International Journal of Bio-resource and Stress Management https://pphouse.org/ijbsm.php

Crossref

IJBSM March 2023, 14(3):443-449 Print ISSN 0976-3988 Online ISSN 0976-4038 **Article** AR3231a

Research Article *Natural Resource Management*

DOI: HTTPS://DOI.ORG/10.23910/1.2023.3231a

Assessment of Genetic Diversity in Sesame (*Sesamum indicum* L.) for Yield and its Components

S. Sasipriya[1], K. Parimala[2], M. Balram[3] and K. B. Eswari[1]

[1]Dept. of Genetics and Plant Breeding, College of Agriculture, [2]Seed Research and Technology Centre, Professor Jayashankar Telangana State Agricultural University, Rajendranagar, Hyderabad, Telangana (500 030), India
[3]Agricultural College, PJTSAU, Warangal, Telangana (506 007), India

Open Access

Corresponding kparimala74@gmail.com

0009-0008-4423-6062

ABSTRACT

A field experiment was conducted to assess the diversity among sesame genotypes for yield and yield component traits during late *kharif*, 2017 (August-November) at Seed Research and Technology Centre, Rajendranagar, Hyderabad, Telangana State, India. Genetic diversity among the genotypes were estimated based on the data recorded for eight yield and yield attributing characters in 51 genotypes using Mahalanobis's D^2 statistics. The percent contribution of characters towards divergence showed that the character days to 50% flowering contributed maximum followed by seed yield plant^{-1}, capsule length and number of seeds capsule^{-1}. Selection of parents based on these traits would be useful to achieve a wide range of genetic variability in crop improvement programmes. The 51 genotypes were grouped into ten clusters and out of them, cluster I was the largest comprising of eighteen genotypes followed by cluster III with fifteen genotypes, cluster IV with seven genotypes, cluster II with five genotypes. The clusters *viz.*, V, VI, VII, VIII, IX and X represented by single genotype indicating high degree of diversity among the genotypes. The maximum inter cluster distance was observed between cluster IX and cluster X (219.39) followed by cluster VII and cluster VIII (190.41). Among the ten clusters, the cluster X had highest mean value for capsule length, number of capsules plant^{-1}, number of seeds capsule^{-1} and seed yield plant^{-1}. The genotypes from these divergent clusters with favourable mean values for different traits could be used as parents in hybridization programme to get superior transgressive segregants.

KEYWORDS: Sesame, diversity, cluster distance, cluster mean

Citation* (VANCOUVER)*: Sasipriya et al., Assessment of Genetic Diversity in Sesame (*Sesamum indicum* L.) for Yield and its Components. *International Journal of Bio-resource and Stress Management,* 2023; 14(3), 443-449. HTTPS://DOI.ORG/10.23910/1.2023.3231a.

Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

Conflict of interests: The authors have declared that no conflict of interest exists.

RECEIVED on 18th August 2022 RECEIVED in revised form on 30th January 2023 ACCEPTED in final form on 28th February 2023 PUBLISHED on 19th March 2023

1. INTRODUCTION

Sesame is an ancient oilseed crop and it is widely cultivated in Asia and Africa (Kurdistani and Tohidinejad, 2011). Asia is rich in diversity of cultivated sesame while Africa is prosperous in wild relatives (Sharma et al., 2014). Sesame seed is an important source of high quality oil and protein (Elleuch et al., 2007) and the oil content ranges from 34 to 63% (Were et al., 2006). The seeds contain two unique substances namely sesamin and sesamolin known to have a cholesterol lowering effect in human and to prevent high blood pressure (Anilakumar et al., 2010). Presence of sesamol, an anti-oxidant and more polyunsaturated fatty acid, have made it to 'queen of oilseed crop' (Ashri, 1998 and Fukuda *et al.*, 1986). Also, it is rich in micronutrients such as minerals, liganans, tocopherol and phytosterol (Hassan et al., 2018). In India, sesame occupies an area of 1.73 m ha with production 0.82 mt and productivity of 474 kg ha^{-1} (Anonymous, 2021). The productivity of sesame is low in India (431 kg ha^{-1}) compared to the world average (512 kg ha^{-1}) (Anonymous, 2018). Low productivity in sesame is attributed to lack of high yielding varieties and traditional production technologies. The major constraints in sesame cultivation are lack of high yielding varieties, poor stand establishment and poor fertilizer response (Alex et al., 2017). Sesame crop offers several advantages by virtue of its faster growth, short duration and drought tolerant capacity cultivated throughout the year in sub-tropical and tropical conditions. Sesame had more preference from farmers because of low input requirement and high price of produce (De et al., 2013). Hence, there is a need to enhance the productivity of this crop by developing high yielding varieties, which depends on the availability of variability for seed yield and its component traits in the populations (Gopal et al., 2020). Earlier researchers, Begum et al. (2011), Jadhav and Mohrir (2013), Tripathi et al. (2013) and Shwetha et al. (2022) were studied the genetic diversity in sesame for yield and its component characters to identify the more diverse genotypes to use in crop improvement programmes.

Assessment of diversity is an important first step in crop improvement programme. The success of any crop improvement programme depends upon the nature and magnitude of genetic variability present in the crop. The phenotypic and genotypic variations of the yield contributing traits are considerably high in sesame (Gangadhara et al., 2012; Sivaprasad et al., 2013 and Teklu et al., 2014), which indicates the possibility of developing a variety with high yield. Sarkar and Saha, (2014) reported high level of polymorphism in sesame regarding its morphology. Several biometrical methods have been found to be useful in assessing the genetic diversity for selection of parents for crop breeding programmes. The Mahalanobis's D^2 statistic considered as a useful statistical tool for measuring the genetic diversity in genotypes. In view of the above, the present investigation was undertaken to study the diversity among sesame genotypes and to identify diverse parents to utilize in crop improvement programmes.

2. MATERIALS AND METHODS

The experimental material for the present study consists of 51 sesame genotypes sown during *kharif*, 2017 (August-November) at Seed Research and Technology Centre, Rajendranagar, Hyderabad, Telangana State, India. The experimental farm is geographically located at 17^{0}19'52.6"N latitude and 78^{0}24'35.6"E longitude and falls under Southern Telangana Agro-Climatic Zone. The trial was laid out in randomized block design with two replications. Each genotype was sown in two rows of 4 m length with a spacing of 30 cm between rows and 10 cm between plants. Recommended package of practices were followed to raise the healthy crop. Observations were recorded for days to 50% flowering, plant height (cm), number of branches plant^{-1}, number of capsules plant^{-1}, number of seeds capsule^{-1}, capsule length (cm), 1000-seed weight (g) and seed yield plant^{-1} (g). The data was recorded for each entry from each replication by selecting five plants at random while data on days to 50% flowering was recorded on plot basis. The mean data was subjected to analysis of variance as per the method proposed by Panse and Sukhatme (1967). To estimate the diversity of genotypes, statistical analysis was performed as suggested by Mahalanobis (1936) and genotypes were grouped into clusters following the Tochers' method as described by Rao (1952) and Singh and Chaudhary (1977).

3. RESULTS AND DISCUSSION

The multivariate analysis developed by Mahalanobis (1936) has been found to be most suitable to measure the degree of divergence in genotypes. The results of percent contribution of eight characters towards genetic divergence showed that the character days to 50% flowering (39.84%) contributed maximum followed by seed yield plant^{-1} (19.61 %), capsule length (11.92%) and number of seeds capsule^{-1} (11.53) (Table 1). Hence, it is advisable to select the parents based on these traits to achieve a broad spectrum of genetic variability in crop improvement programmes. Whereas the characters such as plant height (6.98 %), 1000 seed weight (6.59 %), number of branches plant^{-1} (2.04 %) and number of capsules plant^{-1} (1.49 %) have very less role towards genetic divergence of the genotypes studied.

Fifty-one genotypes were grouped into ten clusters based on D^2 values (Table 2). Out of ten clusters, cluster I was the largest comprising of eighteen genotypes followed by

Table 1: Per cent contribution of each character towards divergence in sesame

Character	Times ranked first	Per cent contribution
Days to 50% flowering	508	39.84
Plant height (cm)	89	6.98
Number of branches plant^{-1}	26	2.04
Capsule length (cm)	152	11.92
Number of capsules plant^{-1}	19	1.49
Number of seeds capsule^{-1}	147	11.53
1000 seed weight (g)	84	6.59
Seed yield plant^{-1} (g)	250	19.61

cluster III with fifteen genotypes, cluster IV with seven genotypes, cluster II with five genotypes and cluster V, VI, VII, VIII, IX and X with one genotype each. The cluster V, VI, VII, VIII, IX and X were represented by single genotype indicating high degree of diversity among the genotypes. The discrimination of germplasm lines into many clusters suggested presence of high degree of genetic diversity in the material studied. The choice of parents based on genetic diversity analysis would be more useful than the choice made on the basis of origin of materials. Similar findings were reported by Sheriff and Shivashankar (1992), Patil and Sheriff (1994). The dendrogram revealed the relative magnitude of resemblance among the different clusters (Figure 1). Similar findings were observed by the Parameswarappa et al. (2010) and Ahadu (2012) though the number of clusters differed depending on the number of genotypes and characters studied.

Table 2: Clustering composition of 51 sesame genotypes in Mahalanobis D^2 analysis

Cluster Number	No. of genotypes	Name of the genotypes
I	18	AVTS-10-5, ES-36-A, GRI-83147, GRM-53, Hima, IC-14120-1, IC-14146-C, IC-96239, IS-191-A, IS-216-1, IS-24-A, IS-673, KMR-83-A, NIC- 17293, NIC-16190-A, NIC-8368, RT-351, S-0484
II	5	IS-133-A, KMS-4-258, RT-346, SI-2039-A, SI-264
III	15	CT-51, DI-314, GRM-18, GRM-48, IC-204595, IS-157-A-1, KMS-423, NIC-13590, NIC-16204, NIC-16386, NIC-8060, NIC-8262, NIC-8591, SI-178, Swetha Til
IV	7	EC-182833, IS-101-3-B, IS-205, KMR-8, NIC-16281, VRI-1, CT-27
V	1	MT-13-7
VI	1	GRM-47
VII	1	GRM-54
VIII	1	GT-4
IX	1	SI-3299-A
X	1	GT-10

The average intra and inter cluster distances of ten clusters are presented in Table 3. The maximum intra cluster distance was observed in cluster IV (44.01) and cluster III (40.68) followed by cluster I (30.77) and cluster II (25.14). It reveals the existence of some genetic diversity among the genotypes within each of the clusters. The maximum inter cluster distance was found between cluster IX and cluster X (219.39) followed by cluster VII and cluster VIII (190.41), cluster IV and cluster IX (169.09), cluster II and cluster IV (163.64), cluster IV and cluster V (162.30), cluster V and cluster X (152.55), cluster VI and cluster VIII (152.20) and cluster IV and cluster VI (150.15). It indicates that the crosses involving genotypes from these clusters would give wider and desirable recombination. Greater the distance between two clusters wider the genetic diversity among the genotypes of these clusters and such highly divergent genotypes would be of great use in recombination breeding programme in order to get high heterotic recombinants. The minimum inter cluster distance was observed between cluster V and cluster VI (15.21), cluster VI and cluster VII (16.02) and cluster V and cluster VII (27.59) indicated that the genotypes included in them were closely related. These results are accordance with the findings of Hika et al. (2015) and Shwetha et al. (2022) who reported clusters with largest and lowest inter cluster distance among the sesame genotypes in their studies. Murty and Arunachalam (1966) reported that genetic drift and selection, both natural and artificial in different environments could cause greater diversity among genotypes than geographic distances.

The cluster means for eight characters are presented in Table 4 and revealed the existence of considerable differences for the characters studied. The data indicated that the cluster

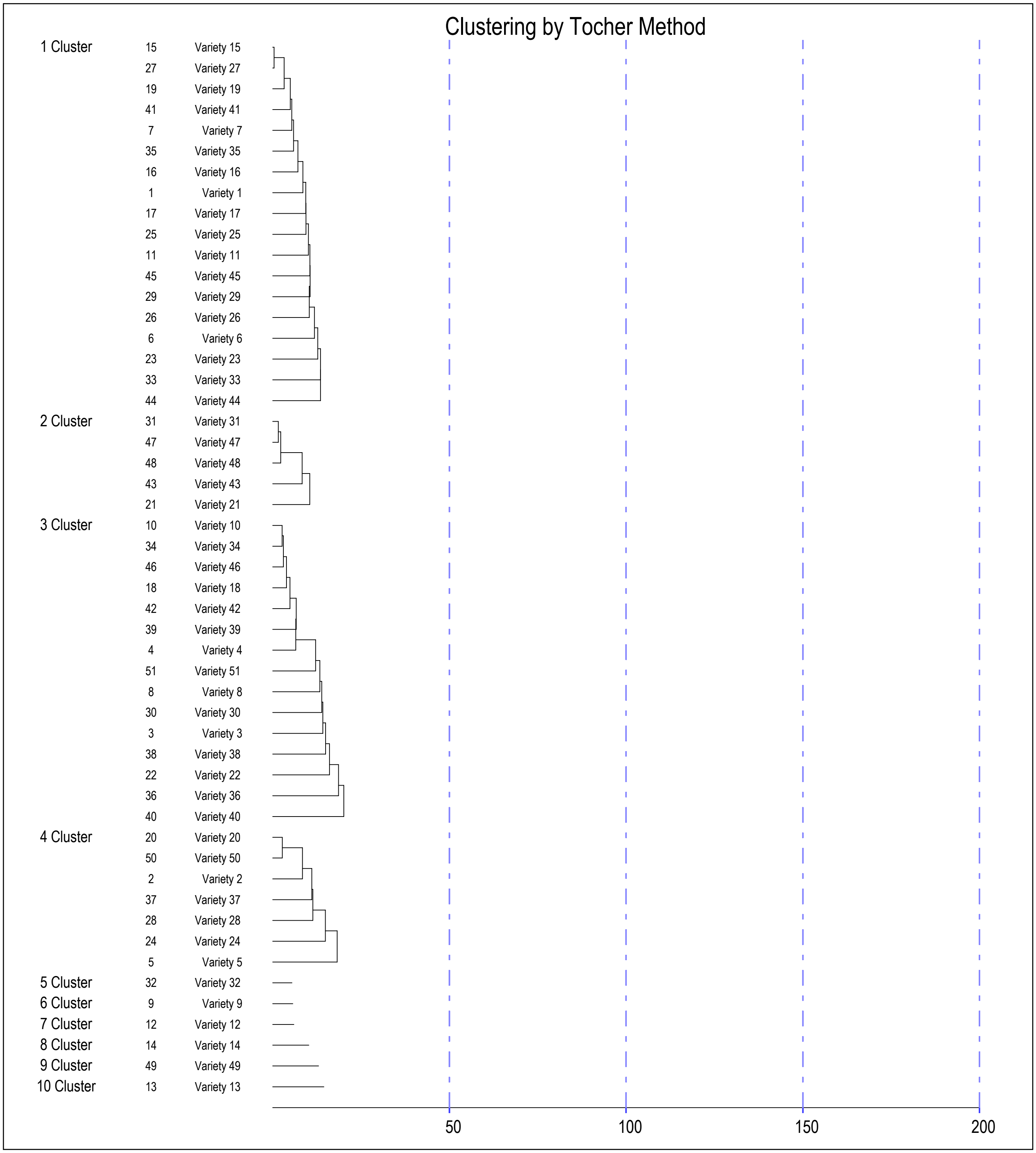

Figure 1: Clustering pattern of 51 sesame genotypes by tocher's method

mean for days to 50% flowering was highest in cluster IV (40.64) and lowest in cluster II (29.40). For plant height, the cluster mean exhibited a range from 81.71 cm (cluster VIII) to 115.95 cm (cluster VII). The cluster VII showed highest mean for number of branches plant^{-1} (3.98) while lowest was in cluster IX (1.75). The cluster X was found to have highest mean values for capsule length (2.80 cm), number of capsules plant^{-1} (59.26), number of seeds capsule^{-1} (70.50) and seed yield plant^{-1} (5.47 g). Selection of genotypes with high cluster mean values for particular trait could be utilized in hybridization programme for improvement of that character.

Table 3: Intra and inter cluster distances of ten clusters from 51 genotypes of sesame

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X
Cluster I	30.77	57.59	70.66	72.42	69.59	64.37	66.59	79.56	82.89	81.93
Cluster II		25.14	138.08	163.64	63.11	64.07	76.10	115.15	53.32	97.98
Cluster III			40.68	80.86	72.07	63.21	66.96	131.81	128.41	145.61
Cluster IV				44.01	162.30	150.15	147.85	109.63	169.09	143.85
Cluster V					0	15.21	27.59	129.25	49.36	152.55
Cluster VI						0	16.02	152.2	77.84	105.66
Cluster VII							0	190.41	99.08	108.53
Cluster VIII								0	122.25	143.80
Cluster IX									0	219.39
Cluster X										0

Table 4: Mean performance of ten clusters for yield and its components in sesame

Cluster No.	Days to 50% flowering	Plant height (cm)	No. of branches plant^{-1}	Capsule length (cm)	No. of capsules plant^{-1}	No. of seeds capsule^{-1}	1000 seed weight (g)	Seed yield plant^{-1} (g)
I	35.17	94.96	3.47	2.48	53.87	49.30	2.34	4.51
II	29.40	87.95	2.51	2.45	53.42	46.40	2.23	4.35
III	40.57	111.64	3.33	2.69	42.36	54.25	2.09	3.52
IV	40.64	103.59	3.69	2.32	53.63	54.93	2.59	4.86
V	34.00	108.29	3.10	2.70	33.17	42.50	2.03	2.58
VI	34.00	99.55	3.05	2.78	34.60	55.00	1.67	2.91
VII	33.50	115.95	3.98	2.71	47.45	55.34	1.58	3.22
VIII	37.50	81.71	2.35	2.50	49.32	38.00	4.30	4.33
IX	33.00	90.45	1.75	2.22	48.05	36.00	1.72	3.18
X	31.50	95.34	3.25	2.80	59.26	70.50	3.46	5.47

A critical appraisal of the observations indicated that none of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits. The study reveals that the character days to 50% flowering contributed maximum towards divergence followed by seed yield plant^{-1}, capsule length and number of seeds capsule^{-1}. The 51 genotypes were distributed into ten clusters and indicated the existence of wide variability among the genotypes evaluated. The study indicated that hybridization between the genotype of SI-3299-A of cluster IX with GT-10 of cluster X; GRM-54 of cluster VII and with GT-4 of cluster VIII; EC-182833, IS-101-3-B, IS-205, KMR-8, NIC-16281, VRI-1, CT-27 of cluster IV with SI-3299-A of cluster IX; IS-133-A, KMS-4-258, RT-346, SI-2039-A, SI-264 of cluster II with EC-182833, IS-101-3-B, IS-205, KMR-8, NIC-16281, VRI-1, CT-27 of cluster IV; EC-182833, IS-101-3-B, IS-205, KMR-8, NIC-16281, VRI-1, CT-27of cluster IV with MT-13-7 of cluster V; MT-13-7 of cluster V with GT-10 of cluster X; GRM-47 of cluster VI with GT-4 of cluster VIII; EC-182833, IS-101-3-B, IS-205, KMR-8, NIC-16281, VRI-1, CT-27 of cluster IV with GRM-47 of cluster VI would yield desirable recombinants.

The cluster X showed highest mean value for capsule length, number of capsules plant^{-1}, number of seeds capsule^{-1} and seed yield plant^{-1}. The cluster II showed desirable mean values for days to 50% flowering and the cluster VII exhibited higher mean values for plant height and number of branches plant^{-1}. The promising genotypes from these clusters with favourable mean values for different traits may be used directly for adaptation or may be used as parents in hybridization programme, depending upon the objective of the breeding programme to obtain superior transgressive segregants.

4. CONCLUSION

The traits such as days to 50% flowering, seed yield plant^{-1}, capsule length and number of seeds capsule^{-1} contributed more towards divergence and selection of parents based on these traits would be useful to achieve a wide genetic variability in crop improvement programme. Among the ten clusters studied, maximum inter cluster distance was observed between cluster IX and cluster X followed by cluster VII and cluster VIII. The genotypes from these clusters could be used in crossing programme to obtain superior recombinants.

5. REFERENCES

Ahadu, M.A., 2012. Phenotypic variability, divergence analysis and heritability of characters in sesame (*Sesamum indicum* L.) genotypes. Nature Science 1, 117–26.

Alex, T., Srinivasan, K., Arthanari, P.M., 2017. Effect of seed pelleting and foliar nutrition on growth and yield of summer irrigated sesame (*Sesamum indicum* L.). Madras Agricultural Journal 104(10/12), 350–353.

Anilakumar, K.R., Pal, A., Khanum, F., Bawa, A.S., 2010. Nutritional, medicinal and industrial uses of sesame (*Sesamum indicum* L.) seeds - An overview. Agriculturae Conspectus Scientificus 75, 159–168.

Anonymous, 2018. India position in yield of sesame seed in the world. https://www.indiastat.com/top-10-countries/data/agriculture/sesamum/data-year/2018 and https://www.indiastat.com/table/top-10-countries/agriculture/india-position-yield-sesame-seed-world-2018/1343280. Accessed on 25.03.2023.

Anonymous, 2021. Area, production and productivity of sesame in India. Available https://www.indiastat.com/data/agriculture and https://www.indiastat.com/data/ agriculture/sesamum and https://www.indiastat.com /table/agriculture/area-production-productivity-sesamum-india-1950-19/36611. Accessed on 25.03.2023.

Ashri, A., 1998. Sesame breeding. Plant Breeding Reviews. John Wiley and Sons 16, 179–228.

Begum, S., Islam, M.A., Husna, A., Hafiz, T.B., Ratna, M., 2011. Genetic diversity analysis in sesame (*Sesamum indicum* L.). Journal of Agriculture 9(2), 65–71.

De, P.S., Bhale, V.M., Khadse, V.A., 2013. Quality and economics of summer sesame (*Sesamum indicum* L.) as influenced by irrigation and nutrient levels. International Journal of Bio-resource and Stress Management 4(2), 369–371.

Elleuch, M., Besbes, S., Roiseux, O., Blecker, C., Attia, H., 2007. Quality characteristics of sesame seeds and by-products. Food chemistry 103(2), 641–650.

Fukuda, Y., Nagata, M., Osawa, T., Namiki, M., 1986. Contribution of lignan analogues to antioxidative activity of refined unroasted sesame seed oil. Journal of the American Oil Chemists' Society 63, 1027–1031.

Gangadhara, K., Chandra, P.J., Rajesh, A.M., Gireesh, C., Somappa, J., Yathish, K.R., 2012. Correlation and path coefficient analysis in sesame (*Sesamum indicum* L.). Bioinfolet 9(3), 303–310.

Gopal Kadvani, J., Patel, A., Patel, J.R., Prajapati, K.P., Patel, P.J., 2020. Estimation of genetic variability, heritability and genetic advance for seed yield and its attributes in sesame (*Sesamum indicum* L.). International Journal of Bio-resource and Stress Management 11(3), 219–224.

Hassan, A.B., Mahmoud, N.S., Elmamoun, K., Adiamo, O.Q., Ahmed, I.A.M., 2018. Effects of gamma radiation on the protein characteristics and functional properties of sesame (*Sesamum indicum* L.) seeds. Radiation Physics and Chemistry 144, 85–91.

Hika, G., Geleta, N., Jalet, Z., 2015. Genetic variability, heritability and genetic advance for the phenotypic traits in sesame (*Sesamum indicum* L.) populations from Ethiopia. Science Technology & Arts Research Journal 4(1), 20–26.

Jadhav, R.S., Mohrir, N.M., 2013. Genetic divergence analysis in sesame. Electronic Journal of Plant Breeding 4(1), 1090-1092.

Kurdistani, R., Tohidinejad, E., 2011. Yield potential evaluation and path analysis of different sesame genotypes under various levels of iron. African Journal of Plant Sciences 5(15), 862–866.

Mahalanobis, P.C., 1936. On the generalized distance in statistics. Proceedings of the National Institute of Science of India 2, 49–55.

Murty, B.R., Arunachalam, V., 1966. The nature of genetic divergence in relation to breeding system in some crop plants. Indian Journal of Genetics 26, 188–198.

Panse, V.G., Sukhatme, P.V., 1967. Statistical method for agricultural workers 2nd edition ICAR Newsletter, 361.

Paremeshwarappa, S.G., Palakshappa, M.G., Salimath, P.M., Paremeshwarappa, K.G., 2010. Studies on genetic variability and character association in germplasm collection of sesame (*Sesamum indicum* L.). Karnataka Journal of Agricultural Sciences 22(2), 252–254.

Patil, R.R., Sheriff, R.A., 1994. Genetic divergence in sesame (*Sesamum indicum* L.). Journal of Agricultural Sciences 28, 106–110.

Rao, C.R., 1952. Advanced statistical methods in biometric research, Edn. 1, John Wiley and Sons. New York.

Sarkar, S., Saha, P.K., 2014. An emerging scenario of Indian sesame seed research. Science and Culture 80(7- 8), 217–226.

Sharma, E., Shah, T.I., Khan, F., 2014. A review enlightening genetic divergence in *Sesamum indicum* based on morphological and molecular studies. International Journal of Agriculture and Crop Sciences 7(1), 1–9.

Sheriff, R.A., Shivashankar, G., 1992. Genetic divergence in foxtail millet (*Setaria italica* B.). Indian Journal of Genetics and Plant Breeding 52(1), 29–32.

Shwetha Yadav, B. P., Thiruvengadam, V., Sasikala, R., Rajendran, L., 2022. Analysis of genetic diversity in sesame (*Sesamum indicum* L.) germplasm for yield and its attributing traits. Electronic Journal of Plant Breeding 13(3), 927–931.

Singh, R.K., Chaudhary, B.D., 1977. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi, 215–218.

Sivaprasad, Y.V.N., Krishna, M.S.R., Yadavalli, V., 2013. Correlation and path analysis in F_2 and F_3 generations of crosses JLSV 4 x TC 25 in sesame (*Sesamum indicum* L.). Advances in Crop Science and Technology 3(5), 370–375.

Teklu, D.H., Kebede, S.A., Gebremichael, D.E., 2014. Assessment of genetic variability, genetic advance, correlation and path analysis for morphological traits in sesame genotypes. Asian Journal of Agricultural Research 8, 181–194.

Tripathi, A., Bisen, R., Ravindra, P., Paroha, A.S., Sahu, R., Ranganatha, A.R.G., 2013. Study on genetic divergence in sesame (*Sesamum indicum* L.) germplasm based on morphological and quality traits. An International Quarterly Journal of Life Sciences 8(4),1387–1391.

Were, B.A., Onkware, A.O., Gudu, S., Welander, M., Carlsson, A.S., 2006. Seed oil content and fatty acid composition in East African sesame (*Sesamum indicum* L.) accessions evaluated over three years. Field Crop Research 97(3), 254–260.