International Journal of Chemical Studies

P-ISSN: 2349–8528
E-ISSN: 2321–4902
www.chemijournal.com
IJCS 2020; 8(2): 133-140

Received: 22-01-2020
Accepted: 24-02-2020

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Characterization of genetic diversity for remodeling of elite accessions of sesame (*Sesamum indicum* L.)

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DOI: https://doi.org/10.22271/chemi.2020.v8.i2b.8759

Abstract
Genetic diversity was studied in 61 white seeded type sesame (*Sesamum indicum* L.) accessions including 4 checks for 9 agro- morphological and 4 biochemical traits under field conditions by cluster and principal component analyses. Accessions were grown in the research field of JN Agricultural University, campus College of Agriculture, Tikamgarh, India in a plot size of 2.0 x 1.50 m^2 (3 rows with 45 cm row x row spacing). Cluster analysis divided the total 61 accessions into eight different non-overlapping clusters during both the years of study i.e. 2015 and 2016. Data based on first and second years, PCs with Eigene value higher that 1.0 contributed 76.33% and 71.75% of the variability amongst accessions, respectively. Cluster pattern demonstrated sufficient diversity among the sesame accessions for various morphological and biochemical traits and some extent of association between different clusters. The results concluded that morpho-biochemical diversity in the studied material is governed by cumulative effect of a number of traits rather than the contribution of few specific traits and this diversity could well be utilized for future breeding strategies and germplasm conservation programs.

Keywords: *Sesamum indicum* L, genetic diversity, morphology, biochemical attributes

Introduction
Sesame (*Sesamum indicum* L.; 2n = 26.) is a popular oilseed crop cultivated for its quality edible oil, high protein, vitamin contents and balanced amino acid profile. It is possibly the most ancient known oilseed crop, whose domestication is lost in the mists of antiquity (Weiss, 2000). Even in the current era, sesame is valued as one of the highest oil content (up to 64%) plant among major oilseed crops in the world (Wei *et al.* 2015; Dossa*et al.* 2017) [31, 10]. Sesame oil is enriched with high valued antioxidants such as sesaminol, sesamolin and tocopherol accounting for longer shelf life with minimal rancidity (Ashri 1998) [6]. Besides, sesame seed finds its application in various important culinary preparations. Studies on antioxidants, blood pressure lowering, anti-aging, the synergistic effect with tocopherols, serum lipid lowering etc. have been extensively reviewed (Namiki 2007) [19]. Despite such high value being placed on sesame seed, neither there have been good numbers of scientific studies validating these claims nor has the saleable gain been affixed to the crop. Moreover, the net outcome in terms of productivity is also not so notable with respect to other sesame growing countries in the world (Rai *et al*. 2016) [23]. The reasons for low productivity in the country might beassociated with lack of high yielding cultivated genotypes (Ram *et al*. 1990) [24] and insufficient germplasm information with respect to exploitable genetic diversity (Were *et al*. 2006) [33]. There exists a wide and valuable morphological diversity for different desirable characters in sesame germplasms (Pathak *et al.* 2014; Pandey *et al.* 2015) [20, 21] however these diversity has not been fully exploited for sesame improvement of the existing cultivars (Wei *et al*. 2015) [31]. Now, in view of its well-known value, there seems an absolute but immediate requirement to develop highly heterotic hybrid and desirable transgressive segregants to achieve a gain in sesame productivity in the country.

Morphological variations in any crop species are the upshot of long term selection for varying objectives in different areas across the globe. Availability of large array of these genetic or morphological variations caters crop improvement programme for better economic characters as ‘quantifying genetic diversity’ and ‘studying the accessiblepatterns of the variability’ are the

leading steps in plant breeding and germplasm conservation (Mohammadi and Prasanna, 2003) [18]. Estimates of genetic diversity and relationships among germplasm accessions are vital for facilitating efficient germplasm selection and management (Siddique *et al*. 2012) [25]. Many advanced tools such as isozymes, and molecular markers are now available at ease for studying variability and relationships among accessions (Trick *et al*. 2009; Cheng *et al*. 2009; Allender and King 2010) [29, 8, 4]. However, morphological characterization is still the primary step in the description and classification of germplasm (Smykal *et al*. 2008) [26]. A number of quantitative taxonomic techniques used to be in practice to classify and measure the patterns of phenotypic diversity in the relationships of species and germplasm collections of variety of crops (Gomez-Campo 1999) [14]. Among these, principal component analysis (PCA) and cluster analysis have analogous efficacy to establish the most suitable cross combinations. The present study attempted to characterize and classify the phenotypic variation and affinities among the different sesame germplasm accessions using these statistical techniques.

Materials and Methods

Sixty one accessions of white seeded sesame accessions including 4 checks were evaluated for 9 agro- morphological and 4 biochemical traits during the years 2015 and 2016 in the research field of JN Agricultural University, campus College of Agriculture, Tikamgarh, India in a plot size of 2.0 x 1.50 m^2 (*i.e.* in 3 rows with 45 cm row x row spacing) (Table 1 and 2). For seed bed preparation pre-sowing irrigation was applied and sowing was carried out under optimum moisture conditions. Recommended doses of all essential fertilizers were applied at the time of land preparation. Planting of the experiments was done by hand drills and thinning was carried out two weeks after germination to maintain optimum plant population. Weeds were controlled manually. The data were recorded on five randomly sampled plants from each accession for days to 50% flowering, days to maturity, plant height (cm), number of branches $plant^{-1}$, capsule length, number of capsules $plant^{-1}$, number of seeds $capsule^{-1}$, 1000-seed weight (g) and seed yield $plant^{-1}$ (g). Biochemical analysis of seed for oil content (%), and fatty acid profile (oleic acid, palmitic acid and linoleic acid content (%) was carried out at Biochemistry laboratory, AICRP (Sesame), JNKVV campus Jabalpur (Table 3).

Statistical Analysis

Basic statistical analysis of different morphological and biochemical characters was carried out (Gomez and Gomez 1984) [13]. Cluster and principal component analyses were carried out on nine morphological and four biochemical traits for the years 2015 and 2016 (Sneath and Sokal 1973) [27]. Basic statistics of all accessions is shown in Table 4.

Results and Discussion

A successful breeding program mainly relies on the magnitude of agro-morphological variability. Investigating the extent of diversity is vital for its conservation and utilization in crop improvement programme (Mohamed *et al*. 2012) [17]. The agro-morphological traits used in the study confirmed a noticeable variation among accessions. The coefficients defining five principal components of the data for *S. indicum* in 2015 are given in (Table 5; Fig.1).

The first principal component contributed 18.85% of total variance and is primarily contributed by days to 50% flowering (0.04), days to maturity (0.30), plant height (0.18), branches $plant^{-1}$ (0.13), capsules $plant^{-1}$ (0.50), seeds $capsule^{-1}$ (0.22) and 1000-seed weight (0.02). The second principal component accounted for 16.30%, having 50% flowering (0.37), days to maturity (0.33), capsules $plant^{-1}$ (0.27), 1000-seed weight (0.83), oleic acid (0.06), palmitic acid (0.047), linoleic acid (0.166). The third component contributed 13.80% of the total variation and positively determined by 50% flowering (0.10), plant height (0.12), capsule length (0.14), capsules $plant^{-1}$(0.14), 1000-seed weight (0.22), seed yield $plant^{-1}$ (0.25), and palmitic acid (0.212). The forth principal component shared for 10.07% of the total variation and contributed by days to 50% flowering (0.28), plant height(0.19), capsules $plant^{-1}$(0.23), seeds $capsule^{-1}$(0.16), seed yield $plant^{-1}$(0.16), oil content(0.06),palmitic acid(0.24), and linoleic acid(0.06). The total contribution of the fifth component were 9.10% having 50% flowering (0. 97), days to maturity (0.16), plant height (0.23), capsules $plant^{-1}$ (0.19), seeds $capsule^{-1}$ (0.25), 1000-seed weight (0.24), seed yield $plant^{-1}$ (0.17) and oleic acid (0.03). The sixth component attributed for 8.23% and determined by days to 50% flowering (0.31), plant height (0. 13), capsule length (0. 14), 1000-seed weight (0. 28), seed yield $plant^{-1}$ (0. 02), oil content (0. 66), linoleic acid (0. 26). All these studies disclosed complex relationships among the accessions and traits, and concluded that the differentiation of the genotypes into different cluster was because of a combined outcome of multiple characters instead of contribution of specific few characters.

The coefficients defining six principal components of the data for *S. indicum* in 2016 is indicated in Table 6 (fig. 2). The first principal component contributes 29.31% of total variance in morphological and biochemical characters and is primarily contributed by 50% flowering (0.18), days to maturity (0.20), capsules $plant^{-1}$ (0.47), 1000-seed weight (0.04), oleic acid (0.08), palmitic acid (0.06) and linoleic acid (0.20).The second component accounted for 14.76% and positively associated with days to maturity (0.35), 50% flowering (0.05),plant height (0.12), capsules $plant^{-1}$ (0.05),1000-seed weight (0.23), palmitic acid (0.17), oleic acid (0.06), linoleic acid (0.17). The third component contributed 10.03% and determined by days to 50% flowering (0.45), days to maturity (0.28), branches $plant^{-1}$ (0.07), capsule length (0.26), capsules $plant^{-1}$ (0.07), seeds $capsule^{-1}$ (0.11) and 1000-seed weight (0.42). The forth component accounted for 9.09% having days to 50% flowering (0.20), capsule length (0.09), seeds $capsule^{-1}$ (0.37), palmitic acid (0.16). The fifth component contributed 8.57% and associated with days to 50% flowering (0.23), plant height (0.06), capsules $plant^{-1}$ (0.09), 1000-seed weight (0.21), oil content (0.62) and linoleic acid (0.25).

It was observed that, in 2015, among the seven principal components, six showed Eigene value higher than 1.0 and accounted for 76.33% of the total variation among 61 genotypes of sesame while in 2016, among the six principal components, five showed Eigene value higher than 1.0 and accounted for 71.755% of the total variation. In 2015, principal component analysis showed association in PCI with number of capsules per plant, days to maturity, number of seeds per capsule, PCII with days to 50% flowering, number of capsules per plant and days to maturity and PCIII with seed yield per plant and 1000-seed weight, whereas in 2016, PCA showed association in PCI with number of capsules per plant, linoleic acid, days to maturity, PCII with days to maturity, 1000 seed weightand PCIII with days to 50% flowering, 1000-seed weight. The comparable results were also reported by Menzir (2012) [16], Tripathi *et al*. (2013) [30], and Hika *et al*.

(2015) [15] in sesame while by Ali *et al*. (2011) [1] in sorghum, Ahlawat *et al*. (2008) [1] and Golabadi *et al*. (2006) [12] in wheat. Here, during both the years, PCI to PCIII accounted for almost 50% of the total variations, therefore traits with high coefficients in the PCI to PCIII should be considered as more significant because these axes explain almost half of the whole variation.

The dendrogram constructed on the basis of *S. indicum* divided the total accessions into eight major groups in the year 2015 (Fig. 3). The 61 genotypes were grouped into eight different non-overlapping clusters. The distribution of 61 sesame accessions into eight clusters is given in Table 7. Maximum number of genotypes grouped in cluster III (12 genotypes) and minimum in cluster VII (2 genotypes). The table revealed that cluster I consisted of 4 genotypes and had the lowest cluster mean values of 1000 seed weight (3.09), whereas it showed no maximum cluster mean values for any trait. Cluster II had 9 genotypes which did not show any maximum and minimum cluster mean values. The cluster mean values under this cluster for days to 50% flowering were (41.24), days to maturity (104.19), plant height (77.65), branching habit (1.96), number of capsules per plant (49.44), number of seeds per capsule (74.66) and seed yield per plant (5.81). Cluster III consisted of 12 genotypes and had the minimum cluster mean values of number of seeds per capsule (57.21), whereas it showed no maximum cluster mean values for any trait. Cluster IV had 11 genotypes which exhibited highest cluster mean values for plant height (92.86), whereas it had minimum cluster mean values for days to 50% flowering (39.82), days to maturity (100.57), capsule length (2.21), and palmitic acid (7.81). Cluster V had 11 genotypes which exhibited highest cluster mean values for number of branches per plant (3.00) and number of seeds per capsule (80.68) whereas it had minimum cluster mean values for 1000 seed weight (2.30). The cluster mean values, for oil content and linoleic acid were 42.02 and 51.40 respectively. Cluster VI had 5 genotypes which exhibited highest cluster mean values for number of days to maturity (106.68) whereas it had minimum cluster mean values for number of capsules per plant (34.75), seed yield per plant (3.15), and oleic acid (23.91). The cluster mean value for palmitic acid was 10.14. Cluster VII had 2 genotypes which exhibited highest cluster mean values for days to 50% flowering (43.20), capsule length (2.40) and palmitic acid (10.27) whereas it had minimum cluster mean values for number of number of branches per plant (0.33), overall oil content (41.02) and linoleic acid (38.28). Cluster VIII had 7 genotypes which exhibited highest cluster mean values for number of capsules per plant (50.75), seed yield per plant (6.71), oil content (54.68), oleic acid (39.08) and linoleic acid (53.08) whereas it had minimum cluster mean values for plant height (48.97).

The dendrogram constructed on the basis of *S. indicum* during the year 2016 revealedeight major groups (Fig. 4). The 61 genotypes were grouped into eight different non-overlapping clusters. The distribution of 61 sesame accessions into eight clusters is given in Table 8. The table revealed that cluster I consisted of 7 genotypes and had the lowest cluster mean values of plant height (72.75), whereas it showed no maximum cluster mean values for any trait. Cluster II had 11 genotypes which showed maximum cluster mean values for 1000 seed weight (3.05) while it did not show minimum cluster mean values for any trait. Cluster III consisted of 4 genotypes which exhibited highest cluster mean values for capsule length (2.56), whereas it had minimum cluster mean values for days to maturity (100.30), seed yield per plant (4.42), oleic acid (22.78) and linoleic acid (36.64). Cluster IV had 11 genotypes which neither exhibited highest cluster mean values nor the minimum cluster mean values for any trait. Cluster V had 12 genotypes which exhibited highest cluster mean values for days to maturity (108.38) and seed yield per plant (6.78) whereas it had minimum cluster mean values for number of branches per plant (0.07), number of capsules per plant (2.02) and overall oil content (40.28). The cluster mean value for palmitic acid was 49.71. Cluster VI had 8 genotypes which exhibited highest cluster mean values for palmitic acid (8.61) whereas it had minimum cluster mean values for number of capsule length (2.03) and number of seeds per capsule (53.63). The cluster mean value for days to 50% flowering was 42.25. Cluster VII had 6 genotypes which exhibited highest cluster mean values for plant height (89.44), number of branches per plant (2.59), number of capsules per plant (37.13) and number of seeds per capsule (73.66) whereas it had minimum cluster mean values for days to 50% flowering (38.95), 1000 seed weight (2.43) and palmitic acid (7.49).Cluster VIII had 2 genotypes which exhibited highest cluster mean values for days to 50% flowering (43.85), overall oil content (54.95), Oleic Acid (39.08) and linoleic acid (53.08).The results of cluster analysis for the years 2012 and 2013 suggested that there is enough variation among the germplasm accessions for different agro-morphological and biochemical traits. Accessions with greater similarity for agro-morphological and seed quality traits were placed in the same cluster; however, the accessions from the nearby/same sites were not necessarily placed in the same cluster. The findings of present studies are in agreement with those of Furat and Uzun (2010) [11] who studied 103 sesame germplasm accessions those were divided into 8 main clusters. They were of the view that Clustering of landraces was not associated with the geographical distribution instead accessions were mainly grouped due to their morphological differences. Similarly, Arriel *et al*. (2007) [5] conducted divergence studies with 108 accessions of sesame germplasm which formed seven conglomerates. They reported that many derivatives of the cross fell into the same cluster but in many cases, in spite of common ancestry, many descendents spread over different clusters. The findings of present studies also coincided with the work of Bedigian *et al*., 1986 [7], Dixit and Swain (2000) [9], Solanki and Gupta, (2003) [28] and Akbar *et al*. (2011) [2]. This may be on account of migration of the sesame materials from one region to another in collection sites. Although a lot of literatures described sesame as an autogamous plant, however, recent findings raise the possibility of sesame being natural out-crossing (Pathirana 1994). Some ecological conditions could also lead to gene flow between populations from different geographical origins. Conclusively, the study indicated existence of high degree of genetic diversity in the germplasm collections. The eight clusters in divergence analysis contained germplasm of heterogeneous origin thereby indicating no parallelism between genetic and geographic diversity. Therefore, crosses between the members of clusters separated by high inter cluster distance are likely to produce desirable segregants. Moreover, the different clusters showed considerable differences in intra-cluster group means for all the thirteen characters. Therefore, crosses between members of cluster having high cluster mean for important characters coupled with high inter-cluster distances between them are likely to be more rewarding.

Table 1: *Sesamum indicum* L. germplasm accessions used in the study

S.#	Accessions	Name under study	S.#	Accessions	Name under study
1	KMR-60	TKGSE-11-1	30	(VKS-272 x SI-250)-2-2-1	TKGSE-11-30
2	KMR-31	TKGSE-11-2	31	(TC-25 x KMR-115)-6	TKGSE-11-31
3	SI-233	TKGSE-11-3	32	VKS-272 x SI-1446)-5-1-1	TKGSE-11-32
4	KMR-51	TKGSE-11-4	33	(GT-1 x TKG-22)-1-2-2	TKGSE-11-33
5	SI-3263-1	TKGSE-11-5	34	(TKG-307 x N-32)-1	TKGSE-11-34
6	KMR-61	TKGSE-11-6	35	(GT-1 x TKG-22)-1-4-2	TKGSE-11-35
7	KMR-394	TKGSE-11-7	36	(GT-1 x TKG-22)-4-1-2	TKGSE-11-36
8	SI-107-B	TKGSE-11-8	37	(JTS-8 x SI-225-3)-2-1-2	TKGSE-11-37
9	IS-405	TKGSE-11-9	38	(RT-46 x N-32)-1-2	TKGSE-11-38
10	IS-8	TKGSE-11-10	39	(SI-911 x N-32)1-1	TKGSE-11-39
11	NIC-10622	TKGSE-11-11	40	(SI-1556 x SI-250)-6-2	TKGSE-11-40
12	IS-35-1-A	TKGSE-11-12	41	(SI-928 x N-32)-3-1-1	TKGSE-11-41
13	EC-303311-1	TKGSE-11-13	42	(SI-928 x N-32)-3-1-2	TKGSE-11-42
14	SI-2039-A	TKGSE-11-14	43	(SI-1556 x TKG-308)-1	TKGSE-11-43
15	SI-8459	TKGSE-11-15	44	(RT-46 x TKG-306)-1-1	TKGSE-11-44
16	SI-1782A	TKGSE-11-16	45	(RT-46 x TKG-306)-2-2	TKGSE-11-45
17	EC-52000145	TKGSE-11-17	46	(AT-66 x TC-25)-1-2	TKGSE-11-46
18	S-01159-B	TKGSE-11-18	47	(AT-66 x TC-25)-2-1	TKGSE-11-47
19	KMR-39	TKGSE-11-19	48	(JLT-7 x CST-785)-1-2-1	TKGSE-11-48
20	KIS-300-A	TKGSE-11-20	49	(JLT-7 x CST-785)-1-2-2	TKGSE-11-49
21	IS-390	TKGSE-11-21	50	(JLT-7 x CST-785)-2-1	TKGSE-11-50
22	SI-3257	TKGSE-11-22	51	(JLT-7 x CST-785)-2-4	TKGSE-11-51
23	KMR-89	TKGSE-11-23	52	(JTS-111 x TC-5252)	TKGSE-11-52
24	NIC-17912-B	TKGSE-11-24	53	(JTS-111 x TC-5252)	TKGSE-11-53
25	NIC-8588	TKGSE-11-25	54	(JTS-111 x N-32)-2	TKGSE-11-54
26	NIC-8584	TKGSE-11-26	55	(K-5142 x HT-36)	TKGSE-11-55
27	NIC-10630	TKGSE-11-27	56	(VK-5262 x CST-785)	TKGSE-11-56
28	KMS-4-258	TKGSE-11-28	57	(VK-5262 x CST-785)	TKGSE-11-57
29	(JTS-8 x SI-225-3)-2-2-1	TKGSE-11-29			

Table 2: Characters of the check entries suitable for export quality traits

Check entries	Promising characters
TKG-55	Resistant to *Phytophthora* blight and *Macrophomina* stem/root rot and free from bacterial diseases and leaf curl diseases,moderately resistant to leaf roller and capsule borer. Oil content –52.56%, Being early in maturity it escapes drought, yield-610 kg/ha.
GT-2	White bold seeded, high Oil content, export quality, resistant to cyst-nematodes.
JTS-08	Bold white seeded,Maturity period-90-100 days, Oil content –53%, yield-610 kg/ha
Phule Til-1	White bold seeded, lustrous, export quality, drought tolerant, yield-600 kg/ha.

Table 3: Morphological and biochemical traits recorded in the 61 accessions of *Sesamum indicum* L.

Trait designation	Code	Description of the trait
Days to 50% flowering	50% DFI	Number of days to 50% plants having 1st flower open from date of planting
Days to maturity	DOM	Number of days to reach physiological maturity from date of planting
Plant height	PH	At maturity, plant height was recorded in cm from ground level to the extremity of plant, determined as mean of 5 random plants
Capsule Length	CL	Recorded in cm from base to the tip of 10 capsules of each accession and average was taken
Number of capsules plant^{-1}	NCPP	Counted from the same 5 plants used for counting number of branches per plant
Number of seeds capsule^{-1}	NSPC	Obtained from the same 10 capsules used for measuring capsule length
Number of branches plant^{-1}	NBPP	Number of branches originated from the main stem which gave rise to other capsule bearing branches
1000- seed weight (gm)	SW	An average of 10 samples per accession using seed counter
Seed yield plant^{-1} (g)	SY	Recorded by harvesting ten individual plants and then averaged to calculate seed yield per plant in each accession
Oil Content (%)	OC	Determined from well cleaned and dried seed samples of 8-10 gm by Gas Liquid Chromatography
Oleic Acid Content (%)	OA	
Palmitic Acid Content (%)	PA	
Linoleic Acid Content (%)	LA	

Table 4: Basic statistics of agro-morphological and biochemical traits of 61 accessions of *Sesamum indicum*

Traits	Range		Mean± SE		Variance	GCV (%)	PCV (%)
	Minimum	Maximum					
Days to 50% Flowering	35.60	47.27	41.20	±0.35	4.91*	1.26	6.71
Days to Maturity	97.52	108.35	103.27	±0.28	3.92*	0.47	2.12
Plant Height (cm)	48.97	107.63	75.49	±1.50	120.63*	5.59	15.55
Branching habit	0.000	5.00	1.81	±0.13	0.88*	20.88	57.16
Capsule Length	1.74	2.85	2.32	±0.02	0.03	7.34	7.93
Capsule/ Plant	31.42	55.42	45.51	±0.78	36.12**	5.61	13.42
Seeds/ Capsule	43.43	90.35	67.98	±1.21	91.54	10.28	13.92
1000 Seed Weight (gm)	2.20	4.24	2.79	±0.06	0.22*	3.88	16.63
Seed Yield/ Plant (gm)	2.05	7.75	5.34	±0.18	1.96*	13.10	26.15
Oil Content (%)	37.52	54.68	42.97	±0.37	7.99*	3.78	6.73
Oleic Acid (%)	21.44	39.08	28.46	±0.49	11.49*	7.92	13.35
Palmitic Acid (%)	6.19	11.00	8.141	±0.16	1.36*	6.65	14.99
Linoleic Acid (%)	35.98	53.20	44.004	±0.66	22.57**	8.07	11.66

* and ** are statistically significant at 0.05 and 0.01 level, respectively

Table 5: Principal components for agro-morphological and biochemical traits in 61 germplasm accessions of sesame during 2015

	1 Vector	2 Vector	3 Vector	4 Vector	5 Vector	6 Vector
Eigene Value (Root)	2.450	2.118	1.794	1.309	1.182	1.070
Proportion of variance (%)	18.846	16.290	13.801	10.068	9.094	8.234
Cumulative Variance (%)	18.846	35.135	48.937	59.005	68.099	76.333
Traits						
Days to 50% Flowering	0.035	0.371	0.101	0.281	0.497	0.306
Days to Maturity	0.303	0.331	0.144	-0.143	0.159	-0.465
Plant Height (cm)	0.184	-0.491	0.124	0.193	0.225	0.128
Branching habit	0.132	-0.441	-0.285	-0.344	-0.041	-0.160
Capsule Length	-0.389	-0.224	0.143	-0.343	-0.143	0.141
Capsule/ Plant	0.493	0.265	0.136	0.229	0.187	-0.116
Seeds/ Capsule	0.217	-0.284	-0.352	0.162	0.246	-0.161
1000 Seed Weight (gm)	0.024	0.083	0.222	-0.676	0.236	0.284
Seed Yield/ Plant (gm)	-0.488	-0.255	0.245	0.161	0.173	0.021
Oil Content (%)	-0.133	-0.103	-0.376	0.063	-0.116	0.656
Oleic Acid (%)	-0.336	0.060	-0.530	-0.017	0.028	-0.100
Palmitic Acid (%)	-0.061	0.047	0.212	0.240	-0.672	0.000
Linoleic Acid (%)	-0.205	0.166	-0.364	0.058	-0.092	0.259

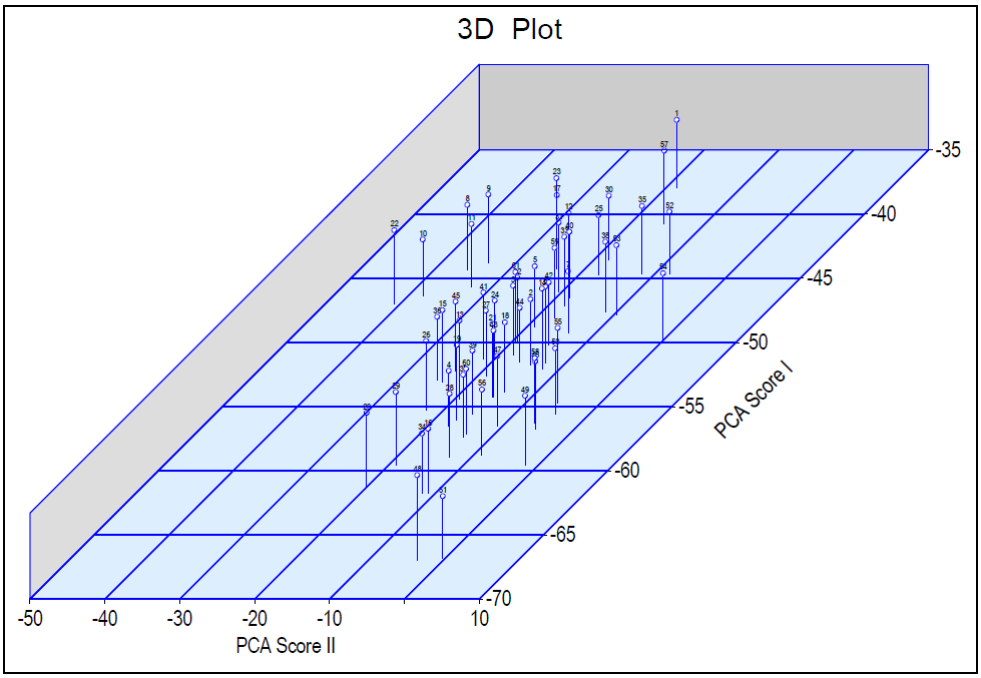

Fig 1: Three dimensional diagram of principal components analysis: Sesame 2015

Table 6: Principal components for agro-morphological and biochemical traits in germplasm accessions of sesame 2015

	1 Vector	2 Vector	3 Vector	4 Vector	5 Vector
Eigene Value (Root)	3.810	1.918	1.304	1.182	1.114
Proportion of variance (%)	29.306	14.755	10.034	9.095	8.566
Cumulative Variance (%)	29.306	44.061	54.094	63.189	71.755
Traits					
Days to 50% Flowering	0.181	0.045	0.445	0.198	0.232
Days to Maturity	0.197	0.347	0.277	-0.068	-0.510
Plant Height (cm)	-0.444	0.108	-0.095	-0.179	0.057
Branching habit	-0.421	-0.095	0.074	-0.109	-0.032
Capsule Length	-0.353	-0.296	0.260	0.086	-0.145
Capsules/ Plant	0.472	0.048	0.072	-0.105	0.091
Seeds/ Capsule	-0.391	-0.205	0.108	0.368	-0.065
1000 Seed Wt (gm)	0.040	0.226	0.420	-0.539	0.214
Seed Yeild/ Plant (gm)	-0.017	-0.104	-0.204	-0.652	-0.280
Oil Content (%)	-0.012	-0.360	-0.266	-0.059	0.617
Oleic Acid (%)	0.076	-0.612	-0.032	-0.097	-0.043
Palmitic Acid (%)	0.061	0.171	-0.556	0.155	-0.279
Linoleic Acid (%)	0.204	-0.361	-0.165	-0.078	0.253

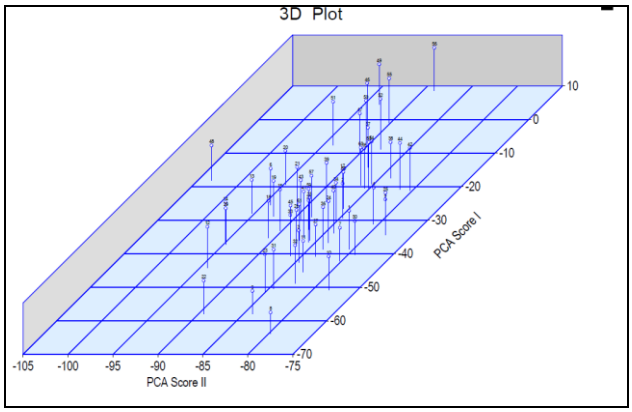

Fig 2: Three dimensional diagram of principal components analysis: Sesame 2016

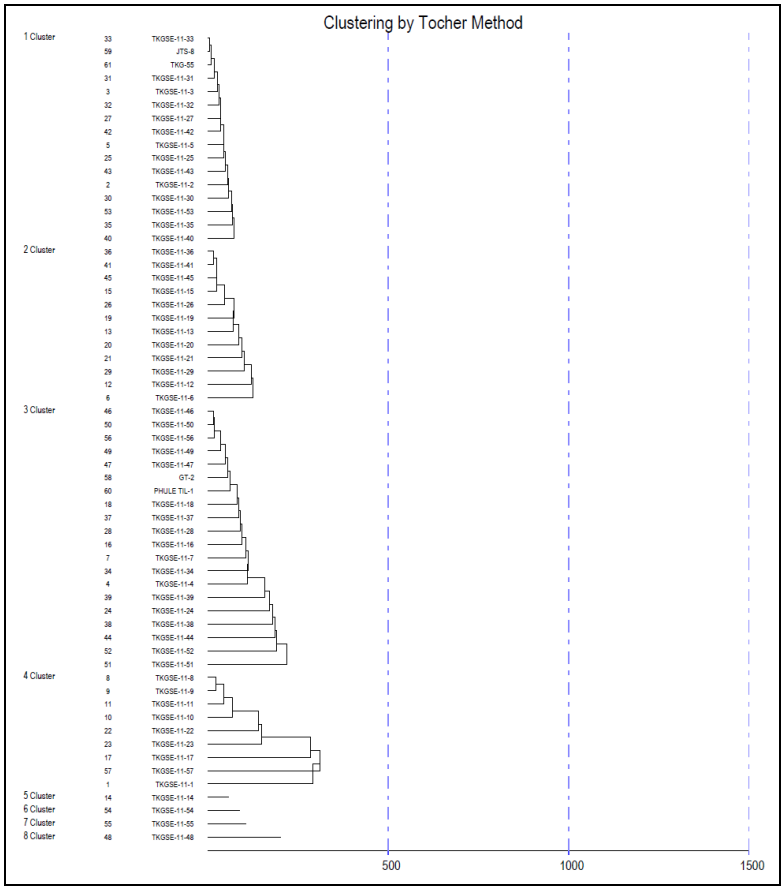

Fig 3: Dendrogram presenting the genetic relationship among different *Sesamum indicum* germplasm accessions used in the study during 2015.

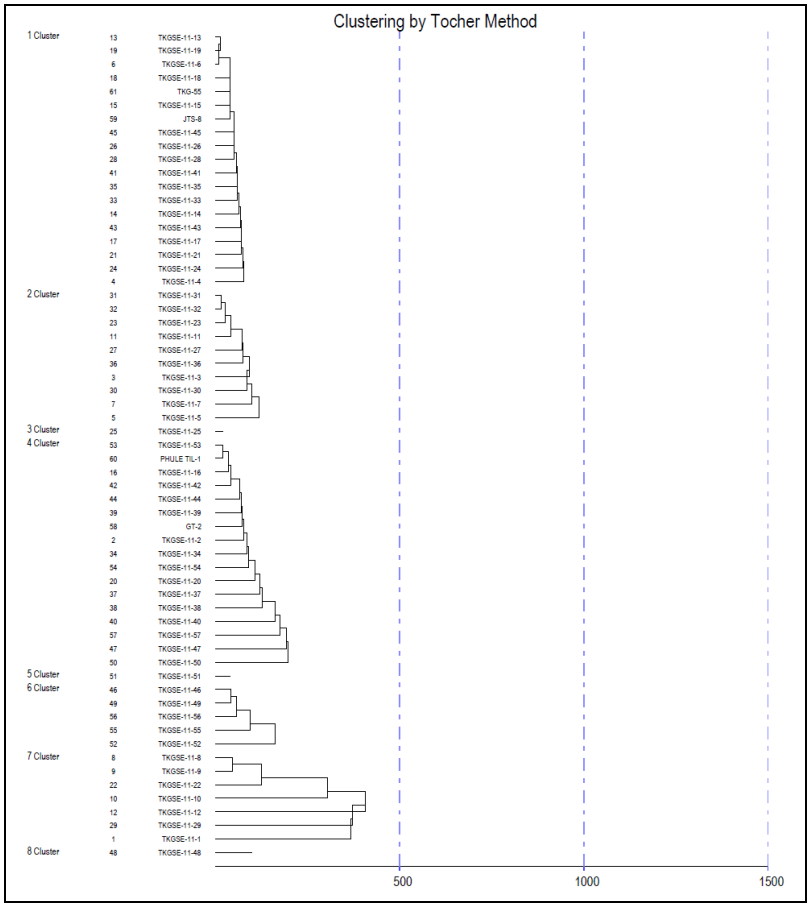

Fig 4: Dendrogram presenting the genetic relationship among different *Sesamum indicum* germplasm accessions used in the study during 2016.

Table 7: Cluster means for different characters in 61 genotypes, 2015

Clusters	Days to 50% Flowering	Days to Maturity	Plant Height (cm)	Branching habit	Capsule Length	Capsule/ Plant	Seeds/ Capsule	1000 Seed Weight (gm)	Seed Yield/ Plant (gm)	Oil Content (%)	Oleic Acid (%)	Palmitic Acid (%)	Linoleic Acid (%)
I	40.95	103.17	74.99	2.01	2.34	42.78	69.87	3.09	4.94	42.43	26.76	8.32	40.69
II	41.24	104.19	77.65	1.96	2.36	49.44	74.66	2.66	5.81	43.18	31.69	7.82	46.56
III	41.73	103.56	70.72	1.43	2.34	46.67	57.21	2.86	5.68	42.34	27.98	8.09	45.30
IV	39.82	100.57	92.86	2.38	2.21	43.78	77.54	2.44	5.00	44.10	26.05	7.81	42.58
V	42.60	105.52	66.72	3.00	2.43	42.42	80.68	2.30	3.69	42.02	33.98	8.63	51.40
VI	41.10	106.68	53.30	1.33	2.34	34.75	63.10	2.48	3.15	42.35	23.91	10.14	42.51
VII	43.20	104.68	53.97	0.33	2.40	43.08	76.43	2.41	4.95	41.02	36.81	10.27	38.28
VIII	43.10	105.35	48.97	1.00	2.37	50.75	70.77	2.45	6.71	54.68	39.08	8.47	53.08

Table 8: Cluster means for different characters in 61 genotypes: Sesame 2016

Clusters	Days to 50% Flowering	Days to Maturity	Plant Height (cm)	Branching habit	Capsule Length	Capsules/ Plant	Seeds/ Capsule	1000 SW (gm)	Seed Yield/ Plant (gm)	Oil Content (%)	Oleic Acid (%)	Palmitic Acid (%)	Linoleic Acid (%)
I	42.14	103.70	72.75	1.99	2.46	24.21	69.76	2.76	5.35	42.37	29.57	8.08	45.12
II	39.93	102.08	84.17	2.43	2.47	30.70	69.17	3.05	5.32	43.24	26.46	8.58	39.01
III	41.52	100.30	74.08	1.57	2.56	21.32	67.57	2.71	4.42	38.03	22.78	7.81	36.64
IV	42.17	103.72	64.27	1.33	2.25	16.30	59.18	2.87	5.39	42.22	27.78	8.08	45.15
V	40.18	108.38	53.92	0.07	2.29	2.02	63.90	2.58	6.78	40.28	30.88	8.34	49.71
VI	42.25	104.25	42.78	0.27	2.03	4.15	55.63	2.71	4.71	43.82	29.72	8.61	45.38
VII	38.95	101.85	89.44	2.59	2.45	37.13	73.66	2.43	5.45	44.91	27.98	7.49	43.23
VIII	43.85	105.38	59.58	1.40	2.39	13.65	66.57	2.45	6.71	54.95	39.08	8.47	53.08

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