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UNRAVELLING THE GENETIC VARIABILITY OF SEED YIELD AND ITS COMPONENTS IN SESAME (*SESAMUM INDICUM* L.) THROUGH MULTIVARIATE ANALYSIS

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ABSTRACT

In this present study, Principal Component Analysis and cluster analysis were employed to assess the genetic variability among ninety-six advanced breeding lines of sesame with four checks *viz*., DS-5, DSS-9, JTS-8 and TKG-22 based on morphological traits. Principal Component Analysis revealed that the first five principal components accounted for 64.10% of the total variation among genotypes. These components were associated with traits such as number of primary branches per plant, number of productive branches per plant, number of productive capsules per plant, seed yield (kg/ha), days to maturity and plant height. A biplot analysis showed distinct grouping patterns of genotypes based on their morphological traits. Cluster analysis further classified the genotypes into eight clusters, indicating a high degree of heterogeneity. By leveraging the diverse genotypes and identifying key traits through multivariate analyses, breeders can make informed selections and develop improved sesame varieties with enhanced productivity and quality.

Key words : Sesame, Principal component analysis, Cluster analysis, Eigen value and Scree plot.

Introduction

Sesame (*Sesamum indicum* L.) belongs to the family Pedaliaceae, having ploidy level 2n = 26 is considered as valuable oilseed crop at global level. Sesame is designated as the “Queen of oilseed crops” because of its high nutritive quality (rich in carbohydrate, protein, calcium, iron and phosphorous) and quantity of oil (40 to 63%). Sesame oil has highest antioxidant content and contains several fatty acids such as oleic acid (43%), linoleic acid (35%), palmitic acid (11%) and stearic acid (7%). Therefore, stability against oxidative rancidity owing to the occurrence of the natural antioxidants namely lignans (sesamin, sesamolin and sesamol) and γ-tocopherol, which offers long shelf life to the sesame, oil (Anilakumar, 2010). Despite its potential, there is still untapped potential in sesame that can be harnessed through aggressive breeding efforts (Furat and Uzun, 2010).

Improvement in yield is normally attained through exploitation of the genetically diverse parents in breeding programmes. Genetic divergence among parents is essentialto realize maximum heterosis and to obtain transgressive segregants in the segregating generations since the crossing programme involving genetically diverse parents. Statistical tools such as 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 to the observed variability in the genotype’s collection. PCA is highly effective and useful for identifying plant features that classify the distinctiveness of promising genotypes (Chakravorty *et al*., 2013). The PCA provides information on the

independent impact of a particular trait to the total variance wherein each coefficient of eigenvalue indicates the degree of contribution of every original variable to which each principal component is associated (Baraki *et al.*, 2020; Teklu *et al.*, 2021).

Materials and Methods

The experiment was conducted during summer 2022 at AICRP on Sesame and Niger, MARS, UAS, Dharwad, India. Ninety-six advanced breeding lines derived from cross DS-5 × DS-28, DS-5 × RMT-496 and DS-5 × NIC-17325 along with four checks *viz.*, DS-5, DSS-9, JTS-8 and TKG-22 (Table 1) were evaluated in randomized complete block design with two replications. The mean phenotypic data were subjected to Principal component analysis using R statistical software. 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).

Table 1 : List of advanced breeding lines of sesame.

S. no.	Genotypes	S. no.	Genotypes	S. no.	Genotypes
1	(DS-5 × DS-28)-1-2-1-2	35	(DS-5 × RMT-496)-1-3-3-1	69	(DS-5 × NIC-17325)-1-1-3-4
2	(DS-5 × DS-28)-1-2-2-1	36	(DS-5 × RMT-496)-1-3-3-2	70	(DS-5 × NIC-17325)-1-3-1-1
3	(DS-5 × DS-28)-2-1-2-2	37	(DS-5 × RMT-496)-1-3-3-3	71	(DS-5 × NIC-17325)-1-3-1-2
4	(DS-5 × DS-28)-2-1-1-2	38	(DS-5 × RMT-496)-3-1-1-1	72	(DS-5 × NIC-17325)-1-3-1-3
5	(DS-5 × DS-28)-2-1-3-1	39	(DS-5 × RMT-496)-3-1-1-2	73	(DS-5 × NIC-17325)-1-3-1-4
6	(DS-5 × DS-28)-2-2-1-1	40	(DS-5 × RMT-496)-3-1-1-3	74	(DS-5 × NIC-17325)-1-3-4-1
7	(DS-5 × DS-28)-2-2-2-2	41	(DS-5 × RMT-496)-3-1-2-1	75	(DS-5 × NIC-17325)-1-3-4-2
8	(DS-5 × DS-28)-2-2-3-1	42	(DS-5 × RMT-496)-3-1-2-2	76	(DS-5 × NIC-17325)-1-3-4-3
9	(DS-5 × DS-28)-3-1-1-1	43	(DS-5 × RMT-496)-3-1-3-1	77	(DS-5 × NIC-17325)-2-1-1-1
10	(DS-5 × DS-28)-3-1-2-1	44	(DS-5 × RMT-496)-3-1-3-2	78	(DS-5 × NIC-17325)-2-1-1-2
11	(DS-5 × DS-28)-3-2-1-1	45	(DS-5 × RMT-496)-3-2-1-1	79	(DS-5 × NIC-17325)-2-3-1-1
12	(DS-5 × DS-28)-3-2-2-2	46	(DS-5 × RMT-496)-3-2-1-2	80	(DS-5 × NIC-17325)-2-3-1-2
13	(DS-5 × DS-28)-3-2-3-2	47	(DS-5 × RMT-496)-3-2-3-1	81	(DS-5 × NIC-17325)-2-3-1-3
14	(DS-5 × DS-28)-3-2-3-3	48	(DS-5 × RMT-496)-3-2-3-2	82	(DS-5 × NIC-17325)-2-3-2-1
15	(DS-5 × DS-28)-4-1-1-1	49	(DS-5 × RMT-496)-3-2-3-3	83	(DS-5 × NIC-17325)-2-3-2-2
16	(DS-5 × DS-28)-4-1-1-2	50	(DS-5 × RMT-496)-3-3-1-1	84	(DS-5 × NIC-17325)-2-3-3-1
17	(DS-5 × DS-28)-4-1-2-2	51	(DS-5 × RMT-496)-3-3-1-2	85	(DS-5 × NIC-17325)-2-3-3-2
18	(DS-5 × DS-28)-4-1-3-2	52	(DS-5 × RMT-496)-3-3-1-3	86	(DS-5 × NIC-17325)-2-3-3-3
19	(DS-5 × DS-28)-4-2-1-2	53	(DS-5 × RMT-496)-3-3-2-1	87	(DS-5 × NIC-17325)-3-2-1-1
20	(DS-5 × DS-28)-4-3-1-2	54	(DS-5 × RMT-496)-3-3-2-2	88	(DS-5 × NIC-17325)-3-2-1-2
21	(DS-5 × DS-28)-4-3-2-1	55	(DS-5 × RMT-496)-3-3-3-1	89	(DS-5 × NIC-17325)-3-2-1-3
22	(DS-5 × DS-28)-4-3-3-2	56	(DS-5 × RMT-496)-3-3-3-2	90	(DS-5 × NIC-17325)-3-2-2-1
23	(DS-5 × DS-28)-5-1-1-1	57	(DS-5 × RMT-496)-3-3-3-3	91	(DS-5 × NIC-17325)-3-2-2-2
24	(DS-5 × DS-28)-5-3-1-2	58	(DS-5 × RMT-496)-3-3-4-1	92	(DS-5 × NIC-17325)-3-2-3-1
25	(DS-5 × DS-28)-5-3-1-3	59	(DS-5 × RMT-496)-3-3-4-2	93	(DS-5 × NIC-17325)-3-2-3-2
26	(DS-5 × DS-28)-5-3-2-1	60	(DS-5 × RMT-496)-3-3-4-3	94	(DS-5 × NIC-17325)-3-2-3-3
27	(DS-5 × RMT-496)-1-1-1-1	61	(DS-5 × NIC-17325)-1-1-1-1	95	(DS-5 × NIC-17325)-3-2-4-1
28	(DS-5 × RMT-496)-1-1-1-2	62	(DS-5 × NIC-17325)-1-1-1-2	96	(DS-5 × NIC-17325)-3-2-4-2
29	(DS-5 × RMT-496)-1-1-1-3	63	(DS-5 × NIC-17325)-1-1-2-1	97	DS-5
30	(DS-5 × RMT-496)-1-2-1-1	64	(DS-5 × NIC-17325)-1-1-2-2	98	DSS-9
31	(DS-5 × RMT-496)-1-2-1-2	65	(DS-5 × NIC-17325)-1-1-2-3	99	JTS-8
32	(DS-5 × RMT-496)-1-3-1-1	66	(DS- 5 × NIC-17325)-1-1-3-1	100	TKG-22
33	(DS-5 × RMT-496)-1-3-1-2	67	DS- 5 × NIC-17325-1-1-3-2		
34	(DS-5 × RMT-496)-1-3-1-3	68	(DS-5 × NIC-17325)-1-1-3-3		

Genotypes 1 to 26 belongs to the cross DS-5 × DS-28, 27 to 60 belongs to cross DS-5 × RMT-496 and 61 to 96 belongs to cross DS-5 × NIC-17325.

Results and Discussion

In PCA analysis, it was found that the first five components contributed cumulatively to a maximum of 64.10per cent of the variation among genotypes evaluated for the different quantitative traits. These five principal components were retained based on the scree plot and

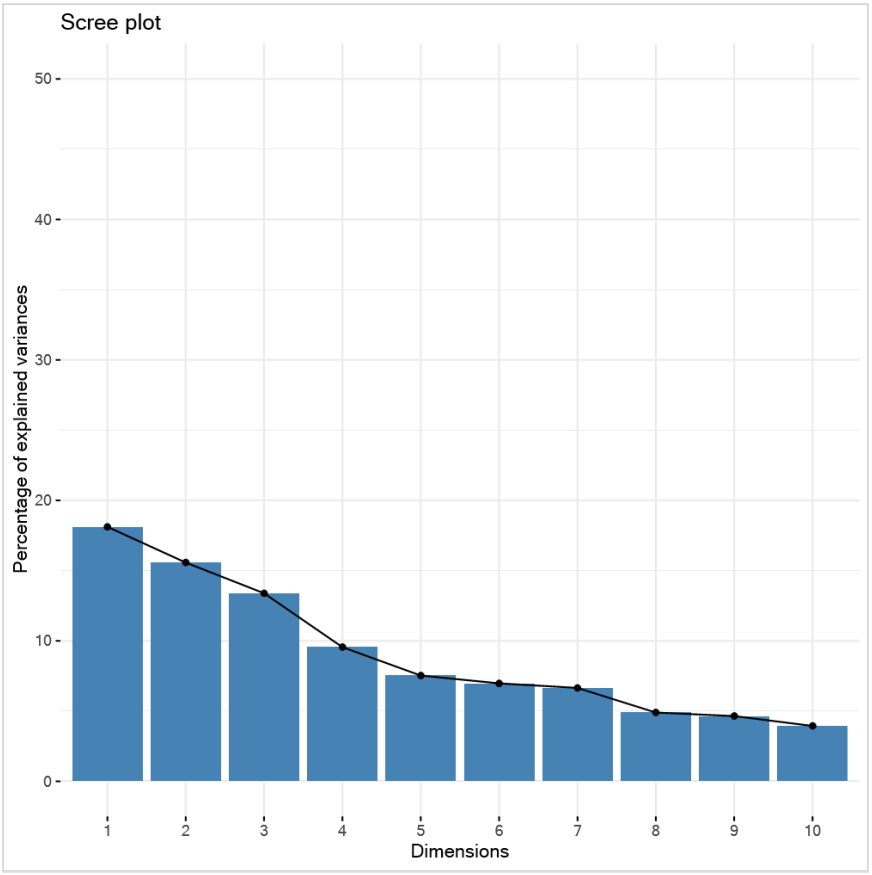

Fig. 1 : Scree plot showing the Eigen value variation for fifteen quantitative traits in sesame.

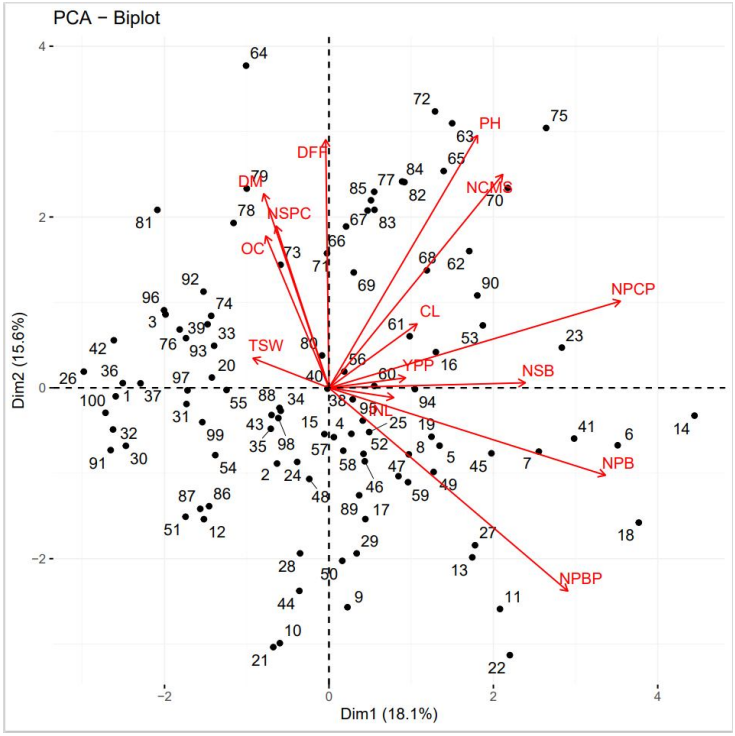

Fig. 2 : Biplot of first two principal components showing the association of genotypes and the quantitative traits.

Table 2 : Eigen value, percent of total variation and component matrix for the principal component axes.

Traits	PC1	PC2	PC3	PC4	PC5
Eigen values	2.55	2.28	2.16	1.51	1.10
Variability (%)	17.00	15.20	14.50	10.10	7.40
Cumulative (%)	17.00	32.20	46.70	56.80	64.10
Component matrix					
DFF	-0.03	0.24	0.41	-0.28	-0.13
DM	-0.13	0.15	0.33	-0.39	-0.32
PH	0.25	0.07	0.44	0.13	0.24
NPB	0.47	-0.02	-0.14	-0.29	-0.24
NSB	0.31	0.17	-0.01	-0.07	0.05
NPBP	0.41	-0.03	-0.35	-0.21	-0.15
NPCP	0.46	0.22	0.12	0.16	-0.10
NCMS	0.27	0.19	0.35	0.34	0.10
CL	0.19	-0.21	0.13	-0.43	0.10
NSPC	-0.06	-0.15	0.30	0.09	-0.20
INL	0.12	-0.14	0.02	-0.24	0.77
TSW	-0.06	-0.31	0.11	-0.32	-0.01
OC	-0.04	-0.36	0.32	-0.07	0.01
YPP	0.21	-0.45	0.07	0.17	-0.18
SY	0.12	-0.52	0.05	0.28	-0.13

DFF-Days to 50% flowering; **DM**- Days to maturity; **PH**: Plant height (cm); **NPB**- Number of primary branches; **NSB**- Number of secondary branches; **NPBP**- Number of productive branches per plant; **NPCP**- Number of productive Capsules per plant; **NCMS**- Number of capsules on main stem; **CL**- Capsule length (cm); **NSPC**- Number of seed per capsule; **INL**- Internodal length (cm); **TSW**-Thousand seed weight (g); **OC**-Oil content (%); **YPP**- Yield per plant (g); **SY**- Seed yield (Kg/ha).

Table 3 : Inter and intra cluster D^2 values for different clusters.

Cluster	Cluster							
	I	II	III	IV	V	VI	VII	VIII
I	0.00	656.37	63.78	241.55	133.96	188.94	410.51	318.29
II		0.00	597.89	415.83	523.46	468.55	246.42	338.39
III			0.00	182.11	74.95	135.03	351.58	259.72
IV				0.00	107.87	62.10	169.50	77.85
V					0.00	62.34	277.21	185.14
VI						0.00	223.86	132.05
VII							0.00	92.30
VIII								0.00

threshold eigenvalue which was greater than 1 (Table 2). The first principal component accounting for 17.00 per cent of the variability. An increase in number of primary branches per plant was associated with an increase in the number of productive branches per plant, number of productive capsules per plantand number of capsules on main stem. The variability accounted by the second component was 15.20 per cent and was mainly attributed to seed yield and thousand seed weight, both in negative directions and days to fifty per cent flowering in a positive direction. The third principal component accounted for 14.50 per cent and was a measure of days to fifty per cent flowering and plant height. The fourth principal component accounting for 10.10% of the variation was a measure of number of productive capsules per plant and number of capsules on main stem resulting in a positive increase of seed yield. The fifth principal component accounted for 7.40 per cent with the plant height exhibiting the largest and positive loading on this axis (Fig. 1). 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 Choi *et al*. (2017) and Baraki *et al*. (2020) for analysing 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 eight clusters. Cluster I comprised of 24 genotypes, which was grouped further into three sub-clusters, cluster II comprised of 8 genotypes, which was grouped further into three subclusters, cluster III comprised of 15 genotypes, cluster IV comprised of 9 genotype and cluster V comprised of 14 genotypes, which was further grouped into three sub-clusters, cluster VI comprised of 9 genotypes, cluster VII comprised of 4 genotypes and cluster VIII comprised of 20 genotypes which was further grouped into three sub-clusters. The cluster-wise mean performance of genotypes for various

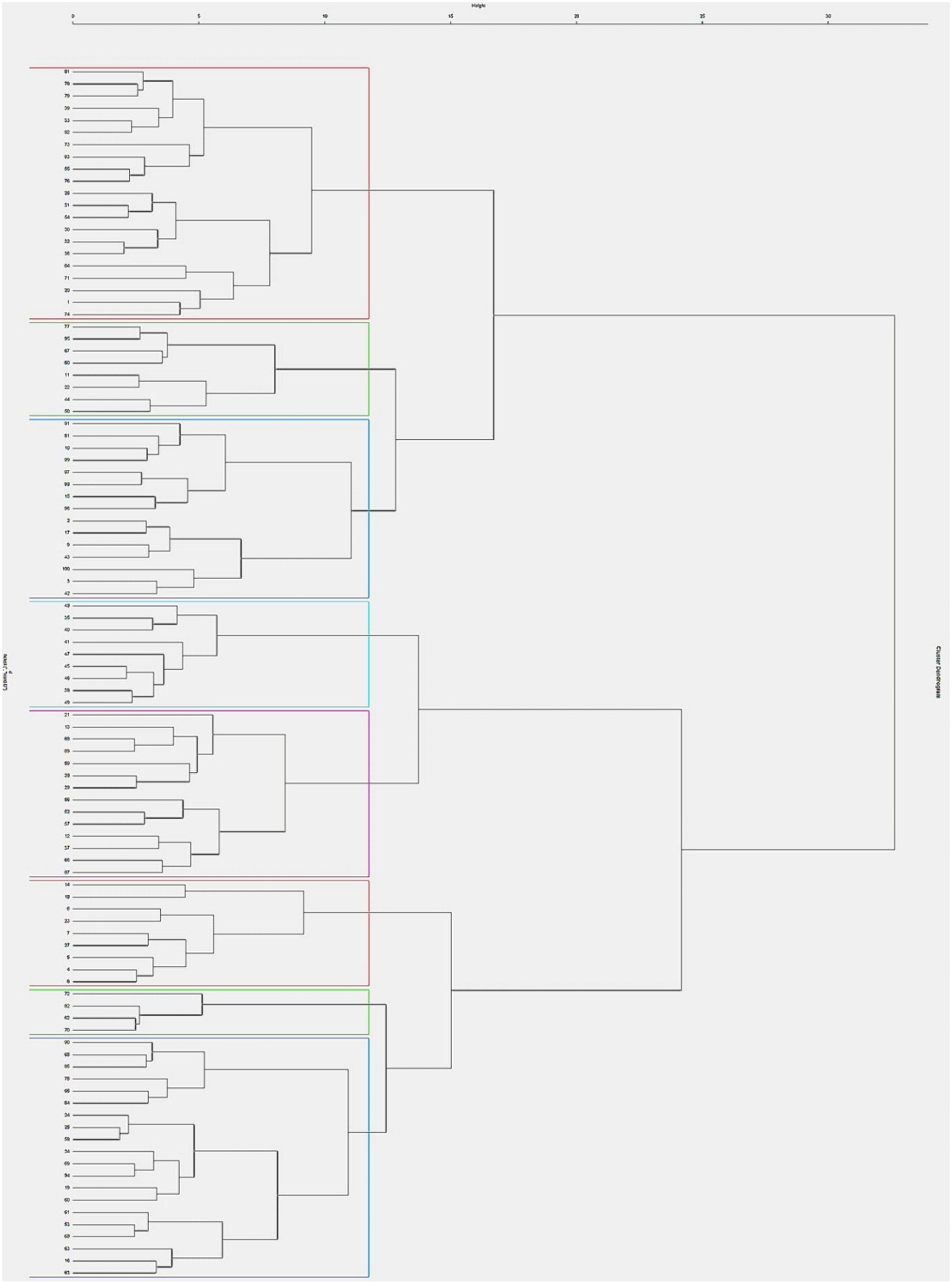

Fig. 3 : Dendrogram based on traits in sesame.

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

Cluster	DFF	DM	PH	NPB	NSB	NPBP	NPCP	NCMS	CL	NSPC	INL	TSW	OC	YPP	SY
I	55.31	105.13	111.10	5.71	2.02	5.00	132.46	30.26	2.99	43.07	3.58	3.08	36.42	5.90	295.40
II	54.08	104.25	114.63	5.65	1.80	5.31	121.30	31.85	3.06	49.70	3.65	3.23	40.53	11.41	951.60
III	55.72	105.22	109.55	5.55	1.53	5.13	107.86	29.18	2.94	39.41	3.60	2.91	33.78	5.47	354.04
IV	54.96	104.38	110.49	5.75	1.76	5.16	111.64	30.40	3.03	40.91	3.59	3.18	38.89	7.24	536.02
V	55.46	105.53	111.45	5.44	1.40	4.99	116.60	31.49	3.02	38.40	3.65	3.11	37.46	6.06	428.33
VI	55.31	105.06	114.06	6.58	2.38	6.23	144.55	32.90	3.16	38.23	3.56	3.12	34.43	7.91	483.82
VII	54.84	104.71	110.70	5.81	1.48	5.22	114.41	29.53	3.01	41.08	3.53	3.21	40.75	8.68	705.48
VIII	54.83	103.89	110.10	5.67	1.60	5.32	119.98	31.47	3.05	39.73	3.63	3.17	38.69	8.11	613.40

morphological traits is presented in Table 4. The dendrogram grouping the 100 genotypes into eight clusters is presented (Fig. 3) indicating high degree of heterogeneity among these genotypes. The average intra and inter cluster D2 values are presented (Tables 3 and 4). Results suggest that useful segregates may be created by crossing genotypes of cluster II with genotypes of cluster VII.

Conclusion

The present study aimed to assess the genetic variability among 96 advanced breeding lines of sesame using PCA and cluster analysis. The first five principal components accounted for a cumulative variation of 64.10%, with the first component primarily associated with an increase in the number of primary branches per plant. The second component was mainly attributed to seed yield and thousand seed weight, while the third component represented days to fifty percent flowering and plant height. The fourth component was related to the number of productive capsules per plant, and the fifth component was primarily influenced by plant height. The biplot analysis based on PCA provided a visual representation of the grouping pattern of genotypes in the factor plane, showing their wide scattering across different quarters. Cluster analysis further grouped the genotypes into eight clusters, indicating high heterogeneity among the genotypes. This information on genetic variability and grouping of genotypes can be valuable for breeding programs aiming to improve yield potential in sesame.

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