

## Diversity in Sesame Accessions

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### ABSTRACT

Sesame known to be the most ancient oilseed crop in the world and well recognized for good quality edible oil due its high PUFA content, antioxidant properties, excellent nutritional and medicinal properties. The present investigation aims at analyzing the genetic diversity of 205 genotypes for 8 morphological characters. Phenotypic coefficients of variation exhibited a bit higher values but maintained a close relation with genotypic variation and genotypic co-efficient of variation for all the traits, indicating low G×E interaction. A combination of high heritability (broad sense) and high genetic advance indicate preponderance of additive gene action which is fixable. Additive gene action was prominent for the traits like no of capsules/plant, seed yield/plant, and primary branches/plant. Hierarchical cluster analysis based on agro-morphological traits results revealed that the inter cluster distance in most cases was larger indicating wider diversity among the germplasm of different groups. The maximum inter cluster distance was found between clusters V and III, followed by clusters V and II, clusters VI and II. The principal component analysis revealed that capsule number and 1000-seed weight had a strong relation with seed yield, suggesting the need for more emphasis on these components for increasing the seed yield in sesame.

### Highlights

- ① Genotypes were significant for all traits as revealed from ANOVA.
- ① Highest PCV was recorded by capsules per plant followed by number primary branches/plant and seed yield per plant.
- ① Hierarchical cluster analysis based on agro morphological traits revealed that the inter cluster distance in most cases was larger indicating wider diversity among the germplasm of different groups
- ① The characters contributing maximum divergence need greater emphasis for deciding on the clusters for the purpose of selection of parents in the respective cluster for hybridization and parents for hybridization should be selected from cluster having high intercluster distance like between cluster V and III or II.
- ① The PCA revealed that emphasis should be given to the traits like 1000 seed weight, branches/plant, plant height and capsules/plant during selection programme.

**Keywords:** Genetic variability, hierarchical clustering, principal components, seed yield, sesame

Sesame (*Sesamum indicum* L.) is one of the most ancient and important oilseed crops known and used by mankind. Oil seeds constitute the major agricultural crop next only to food grains. Among the edible oilseed crops, sesame occupies a unique position as it can be grown throughout the year and

moreover, it's poly-unsaturated fatty acid content makes it beneficial for human health. Sesame was cultivated and domesticated on the Indian subcontinent during Harappan and Anatolian eras around 4,000 years ago. (Bedigian and Van der Mesen 2003). Due to the great stability of its healthy

oil, easiness of extraction and resistance to drought, Sesame was very popular in the ancient world. It is considered as a nutritious oilseed crop being rich source of protein (18–25%), carbohydrate (13.5%), minerals and healthy polyunsaturated fatty acid (Bedigian *et al.* 1985). Sesame oil is favored as a media of cooking by Indians and Africans. Presence of sesamol, a unique anti-oxidant and more polyunsaturated fatty acid, have made it to 'queen of oilseed crop' (Ashri 1998; Fukuda *et al.* 1986). Sesame ranks fifth for important edible oil crop in India after groundnut, rapeseed-mustard, sunflower and soybean. India holds first position in the world in sesame-acreage (24%) and contribution in export (40%) (FAO Statistics Division, 2010; Raikwar and Srivastva (2013). In spite of good production, productivity of sesame in India is low compared to other sesame producing countries. Other than favourable climate of production and remunerative price of the crop one of the simplest approach to increase horizontal expansion of the crop is to boost up productivity of the crop. Genetic up gradation of any crop primarily depends on utilization of existing genetic resource, and hence assessment of genetic diversity gets priority area. A large germplasm resource is always favoured in plant breeding program as many desirable traits may obviously remain in the population on which may be utilized in breeding program. It is difficult to maintain and evaluate large number of germplasm. The idea was to constitute novel variation from large gene pool and concept has been successfully established by Ellis *et al.* (1998). The genetic improvement of any crop is highly dependent on the magnitude of quite a few genetic parameters, such as, phenotypic variances and genotypic variances, phenotypic and genotypic coefficient of variation (PCV and GCV), broad sense heritability and genetic gain on which the breeding methods are designed for its further improvement. Assessing germplasm for diversity has an important implication in plant breeding program.

Different quantitative traits are usually pooled up together in multivariate analysis to reach towards a conclusive outcome of diversity based multivariate analysis is often used in selection of parents for hybridization program in different crops like horsegram (Dasgupta 2005), blackgram (Dasgupta and Das 1991, 1984) and sesame (Akbar *et al.* 2011;

Pham *et al.* 2010). The present study has been conducted to assess the diversity of a core collection in sesame following morphological traits.

## MATERIALS AND METHODS

Two hundred and five sesame genotypes collected from diverse eco-geographical regions of India and abroad, were planted in Randomized Block Design (RBD) with three replications having 10cm spacing between plants and 40cm between rows were studied during Summer 2015 at Agricultural Experimental Farm, University of Calcutta, Baruipur, West Bengal (22°51' N latitude and 88° 24' E longitude). Normal cultural practices were followed during cultivation and irrigations were applied whenever the soils become very dry. All recommended package of practices were followed during the conduct of experiment. Observations were recorded on the basis of five random competitive plants selected from germplasm in every replication for seed yield and its attributing characters. The observations recorded on 8 morphological traits namely plant height (cm), days to 50% flowering, days to maturity, number of primary branches/plant, number of capsules/plant, capsule length (cm), 1000 seed weight (gm) and seed yield/plant (gm). Statistical analysis was computed in SPSS 21.0 to cluster the genotypes based on genetic similarity. Genotypic coefficient of variation, phenotypic coefficient of variation, heritability (broad sense) and genetic advance was measured by the methods described Burton (1968) and Hanson *et al.* (1956). The PCA analysis reduces the dimensions of a multivariate data to a few principal axes, generates an Eigen vector for each axis and produces component scores for the characters (Sneath *et al.* 1973; Ariyo and Odulaja 1991).

## RESULTS AND DISCUSSION

### Components of genetic variability

Genotypes were significant for all traits as revealed from ANOVA. The estimates of GCV and PCV exhibited that PCV was greater than GCV for all traits indicating substantial role of environmental effect in the character expression (Table 1). Highest PCV was recorded by capsules per plant (56.5.) followed by number primary branches/plant (47.6) as well seed yield per plant (41.1). Conversely,

**Table 1:** Components of genetic variability in sesame

Sl. No.	Character	Mean	GCV(%)	PCV(%)	h <sup>2</sup> (%)	GA	GA as %of mean
1	Plant height	87.93	19.85	25.20	62.06	22.31	8.12
2	No. of branches per plant	5.30	42.9	47.6	27.85	1.33	8.01
3	Days to flowering	41.84	6.81	9.51	51.27	3.00	2.40
4	Days to maturity	88.39	3.51	6.22	31.84	2.03	0.76
5	No. of capsules per plant	66.87	47.21	56.77	69.15	44.98	21.96
6	Capsule length	2.33	12.17	16.94	51.62	0.30	4.29
7	1000-seed weight	2.58	23.29	24.99	86.85	1.07	13.55
8	Seed yield per plant	4.95	36.08	41.81	74.46	2.76	19.24

**Table 2:** Cluster means of germplasms

	Cluster												
	1	2	3	4	5	6	7	8	9	10	11	12	13
Plant height	86.50	42.00	65.57	72.33	90.67	134.78	77.00	107.25	107.83	62.78	85.52	90.88	126.67
Days to 50% flowering	42.23	57.00	41.67	41.24	44.00	42.55	41.75	42.43	42.40	41.87	40.84	41.29	40.50
No. of branches/plant	4.23	3.67	3.10	4.79	8.00	8.00	11.66	7.22	4.30	4.40	6.60	6.06	5.67
Days to maturity	87.03	121.33	86.74	89.33	88.00	90.78	88.75	88.87	89.33	86.92	89.92	87.44	88.88
Capsule length	2.24	1.63	2.15	2.52	1.90	2.50	2.16	2.37	2.28	2.39	2.30	2.40	2.38
No. of capsules/plant	41.44	31.00	17.40	62.88	193.00	152.33	157.83	116.91	47.65	42.56	97.71	73.00	78.96
1000 seed weight	2.47	1.47	2.64	2.81	2.16	2.36	2.62	2.73	2.49	2.46	2.46	2.64	2.85
Seed yield /plant	4.07	3.51	3.24	5.21	2.22	5.73	7.43	6.20	4.04	4.98	5.83	5.42	5.58

moderate to low GCV and PCV was observed for the traits like plant height, days to 50% flowering, days to maturity and capsule length (Table 1). The broad sense heritability estimates were found to be higher for 1000 seed weight (88.1%), seed yield/plant (74.4%), number of capsule per plant (65.15%), plant height (60.60%), while capsule length (52.15%), days to flowering (51.57%) and days to maturity (31.99%) exhibited moderate heritability. Thus, in the present study, seed yield/plant, 1000 seed weight, number of branches/plant, number of capsules/plant, showed high GCV and heritability.

Significant variability existed among the genotypes. Higher value of PCV than GCV indicated substantial role of environment in expression of the characters. Similar findings were reported by Reddy *et al.* (2001), Saha *et al.* (2012), Tripathi *et al.* (2013), Begum and Dasgupta (2014) and Iqbal *et al.* (2015, 2016) and in sesame. In the present study, high GCV and PCV estimate for traits like seed yield/plant, 1000 seed weight, number of branches/plant number of capsules per plant and plant height

suggested sufficient variability of these characters and genetic improvement through selection of these traits seemed to be possible. High GCV coupled with high heritability can provide more desirable information than a single parameter alone (Saha *et al.* 1990). In the present study, 1000 seed weight, seed yield/plant, number of capsule per plant, plant height exhibited higher heritability, while moderately high heritability was observed for capsule length, days to flowering, days to maturity. Similar results were reported by Parameshwarappa *et al.* (2010) in sesame for branches per plant, days to maturity, capsule length and capsules per plant. The estimates of heritability (broad sense) include both additive and non-additive gene effect and its higher estimates in broad sense indicates that the trait is least influenced by environmental effects. Traits with high heritability estimates can be utilized for genetic improvement as they have potential for large genetic determination (Vasline *et al.* 2000). In fact, in present study characters like for 1000 seed weight, seed yield/plant, number of capsules per plant and plant height would hopefully leads

towards similar repeatable results and hence more predictable.

### Cluster analysis

Hierarchical cluster analysis based on agro morphological traits revealed that the inter cluster distance in most cases was larger indicating wider diversity among the germplasm of different groups. Cluster I included maximum number of genotypes (45) followed by cluster IV (25), cluster XII (24), cluster IX and cluster VII in such a way that genotypes having minimum genetic distance were grouped in same cluster and *vice versa*. Rest of the clusters were composed of mono-genotypic one. The range of inter cluster distance was 21.24 to 177.47, respectively (Table 3). The maximum inter cluster distance was found between clusters V and III (177.45), followed by clusters V and II (172.95), clusters VI and II (156.51), clusters V and X (153.09). The minimum inter cluster distance was recorded between clusters IV and XII followed by clusters 1 and IX (22.35). Cluster means of germplasm for eight characters (Table 3) revealed that cluster XIII had maximum plant height and 1000 seed weight. Cluster III reported to be early maturing average plant type. Cluster V had maximum number of capsule per plant (Table 2). Highest seed yield per plant were recorded in cluster VII (Table 2).

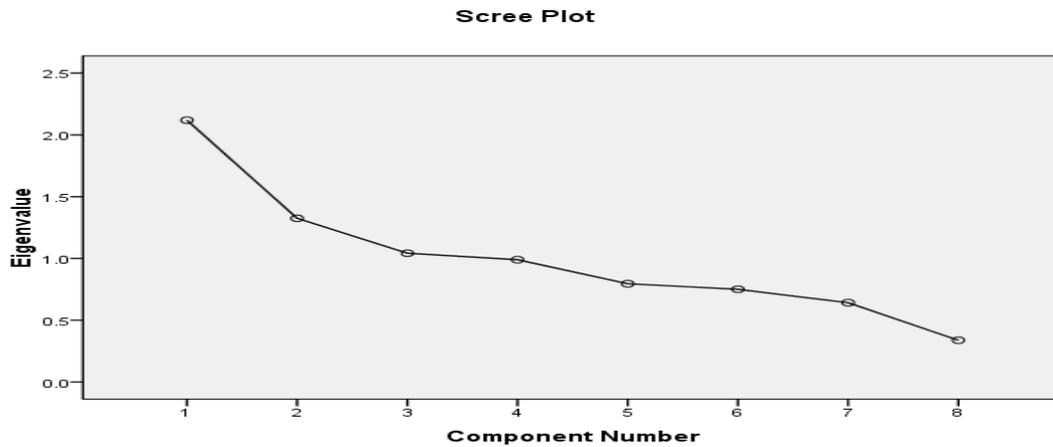
Hierarchical cluster analysis grouped the genotypes into thirteen clusters. The composition of clusters showed that clustering of germplasm was not associated with the geographical distribution

and accessions were mainly grouped due to their morphological differences. Thus geographical isolation is not the only factor causing genetic diversity in sesame rather forces other than geographical origin such as genetic drift, natural and artificial selection, exchange of breeding material might have played an important role in the fixation of diversity among the germplasm lines (Kandamoorthy and Govindarasu 2005; Senapati and Sarkar 2005; Sabesan *et al.* 2009; Banumathy *et al.* 2010). A few ecological conditions could also direct the gene flow between populations from diverse geographical origins. The characters contributing maximum divergence needs greater emphasis for deciding on the clusters for the purpose of selection of parents in the respective cluster for hybridization and parents for hybridization should be selected from cluster having high intercluster distance like between cluster V and III or II.

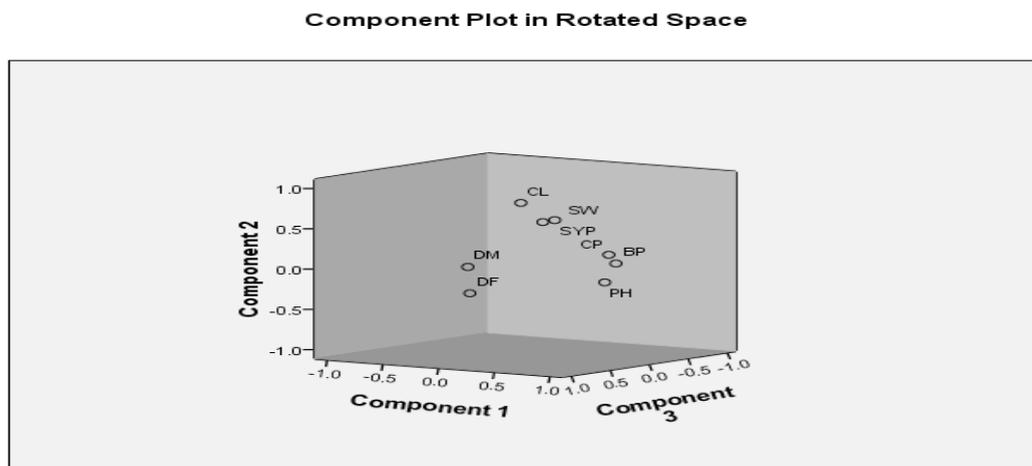
In order to know with which combination type of agronomic traits the sesame would attain high grain yield, PCA was performed (Table 2). The Scree plot of the PCA (Fig. 1) showed that the first three eigen values were correspond to the whole percentage of the variance in the dataset. The first three main PCAs are extracted from the complicated components, the total cumulative variance of these three factors amounted to 56.07% and these components had eigenvalues >1. The PCA simplifies the complex data by transforming the number of associated traits into a smaller number of variables as PCAs. The first PCA accounts for maximum

**Table 3:** Inter cluster distance among the genotypes of sesame

Cluster	1	2	3	4	5	6	7	8	9	10	11	12	13
1													
2	59.03												
3	31.91	46.62											
4	25.84	56.70	46.12										
5	151.68	172.95	177.47	131.51									
6	121.07	156.51	151.80	109.15	60.18								
7	117.07	136.69	141.23	95.34	38.34	58.22							
8	78.37	113.69	108.02	64.39	78.01	44.91	51.10						
9	22.33	76.48	52.06	38.66	146.43	108.17	114.70	69.35					
10	23.76	44.52	25.40	22.60	153.09	131.38	116.41	86.71	45.41				
11	56.44	87.22	82.93	37.30	95.57	73.58	60.96	29.06	54.90	59.79			
12	31.95	74.56	61.20	21.24	120.09	90.75	86.17	46.91	30.65	41.47	25.42		
13	55.06	103.94	86.83	56.67	119.71	73.91	93.42	42.70	36.65	73.58	45.24	36.32	



**Fig. 1:** Scree plot showing eigenvalues



**Fig. 2:** Plot of the first three PCAs showing relation among various sesame traits.

variability in the data with respect to succeeding components. The PCA grouped the estimated sesame variables into three main components which PCA1 accounted for about 26.48% of the variation; PCA2 for 16.56% and PCA3 for 13.06% (Table 2). The first PCA was related to capsule number and its contributing traits such as branch number and plant height, whereas the second PCA was related to days to 50% flowering and its contributing traits such as days to maturity (Table 4).

The traits, which contributed more positively to PCA1, were number of capsules / plant, number of branches/ plant, plant height, and seed yield per plant suggesting that this component reflected the yield potential of each genotype through some yield component aspects. In addition, the traits, which contributed positively to PCA2, were seed yield per plant, capsule length and thousand seed weight

suggesting that this component reflected the yield potential of each genotype. In addition, the traits, which contributed positively to PCA3, were days to maturity, days to flowering, capsule length and seed yield per plant.

The PCA may allow the plant breeder more flexibility in finding the number of plants to be evaluated and the plant breeder could use the multivariate methods by first determining the combination of traits that constitute an ideal plant. By plotting the PCAs that are considered to be important, plants close to the ideal plant would be selected (Yan and Rajcan 2002). The PCA may be deemed important if their associated coefficients are of relative magnitude with breeding targets and given this apparent potential for using PCA, further work is required to compare multivariate methods for reaching actual gains.

**Table 4:** Loadings of PCA for the estimated traits of sesame

Traits	Component		
	PC-1	PC-2	PC-3
Capsule/plant	.863	.164	-.049
Primary branch	.754	.142	-.230
Seed yield/plant	.620	-.215	.353
Plant height	.534	.262	-.355
Days to flowering	-.065	.637	.386
Capsule length	.279	-.562	.441
Seed weight	.207	-.495	.124
Days to maturity	.102	.444	.614
Eigen value	2.119	1.325	1.042
Percentage of variance	26.486	16.560	13.026
Cumulative percentage	26.486	43.047	56.072

The PCA revealed that emphasis should be given to the traits like 1000 seed weight, branches/plant, plant height and capsules/plant during selection programme.

## CONCLUSION

In this study, the estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) revealed that GCV was less than its corresponding estimates of PCV for seed yield and its related traits exhibiting environmental interference. Traits like 1000 seed weight, seed yield/plant, number of capsules per plant and plant height would hopefully leads towards similar repeatable results and hence more predictable because these traits posses high heritability estimates can be utilized for genetic improvement as they have potential for large genetic determination. In this study we conclude that geographical isolation is not the only factor causing genetic diversity in sesame rather forces other than geographical origin such as genetic drift, natural and artificial selection, exchange of breeding material might have played an important role in the fixation of diversity among the germplasm lines.

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