Received: 12 Aug 2022 | Revised: 21 Oct 2022 | Accepted: 22 Oct 2022

Electronic Journal of Plant Breeding

Research Article

Principal component analysis and metroglyph of variation among sesame (*Sesamum indicum* L.) genotypes

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Abstract
A study was carried out by using 45 genotypes of sesame at Seed Research and Technology Centre, Hyderabad during 2018 to evaluate the genetic variability, morphological clustering using Metroglyph and to identify the principle components having a major contribution to the total variation. Analysis of variance indicated appreciable variation among the genotypes for the traits. The genotypes Julang Sesame and NI8-8316 recorded the highest average performance for seed yield per plant and other yield components. The trait, seed yield per plant recorded the highest value for GCV and PCV followed by test weight. High heritability together with high values of genetic advance was showed by 1000 seed weight and seeds per individual pod. Principal component analysis (PCA) indicated three principle components with eigenvalue more than one and contributing 78 % towards the total variability of the population. Metroglyph analysis clustered the genotypes into six groups and group IV being the largest with 20 genotypes. Cluster VI characterized with high seed yield and number of seeds per pod comprised of three genotypes including Julang Sesame and NI8-8316. The overall study indicated that genotypes Julang Sesame and NI8-8316 were superior in performance and could be utilized as parents in hybridization programs.

Keywords: Bi plot, Genetic variability, Metroglyph, PCA, Sesame

INTRODUCTION

Sesame or Gingelly is one of the oldest cultivated oilseed crops in India. It is a warm weather crop often grown under marginal or stressed conditions. The distribution of genetic variability in different plant species depends not only on their evolution and breeding systems but also on ecological, geographical and human factors (Ramanatha and Hodgkin, 2002). Morphological traits were the primary parameters to estimate genetic divergence among sesame cultivars. Several researches based on these visual markers or morphological traits have indicated large genetic diversity of sesame species (Arriel *et al.,* 2007, Pandey *et al*., 2015). Knowledge on the extent and type of variability on genotypic and phenotypic levels along with heritability of the traits present in the population plays an important role in further manipulation of the crop. Traditional landraces and their wild related species are a relevant source of genetic diversity for plant breeders and act as the backbone of efficient agricultural production. The availability of natural diversity also aids in the categorization and utilization of these germplasm for the breeding program. However, the genotypic and phenotypic diversity of sesame has received in appreciable attention.

https://doi.org/10.37992/2022.1304.156

Meteroglyph is a semi-graphical approach for deciphering the morphological variations existing among the population. The results of this technique is more reliable as it is based on the first order statistics and the results can be easily interpreted. There are many quantitative as well as qualitative traits contributing for the total variation among the individuals of a population. In such cases, it is important to know the characters accounting for the major source of variations. Principle component analysis (PCA) is a multivariate analysis which helps in data transformation and reduction. PCA results in a smaller number of linear uncorrelated variables from a large number of correlated variables. These linear variables are known as principle components and are essentially used as criteria for plant selection. This technique has been widely used for studying genetic variability in sesame (Teklu *et al.,* 2021, Durge *et al.,* 2022).

In the present study, 45 genotypes of sesame were evaluated for their genetic and morphological variances and to identify major contributing components of variability.

MATERIALS AND METHODS

The seed material for the study consisted of 43 genotypes with two checks namely Swetha Til and Rajeswari. The study was carried out at the experimental farm of Seed Research Centre, Hyderabad and the crop was raised in RBD with three replications during August, 2017. The spacing adopted was 30 cm between each entry rows and 10 cm among the plants. Necessary cultural practices were practised as required for a successful crop. Observations on days to fifty per cent flowering, height of the plant, branches number per plant, the number of pods per plant, seeds number per pod, pod length (cm), seed yield per plant and test weight (g) were recorded. Data were collected in all genotypes by averaging five plants selected randomly from all three replication for the characters except days to fifty per cent flowering which was documented on plot wise.

The coefficients of genotypic and phenotypic variations were estimated using the formulae suggested by Falconer (1981) and the assigning the level of variation was carried out as given by Sivasubramanian and Madhavamenon (1973). Broad sense heritability (h^2bs) was estimated according to the formula proposed by Allard (1960) and the genetic advance was categorized as per cent of mean, given by Johnson *et al.* (1955).

Data from 45 genotypes for eight quantitative traits were used for principle component Analysis (PCA) in the R program. The eigenvalue and percentage of contribution of each trait towards the total genetic variation were calculated. Major principle components with an eigenvalue more than one were selected for further interpretations.

The pattern of morphological variation among the 45 genotypes for eight quantitative characters was computed as given by Anderson (1957). Two characters with high GCV and PCV were selected out of eight characters for plotting the graph. One of the characters is used on the X axis and the other one on the Y axis. The mean values of X for each genotype are plotted on the graph against the mean values of Y. The plotted glyphs are open since the genotypes are indigenous. Index scores were developed for all traits and divided into low, medium and high classes (**Table 1**). The remaining six traits were represented as rays on glyphs with varied length depending upon the index score.

RESULTS AND DISCUSSION

The examination of variance data among the genotypes for all the investigated characters revealed significant deviations. (**Table 2**). It suggests the existence of a considerable level of genetic divergence among the genotypes under study.

The average potential of forty-five genotypes for the trait seed yield and yield components are tabulated (**Table 3**). It was evident that the entry Julang Sesame set the highest average value for characters like branches number per plant, the number of pods per plant, seed number per pod and test weight. The entry NI8-8316 scored the highest average value for seed yield and performed superior for other yield components such as the number of branches per plant, pod number per plant and the number of seeds per pod. KMS-4-323-B, SI-241, NIC-16220, PKDS-11,

Table 1. Index score and signs used for metroglyph analysis of sesame genotypes

S. No	Trait	Range	Score 1		Score 2		Score 3	
			Value less than	Sign	Value from-to	Sign	Value more than	Sign
1	DFF	31.66-43.66	35.66	○	35.66-39.66		39.66	
2	PH	74.06-141.43	96.52	○	96.52-118.98		118.98	
3	NB	1.35-4.95	2.55	○	2.55-3.75		3.75	
4	NF	21.54-88.29	43.79	○	43.79-66.04		66.04	
5	FL	2.06-2.84	2.32	○	2.32-2.58		2.58	
6	TW	0.55-2.69	1.26	○	1.26-1.97		1.97	

Table 2. ANOVA for yield and yield governing traits of sesame

S. No.	Traits	Mean sum of squares (MSS)		
		Replications (df=2)	Treatments (df= 44)	Error (df= 88)
1	Days to fifty percent flowering	1.16	27.61**	1.57
2	Height of plant (cm)	12.91	615.49**	64.53
3	No. of branches/ plant	0.086	1.56**	0.060
4	No. of pods/ plant	17.95	394.10**	32.97
5	pod length (cm)	0.024	0.142**	0.01
6	No. of seeds/ pod	11.64	548.24**	13.50
7	Seed yield/ plant (g)	0.12	2.99**	0.18
8	Test weight(g)	0.014	0.59**	0.07

Table 3. Average performances of 45 sesame genotypes for yield and its governing traits

Entry	DFF	Height of plant (cm)	branches / plant	Number of pods/ plant	pod length (cm)	Number of seeds / pod	Test weight (g)	Seed yield per plant (g)
Nirmala	37.66	94.27	4.56	75.90	2.73	79.01	1.90	4.99
Smarak	36.66	101.10	3.81	52.54	2.83	64.59	1.54	4.33
Krishna	36.33	96.72	4.15	57.94	2.48	67.16	2.55	4.50
TMV-7	37.00	90.82	3.11	56.30	2.69	45.37	1.53	2.87
RT-54	37.00	91.19	3.50	55.30	2.09	62.37	2.03	4.32
Rama	34.00	91.74	3.10	54.60	2.41	51.93	1.66	3.80
Chandana	34.00	102.04	4.08	54.30	2.49	61.81	2.17	4.47
DS-1	38.00	120.16	3.81	59.70	2.68	53.61	1.97	3.99
PKDS-11	37.33	115.13	4.42	56.60	2.61	58.16	2.23	4.48
Savitri	33.33	96.82	4.66	60.00	2.36	75.08	2.44	4.53
Guatama	39.00	110.51	3.85	56.90	2.32	41.96	2.31	3.97
IC-56196	36.66	107.88	3.90	53.64	2.66	49.54	1.69	3.98
IC-205439	34.00	96.27	4.05	52.50	2.27	53.98	1.61	3.79
IC-41945	31.66	116.81	4.02	49.67	2.62	50.18	1.79	3.64
IC-205311	37.33	100.40	4.45	68.36	2.44	75.69	2.03	4.60
IC-205071	37.33	103.50	2.80	46.95	2.51	43.82	1.52	3.35
KMR-43-A	37.66	133.12	3.96	48.70	2.46	53.22	1.21	3.33
CT-60	43.66	74.06	1.35	44.00	2.09	31.66	1.59	2.06
FRP-8351-B	39.66	91.36	3.50	54.60	2.22	54.66	2.24	4.08
IS-476	42.00	102.45	4.12	53.75	2.58	57.26	2.28	4.40
IS-195	42.33	89.70	3.95	53.20	2.36	50.33	2.11	3.97
NI8-8316	36.66	97.74	4.75	77.83	2.51	86.02	2.14	5.75
CT-40	37.00	108.23	3.40	56.02	2.74	51.22	1.60	3.62
IS-54039-B	37.33	110.87	3.36	49.53	2.57	44.63	1.89	3.49
NIC-16220	37.66	116.30	4.20	72.03	2.72	76.33	1.95	4.63
DS-37	36.66	106.84	4.15	50.45	2.67	44.82	2.32	3.90
AT-238	33.66	89.36	3.55	52.70	2.83	51.12	1.69	3.62
KMR-38	36.33	104.84	4.35	55.50	2.58	45.00	1.24	3.39
ES-33477	41.00	122.69	3.86	48.59	2.36	48.97	2.14	3.65
Kanpur local	36.00	103.51	3.47	52.85	2.17	47.93	1.21	2.88
IS-644-A	42.33	105.34	4.45	29.61	2.59	49.16	0.92	0.78

Table 3. Continued..

Entry	DFF	Height of plant (cm)	branches / plant	Number of pods/ plant	pod length (cm)	Number of seeds / pod	Test weight (g)	Seed yield per plant (g)
IC-310438-B	38.00	109.36	4.64	21.54	2.06	40.00	0.55	0.58
IS-112	33.00	78.60	3.30	52.35	2.19	47.49	1.56	3.06
Julang Sesame	41.66	107.39	4.95	88.29	2.46	88.83	2.69	5.64
KMS-4-323-B	43.00	111.28	4.43	69.60	2.84	77.40	1.97	4.69
SI-241	36.33	132.88	4.58	81.00	2.80	83.06	2.24	5.28
CT-27	36.66	97.92	3.90	56.60	2.48	60.16	2.44	4.50
EC-208652	40.66	123.10	4.05	57.49	2.29	59.77	2.31	4.46
IS-469-1-84-A	33.33	81.66	1.55	45.90	2.25	32.42	1.33	2.74
FFAT-10-20	42.33	92.45	3.24	49.35	2.57	50.49	1.51	3.60
IS-54034-B	37.00	102.40	3.76	53.63	2.49	44.66	1.53	3.55
Gowri	37.33	130.58	3.86	55.63	2.81	50.73	1.62	3.95
Madhavi	41.33	141.43	4.03	50.24	2.79	57.40	1.80	3.75
Rajeshwari (C)	41.66	104.72	3.15	51.95	2.22	56.33	1.59	3.46
Swetha Til (C)	42.00	101.47	3.05	55.01	2.56	61.12	1.51	3.74
Mean	37.81	104.59	3.80	55.53	2.50	56.36	1.82	3.82
SEm ±	0.72	4.63	0.14	3.31	0.06	2.12	0.05	0.24
CV (%)	3.32	7.68	6.46	10.33	4.15	6.52	1.82	11.25
CD at 5%	2.03	13.03	0.39	9.31	0.16	5.96	0.14	0.69

DFF : Days to Fifty percent Flowering

Savitri, Krishna, IC-205311, Nirmala, CT-27 and DS-1, are the other elite genotypes identified for seed yield and yield traits, suggesting that these entries can be well utilized in hybridization programs as parents. The genotypes Kanpur Local, CT-60, IS-644-A, IC-310438-B, IS-469-1-84-A and IC-205071 recorded lower mean values for most of the traits compared to other genotypes.

The coefficients of variation at genotypic and phenotypic levels, broad sense heritability and genetic advance and genetic advance as per cent of mean were calculated for all the entries (**Table 4**). The trait, seed yield/ plant recorded very high genotypic (25.25 %) and phenotypic (27.64 %) coefficients variation followed by test weight (GCV= 24.19 and PCV = 24.66) and the number of seeds/ pod (GCV= 23.68 and PCV = 24.56). Similar findings were recorded by Kalaiyarasi *et al.* (2019), Manjeet *et al.* (2020) and Vivek *et al.* (2022). Moderate estimates of GCV and a large estimate of PCV were recorded for the number of branches per plant (18.58 and 19.67) and plant height (12.95 and 15.06). These findings were in line with that of Chandramohan (2014), Mahmoud *et al.* (2015) and Saravanan *et al.* (2020). Low genotypic and phenotypic coefficients of variation were recorded for days to fifty per cent flowering (7.79 and 8.47 %) and pod length (8.38 % and 9.36 %). The results are in accordance with that of Bharathi *et al*. (2014) and Abate and Mekbib (2015).

Broad sense heritability and high genetic advance as per cent of mean estimates for the character, test weight was found high (96.2 % and 48.90 %) suggesting the predominance of additive type of gene action governing the trait. Hence, direct selection for this character is rewarding for yield. Begum *et al.* (2017) and Saravanan *et al.* (2020) also recorded high heritability combined with high genetic advance as per cent of mean for test weight. Other traits like the number of seeds per pod (93.00 % h^2, 47.04 % GAM), the number of branches per plant and the number of pods per plant also recorded appreciable levels of heritability together with high genetic advance indicating the prevalence of additive gene action. A simple phenotypic selection can be suggested for the improvement of these traits. Iqbal *et al.* (2016) Abhijatha *et al.* (2017) Patil and Lokesha (2018) and Saravanan *et al.* (2020) also noticed high heritability values combined with high genetic advance as per cent of mean in their studies for the above mentioned traits.

High heritability (86.4%) combined with mild genetic advance as detected per cent of mean (14.76) was estimated for fifty per cent flowering. Abhijatha *et al.* (2017) and Saxena and Rajani Bisen, (2017) also reported similar findings. The trait pod length scored high values of broad sense heritability (80.30%) and reasonable values of genetic advance

Table 4. Genetic variability parameters in 45 sesame genotypes

Character	Coefficient of variation		Heritability (%)	Genetic advance at 5%	Genetic advance as per cent mean at 5%
	Genotypic (GCV)	Phenotypic (PCV)			
DFF	7.79	8.47	86.40	5.58	14.76
Plant height (cm)	12.95	15.06	74.00	24.01	22.95
Number of branches per plant	18.58	19.67	89.20	1.376	36.15
Number of pods per plant	19.75	22.29	78.50	20.02	36.05
Pod length (cm)	8.38	9.36	80.30	0.387	15.47
Number of seeds per pod	23.68	24.56	93.00	26.51	47.04
Seed yield per plant (g)	25.25	27.64	83.40	1.81	47.51
Test weight (g)	24.19	24.66	96.20	0.89	48.90

DFF : Days to Fifty percent Flowering

(15.47) indicating their governance by non-additive type of gene action. Chandramohan (2014) and Abate and Mekbib (2015) also noticed high heritability together with reasonable values of genetic advance for pod length.

Principle component analysis is one of the popular and important non-parametric techniques (Chang and Keinan, 2014) which helps to transform a set of observations to several inter dependent variables (Baraki *et al.,* 2020). The analysis of principle components revealed that the first three principle components had eigenvalues more than one and accounts for most of the variability among the sesame population. The first component (PC1) had the highest eigenvalue (3.796) contributing about 47.46% of the total variance. The PC2 had an eigenvalue of 1.418 contributing 17.73% towards the variability and PC3 had an eigenvalue of 1.024, with 12.80% of the variability. The three major principle components explained 78.00% of the total variability of the population (**Table 5**). From the data of individual trait scores, it is clear that test weight (0.471), the number of seeds per pod (0.457), the number of pods per plant (0.454) and seed yield per plant (0.383) are positively influenced by the first principle component. The positive influence of the number of pods per plant and seed yield on the first principle component was also recorded by Iqbal *et al.* (2018). On the other hand, the second principle component had a negative impact on traits such as seed yield (-0.313), test weight (-0.226) and a number of pods per plant (-0.216). Plant height (0.671), pod length (0.444) and a number of branches per plant (0.329) were the traits with a relatively higher contribution towards the second principle component. The third component had a negative influence on most of the characters especially the days to fifty per cent flowering (-0.939) and seed yield per plant (-0.189). Pod length (0.260) was the trait which was largely and positively influenced by principle component 3. The fourth principle component with eigenvalue 0.718 and a relative contribution of 8.98% of variability can also be considered informative. The component had a positive influence on pod length (0.692) and a strong negative influence on a number of branches per plant (-.0.632).

Table 5. Principle component analysis for eight quantitative traits in sesame genotypes

	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7	PC 8
Eigenvalue	3.796	1.418	1.024	0.718	0.534	0.333	0.104	0.068
Percentage of variance (%)	47.46	17.73	12.80	8.98	6.67	4.16	1.30	0.860
Cumulative percentage of variance (%)	47.46	65.19	78.00	86.98	93.66	97.83	99.13	100
Days to fifty percent flowering	0.002	0.208	-0.939	0.139	-0.177	0.077	-0.083	0.100
Height of plant (cm)	0.184	0.671	-0.019	-0.095	0.538	-0.450	0.083	-0.073
Number of branches/ plant	0.343	0.329	0.098	-0.632	-0.213	0.425	-0.354	0.100
Number of pods/ plant	0.454	-0.216	-0.009	0.179	-.0.172	-0.432	-0.601	-0.368
pod length (cm)	0.248	0.444	0.260	0.692	-0.206	0.379	0.053	-0.061
Number of seeds/ pod	0.457	-0.049	-0.052	-0.194	-0.441	-0.214	0.691	-0.169
Seed yield/ plant (g)	0.383	-0.313	-0.189	0.004	0.577	0.473	0.133	-0.378
Test weight(g)	0.471	-0.226	0.0185	0.146	0.179	-0.094	-0.001	0.814

The scree plot (**Fig. 1**) indicated a sudden decline in the variability from the first principle component to the second component. The graph continues to decline after the third principle component, indicating the gradual reduction in the total variability The genotype distribution and the direction of character distribution are depicted in the PCA bi-plot (**Fig. 2**). The bi plot indicates the division of eight traits two distinct groups with four characters each. In the first group, traits such as days to first flowering, plant height, pod length and the number of branches are involved. A number of pods per plant, the number of seeds per pod, seed yield and test weight belong to the second group. Genotype 34 (Julang sesame), 22 (N18-8316) and 1 (Nirmala) form a distinctive class with high seed yield per plant, test weight and the number of seeds peter pod**.**

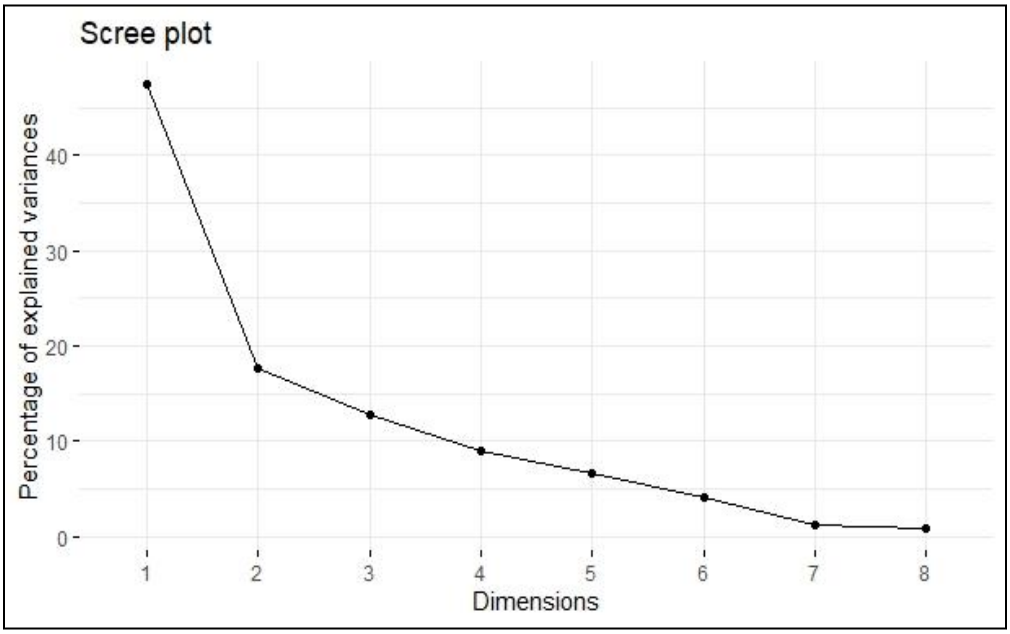

Fig. 1. Scree plot of PCA for eight characters in sesame

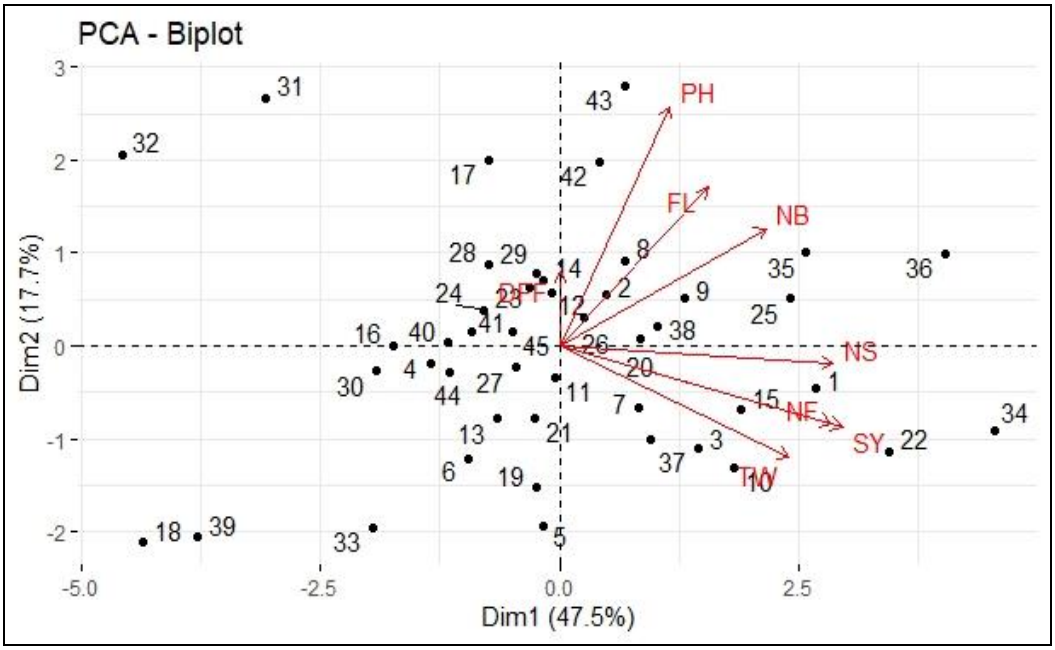

Fig. 2. Biplot for quantitative traits in sesame genotypes

Table 6. Distribution of 45 sesame genotypes based on metroglyph analysis

Group	Number of genotypes	Genotype names	Characteristics
I	8	CT-60, IS- 469- 1- 84- A, IC-205071, KMR- 38, IS-112, TMV-7, Kanpur Local, IS-54039-B	Low seed yield per plant and low number of seeds per pod
II	2	KMR-43-A, Rajeshwari	Low seed yield per plant and medium number of seeds per pod
III	5	IC-56196, DS- 37, Gautama, ES- 33477, IS- 54034-B	Medium seed yield per plant and low number of seeds per pod
IV	20	IC-41945, FRP-8351-B, IS-476, IS-195, CT-40, AT- 238, FFAT- 10- 20, IC-205439, Gowri, Madhavi, DS-1, PKDS-11, EC- 208652, CT- 27, RT-54, Smarak, Swetha Til, Krishna, Chandana, Rama	Medium seed yield per plant and medium number of seeds per pod
V	5	IC-205311, CT-40, NIC-16220, KMS- 4- 232-B, Savitri, Nirmala,	Medium seed yield per plant and high number of seeds per pod
VI	3	NI8-8316, Julang sesame, SI- 241	High seed yield per plant and high number of seeds per pod

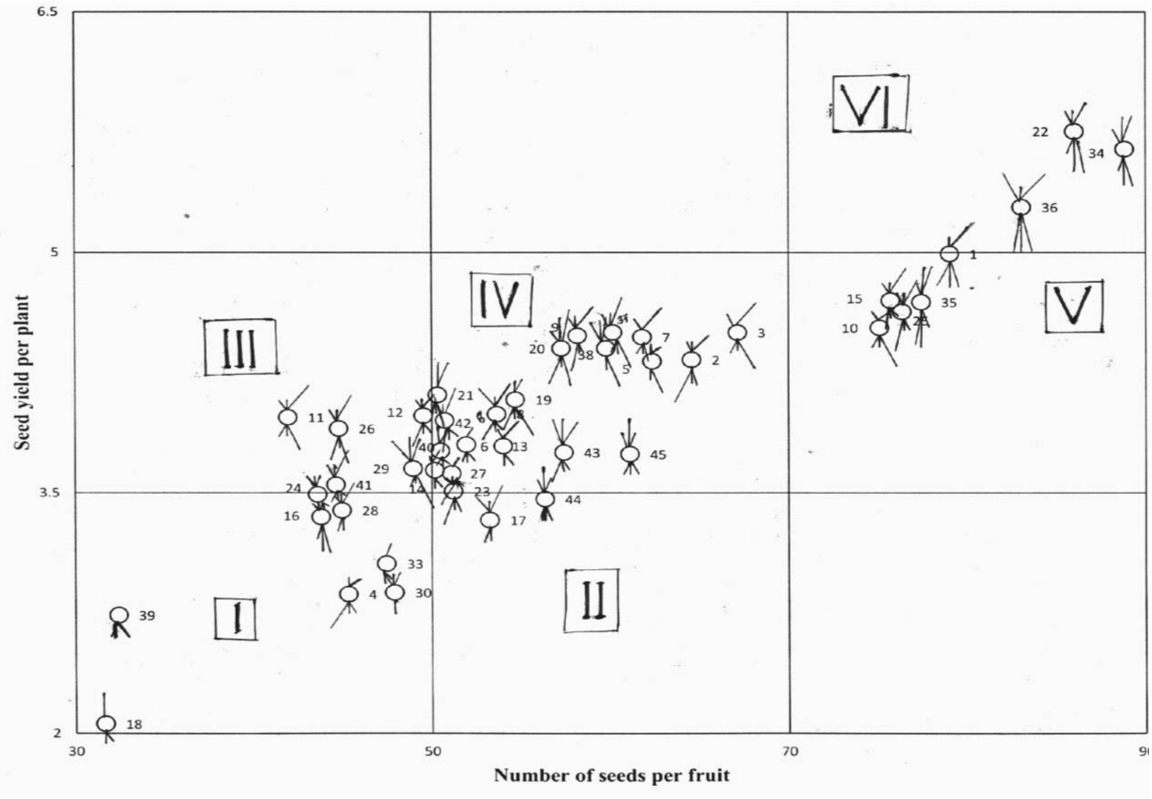

Fig. 3. Scattered diagram of metroglyph analysis in sesame genotypes

Metroglyph analysis categorized the 45 genotypes into six different groups based on the morphological diversity (**Table 6**). From the scatter diagram (**Fig. 3**) it is clear that, group IV has the highest number of genotypes (20) with a moderate number of seeds per pods and seed yield close to the mean yield of the population (3.80 g). The plants of this cluster are medium to tall in height with more number of branches and seeds with higher test weight. Group I composed of eight genotypes characterized by early maturing dwarf plants with small pods having a lesser number of low weighing seeds. Group III and V comprised of five genotypes each. Genotypes of group III had a medium blooming period and produced fewer seeds with considerably higher weight. Group V contained genotypes which were medium tall with more number of branches, superior in a total number of pods and seeds produced, pod length and mean seed yield per plant. Group VI comprised the three most productive lines such as Julang sesame (34), NI8-8316 (22) and SI-241(36). They were characterized with tall stature plants with many branches and produced the highest number of medium to long pods carrying more than an average number of seeds. The seeds had greater seed weight such that the total seed yield per plant and thousand seed weight was more than other genotypes. Group II included the lowest number of genotypes (two) and two genotypes (Kanpur Local and IS-644-A) were not included in any of these groups. Dhanraj (1999) in sesame used metroglyph analysis among sesame genotypes to cluster them into eight groups based on morphological diversity. The application of this technique is still valid in many crops like mungbean (Ahmad *et al.,* 2019), okra (Olayiwola *et al.,* 2021), and rice (Soharu *et al.,* 2021) for the preliminary classification.

The study revealed the existence of a large amount of noticeable variations among the genotypes for the traits considered. From the results it was clear that the entry Julang Sesame recorded the highest mean value for traits like the number of branches, the number of pods, seed number per pod and test weight followed by the entry NI8-8316. The PCA analysis and Metroglyph analysis also revealed the superior performance of both genotypes. The traits such as seed yield per plant, test weight, the number of seeds per pod and the number of branches per plant documented detectable amounts of GCV, PCV coupled with a high range of broad sense heritability and genetic advance. Therefore, more emphasis should be given on these traits for predicting the authentic selection process for the development of desirable sesame genotypes.

REFERENCES

Abate, M. and Mekbib, F. 2015. Study on genetic divergence in low-altitude sesame (*Sesamum indicum* L.) germplasm of Ethiopia based on agro morphological traits. *Journal of Advanced Studies in Agricultural, Biological and Environmental Sciences,* **2**(3): 78-90.

Abhijatha, A., Arya, K., Madhukar, K. and Gogineni, S. 2017. Evaluation of sesame (*Sesamum indicum* L.) genotypes to the shaded uplands of southern region. *International Journal of Current Microbiology and Applied Sciences,* **6**(7): 332-339. [Cross Ref]

Ahmad, H. B., Rauf, S., Chattha, W. S., Hussain, B., Hussain, I. and Rasool, I. 2019. Diversity analysis of mungbean (*Vigna radiata*) germplasm using a semi-graphical technique. *South African Journal of Plant and Soil*, **36(**5): 393-396. [Cross Ref]

Allard, R. W. 1960. Principles of plant breeding. Pp: 485. John Wiley and Sons, New York, USA.

Arriel, N. H. C, Mauro, A. O., Arriel, E. F., Helena, S., Trevisoli, U., Costa,M. M., Bárbaro, I. M. and Muniz, F. R. S. 2007. Genetic divergence in sesame based on morphological and agronomic traits. *Crop Breeding and Applied Biotechnology,* **7**: 253-261. [Cross Ref]

Baraki, F., Gebregergis, Z., Belay, Y., Berhe, M., Teame, G., Hassen, M., Gebremedhin, Z., Abadi, Z., Negash, W, Atsbeha, A. and Araya, A. 2020. Multivariate analysis for yield and yield-related traits of sesame (*Sesamum indicum* L.) genotypes. *Heliyon.* **6**, e5295. [Cross Ref]

Begum, T., Iqbal, A. and Dasgupta, T. 2017. Genetic variability and divergence among genotypes of sesame (*Sesamum indicum* L.). *Bangladesh Journal of Botany,* **46**(3): 955-962.

Bharathi, D., Thirumala Rao, V., Chandra Mohan, Y., Bhadru, D. and Venkanna, V. 2014. Genetic variability studies in sesame (*Sesamum indicum* L.). *International Journal of Applied Biology and Pharmaceutical Technology,* **5**(4): 31-33.

Chandramohan, Y. 2014. Variability and genetic divergence in sesame (*Sesamum indicum* L.). *International Journal of Applied Biology and Pharmaceutical Technology,* **5**(3): 222-225.

Chang, D. and Keinan, A. 2014. Principal component analysis characterizes shared pathogenetics from genome wide association studies. *PLOS computational biology,* **9**(10): 1- 14. [Cross Ref]

Dhanraj, A. 1999. Metroglyph canonical analysis studies sesame (*Sesamum indicum* L.) Germplasm. MSc. Thesis, Professor Jayashankar Telangana State Agricultural University, Hyderabad, 500030.

Durge, B. D., Geethanjali, S. and Sasikala, R. 2022. Assessment of genetic variability for seed yield and its components in sesame (*Sesamum indicum* L.) based on multivariate analysis. *Electronic Journal of Plant Breeding,* **13**(3): 974 – 982. [Cross Ref]

Falconer, D. S. 1981. *Introduction to Quantitative Genetics*. Oliver and Boyd, London, Pp: 340.

Iqbal, A., Ahktar, R., Begum, T. and Dasgupta, T. 2016. Genetic estimates and diversity study in Sesame (*Sesamum indicum* L.). *IOSR Journal of Agriculture and Veterinary Science*, **9**(8): 1-5. [Cross Ref]

Johnson, H. W., Robinson, H. F. and Comstock, R. E. 1955. Estimates of genetic and environmental variability in soybean. *Agronomy Journal*, **47**: 314-318. [Cross Ref]

Kalaiyarasi, R. Rajasekar, R. Lokeshkumar, K. Priyadharshini, A. and Mohanraj, M. 2019. Correlation and path analysis for yield and yield traits in sesame (*Sesamum indicum* L.) genotypes. *International Journal of Current Microbiology and Applied Sciences,* 8(11): 1251-1257. [Cross Ref]

Mahmoud, M. W. S. H., Elezz, A. A. and Hassan, T. H. A. 2015. Genetic variability, heritability and correlation coefficients of yield and its components in sesame. *Egyptian Journal of Plant Breeding,* **19**(4): 1101-1116. [Cross Ref]

Manjeet, Verma, P. K., Sheoran, R. K., Nain, M. and Avtar, R. 2020. Evaluation of sesame (*Sesamum indicum* L.) genotypes for genetic variability based on different traits under rainfed conditions. *Electronic Journal of Plant Breeding,* **11***:* 54-59. [Cross Ref]

Olayiwola, O., Yusuf, R. A., Oyetunde, O. A., Sosanya,O. S., Johnson, O. and Ariyo. 2021. Assessment of genetic variability among accessions of okra (*Abelmoschus esculentus* L. Moench). *Acta horticulturae et regiotecturae,* **24**(2): 141–147. [Cross Ref]

Pandey, S. K., Das, A., Rai, P. and Dasgupta, T. 2015. Morphological and genetic diversity assessment of sesame (*Sesamum indicum* L.) accessions differing in origin. *Physiology and Molecular Biology of Plants,* **21**(4): 519–529. [Cross Ref]

Patil, M. K. and Lokesha, R. 2018. Estimation of genetic variability, heritability, genetic advance, correlations and path analysis in advanced mutant breeding lines of sesame (*Sesamum indicum* L.). *Journal of Pharmacognosy and. Natural Products,* **4**: 1-4. [Cross Ref]

Ramanatha, R. and Hodgki, T. 2002. Genetic diversity and conservation and utilization of plant genetic resources. *Plant Cell, Tissue and Organ Culture*, **68**: 1-19. [Cross Ref]

Saravanan, M., Kalaiyarasi, R. and Viswanathan, P. L. 2020. Assessment of genetic variability, character association and path analysis in F_2 population of sesame (*Sesamum indicum* L.). *Electronic Journal of Plant Breeding,* **11**(02): 447-450. [Cross Ref]

Saxena and Rajani Bisen. 2017. Genetic variability, heritability and genetic advance for the phenotypic traits in sesame (*Sesamum indicum* L.). *International Journal of Pure and Applied Sciences,* **2**: 1126-1131. [Cross Ref]

Sivasubramanian, S. and Madhavamenon, P. 1973. Combining ability in rice. *Madras Agriculture Journal,* **60**: 419-421.

Soharu, A., Sanadya, S. K., Dwivedi, A. and Pandey, D. P. 2021. Clustering of upland rice genotypes by different biometrical methods. *Journal of crop and weeds,* **17**(1): 143-151. [Cross Ref]

Teklu, D.H., Shimelis, H., Tesfaye, A., Mshilo, J., Zhang, X., Zhang, Y., Dossa, K. and Shayanowako, T. 2021. Genetic variability and population structure of Ethiopian sesame (*Sesamum indicum* L.) germplasm assessed through phenotypic traits and simple sequence repeats markers. *Plants*, **10**(6): 1129. [Cross Ref]

Vivek, K., Sima, S., Satyendra, Sweta, S., Ravi, S., Shankar and Singh, S. N. 2022. Assessment of genetic variability, correlation and path analysis in sesame (*Sesamum indicum* L.). *Electronic Journal of Plant Breeding,* **13**(1): 208- 215. [Cross Ref]

https://doi.org/10.37992/2022.1304.156