Assessment of genetic diversity in sesame genotypes based on morphological characters

Abstract

Fifty sesame genotypes were evaluated to assess the extent of genetic diversity based on morphological characters. Analysis of variance revealed significant differences among the genotypes. Plant height (62.20 %) contributed most to the genetic divergence followed by number of capsules per plant (20.40 %). No relationship between geographic origin and genetic diversity was observed as genotypes from different sources were grouped in same clusters in spite of difference in their origin. Based on the intercluster distances, diverse parents from different clusters were identified for further use as parents in future breeding programmes.

Key words: Sesame, genetic diversity, cluster analysis, Tocher′s method

Introduction

Sesame (*Sesamum indicum* L.) stands as one of the oldest cultivated oilseed crops, contributing significantly to human nutrition and agro-economic sustainability across diverse regions of the world. Its global importance lies not only in nutritive value but also in adaptability to a wide range of agroclimatic conditions. The genetic resources within the sesame genus possess a rich and unexplored repository of morphological diversity, offering a valuable asset for agricultural advancement and food security.

“In India, sesame was grown over an area of 16.27 lakh hectares with the production of 7.89 lakh tonnes and productivity of 485 kg ha^{-1} (Indiastat, 2022). In Telangana, it is grown over an area of 0.34 lakh hectares with an annual production of 0.26 lakh tonnes and productivity of 766 kg ha^{-1}” (Indiastat, 2022).

“Genetic variability and divergence are of great importance to plant breeders as they play a crucial role in implementing a successful hybridization programme through selection of genetically diverse parents. Moreover, genetic diversity in crop plants is essential to sustain high productivity” (Rabbani *et al*., 2010). “Genetic divergence analysis helps in categorizing genotypes into distinct genotypic classes and identifying parents for hybridization” (Rao et al., 1981, Jatasra and Paroda, 1983). “It is determined by using cluster analysis, which assigns genotypes into different groups. Mahalanobis D^2 statistic is a powerful tool in quantifying the degree of divergence at genotypic level. D^2 analysis would consolidate in identification of genetically diverse high yielding genotypes which could be useful in cross breeding programme for producing more transgressive segregants” (Mahalanobis, 1936).

By keeping this in view, the present investigation was carried out to ascertain the nature and magnitude of genetic divergence among fifty sesame genotypes to identify the genetically diverse parents which can be used as parents in future breeding programmes.

Materials and methods

The experiment was carried out at Regional Agricultural Research Station, Polasa, Jagtial, during late *kharif*, 2022. The experiment was laid out in Randomized Block Design (RBD) in two replications with inter-row spacing of 30 cm and intra-row spacing of 15 cm with plot size of 2 rows of each 3m length. The experimental material consisted of 50 genotypes collected from different sources. Details of 50 genotypes is listed below in Table 1.

Table 1. Details of 50 genotypes of sesame

S.No.	Genotype	Source
1	TKG 21	Tikamgarh, Madhya Pradesh
2	TKG 55	Tikamgarh, Madhya Pradesh
3	TKG 306	Tikamgarh, Madhya Pradesh
4	TKG 308	Tikamgarh, Madhya Pradesh
5	JTS 8	Tikamgarh, Madhya Pradesh
6	EC3349997	PC unit, JNKVV, Jabalpur
7	NIC 9843	PC unit, JNKVV, Jabalpur
8	EC 3349998	PC unit, JNKVV, Jabalpur
9	NIC 16095-A	PC unit, JNKVV, Jabalpur
10	ES 3196	PC unit, JNKVV, Jabalpur
11	ES 81	PC unit, JNKVV, Jabalpur
12	FFAT 17	PC unit, JNKVV, Jabalpur
13	ES 28	PC unit, JNKVV, Jabalpur
14	Madhavi	ARS, Yelamanchili
15	EC 182833	PC unit, JNKVV, Jabalpur
16	FFAT 04	PC unit, JNKVV, Jabalpur
17	FFAT 16	PC unit, JNKVV, Jabalpur
18	EC 330005	PC unit, JNKVV, Jabalpur
19	EC 182835	PC unit, JNKVV, Jabalpur

S.No.	Genotype	Source
20	FFAT 13	PC unit, JNKVV, Jabalpur
21	IS 35-1-A	PC unit, JNKVV, Jabalpur
22	JCS 3880	RARS, Polasa, Jagtial
23	Swetha	RARS, Polasa, Jagtial
24	JCS 3287	RARS, Polasa, Jagtial
25	JCS 4047	RARS, Polasa, Jagtial
26	JCS 4026	RARS, Polasa, Jagtial
27	JCS 4022	RARS, Polasa, Jagtial
28	JCS 4018	RARS, Polasa, Jagtial
29	JCS DT 26	RARS, Polasa, Jagtial
30	JCS 3889	RARS, Polasa, Jagtial
31	JCS 4020	RARS, Polasa, Jagtial
32	JCS RF2	RARS, Polasa, Jagtial
33	Pragathi	Mauranipur, Uttar Pradesh
34	JCS RF4	RARS, Polasa, Jagtial
35	Jagtiala Til-1 (JCS 1020)	RARS, Polasa, Jagtial
36	JCS 4894	RARS, Polasa, Jagtial
37	JCS 4904	RARS, Polasa, Jagtial
38	JCS 4911	RARS, Polasa, Jagtial
39	JCS 4917	RARS, Polasa, Jagtial
40	TKG 22	Tikamgarh, Madhya Pradesh
41	JCS 3890	RARS, Polasa, Jagtial
42	JCS 3604	RARS, Polasa, Jagtial
43	JCS 3888	RARS, Polasa, Jagtial
44	JCS 3758	RARS, Polasa, Jagtial

S.No.	Genotype	Source
45	JCS 3605	RARS, Polasa, Jagtial
46	Jagtiala Til-2 (JCS 2454)	RARS, Polasa, Jagtial
47	JCS 4862	RARS, Polasa, Jagtial
48	Telangana Til-1 (JCS 3202)	RARS, Polasa, Jagtial
49	GT 10	ARS, Amreli, Gujarat
50	JCS 2698	RARS, Polasa, Jagtial

All the standard packages of practices were followed during the crop growth period. Variation in eight characters of fifty sesame genotypes was tested for assessing the nature of genetic divergence. The aggregate effect of all the eight characters tested by Wilk's criterion indicated highly significant differences among the genotypes and clustering pattern was estimated according to the procedure provided by Mahalnobis D^2 (1936) statistics and Tocher′s method (Rao., 1952). The data collected for yield and yield contributing traits was analysed through WINDOSTAT statistical package.

Results and Discussion

Analysis of variance revealed highly significant differences among the genotypes in respect eight characters, thus revealing existence of considerable genetic variation in the studied genotypes.

Clustering pattern

Based on the D^2 values, the genotypes were grouped into six clusters (Table 2 and Fig 1). Among the six clusters, cluster I was the largest comprising of 37 genotypes followed by cluster II with 5 genotypes, cluster III with 5 genotypes and cluster IV, V and VI were solitary represented by single genotype, showing high degree of heterogeneity. Solitary clusters may be of distinct recombinant or rare segregants (Soundharya *et al*., 2017; Mohanty *et al.,* 2020). There was no correspondance between geographic diversity and genetic diversity, as shown by the pattern of dispersion of genotypes from diverse eco-geographical groupings into one another. This implies that factors including the trade of breeding stock, natural and artificial selection, genetic drift, migration, gene flow and environmental variation could be the reason for this diversity.

Table 2. Clustering pattern of sesame genotypes based on D^2 values

Clusters	No of genotypes	Name of genotypes
Cluster 1	37	EC 3349997, NIC 9843, EC 3349998, NIC 16095-A, FFAT 04, FFAT 17, EC 330005, FFAT 13, IS 35-1-A, ES 28, FFAT 16, EC 182835, ES 81, JCS 3287, JCS 3880, Swetha, Madhavi, JCS 4022, JCS 4020, JCS 4018, JCS RF2, Pragathi, JCS RF4, JCS 4026, JCS 3889, JCS 4894, JCS 3605, JCS 3202, JCS 3758, JCS 3888, JCS 4862, JCS 3604, JCS 4904, GT 10, JCS 2698, JCS 1020 and JCS 2454.
Cluster 2	05	JCS 4917, JCS 3890, JCS 4911, EC 182833 and TKG 22.
Cluster 3	05	TKG 55, JTS 8, TKG 21, TKG 306 and TKG 308.
Cluster 4	01	JCS DT 26
Cluster 5	01	JCS 4047
Cluster 6	01	ES 3196

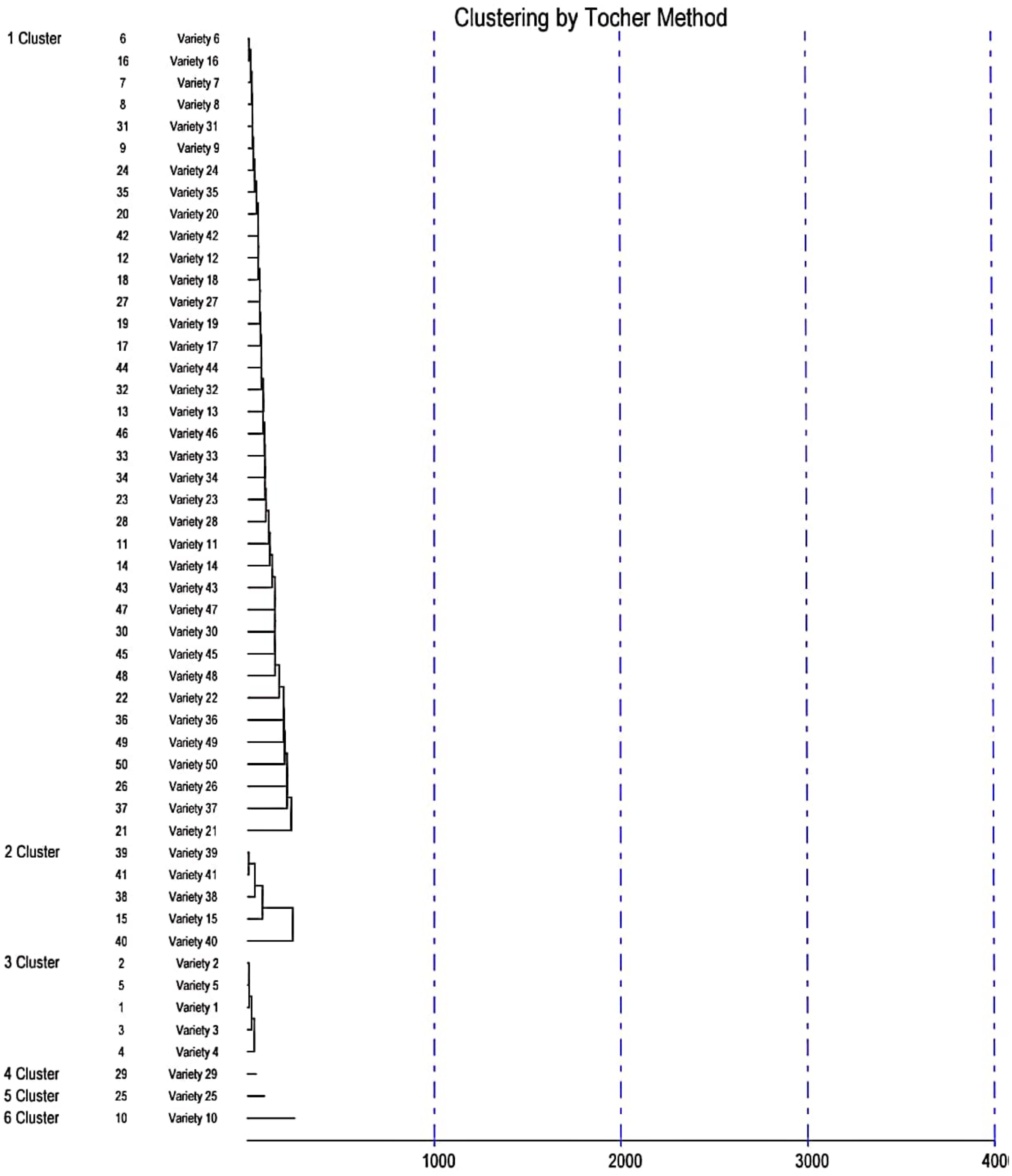

Fig. 1. Clustering pattern of sesame genotypes based on Tocher's method.

Average intra and inter cluster distance

The average intra and inter cluster D^2 values are presented in Table 3 and Fig 2. The maximum intra cluster distance was recorded for cluster II (436.41) followed by cluster I (385.90) and cluster III (76.22) indicating that some diversity still existed among the genotypes. This could be made use of in the yield improvement through recombination breeding. Because of solitary nature clusters IV, V and VI recorded zero intra cluster distances which were in conformity with the results of Venkatesh *et al.* (2011) and Ahadu Menzir (2012).

From the inter Cluster D^2 values of six clusters, the highest inter cluster distance (7021.21) was observed between clusters III and IV whereas, the lowest inter cluster distance was observed between cluster I and IV (979.49). Therefore, it is suggested that the hybridization of cluster III (TKG 55, TKG 308, TKG 21, TKG 306 and JTS 8) and cluster IV (JCS DT 26) will result in a promising segregation for yield and yield-contributing characters. The genotypes of these clusters may be used as parents in the crossing programme to generate breeding material with high diversity.

Table 3. Average intra (diagonal) and inter cluster distances of sesame genotypes

Clusters	**Cluster 1**	**Cluster 2**	**Cluster 3**	**Cluster 4**	**Cluster 5**	**Cluster 6**
Cluster 1	**365.9**	1272.22	3437.35	979.49	1003.12	1577.15
Cluster 2		**436.41**	983.67	3385.19	2961.77	2636.06
Cluster 3			**76.22**	7021.21	6099.03	5459.71
Cluster 4				**0**	249.04	1144.04
Cluster 5					**0**	993.06
Cluster 6						**0**

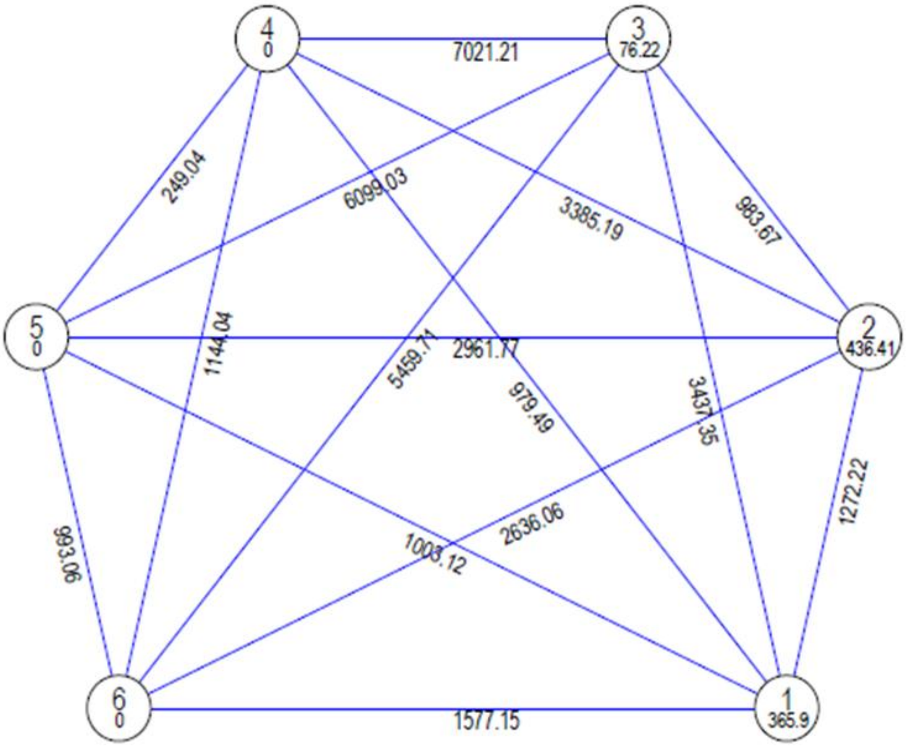

Fig 2. Cluster diagram of sesame genotypes

Cluster mean

The cluster means in respect of eight yield and yield contributing traits across six clusters are presented in Table 4. Genotypes of cluster III showed early flowering habit with 36.00 number of days to flowering while, genotypes of cluster IV had late flowering habit with 44.00 days. Genotypes under cluster III was of early maturity type with number of days to mature being

82.00 days, while that under cluster VI were of late maturity types (97.50 days). With regards to plant height, the genotypes of cluster III exhibited the lowest mean plant height (71.65 cm) whereas, cluster IV showed the highest mean plant height (147.20 cm). Cluster VI showed the highest mean value for both number of capsules per plant (89.00) and seed yield per plant (10.93 g). Therefore, the genotypes of cluster VI may be used as parents for improvement of yield in sesame.

Table 4. Cluster means for yield and yield attributing traits using Tocher's method

Clusters	Days to 50% flowering	Days to maturity	Plant height	Number of branches per plant	Number of capsules per plant	Number of seeds per capsule	1000 seed weight	Seed yield per plant
Cluster 1	41.43	95.41	124.34	4.59	54.73	56.61	3.19	5.86
Cluster 2	40.30	92.00	95.08	4.88	48.50	59.99	3.16	5.07
Cluster 3	36.10	82.00	71.65	3.81	39.37	55.02	3.45	3.42
Cluster 4	44.00	97.00	147.20	5.56	69.35	63.85	3.36	7.38
Cluster 5	39.00	84.00	141.55	5.56	70.40	68.45	3.27	8.30
Cluster 6	43.00	97.50	120.60	7.30	88.95	69.80	3.39	10.93

Relative contribution of different traits towards genetic divergence

The per cent contribution towards genetic divergence by all the yield and yield contributing traits is presented in Table 5. The maximum contribution towards genetic divergence was shown by plant height (62.20 %), number of capsules per plant (20.40 %), number of seeds per capsule (10.61 %), days to maturity (5.63 %) and number of branches per plant, 1000 seed weight, and seed yield per plant contributed zero. These results corroborated with the reports of Rajani Bisen *et al*. (2013), Tanwar and Bisen (2018) and Gogoi *et al*. (2018).

Table 5. Relative contribution (%) of yield and yield attributing traits towards divergence

Character	**Times ranked 1st**	**Contribution %**
Days to 50% flowering	14	1.14
Days to maturity	69	5.53
Plant height (cm)	762	62.20
Number of branches per plant	-	0
Number of capsules per plant	250	20.40
Number of seeds per capsule	130	10.61
1000 seed weight (g)	-	0
Seed yield per plant (g)	-	0

Conclusion

Analysis of variance revealed significant differences between the 50 genotypes for all the 8 characters. The genotypes from diverse clusters like III and IV having high inter cluster distances may be used as parents to create variability in future breeding programmes. In addition, these genotypes may be screened by using molecular markers to confirm the results obtained in the present investigation.

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