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Characterization and Evaluation of Sesame Landraces

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Abstract

Availability of genetic variability is the prerequisite of any crop improvement program. Thus, the experiment was conducted to characterize and evaluate sesame landraces based on their qualitative and quantitative traits. Forty-nine sesame genotypes were evaluated at Kamashi research sub-station during 2017/18 cropping season. The experiment was laid out on 7 × 7 simple lattice design. Each experimental material was planted on a plot consisted of 5 rows with 4 m length, and 10 cm and 40 cm intra and inter row spacing, respectively. Data was recorded on 10 qualitative and 14 quantitative traits. Statistical analysis was computed using R and SAS university edition. In the present study, genetic variation was exhibited among sesame genotypes for eight qualitative traits such as leaves hairiness, stem hairiness, capsule hairiness, number of flower/leaf axil, number of capsules/leaf axil, number of carpels/capsule, number of locules/capsule and seed coat color. In addition, analysis of variance on quantitative traits revealed the presence of genetic variability among sesame genotypes for days to flowering, bacterial blight disease resistance, days to maturity, plant height to first branching, length of capsule bearing zone, internode length, capsule length, number of capsules/plant, 1000 seeds weight and seed yield. Factor analysis confirmed that bacterial blight disease resistance, plant height, length of capsule bearing zone, number of branches/plant, number of capsules/plant and seed yield were the most important traits those highly contributed to an observed genetic variation. Further, cluster analysis based on 14 quantitative traits grouped the 49 sesame genotypes into seven groups which indicate the presence of genetic diversity.

Keywords: Cluster analysis; Factor analysis; Genetic diversity; Qualitative trait; Quantitative trait

Introduction

Sesame (*Sesamum indicum*, 2n=26) is among the oldest oilseeds crops widely grown in Africa and Asia. Sesame is the major agricultural commodity crop in Ethiopian global market next to coffee as well as source of cash for farmers growing it. Africa is considered as the primary center of origin for sesame hence there is diversified wild species in the continent [1]. Further, availability of wild forms of sesame such as *S. alatum* and *S. latifolium* in Ethiopia as reported by Ayana indicates the existence of genetic diversity in the country as well [2]. Most of improved varieties which have been cultivated in Ethiopia were derived from local landraces through selection. Abate, et al. reported the presence of genetic diversity for different traits among the tested Ethiopian germplasm [3].

Besides the presence of genetic diversity in sesame, its genetic potential has not been exploited yet. Sesame productivity has been constrained due to low yielding performance of cultivars, diseases and insect pests, and seed shattering [4]. Assessment of genetic diversity through collection, characterization and evaluation of local landraces is the prerequisite to meet crop improvement goals of any crop. Assessment of genetic diversity provides information for effective selection of starting materials for breeding programs [5]. Study of genetic diversity enables to formulate selection of parents [6], in attempt to combine desirable traits through hybridization. In addition, available genetic diversity can be used for direct variety release through selection [7]. Thus, any available genetic potential would be exploited through collection, characterization and evaluation of local landraces that have not been addressed.

Therefore, the objective of the experiment was to characterize and evaluate sesame landraces based on their qualitative and quantitative traits in attempt of identifying and selecting sesame genotypes with desirable traits.

Materials and Methods

Experimental materials and design

The experiment was conducted at Kamashi research sub-station of Assosa Agricultural Research Center in 2017/18 cropping season. Forty-nine sesame genotypes were the experimental materials of the experiment (Table 1). The experiment was laid out on 7 × 7 simple lattice designs. Each sesame genotype was planted on a plot consisted of five rows of 4 m length with 10 cm and 40 cm intra and inter row spacing, respectively.

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S. No.	Genotype	Administrative zone	Source	S.No.	Genotype	Administrative zone	Source
1	202514	Assosa	IBC	26	202517	Eastern Wellega	IBC
2	23559	Metekel	IBC	27	17710	Eastern Wellega	IBC
3	23557	Metekel	IBC	28	17703	Eastern Wellega	IBC
4	23552	Metekel	IBC	29	111520	Eastern Wellega	IBC
5	23554	Metekel	IBC	30	17699	Eastern Wellega	IBC
6	23561	Metekel	IBC	31	17702	Eastern Wellega	IBC
7	23546	Metekel	IBC	32	111522	Eastern Wellega	IBC
8	23558	Metekel	IBC	33	17711	Eastern Wellega	IBC
9	23548	Metekel	IBC	34	111521	Eastern Wellega	IBC
10	23555	Metekel	IBC	35	207954	Eastern Wellega	IBC
11	23547	Metekel	IBC	36	17697	Eastern Wellega	IBC
12	23564	Metekel	IBC	37	17701	Eastern Wellega	IBC
13	23556	Metekel	IBC	38	17713	Eastern Wellega	IBC
14	23565	Metekel	IBC	39	215816	Eastern Wellega	IBC
15	23551	Metekel	IBC	40	202518	Eastern Wellega	IBC
16	23560	Metekel	IBC	41	208671	Western Hararge	IBC
17	207955	Zone 1	IBC	42	19039	Western Hararge	IBC
18	207957	Zone 1	IBC	43	208751	Western Wellega	IBC
19	222876	Zone 1	IBC	44	17708	Western Wellega	IBC
20	207956	Zone 1	IBC	45	208752	Western Wellega	IBC
21	216733	Zone 2	IBC	46	207953	Western Wellega	IBC
22	202512	Eastern Hararge	IBC	47	237994	Western Wellega	IBC
23	228816	Eastern Hararge	IBC	48	17704	Western Wellega	IBC
24	208673	Eastern Hararge	IBC	49	Abasena	Western Wellega	WARC
25	17712	Eastern Wellega	IBC				

IBC: Institute of Biodiversity Conservation; WARC: Werer Agricultural Research Center

Table 1: Sesame genotypes used in the experiment conducted at Kamashi during 2017/18 cropping year.

Data collection

Data was collected on 10 qualitative and 14 quantitative traits following IPGRI and NBPGR [8] sesame descriptor. Qualitative traits those considered for data collection were Plant Growth Type (PGT), Branching Habit (BH), Stem Hairiness (SH), Leaves Hairiness (LH), Capsule Hairiness (CH), number of Flower/Leaf Axil (FPA), number of Capsules/Leaf Axil (CPA), number of Carpel/Capsule (CPC), number of Locule/Capsule (LPC), and Seed Coat Color (SCC). In addition, data was collected on quantitative traits such as Bacterial Blight Disease Severity 1-9 scale (BBDS), Days to Flowering (DF), Days to Maturity (DM), Plant Height to First Branching (PHFB) in cm, Plant Height (PH) in cm, Length of Capsule Bearing Zone on main stem (LCBZ) in cm, Internode Length (IL) in mm, Capsule Length (CL) in mm, Capsule Width (CW) in mm, number of Branches/Plant (BPP), number of Capsules/Plant (CPP), number of Seeds/Capsule (SPC), Thousand Seed Weight (TSW) in gm and Seed Yield (SY) kg ha^{-1}. Resistance of sesame genotypes against bacterial blight was scored was recorded at flowering stage in 0-6 disease susceptibility scale as applied by Sarwar and Haq [9] where 0=0% (immune), 1=0.10-5% (highly resistant); 2=5.10-10% (resistant); 3=10.10-20% (moderately resistant); 4=20.10-50% (moderately susceptible); 5=50.10-70% (susceptible) and 6=>70 % (highly susceptible). Disease susceptibility scales recorded 0–6 were converted to Percentage of Severity Index (PSI) according to Wheeler [10] as follows:

$$PSI\ (\%) = \frac{\text{Sum of all disease scores}}{\text{Number of ratings} \times \text{Maximum disease grade}} \times 100$$

Data analysis

Summary statistics, factor analysis and cluster analysis were computed using SAS university edition [11]. Mean and range in quantitative traits, and dominance of observed phenotypic classes in regard of qualitative traits were summarized by using "proc summary" and "proc freq" procedures, respectively. Contribution of traits for explained genetic variability and interrelationship among traits were determined by factor analysis. Mean values of quantitative traits were subjected to factor analysis using "proc factor" procedure. SAS rotation method *i.e.,* "varimax" rotation as suggested by Cody and Smith [12] was used to maintain orthogonality of the factors and then to get the traits to load high on one of their respective factor and low on the consecutive factors. Significance of association between a factor and loadings scores of traits was tested by Pearson correlation. Clustering of genotypes and identification of member genotypes belongs to each cluster based on quantitative traits were determined by using "proc cluster'' (Euclidean average linkage method) and "proc tree" procedures, respectively. Genetic divergence in sesame genotypes included in the study was estimated from Mahalanobis [13] squared distances by using "proc distance" procedure.

Analysis of Variance (ANOVA): Analysis of variance was carried out by using "PBIB test" (variance component estimation) function of R 3.4.3 software [14] which is applicable for families of partially balanced designs like lattices and alpha designs. The model used in analysis of variance was:

$$Yijk = \mu + Repj + Blockk\,(Repj) + Geni + eijk$$

where Yijk is an observation for trait of interest; μ is the mean; Repj is the effect of the j^{th} replication; Blockk (Repj) is the effect of the k^{th} incomplete block within the j^{th} replication; Geni is the effect of the i^{th} genotype, and eijk is the residual term.

Results and Discussion

Genetic variability in sesame based on quantitative and qualitative traits

Sesame genotypes showed genetic variability in terms of their mean performance for quantitative traits as well as in their phenotype of qualitative traits (Table 2). Sesame genotypes showed genetic variation for days to flowering with a range of 46.27 days to 59.87 days whereas number of days to maturity was ranged from 98.48 to 136.53 days. Mean bacterial blight disease severity in sesame genotypes was ranged from 30.19% to 77.74%. Sesame genotypes were varied in terms of length of capsule bearing zone from 25.82 cm to 76.25 cm whereas the genetic variation for number of branches/plant was ranged from 2.85 to 8.49. In addition, Number of capsules/plant was ranged from 21.65 to 95.17 while number of seeds/capsule showed variation ranging from 52.11 to 91.38. Further, 1000 seeds weight was ranged from 1.84 g to 2.72 g with mean 1000 seeds weight of 2.13 g. Sesame genotypes showed genetic variation for seed yield in a magnitude of 179.17 kg ha-1 to 929 kg ha^{-1} with mean seed yield of 573.22 kg ha^{-1}.

In terms of qualitative traits, sesame genotypes were with varying phenotype in leaf hairiness (51.02% sparse and 48.98% glabrous); stem hairiness (91.84% glabrous and 8.12% sparse); capsule hairiness (81.63% sparse, 10.20% medium, 6.12% glabrous and 2.02% profuse); number of flowers/leaf axil (93.88% one and 6.12% more than one); number of capsules/leaf axil (93.88% monocapsular and 6.12% multicapsular); number of carpels/capsule (93.88% bicarpellate and 6.12% tetracarpellate) and number of locules/capsule (98.88% four, 4.10% eight and 2.02% six). In addition, sesame genotypes were with varying phenotypes in terms of seed coat color (38.77% white, 34.69% cream, 6.12% tan, 6.12% mixed, 4.10% black, 4.10% light brown, 2.02% medium brown, 2.02% dark brown and 2.02% beige). However, there was no variability among sesame genotypes for growth type (100% indeterminate), branching pattern (100% basal branching). Langham [15] reported the presence of genetic variability in sesame for number of capsules/leaf axil. Similarly, genetic variability among sesame genotypes have been reported for number of capsules/leaf axil and seed coat color [6], and for seed coat color ranging from white to black [16]. The result of the present study revealed that sesame genotypes with indeterminate growth type; basal branching pattern; one flower/leaf axil; monocapsular node; bicarpellate capsule and four loculed capsules were abundant. On the other hand, sesame genotypes with more than one flower/leaf axil; multicapsular node, teteracarpellate capsule and six loculed capsules were rarely found whereas sesame genotypes were entirely indeterminate and basal branching in terms of their growth type and branching pattern. Similar results were reported by Furat and Uzun [17] in which all genotypes were indeterminate while multicapsuled genotypes and genotypes with tetracarpellate capsules were found in low proportion. Genotypes with three flower/leaf axil are an important resource for plant breeding programs in increasing capsule density per unit length hence number of capsules/plant is the most contributing trait of sesame seed yield.

Quantitative trait	Minimum	Maximum	Mean	SE	CV (%)
DF	46.27	59.87	49.1	1.34	2.7
BBDS	30.19	77.74	48.75	10.48	21.5
DM	98.47	136.53	104.23	2.24	2.1
PH	114.8	158	139.62	12.34	8.8
PHFB	35.1	78.6	49.86	7.69	15.4
LCBZ	25.82	76.25	61.68	8.25	13.4
IL	25.4	64.45	52.56	5.96	11.3

CL	19	30.5	23.78	1.81	7.6
CW	4.54	8.76	6.8	0.92	13.5
BBP	2.85	8.49	6.01	1.35	22.5
CPP	21.65	95.17	63.28	15	23.7
SPC	52.11	91.38	72.4	8.4	11.6
TSW	1.84	2.72	2.13	0.17	8.4
SY	179.17	929.76	573.22	122.21	21.3
Qualitative trait					
Growth type	Indeterminate (100%)				
Branching pattern	Basal (100%)				
Leaves hairiness	Sparse (51.02%) and glabrous (48.98%)				
Stem hairiness	Glabrous (91.84%) and sparse (8.12%)				
Capsule hairiness	Sparse (81.63%), medium (10.20%), glabrous (6.12%) and profuse (2.02%)				
Number of flowers/leaf axil	One (93.88%) and more than one (6.12%)				
Number of capsules/leaf axil	Monocapsular (93.88%) and multicapsular (6.12%)				
Number of carpels/ capsule	Bicarpellate (93.88%) and tetracarpellate (6.12%)				
Number of locule/capsule	Four (93.88%), eight (4.10%) and Six (2.02%)				
Seed coat color	White (38.77%), cream (34.69%), tan (6.12%), mixed (6.12%), black (4.10%), light brown (4.10%), medium brown (2.02%), dark brown (2.02%) and beige (2.02%)				

DF: Days to Flowering; BBDS: Bacterial Blight Disease Severity (%); DM: Days to Maturity; PH: Plant Height in cm; PHFB: Plant Height to First Branch in cm; LCBZ: Length of Capsule Bearing Zone in cm; IL: Internode Length in mm; CL: Capsule Length in mm; CW: Capsule Width in mm; BPP: Number of Branch/Plant; CPP: Number of Capsules/Plant; SPC: Number of Seeds/Capsule; TSW: Thousand Seed Weight in g; SY: Seed Yield in kg ha^{-1}; SE: Standard Error and CV(%): Coefficient of Variation

Table 2: Genetic variability in sesame genotypes for 14 quantitative and 10 qualitative traits at Kamashi during 2017/18 cropping season.

Analysis of variance and mean performance of sesame genotypes

Analysis of variance revealed a significant genetic variability among sesame genotypes for days to 50% flowering, bacterial blight disease severity (%), days to maturity, plant height to first branching, length of capsule bearing zone, internode length, capsule length, number of branches/plant, number of seeds/capsule, 1000 seeds weight and seed yield kg ha^{-1} (Table 3). Similar results were reported by Bandila, et al. [18] and Gidey, et al. [19] for plant height, number of branches/plant, number of capsules/plant, number of seeds/capsule, 1000 seeds weight and seed yield. The shortest and tallest sesame genotypes were 23561 (114.80 cm) and 111521 (158.00 cm), respectively. The highest number of capsules/plant (95.17) was recorded from 17701 while the highest number of seeds/capsule (91.38) was recorded from 202517. The genotype with larger seeds (2.72 g) was Abasena which have been widely grown in high rainfall and humid sesame growing areas of Ethiopia. The highest seed yield/plant (929 kg ha^{-1}) was recorded on 17703 followed by Abasena (Table 4). Thus, the present study confirmed the presence of genetic variability that can be exploited to enhance seed yield through selection for seed yield and seed yield related traits.

Trait	Replication	Block/Rep adj.	Genotype undj.	Residual
DF	4.08	13.48	2.77^{**}	1.8
BBDS	1936.2	259.05	149.34^{**}	109.91
DM	77.24	81.02	12.41^{**}	5.01
PH	0.83	168.27	102.08^{ns}	152.27

PHFB	724.17	105.97	58.98*	59.2
LCBZ	788.61	135.12	84.83*	68.07
IL	186.52	70.3	52.20*	35.5
CL	13.37	9.53	1.09**	3.28
CW	0.77	1.32	1.44ns	0.85
BBP	15.64	2.72	2.25ns	1.83
CPP	759.39	537.49	234.97**	225.15
SPC	583.84	99.58	80.72ns	70.61
TSW	0.05	0.08	0.03**	0.03
SY	36494	10130	77722**	14935

DF: Days to Flowering; BBDS: Bacterial Blight Disease Severity (%); DM: Days to Maturity; PH: Plant Height in cm; PHFB: Plant Height to First Branch in cm; LCBZ: Length of Capsule Bearing Zone in cm; IL: Internode Length in mm; CL: Capsule Length in mm; CW: Capsule Width in mm; BPP: Number of Branch/Plant; CPP: Number of Capsules/Plant; SPC: Number of Seeds/Capsule; TSW: Thousand Seed Weight in g; SY: Seed Yield in kg ha^{-1}; **: highly significant; *: significant; ns: non-significant

Table 3: Analysis of variance on 14 quantitative traits of sesame at Kamashi during 2017/18 cropping season.

Genotype	DF	BBDS	DM	PH	PHFB	LCBZ	IL	CL	CW	BPP	CPP	SPC	TSW	SY
17703	48.87	35.39	106.68	145	56.5	61.83	52.45	22.3	7.69	7.26	68.6	76	1.98	929.76
Abasena	49.65	42.22	103.62	150.9	54.4	66.01	54.94	23.1	7.18	7.3	92.02	86.57	2.72	915.05
17704	46.75	34.72	105.28	137.5	55.3	62.07	48.37	21.8	6.43	6.58	56.79	77.05	2.05	857.24
208752	47.03	50.86	100.16	137.9	50.2	64.22	51.61	24	6.95	6.54	60.68	68.08	2.05	825
202514	49.2	45.37	106.89	144.9	49.4	69.13	52.77	23.9	7.31	6.62	82.49	73.11	2.01	805.21
17701	51.32	48.3	105.37	143.3	47.1	71.97	60.46	22.9	6.86	8.49	95.17	70.34	2.06	786.97
207956	47.37	51.15	101.49	141.7	49	57.6	50.45	25.6	7.03	7.89	76.12	74.66	2.13	756.25
17697	47.6	38.53	102.46	155.8	47.8	68.16	54.11	22.6	6.71	6.65	71.84	85.64	1.94	755.21
111522	47.85	30.52	102.63	145.9	55.2	59.73	46.09	23	6.69	6.5	69.15	81.63	1.94	751.04
207955	47.92	38.11	102.48	138.5	35.1	74.73	50.31	26.5	5.82	6.94	92.38	75.49	1.84	747.92
111521	47.85	40.04	103.73	158	43.9	76.25	56.83	24.8	6.41	6.68	77.04	67.47	1.91	746.88
237994	48.18	30.19	103.24	151.3	48.5	72.81	50.01	23.5	7.94	6.12	86.14	71.72	2	737.83
17708	46.63	45.2	102.71	153.7	52.2	68.91	56.14	23.7	6.53	6.16	89.52	68.44	1.97	722.92
23546	50.25	46.92	105.96	131.9	55.5	58.93	52.25	24.2	7.65	6.29	62.3	73.32	2.15	714.44
17710	48.52	36.01	105.24	141.8	46.7	70.23	56.82	23.7	6.41	6.88	70.9	74.9	2.14	712.5
17713	48.92	47.26	102.01	147.3	48	64.4	61.53	23	6.84	6.55	61.14	66.14	2.16	711.46
23556	49.05	35.3	104.41	139.9	55.4	64.47	54.44	22.9	7.58	6.65	67.26	79.27	2	707.41
Grand mean	49.1	48.75	104.23	139.62	8.8	61.68	52.56	23.78	6.8	6.01	63.28	72.4	2.13	573.22
SE	1.34	10.48	2.24	12.34	7.69	8.25	5.96	1.81	0.92	1.35	15	8.4	0.17	122.21
LSD at 5%	2.64	20.65	4.41	ns	15.16	16.25	11.74	3.57	ns	ns	29.56	ns	0.34	240.75
CV (%)	2.7	21.5	2.1	8.8	15.4	13.4	11.3	7.6	13.5	22.5	23.7	11.6	8.4	21.3

DF: Days to Flowering; BBDS: Bacterial Blight Disease Severity (%); DM: Days to Maturity; PH: Plant Height in cm; PHFB: Plant Height to First Branch in cm; LCBZ: Length of Capsule Bearing Zone in cm; IL: Internode Length in mm; CL: Capsule Length in mm; CW: Capsule Width in mm; BPP: Number of Branch/Plant; CPP: Number of Capsules/Plant; SPC: Number of Seeds/Capsule; TSW: Thousand Seed Weight in g; SY: Seed Yield in kg ha-1; SE: Standard Error and CV(%): Coefficient of Variation

Table 4: Mean performance elite sesame genotypes for 14 quantitative traits at Kamashi during 2017/18 cropping season.

Factor analysis

Factor analysis (Table 5) partitioned the data into five factors with an eigenvalue greater than one. A total of 70.80% of a genetic variation was explained in these five factors where the first one, the second and third factors were contributed 22.43%, 17.08% and 11.52% of the total explained variation, respectively. The first factor was with highly significant correlation with loading scores of bacterial blight disease severity (-0.53), plant height (0.65), length of capsule bearing zone (0.68), number of branches/plant (0.81), number of capsules/plant (0.85), and seed yield/plant (0.64). On the other hand, the second factor was with highly significant correlation with loading scores of days to flowering (0.62), days to physiological maturity (0.78), plant height to first branch (0.65) and internode length (-0.73) whereas the third factor highly and significantly correlated with capsule length (0.77) and number 1000 seeds weight (0.71). The fourth and fifth factors were with highly significant correlation with capsule width (0.79) and number of seeds/capsule (0.83), respectively. The result was in agreement with factor analysis of Tabatabaei et al. [20] for seed yield/plant, plant height and number of capsules/plant which loaded higher in the first factor. Significance of traits and interrelationship of traits can be simultaneously understood through data reduction multivariate techniques such as factor analysis [21]. The result of factor analysis revealed that bacterial blight disease severity (%), plant height, length of capsule bearing zone, number of branches/plant, number of capsules/plant and seed yield/plant were the most determinant traits of explained genetic variation. Therefore, selection underlying these traits would result promising sesame genotypes. Highest loading scores for several traits in a particular factor indicate co-inheritance of traits while the sign of loading scores in a factor indicate the direction of relationship of loading scores and factors. So, loading scores of first factor indicates that higher seed yield/plant associated with bacterial blight disease resistance, tallness, longer capsule bearing zone, high number of branches/plant, and high number of capsules/plant.

	Factor				
	1	**2**	**3**	**4**	**5**
Eigenvalue	3.14	2.39	1.61	1.58	1.19
Proportion of variation (%)	22.43	17.08	11.52	11.26	8.51
Total percent of variation (%)	22.43	39.51	51.03	62.29	70.8
DF	-0.16	0.62**	0.19	-0.53**	-0.15
BBDS	-0.53**	0.16	0.34**	-0.27**	-0.19
DM	0.05	0.78**	0.11	-0.40**	0.03
PH	0.65**	0.04	-0.16	-0.29**	0.37**
PHFB	-0.25*	0.65**	-0.30**	-0.08	0.43**
LCBZ	0.68**	-0.52**	-0.04	-0.15	0.05
IL	0.14	-0.73**	-0.09	-0.24*	0.15
CL	0.05	-0.1	0.77**	0.15	0.15
CW	0.12	-0.02	0.12	0.79**	0
BPP	0.81**	0.04	0.21*	0.16	-0.18
CPP	0.85**	-0.29**	-0.03	0.16	0.06
SPC	0.13	-0.06	0.16	0.07	0.83**
TSW	-0.15	0.24*	0.71**	-0.06	-0.01
SY	0.64**	0.02	-0.36**	0.41**	0.194

DF: Days to Flowering; BBDS: Bacterial Blight Disease Severity (%); DM: Days to Maturity; PH: Plant Height in cm; PHFB: Plant Height to First Branch in cm; LCBZ: Length of Capsule Bearing Zone in cm; IL: Internode Length in mm; CL: Capsule Length in mm; CW: Capsule Width in mm; BPP: Number of Branch/Plant; CPP: Number of Capsules/Plant; SPC: Number of Seeds/Capsule; TSW: Thousand Seed Weight in g; SY: Seed Yield in kg ha-1; ** : highly significant Pearson correlation; * : significant Pearson correlation

Table 5: Factor eigenvalues and factor loading scores of 14 quantitative traits of sesame at Kamashi during 2017/18 cropping season.

Cluster analysis

The plot of the Pseudo-F against the number of clusters suggests that 7 clusters would be an appropriate classification for the 49 sesame genotypes (Figure 1). A dendogram of 49 sesame genotypes based on cluster analysis on data of 14 quantitative traits is shown on Figure 2. The majority of sesame genotypes (44.90%) were classified into Cluster-II and Cluster-IV where each cluster consisted of 11 sesame genotypes (Table 6).

Cluster-I and cluster-VI each consisted of 6 sesame genotypes totally accounted for 24.48% of the total sesame genotypes whereas cluster-V and cluster-VII comprised 7 (14.28%) and 2 (4.08%) sesame genotypes, respectively. Cluster analysis order genotypes in groups that are similar with respect to some measure [22]. Cluster analysis based on similarity or dissimilarity of traits classifies genotypes into different clusters each comprised genotypes having unique characters in contrast with that of the other clusters. Thus, the result of cluster analysis revealed an availability of genetic diversity in the studied sesame population. Similarly, the previous study carried out by Abate, et al. [3] indicated the presence of genetic diversity in Ethiopian sesame germplasm. Therefore, the study indicates the possibility to find out parental materials from different clusters to combine traits those discriminated the studied materials to be grouped in different clusters.

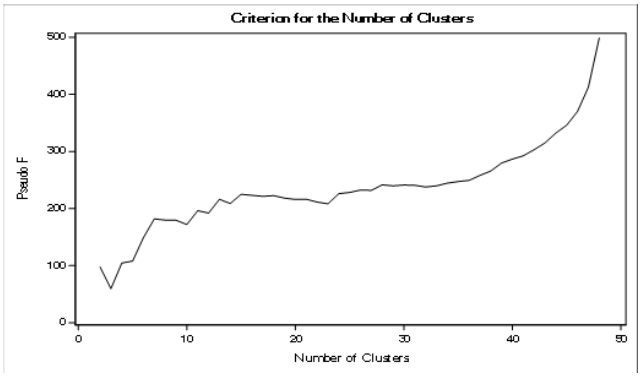

Figure 1: Plot of Pseudo F (Y-axis) against the number of clusters (X-axis).

Cluster	List of member genotypes
I	17701, 202514, 17703, Abasena, 17704 and 208752
II	17712, 17713, 207953, 215816, 17711, 207954, 23560 17702, 17699, 207957 and 222876
III	23554, 111520, 23564, 202518, 23552 and 23548
IV	17708, 111521, 17710, 207955, 23556, 23565, 207956 237994, 17697, 111522 and 23546
V	23558, 23561, 208671, 208673, 23555, 23551 and 23547
VI	23557, 208751, 23559, 216733, 202517 and 19039
VII	202512 and 228816

Table 6: Pattern of clustering of 49 sesame genotypes based on 14 quantitative traits grown at Kamashi during 2017/18 cropping year.

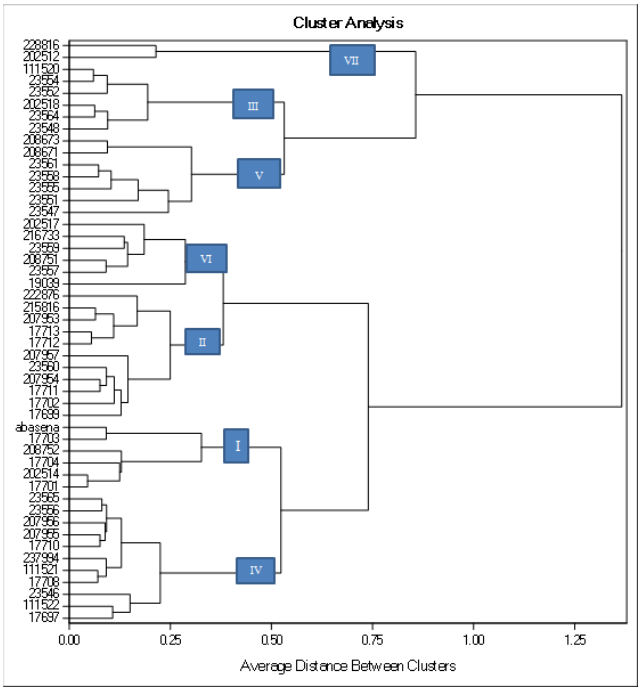

Figure 2: Dendrogram clustering 49 sesame genotypes based on 14 quantitative traits grown at Kamashi during 2017/18 cropping year.

As cluster means of traits shown in Table 7, bacterial blight disease severity, days to maturity, plant height, length of capsule bearing zone, number of branches/plant, number of capsules/plant, number of seeds/capsule, 1000 seeds weight and seed yield were the most discriminating traits of sesame genotypes grouped in different clusters. Similarly, the study of Abate, et al. [3] showed that seed yield/plant, number of branches/plant, number of capsule/plant, maturity period, and plant height are the most distinguishing traits used to characterize sesame genotypes belonging to different clusters. Sesame genotypes belongs to Cluster-I were characterized by moderate susceptibility to bacterial blight disease, longer capsule bearing zone on main stem, high number of branches/plant, high number of capsules/plant, high number of seeds/capsule and high seed yield kg ha^{-1}. Cluster-I includes a variety (Abasena) which was incorporated in the study as a standard check for its higher yielding and adaptability in high rainfall and bacterial blight disease prone areas of Western Ethiopia. Sesame genotypes grouped in Cluster-IV are the second in respect of seed yield (732.42 ± 218.45 kg ha^{-1}) and other seed yield contributing traits next to Cluster-I. Among the 17 highest yielding genotypes presented in Table 4, the first 6 highest yielding genotypes (17703, Abasena, 17704, 208752, 202514, and 17701) were found in Cluster-I whereas the second group of highest yielding genotypes (10 genotypes) were belonging to Cluster-IV. Thus, Cluster-I and Cluster-IV consisted of 35.29% (6 genotypes) and 58.82% (10 genotypes), respectively which totally accounted of 94.11% (16 genotypes) of the highest yielding 17 genotypes. Sesame genotype (202512 and 228816) which belongs to Cluster-VII characterized by late maturity, tallness, bacterial blight disease susceptible, lowest seed yield has an advantage of long capsule (25.54 ± 0.56 mm) and larger seed size (2.41 ± 0.43 g). Thus, the study indicated that some genotypes such as genotypes which belongs to Cluster-I can be considered for their overall performance whereas sesame genotypes belong to Cluster-VII being considered for specific traits like big seed size. The available genetic diversity can be exploited either through selection of genotypes for their desirable traits or for combining of desirable genes through hybridization [7]. Promising sesame genotypes with cumulative desirable performance in regard of key traits could be selected and evaluated further for direct release as a variety. Further, sesame genotypes with improved performance for a corresponding desirable trait of interest can be selected as parental line for hybridization.

	Cluster						
Quantitative traits	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**
DF	48.75 ± 1.43	48.19 ± 3.45	48.63 ± 1.16	48.03 ± 1.94	51.59 ± 3.44	49.93 ± 1.81	51.32 ± 1.01
BBDS	42.38 ± 5.26	47.36 ± 9.98	48.31 ± 9.92	41.96 ± 7.59	59.82 ± 12.20	52.70 ± 12.14	63.65 ± 10.33
DM	104.89 ± 1.65	103.09 ± 10.16	100.92 ± 1.78	103.56 ± 5.12	103.58 ± 3.68	106.96 ± 6.14	116.29 ± 0.51
PH	143.95 ± 9.04	136.76 ± 9.12	135.77 ± 10.50	143.50 ± 8.00	132.79 ± 6.46	143.42 ± 6.02	145.04 ± 0.82
PHFB	52.08 ± 2.62	46.96 ± 12.31	47.86 ± 6.25	50.05 ± 5.36	48.89 ± 10.02	56.07 ± 8.20	49.07 ± 7.16
LCBZ	66.70 ± 4.88	61.35 ± 11.84	61.31 ± 7.68	65.72 ± 7.34	59.18 ± 5.22	55.57 ± 5.73	54.37 ± 5.38
IL	53.57 ± 3.31	54.33 ± 9.10	52.71 ± 6.25	51.86 ± 3.73	52.29 ± 3.70	50.32 ± 2.37	50.93 ± 4.59
CL	22.79 ± 0.61	23.26 ± 1.74	23.89 ± 2.59	23.92 ± 2.29	24.57 ± 2.60	23.83 ± 2.11	25.54 ± 0.56
CW	7.11 ± 0.88	7.30 ± 0.75	6.54 ± 0.65	7.01 ± 0.79	6.28 ± 1.17	6.73 ± 1.01	4.91 ± 0.35
BPP	7.13 ± 0.53	6.12 ± 1.28	5.59 ± 1.02	6.46 ± 0.85	4.87 ± 2.32	5.76 ± 1.02	5.54 ± 1.09
CPP	75.74 ± 11.98	67.29 ± 18.43	59.58 ± 12.25	73.56 ± 10.84	46.38 ± 21.39	52.25 ± 16.36	50.72 ± 2.07
SPC	75.96 ± 6.13	71.06 ± 5.78	71.74 ± 4.99	73.01 ± 5.13	67.81 ± 7.16	75.40 ± 6.22	74.71 ± 11.76
TSW	2.15 ± 0.05	2.04 ± 0.12	2.07 ± 0.29	2.06 ± 0.17	2.23 ± 0.12	2.20 ± 0.25	2.41 ± 0.43

SY	875.48 ± 139.65	622.60 ± 162.12	427.36 ± 163.38	732.42 ± 218.45	281.85 ± 212.26	527.83 ± 261.43	112.87 ± 141.36

DF: Days to Flowering; BBDS: Bacterial Blight Disease Severity (%); DM: Days to Maturity; PH: Plant Height in cm; PHFB: Plant Height to First Branch in cm; LCBZ: Length of Capsule Bearing Zone in cm; IL: Internode Length in mm; CL: Capsule Length in mm; CW: Capsule Width in mm; BPP: Number of Branch/Plant; CPP: Number of Capsules/Plant; SPC: Number of Seeds/Capsule; TSW: Thousand Seed Weight in g; SY: Seed Yield in kg ha^{-1}

Table 7: Mean and standard deviation of 7 clusters for 14 quantitative traits of sesame genotypes studied at Kamashi during 2017/18.

The pair wise generalized squared distances (D^2) between the clusters (Table 8) showed that the distance between most of the clusters was big. The highest distance between Cluster-I and Cluster-VII (759.83) showed that these clusters are the most distant which indicating divergence between the genotypes that belonging to these two different clusters. The second most distant clusters are Cluster-IV and Cluster-VII (519.56) followed by Cluster-I and Cluster-V (502.82).

Crossing of elite accessions from distant clusters and characterized by specific desirable traits of breeder's interest is expected to result an ideal plant. For example, crossing between sesame genotypes grouped in Cluster-I such as 17703 which are characterized by highest seed yield and sesame genotypes of Cluster-VII is expected to produce a hybrid with desirable seed quality and highest seed yield. The nearest neighbor of Cluster-I is Cluster-IV which constituted the second highest yielding genotypes.

Cluster	**Cluster**						
	I	**II**	**III**	**IV**	**V**	**VI**	**VII**
I	0	86.74	280.44	27.09	502.82	178.81	759.83
II		0	60.16	19.93	180.28	22.6	361.48
III			0	137.41	36.45	18.02	160.64
IV				0	306.49	72.17	519.56
V					0	91.9	81.99
VI						0	223.09
VII							0

Table 8: Distance matrix of clusters formed from 49 sesame genotypes grown at Kamashi in 2017/18 cropping year.

Conclusion

The ANOVA and mean performance of sesame genotypes indicated an availability of genetic potential to improve seed yield through selection of promising sesame genotypes. Further, the presence of genetic diversity both in qualitative and quantitative traits of sesame revealed the possibility to select candidate parents which can be used in improving sesame through combining desirable traits to meet the productivity and quality demands in sesame. In addition, the most discriminating quantitative traits which would be considered in sesame improvement were identified through factor analysis. Bacterial blight disease severity, plant height, length of capsule bearing zone, number of branches/plant, number of capsules/plant and seed yield/plant were the most important traits which largely accounted for explained genetic variation.

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