



Assessment of genetic diversity for various morpho-phenological traits in sesame (*Sesamum indicum*)

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Sesame (*Sesamum indicum* L.) belongs to the family Pedaliaceae, having polidy level $2n = 26$ is considered as valuable oilseed crop at global level. Sesame seeds are an important source of good quality edible oil which is widely used as ingredient in food products especially in bakery and sweets. The seeds contain substantial amount of oil (45–55%), protein (18–25%), carbohydrates (16–18%), fibers, phenolic compounds and also possess considerable quantity of mineral nutrients (Ojiako *et al.* 2010). Among the edible oils, sesame oil has the highest antioxidants potential (Cheung *et al.* 2007) and contain plentiful unsaturated fatty acids mainly linoleic acid and oleic acid which enhance the quality of the oil for human consumption.

India ranks first in world with 1.95 million ha area and 0.87 million tonnes production. The average yield of sesame in India is 413 kg/ha, low as compared with other countries in the world is 535 kg/ha (Singh *et al.* 2022). However, the productivity of sesame crop is generally very low as compared to other oilseed crops which is mainly due to lack of high yielding cultivars. In present scenario, more aggressive breeding efforts are required to harness the untapped potential of this crop for further yield enhancement (Furat and Uzun 2010). Under changing climatic conditions, breeding of climate resilient varieties is becoming more important. Knowledge about genetic diversity is necessary not only in selecting elite parents for high grain and oil yield but also for development of disease and pest resistant varieties. Genetic diversity between two parents is essential to realize maximum heterosis and to obtain transgressive segregants in the segregating generations. Yield improvement is normally attained through exploitation of the genetically diverse parents. Thus, information on the genetic diversity in the source material is highly essential prior to formulating any crossing programme. Therefore,

the present study was carried out with the objectives to analyze genetic diversity among 60 sesame accessions and identification of potential genotypes based on yield and its component traits.

Sixty genotypes of sesame were collected from the Oilseeds Section, Chaudhary Charan Singh, Haryana Agricultural University, Hisar and evaluated during *kharif* 2017 (Supplementary Table 1). All the genotypes were evaluated in Randomized Block Design (RBD) with three replications. Each genotype was sown in a rows of 3-meter length with spacing of 30 cm × 15 cm (row-to-row and plant-to-plant). Morphological data for all the 12 characters were subjected to Analysis of variance, Coefficient of variation and mean performance of all the genotypes for various morphological characters as per the standard statistical methods. Genetic divergence assessment was made by adopting Mahalanobis D^2 statistic (1936) for yield and its attributing characters. Sesame genotypes were grouped into different clusters based on D^2 values using Tocher's method as described by Rao (1952).

Morphological traits diversity: Genetic diversity based on morpho-physiological traits have direct practical value in sesame crop improvement. In our study, analysis of variance showed highly significant differences among the studied genotypes (Table 1). The mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (broad sense) and expected genetic advance as per cent of mean for various morphological characters have been given in Table 2. Phenotypic coefficient of variation (PCV) was found to be greater than the genotypic coefficient of variation (GCV) for all the characters studied, which reflected the role of environment in the expression of the observed traits. High PCV & GCV estimates were observed for number primary and secondary branches per plant, number of capsules per plant, number of seeds per capsule and seed yield per plant. These results suggested that there is considerable possibility of further improvement for these characters through hybridization and phenotypic selection. Similarly, Manjeet *et al.* (2020) also reported the high genotypic and phenotypic coefficient of variation for

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these traits in sesame. High heritability coupled with high genetic advance observed for number of capsules per plant and number of seeds per capsule indicating predominance of additive gene action for controlling these traits and direct selection is rewarding for improvement of these traits. Similar findings in sesame were also made by Mahmoud

Table 1 Analysis of variance (ANOVA) for various morphological traits in sesame

Source of Variation	Mean sum of square			Coefficient of Variation (%)
	Repli- cations	Geno- types	Error	
	2	59	118	
Days to 50% flowering	0.16	26.04**	0.61	1.49
Days to maturity	0.22	31.67**	0.45	0.66
Plant height	0.32	3.22*	0.75	5.01
Primary branches per plant	0.18	6.55**	0.15	7.48
Secondary branches per plant	0.04	46.72**	0.04	11.94
Number of capsules per plant	0.17	31.84**	0.19	5.50
Number of seeds per capsule	1.27	14.54**	4.16	5.06
Capsule length	1.63	3.45*	1.46	5.71
Capsule width	0.03	3.56*	0.04	2.56
1000-seed weight	0.04	4.72*	0.01	3.75
Oil content	0.57	4.19*	1	2.09
Seed yield per Plant	2.41	42.71**	0.26	6.30

Table 2 Estimates of mean performance, range, genotypic coefficient of variation (GCV), phenotypic, coefficient of variation (PCV), heritability (broad sense) and genetic advance (GA) as per cent of mean for morphological characters in sesame

Trait	Mean	Range		Coefficient of variation (%)		Heritability (%) (b.s.)	Genetic advance as per cent of mean (%)
		Lowest	Highest	Genotypic	Phenotypic		
DF	52.41	46.67	58.67	4.30	4.38	96.16	8.68
DM	101.85	96.67	109.33	2.10	2.13	96.84	4.26
PH	173.08	139.47	192.97	4.31	5.19	68.91	7.36
PBP	5.15	4.07	6.60	10.18	11.06	84.14	19.30
SBP	1.61	0.42	3.57	46.60	47.10	97.86	94.96
NCP	79.74	53.42	118.49	17.64	17.93	96.86	35.77
NSC	40.37	29.83	51.53	10.74	11.13	93.12	21.35
CL	21.17	18.00	24.00	5.16	6.12	71.04	8.96
CW	7.57	7.20	8.00	2.36	2.79	71.91	4.13
1000 SW	2.99	2.66	3.22	4.18	4.71	78.84	7.65
OC	47.99	45.60	50.70	2.16	2.47	76.14	3.87
SYP	8.12	4.57	12.13	23.50	23.78	97.66	47.84

DF, Days to flowering (50%); DM, Days to maturity; PH, Plant height (cm); PBP, Primary branches per plant; SBP, Secondary branches per plant; NCP, No. of capsules per plant; NSC, No. of seeds per capsule; CL, Capsule length; CW, Capsule width; 1000-SW, 1000 Seeds weight (g); OC, Oil content; SYP, Seed yield per plant (g).

and Ghareeb (2015), Abate *et al.* (2015), Saxena and Bisen (2017), Manjeet *et al.* (2020).

Grouping of genotypes into various clusters: Sixty genotypes were grouped into eight clusters based on D^2 values using Tocher's method (Supplementary Table 2 and Fig 1). Out of eight clusters, cluster I was the largest one comprising of 23 genotypes followed by Cluster II with 19 genotypes, cluster III with 13 genotypes. Cluster IV, V, VI, VII and VIII each with single genotype indicating high degree of heterogeneity among these genotypes.

Average intra and inter cluster distances: The average intra and inter cluster D^2 values are presented in Supplementary Table 3. Results suggest that useful segregates may be created by crossing genotypes of cluster V with genotypes of cluster VIII, and genotypes of cluster III with genotypes of cluster VIII.

Relative contribution of characters towards genetic divergence: The percentage of contribution towards genetic divergence by all the 12 characters is presented in Supplementary Table 4. The characters contributing maximum towards divergence should be given emphasis for the selection of parents for hybridization programmes. The results are in agreement with reports of Kumhar *et al.* (2013), Mohan (2014), Soundharya *et al.* (2017) and Patil *et al.* (2017) in sesame. This study will provide valuable information to breeders for the development of high yielding sesame genotypes.

The presence of genetic diversity among the evaluated germplasm material might play an important role in exploiting maximum heterosis and to produce desirable transgressive segregants in F_2 generation for future sesame improvement programmes. The present study will help

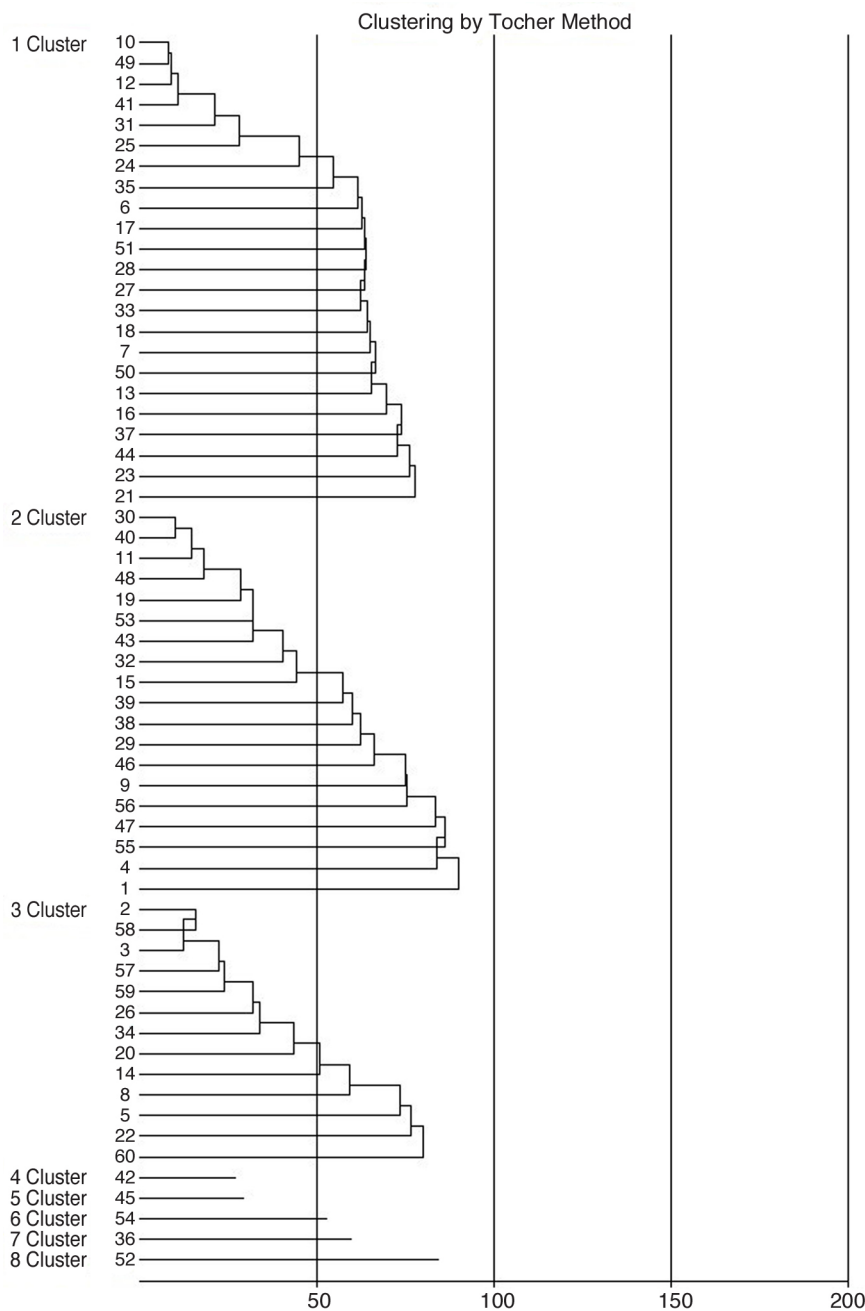


Fig 1 Dendrogram of 60 sesame genotypes based on morphological characters.

geneticist and breeders to select diverse parents in crossing for development of high yielding genotypes of sesame.

SUMMARY

Sesame (*Sesamum indicum* L. 2n = 26) is considered as valuable oilseed crop known to humans since ancient times. Despite having high oil quality, it is grown in small area due to lack of high yielding varieties with inbuilt resistance to biotic and abiotic stresses. Therefore an experiment was conducted to study the genetic diversity for yield and its component traits using 60 sesame (*Sesamum indicum* L.) genotypes collected from the Oilseeds Section, CCS Haryana Agricultural University, Hisar, during *kharif*

2017. Analysis of variance showed highly significant differences among the studied genotypes. Phenotypic coefficient of variation (PCV) was found to be greater than the genotypic coefficient of variation (GCV) for all the characters studied, which reflected the role of environment in the expression of the observed traits. High heritability coupled with high genetic advance was observed for number of capsules per plant and number of seeds per capsule indicating predominance of additive gene action for controlling these traits. Cluster analyses based on D² values using Tocher’s method was used to make a dendrogram of the morphological data. The presence of genetic diversity among the evaluated germplasm will help geneticist and breeders to select diverse parents in crossing for development of high yielding genotypes of sesame.

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