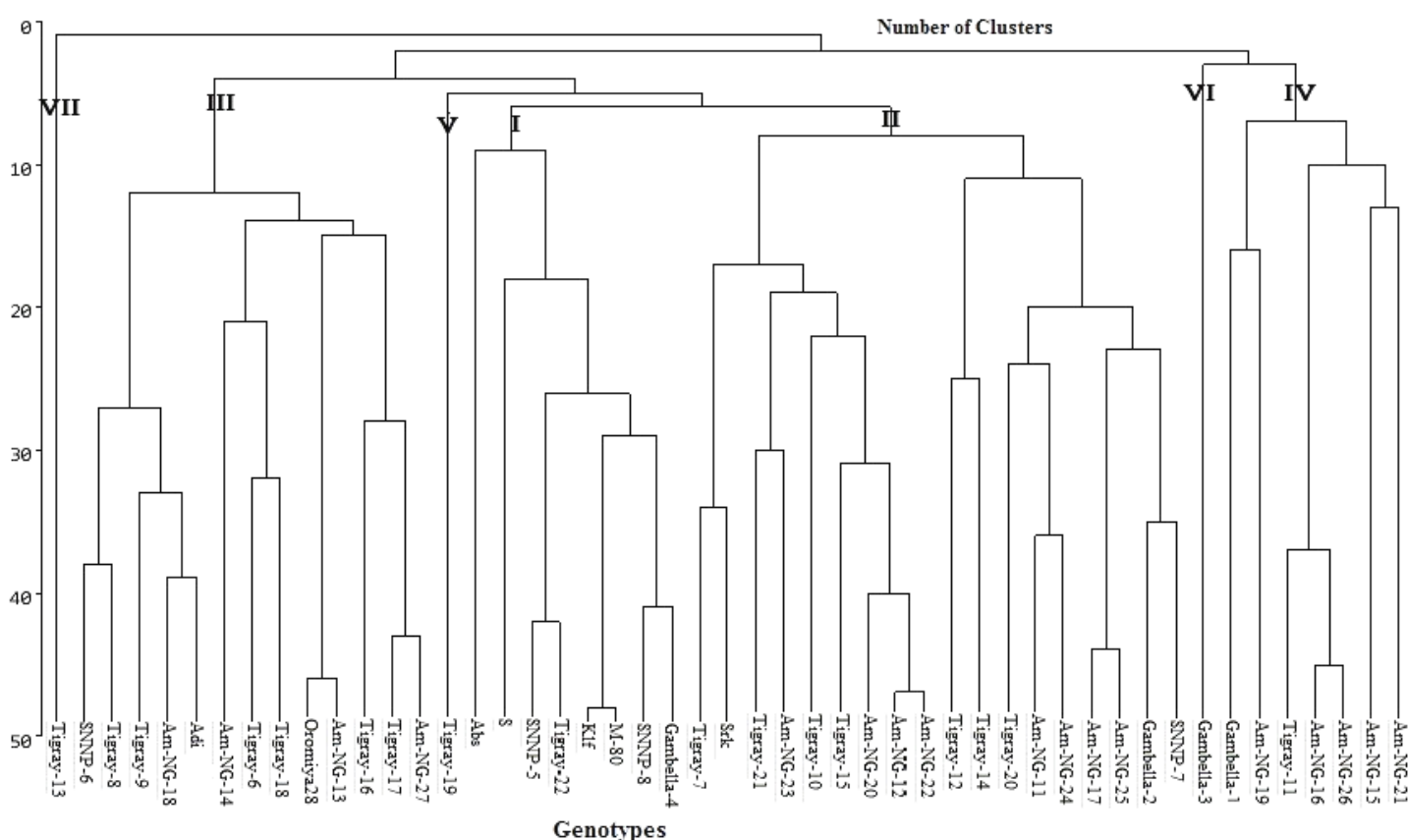


Figure 1. Dendrogram generated based on mean values of quantitative traits illustrating the clustering pattern of 49 low-altitude sesame genotypes.

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The range of inter and intra cluster distances were 19.61 to 665.46 and 0.00 to 3.89, respectively (Table 6). The maximum inter cluster distance was found between Clusters VI and VII, followed by Clusters IV and VII (577.97), Clusters II and VII (420.56), Clusters V and VII (397.58), and Clusters I and VII (397.03). Selection of parents from such clusters for hybridization program would help to achieve novel recombinants. Hybridization between genetically distant genotypes to generate promising breeding material has been suggested by Alarmelu and Ramanathan [41]. The hybridization between the genotypes falling in the most distant clusters i.e., VI (Gambella-3) and VII (Tigray-13) could result in maximum hybrid vigor and eventually may give rise desirable recombinants. The minimum inter cluster distances were recorded between Clusters I and III, Clusters II and IV (24.64) and Clusters I and II (28.26). The highest intra cluster distance was observed for Cluster IV (Table 5). It indicates that the germplasm lines of Cluster IV were more diverged than any other cluster. Thus, the germplasm lines belonging to the distant clusters could be used for breeding program to obtaining a wider range of variability.

Table 6. Average intra- (bold face) and inter-cluster distance (D^2 values) in 49 sesame genotypes

Clusters	I	II	III	IV	V	VI	VII
I	3.62	28.26*	19.61*	68.74	43.91	85.84	397.03
II		2.00	35.40	24.64*	82.18	92.19	420.56**
III			2.65	101.32	46.06	156.75	289.83
IV				3.89**	135.92	61.62	577.97**
V					0.00	148.21	397.58
VI						0.00	665.46**
VII							0.00

** , * = maximum and minimum cluster distances respectively.

The contribution of individual characters towards genetic divergence was estimated from the number of times that character appeared in first rank (Table 7). It was observed that harvest index contributed highest (13.97%) towards genetic divergence, followed by seed yield/plant and seed yield/plot (13.78%), biomass/plant (13.73%), plant height (8.10%) and 1000 Seed weight (7.31%). These characters showed highest contribution in total genetic divergence. The remaining characters, days to emergence, days to flowering, number of branches/plant, number of seeds per capsules, capsule length and oil content showed negligible contribution. Similar observations have been recorded by previous researchers [36, 41 and 42]. Thus, six characters viz., harvest index, seed yield, biomass/plant, plant height, 1000 seed weight and days to maturity were important since they together contributed about 64% towards total divergence. These results are in agreement with that given by Velusami *et al.* [43] for seed yield followed by 1000 seed weight. In sesame, Solanki and Gupta [44] reported that seed yield, number of capsules, plant height and 1000 seed weight are the important contributing factors.

The result of principal component analysis indicated that seed yield, biomass/plant, harvest index, days to maturity, plant height, number of capsules/plant, number of Primary branches/plant and 1000-seed weight were among the most important descriptors which accounted for more than 50% of the phenotypic variation expressed in these germplasm collections (Table 8). These traits are therefore found to be most useful for studying the variability of populations. Akbar *et al.* [45] suggested that the use of these characters will save considerable amount of time for identification of sesame germplasm for downstream breeding works.

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Vol.2.Issue.3.2015 (July-Sept.)**ISSN:2394-2606****Table 7. Percent contribution of different traits towards divergence in 49 sesame genotypes**

No	Character	Times ranked first	Percent contribution
1.	Days to Emergence	26	2.22
2.	Days to Flowering	19	1.62
3.	Days to Maturity	81	6.92
4.	No. of Pr. Branches	53	4.53
5.	No. of Capsules/plant	59	5.01
6.	No. of Seeds/capsule	23	1.91
7.	Capsule Length (cm)	58	4.90
8.	Plant Height (cm)	95	8.10**
9.	Biomass/plant (g)	162	13.73**
10.	Harvest Index (%)	164	13.97**
11.	1000 Seed weight (g)	86	7.31
12.	Seed Yield/plant (g)	162	13.78**
13.	Seed Yield/plot (g)	162	13.78**
14.	Oil Content (%)	26	2.21

** indicates percent of high contribution.

Table 8. Principal component analysis of quantitative traits for 49 sesame genotypes

Characters	PC I	PC II	PC III	PC IV	PC V
Days to Emergence	-0.012	-0.046	-0.119	0.493*	0.260
Days to Flowering	0.001	-0.245	-0.142	0.398	0.433*
Days to Maturity	-0.165	0.315	0.424*	0.283	-0.030
No. of Branches/ plant	-0.037	0.350*	0.176	0.157	0.275
No. of Capsules/plant	0.125	0.366*	-0.465	0.107	-0.265
No. of Seeds/capsule	0.128	-0.398	0.180*	0.025	0.272
Capsule Length (cm)	0.076	-0.351	-0.424	-0.244	0.219
Plant Height (cm)	0.106	0.409*	-0.214	-0.164	0.315
Biomass/plant (g)	0.459*	0.061	0.034	0.043	-0.026
Harvest Index (%)	0.445*	0.001	0.074	0.049	-0.027
1000 Seed weight (g)	0.280	-0.089	0.391*	-0.081	0.072
Seed Yield/plant (g)	0.461*	0.050	0.043	0.050	-0.025
Seed Yield/plot (g)	0.460*	0.049	0.043	0.052	-0.029
Oil Content (%)	-0.092	0.128	0.261	-0.283	0.405*
Eigen value	4.601	2.192	1.937	1.555	1.305
Proportion	28.75%	13.70%	12.10%	9.72%	8.16%
Cumulative	28.75%	42.45%	54.56%	64.28%	72.43%

* indicates high vector value of the trait. PC (I-V) is principal component axis from one to five.

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CONCLUSION

The study showed that there is high level of genetic variability with regard to seed yield and its component characters in the studied germplasm. It indicates the presence of a huge scope for selection of promising genotypes with different agronomic traits from the present collection pool. The value of PCV was higher than GCV for all the observed traits, indicating that genotypic expression was superimposed by environmental influences. Most of the traits in low-altitude genotypes showed moderate heritability with minimum genetic advance, which makes the yield improvement programme through important traits difficult. Biomass/plant, harvest index and 1000 seed weight exerted highest positive direct effect on seed yield. Improving these traits may increase seed yield in sesame. D^2 values and clustering pattern revealed the existence of considerable amount of genetic diversity among the studied genotypes. Genotypes from different regions were closely related while genotypes from the same region were grouped in different clusters, indicating the absence of relationship between genetic diversity and geographic diversity. There was a wide range of variation in the cluster mean values for most of the traits under study. Hybridization between genotypes of divergent clusters is likely to produce wide variability with desirable segregants. Seed yield/plant, seed yield/plot, harvest index and biomass/plant had greater contribution to divergence in the present sets of sesame genotypes.

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