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## Research Article

### Assessment of genetic variability for seed yield and its components in sesame (*Sesamum indicum* L.) based on multivariate analysis

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#### Abstract

Sesame is an important oilseed crop in India. The productivity of sesame is considerably low owing to several production challenges. Developing high yielding varieties with resistance to biotic and abiotic stresses remains a major goal in sesame breeding. In this study, a total of 55 sesame genotypes were evaluated for 16 quantitative traits related to seed yield. Genetic relationship and variability in the genotypes were assessed based on correlation, principal component analysis (PCA) and cluster analysis. The results showed that seed yield had a high positive correlation with the number of capsules per plant and a high negative correlation with days to maturity. The PCA revealed six components contributing to the total variance, which were components 1 (plant height, the number of primary branches, leaf length and leaf width), 2 (seed yield per plant and thousand seed weight in the positive direction and days to maturity in the negative direction), 3 (days to flower initiation and days to 50 per cent flowering), 4 (capsule width and seeds per capsule), 5 (the number of capsules per plant) and 6 (the number of seeds per capsule) in the order of importance. Cluster analysis showed five clusters of genotypes in accordance with the phenotypic traits. Overall results indicated that the number of capsules per plant, the number of seeds per capsule and thousand seed weights were the most critical traits for selecting high yielding genotypes in sesame.

**Keywords:** Correlation, principal component analysis, cluster, genetic resources, evaluation, sesame

#### INTRODUCTION

Sesame (*Sesamum indicum* L.) is a traditional oilseed crop of India. It belongs to the family Pedaliaceae with a chromosome number of  $2n=26$ . It is commonly called as gingelly, til, nuvvulu, ellu etc. in India. The sesame seed and its oil possess excellent nutritional, medicinal and industrial values (Anilakumar *et al.*, 2010). The seed oil contains a balanced composition of unsaturated fatty acids (oleic acid: 36-52%; linoleic acid: 30-52%) (Mondal *et al.*, 2010). Seed is also a rich source of

protein and antioxidants like lignans and tocopherols (Hemalatha and Ghafoorunnisa, 2004; Anilakumar *et al.*, 2010). The seeds earned high export potential (Wacal *et al.*, 2021). During 2020-21, India's export of sesame seeds was worth of 425.60 million USD (INR 2766 crore) (<https://www.pib.gov.in/PressReleasePage.aspx?PRID=1738172>). Despite huge potential, sesame is underexploited in India (Pathak *et al.*, 2014).

The area, production and productivity of sesame were 14 million ha, 6.8 million tonnes and 487 kg/ha, respectively during 2020 at the world level (FAOSTAT, 2020). It is grown in several countries including India, Myanmar, Nigeria, China, Ethiopia and Uganda. In India, it is grown in an area of 1.52 million ha with a production of 0.66 million tonnes and productivity of 433 kg/ha (FAOSTAT, 2020). Major sesame growing states in India are West Bengal, Madhya Pradesh, Rajasthan, Uttar Pradesh, Gujarat, Andhra Pradesh, Telangana and Tamil Nadu. It is grown either as a sole crop or as an intercrop with groundnut, pearl millet, cotton, greengram, blackgram, pigeonpea or soybean in different states. More than 30 varieties of sesame have been notified for cultivation across states. Low and unstable yield, non-synchronous maturity and susceptibility to biotic and abiotic stresses are major challenges of sesame cultivation in India. Therefore, developing varieties with high seed yield coupled with resistance to biotic and abiotic stresses remains a major goal in sesame breeding. Genetic variability in germplasm is fundamental for crop breeding

programmes aiming at improving yield potential. More than 6000 accessions are maintained at the ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR) which underscores the potential for broadening the genetic base of sesame (Bisht *et al.*, 2002). Genetic variability in a germplasm collection can be assessed using morphological or molecular data or a combination of both (Pandey *et al.*, 2015). Statistical tools such as correlation and multivariate grouping techniques namely cluster analysis and Principal Component Analysis (PCA) reveals the pattern of relationships between genotypes and explain the relative contribution of traits or genotypes to the observed variability in the genotype's collection. PCA has been widely used for studying genetic variability in sesame (Pandey *et al.*, 2015; Baraki *et al.*, 2020; Teklu *et al.*, 2021). With this background, the present study was taken up with the main objective to analyze the genetic relationship and variability for seed yield and its related traits in a collection of 55 genotypes through correlation and multivariate analysis.

**Table 1. List of sesame genotypes used in the study**

Code	Entries	Code	Entries
G1	NIC-16106	G29	SI-1769
G2	NIC-2939	G30	PAIYUR-1
G3	SI-2186	G31	KMR-87
G4	G-53	G32	SI-1771
G5	PSR-2000	G33	ES-71
G6	SI-9185	G34	TC-25
G7	NAE-79114/7	G35	SI-1236
G8	SI-801	G36	SI-1143-1
G9	NIC-8252	G37	SI-1214
G10	KMR-95	G38	RT-146
G11	IS-1516	G39	RT-106
G12	NIC-8283	G40	IS-249
G13	DS-1	G41	S-861
G14	NIC-8261	G42	SI-1967
G15	SI-769-2	G43	NIC-8317
G16	SI-395	G44	BS-27
G17	GUN-3-NL-1	G45	SI-2334
G18	DP1-15-25	G46	SI-533
G19	SI-9185	G47	SI-212
G20	SI-2289-2	G48	SI-328
G21	OTS-2	G49	SI-7613
G22	JTS-80	G50	SI-80-1
G23	SI-1760/1	G51	ANNAMALAI-NC-1
G24	SO-233	G52	SI-3171
G25	KMR-342	G53	SI-987/1
G26	SI-70	G54	KANDAPPAN KURICHY
G27	IC-2046-18	G55	CO-1
G28	SI-702		

## MATERIALS AND METHODS

A total of 55 sesame genotypes (**Table 1**) were used for evaluation in this study. The experiment was conducted during summer 2022 at the Department of Oilseeds, Tamil Nadu Agricultural University, Coimbatore, India (11°N latitude and 77°E longitude at an altitude of 427 metres above MSL) in Alpha Lattice Design with two replications (11 genotypes/ block/replication). Each genotype was raised in a single row of three meters in length with a spacing of 30 cm between rows and 30 cm between plants, following the recommended agronomic packages of practices during the experimental period.

Sixteen quantitative traits connected to yield and yield components were recorded on five randomly selected plants of each genotype in each replication as per the standard procedures described for sesame (IPGRI and NBPGR, 2004). The traits measured were: plant height (cm), the number of primary branches per plant, the number of secondary branches per plant, basal leaf length (cm), basal leaf width (cm), top leaf length (cm), top leaf width (cm), days to first flower initiation, days to 50 per cent flowering, days to maturity, capsule length (cm), capsule width (cm), the number of capsules per plant, the number of seeds per capsule, 1000 seed weight (g) and seed yield per plant (g). The data were

subjected to the following statistical analyses. The mean phenotypic data were subjected to simple correlation using R statistical software (v4.1.2; R Core Team 2021). Principal component analysis was done using EXCEL\_STAT (Trial version). The Manhattan coefficient and the UPGMA method of hierarchical clustering technique were employed to group the accessions based on the similarity matrix as implemented in Darwin software version 5 (Dissimilarity Analysis and Representation for windows) V.5.0.158 (Perrier and Jacquemoud-Collet, 2006) (<http://darwin.cirad.fr/darwin>).

## RESULTS AND DISCUSSION

Correlation analysis helps to measure the genetic association between two or more traits; thus, allowing indirect selection in plant breeding (Hallauer and Miranda Filho, 1988). Results of correlation observed among traits in this study are provided in **Table 2**. Plant height showed positive correlation with the number of primary branches ( $r=0.3490$ ), basal leaf length ( $r=0.2646$ ), basal leaf width ( $r=0.2644$ ), top leaf length ( $r=0.3432$ ) and top leaf width ( $r=0.3138$ ). Days to initial flowering showed a positive correlation with days to 50 per cent flowering ( $r=0.8274$ ). Seed yield per plant showed a positive correlation with basal leaf width ( $r=0.2791$ ), the number of capsules per plant ( $r=0.5014$ ) and thousand seed

**Table 2. Simple correlation coefficients for yield and yield components in sesame**

	NPB	NSB	BLL	BLW	TLL	TLW	DTIF	DTFF	DTM	CL	CW	CPP	SPC	TSW	SYP
PHT	0.3490	0.0063	0.2646	0.2644	0.3432	0.3138	0.2556	0.2222	-0.1652	0.0771	-0.0761	0.1033	-0.1013	0.2387	0.2423
NPB		0.4288	0.2589	0.1644	0.1882	0.2483	0.1742	0.0878	-0.2388	0.1129	-0.1930	-0.0013	-0.1335	0.1384	0.1633
NSB			0.0754	0.0734	-0.1205	-0.0763	0.0959	0.1078	-0.0813	0.1284	-0.2260	0.2107	0.0109	0.0095	0.0653
BLL				0.6072	0.3992	0.4426	0.1776	0.1334	-0.0062	-0.3213	-0.1524	0.1576	-0.0746	-0.3293	0.1215
BLW					0.3072	0.4585	0.1293	0.2110	0.0593	-0.2190	0.0840	0.2827	0.1196	-0.0539	0.2791
TLL						0.5918	-0.0598	0.0643	-0.0463	-0.3734	0.0084	-0.0634	-0.0524	-0.1050	0.0494
TLW							0.2263	0.3254	-0.0290	-0.2382	0.0471	0.0963	0.0449	-0.1803	0.1241
DTIF								0.8274	0.0820	-0.0118	0.0230	0.1561	0.1332	-0.1426	0.0817
DTFF									0.2104	-0.0985	0.1169	0.0576	0.2191	-0.2796	0.0551
DTM										-0.1089	0.0984	-0.1163	0.0979	-0.3725	-0.4775
CL											-0.1286	-0.0922	0.0409	0.2430	-0.0904
CW												-0.0684	0.2811	0.0640	0.2483
CPP													-0.0875	0.0427	0.5014
SPC														0.0663	-0.0422
TSW															0.3403

PHT=Plant height, NPB=Number of primary branches per plant, NSB=Number of secondary branches per plant, BLL=Basal leaf length, BLW=Basal leaf width, TLL=Top leaf length, TLW=Top leaf width, DTIF=Days to first flower initiation, DFF=Days to 50 per cent flowering, DTM=Days to maturity, CL=Capsule length, CW=Capsule width, CPP=Number of capsules per plant, SPC=Number of seeds per capsule, TSW=1000 seed weight and SYP=Seed yield per plant.

Tabulated values of Pearson correlation coefficients are 0.263447 ( $\alpha=0.05$ ) and 0.34177 ( $\alpha=0.01$ ) at  $df=54$ ; the tabulated values at  $df=50$  and  $60$  were interpolated to arrive at the value at  $df=54$  (<https://www.real-statistics.com/statistics-tables/interpolation/>)

weight (0.3403). Similar observations were made by Pham *et al.* (2010), Goudappagoudra *et al.* (2011), Ukaanand Ogbonna (2012), Ismaila and Usman (2014), Fazal *et al.* (2015), Sasipriya *et al.* (2018), Patil and Loksha (2018) and Umamaheshwari *et al.* (2019). Days to maturity showed a negative correlation with thousand seed weight and seed yield per plant. This result is in line with the report of Baraki *et al.* (2020).

Overall, seed yield had a high positive correlation with the number of capsules per plant ( $r=0.5014$ ) and a high negative correlation with days to maturity ( $r=-0.4775$ ). In general, plant breeders would seriously consider the correlations between traits if more than 0.5. However, Gilbert (1961) suggested that even small correlations can have important effects depending on the progeny size. Therefore, careful consideration of trait's correlation found in this study would help in exercising desirable plant selections in sesame breeding.

Principal Component Analysis was applied as a reductionist approach of the multivariate data to measure the importance and contribution of each component to total variance. The PCA provides information on the independent impact of a particular trait to the total

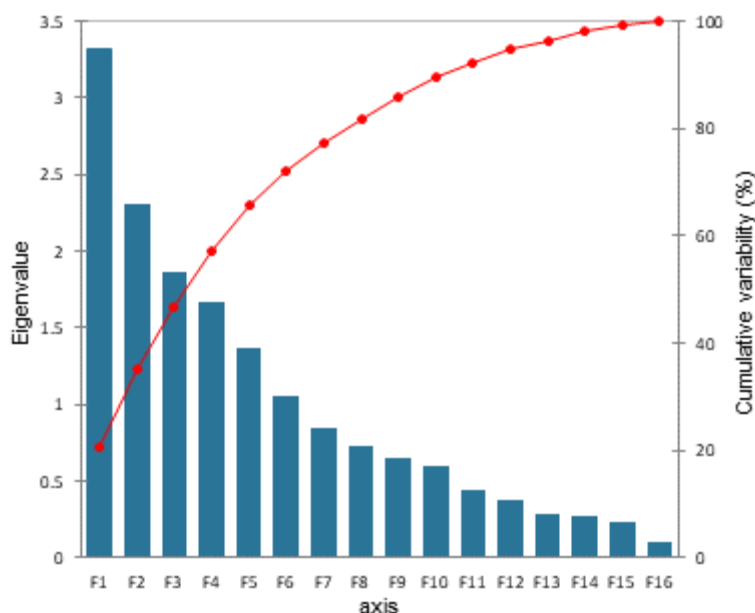
variance wherein each coefficient of eigenvectors indicates the degree of contribution of every original variable to which each principal component is associated with. Based on PCA analysis, it was found that the first six components contributed cumulatively to a maximum of 72.11 per cent of the variation among genotypes evaluated for the different quantitative traits. These six principal components were retained based on the scree plot and threshold eigenvalue which was greater than 1 (Fig.1 and Table 3).

The first principal component accounting for 20.73 per cent of the variability measured vegetative traits in a positive direction. An increase in plant height was associated with an increase in the number of primary branches, leaf length and leaf width. The variability accounted by the second component was 14.40 per cent and was mainly attributed to seed yield per plant and thousand seed weight, both in positive directions and days to maturity in a negative direction. The third principal component accounted for 11.58 per cent and was a measure of days to flower initiation and days to 50 per cent flowering. The fourth principal component accounting for 10.37% of the variation was a measure of capsule width and seeds per capsule resulting in a positive increase of seed

**Table 3. Eigen value and percent of total variation and component matrix for the principal component axes**

Traits	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6
Eigenvalue	3.317	2.304	1.853	1.660	1.355	1.048
Variability (%)	20.733	14.401	11.584	10.374	8.471	6.552
Cumulative %	20.733	35.134	46.718	57.092	65.563	72.115
Component matrix						
PHT	0.541	-0.347	0.056	-0.097	-0.423	-0.249
NPB	0.419	-0.441	0.124	-0.456	-0.213	0.265
NSB	0.132	-0.308	0.359	-0.433	0.331	0.489
BLL	0.723	0.108	-0.278	-0.208	0.205	0.123
BLW	0.708	0.013	-0.129	0.166	0.180	0.314
TLL	0.583	0.103	-0.524	-0.025	-0.339	0.014
TLW	0.747	0.140	-0.186	0.026	-0.236	0.012
DTIF	0.482	0.186	0.729	-0.025	-0.053	-0.300
DTFF	0.523	0.361	0.671	0.040	-0.094	-0.189
DTM	-0.068	0.721	0.109	-0.090	0.087	0.103
CL	-0.352	-0.364	0.412	-0.216	-0.282	0.081
CW	0.035	0.157	0.081	0.745	-0.156	0.182
CPP	0.324	-0.333	0.126	0.210	0.675	-0.160
SPC	0.016	0.228	0.337	0.419	-0.207	0.586
TSW	-0.181	-0.693	0.046	0.294	-0.318	0.066
SYP	0.368	-0.605	0.043	0.516	0.232	-0.115

PHT=Plant height, NPB=Number of primary branches per plant, NSB=Number of secondary branches per plant, BLL=Basal leaf length, BLW=Basal leaf width, TLL=Top leaf length, TLW=Top leaf width, DTIF=Days to first flower initiation, DFF=Days to 50 per cent flowering, DTM=Days to maturity, CL=Capsule length, CW=Capsule width, CPP=Number of capsules per plant, SPC=Number of seeds per capsule, TSW=1000 seed weight and SYP=Seed yield per plant.



**Fig.1. Scree plot showing the Eigen value variation for sixteen quantitative traits in sesame**

yield per plant. The fifth principal component accounted for 8.47 per cent with the number of capsules per plant exhibiting the largest and positive loading on this axis. The number of secondary branches and basal leaf length parameters resulted in more number of capsules per plant thereby led to a yield increase in a positive direction. However, the proportion of seed yield increase was found to be nominal, since an increase in the number of capsules per plant resulted in a reduction of seeds per capsule and thousand seed weight. The variability attributed by the sixth component was to the tune of 6.55 per cent with the highest positive loading for seeds per capsule in this axis. The number of primary and secondary branches and increase in basal leaf area contributed to the increase in seeds per capsule in a positive direction. Similar results were reported by Singh *et al.* (2018), Baraki *et al.* (2020) and Deepak Gupta *et al.* (2021). The important yield traits both through correlation and PCA analyses showed a negative association with days to maturity which was also observed by Baraki *et al.* (2020).

A biplot representing the ordination of genotypes and the morphological traits with PC1 in the abscissa and PC2 in the ordinate depicted a clear pattern of grouping of genotypes in the factor plane. All the genotypes were widely scattered across different quarters (Fig.2). The prominent characters identified in a particular principal component are prime contributors to total variability and have the tendency to hang together and can be used effectively for selection in crop breeding programmes. Such biplots based on PCA analysis were used by Furat and Uzan, (2010), Choi *et al.* (2017) and Baraki *et al.* (2020) for analyzing the association of

genotypes and quantitative traits. Cluster analysis is another commonly used multivariate analysis to group the genotypes based on their similarity. Based on cluster analysis, the genotypes were grouped into five clusters. Cluster I comprised of 17 genotypes, which was grouped further into three sub-clusters, cluster II comprised of 20 genotypes, which was grouped further into three sub-clusters, cluster III comprised of 13 genotypes, cluster IV comprised of one genotype and cluster V comprised of 4 genotypes which was further grouped into two sub-clusters. The cluster-wise mean performance of genotypes for various morphological traits is presented in Table 4. The dendrogram grouping the 55 genotypes into five clusters is presented in Fig. 3.

Cluster I comprised of early flowering genotypes with long basal leaves and reduced plant height. The genotypes belonging to this cluster had a moderate single plant yield contributed by more than 120 capsules per plant. Cluster II and III were characterized by tall genotypes bearing more number of primary branches and recording higher thousand seed weights. However, the genotypes belonging to cluster II recorded a lesser number of capsules per plant with a mean value of less than 100 capsules, while Cluster III comprised of high yielding genotypes producing on an average more than 150 capsules per plant. Cluster IV included a single high yielding genotype which was late flowering and late maturing, and recorded more than 200 capsules per plant with more number of seeds per capsule and thousand seed weight. Cluster V comprised of early flowering and short genotypes possessing poor yield attributes. These findings are in line with the reports of Baraki *et al.* (2020).

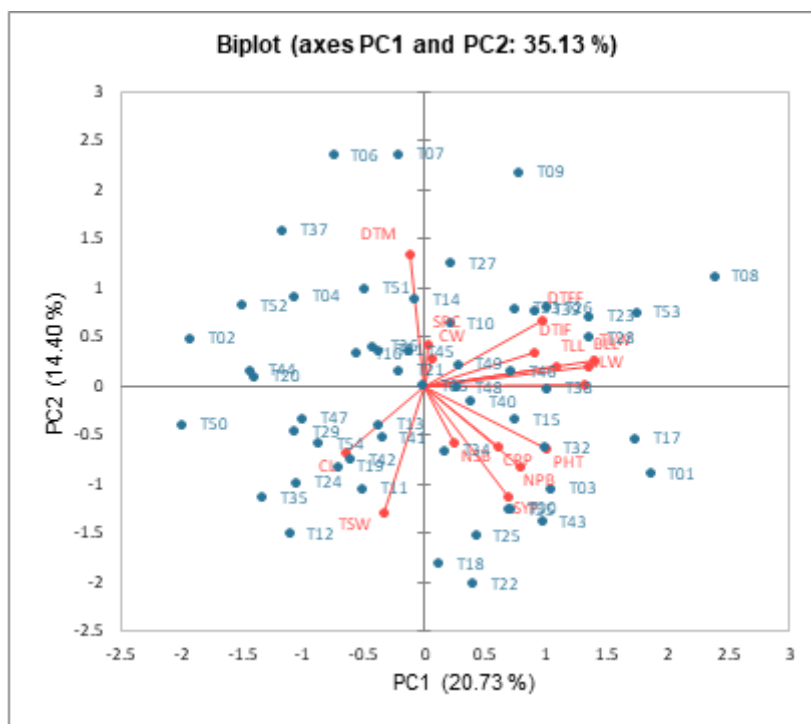


Fig. 2. Biplot of first two principal components showing the association of genotypes and the quantitative traits

Table 4. Cluster-wise mean values of the morphological traits used for grouping the sesame genotypes

Traits	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
PHT	128.30	140.94	142.95	134.88	124.28
NPB	5.79	6.33	6.12	6.20	5.60
NSB	4.27	4.03	4.56	5.50	3.48
BLL	13.87	12.95	13.34	13.54	12.28
BLW	7.11	6.57	6.91	7.61	5.78
TLL	7.23	7.58	7.38	7.38	7.40
TLW	1.85	1.87	1.94	2.29	1.78
DTIF	39.50	40.93	41.12	45.00	39.63
DTFF	43.53	45.14	44.81	48.00	43.88
DTM	112.24	111.77	111.75	114.10	113.83
CL	2.48	2.48	2.46	2.40	2.44
CW	0.62	0.62	0.61	0.64	0.62
CPP	127.33	96.17	157.20	206.00	41.33
SPC	52.72	53.49	50.94	57.50	53.40
TSW	2.78	2.97	2.85	3.00	2.71
SYP	7.82	7.37	9.63	8.72	4.34

PHT=Plant height(cm), NPB=Number of primary branches per plant, NSB=Number of secondary branches per plant, BLL=Basal leaf length (cm), BLW=Basal leaf width (cm), TLL=Top leaf length (cm), TLW=Top leaf width (cm), DTIF=Days to first flower initiation, DFF=Days to 50 per cent flowering, DTM=Days to maturity, CL=Capsule length (cm), CW=Capsule width (cm), CPP=Number of capsules per plant, SPC=Number of seeds per capsule, TSW=1000 seed weight (g) and SYP=Seed yield per plant (g).

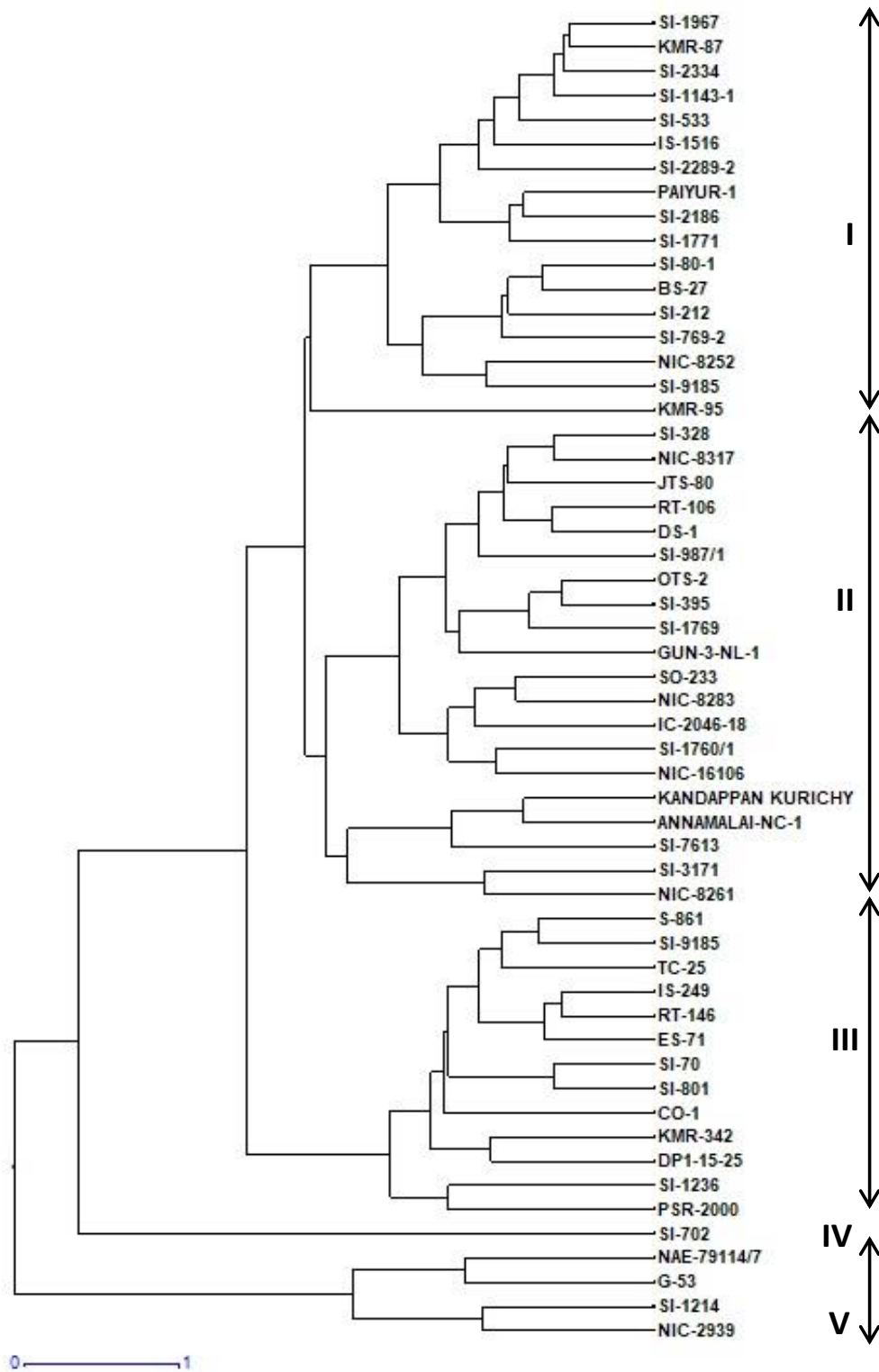


Fig. 3. Dendrogram based on biometrical traits in sesame



Seed yield in sesame is a polygenic trait and is highly influenced by environmental factors. Practising direct selection for seed yield may not be effective in sesame. Indirect selection for seed yield by analyzing the inter-relationship among the different agro-morphological traits and their association with yield can help to improve the productivity of sesame. The multivariate analysis has helped in reducing a large number of variables and results of the present study revealed that the number of capsules per plant, seeds per capsule and thousand seed weights should be considered as important component traits while selecting for high yielding genotypes in sesame.

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