

Genetic diversity studies in indigenous and exotic sesame (*Sesamum indicum* L.) germplasm

Vallepu Ashok, A L Rathnakumar, D Ratna Babu and A Alivelu

Department of Genetics and Plant Breeding, Acharya N G Ranga Agricultural University,
Agricultural College, Bapatla-522101, Andhra Pradesh, India

ABSTRACT

Sesamum is an important and ancient seed crop of world. Huge variability was noted different parts of the world. On the present study, ICAR-IIOR indigenous land races and exotic germplasm accessions representing 15 different countries were evaluated to identify superior genotypes for further improvement program. A total of sixty sesame accessions, 30 indigenous and 30 exotic were evaluated in Augmented Block Design at Hyderabad. Data were recorded and analyzed by R software. The combined analysis showed significant differences among the accessions for all the traits except for number of flowers per leaf axil. Principal Components Analysis showed that the first five PCs with eigen values greater than unity about 62.8% of the total variations among sesame genotypes. Based on PCA score/loadings, the characters such oil content, seed yield, thousand seed weight, days to maturity, days to 50% flowering and seed coat colour contributed to the diversity and these traits were found to be important factors for genetic differentiation in the accessions studied. Shannon-Weiner's diversity index (H_2) for individual traits indicated capsule number per plant, thousand seed weight, capsule width, internode length and days to 50% flowering were more diverse among the lines studied. Interestingly, the trait thousand seed weight in both multivariate analyses (PCA and Shannon-Weiner's diversity index) proved to contribute more towards the diversity. The present material may be exploited further selection of contrasting parents from these accessions to develop mapping populations or MAGIC populations for marker aided breeding schemes.

Keywords: Cluster analysis, Genetic diversity, Principal Component analysis and Shannon-Weiner's diversity index

Sesame (*Sesamum indicum* L.) is an annual plant of the Pedaliaceae family with diploid chromosomes ($2n = 26$) and considered as the oldest oilseed crops cultivated by man (Bedgian and Harlan, 1986). It is a self-pollinated crop containing 60 species organized into 16 genera (Zhang *et al.*, 2013). Hildebrandt (1932) considered Africa as the original home of sesame, since this continent hosts high number of wild species. Later evidences from inter-specific hybridization, molecular and lignans analyses suggested that the Indian subcontinent as the center of domestication and the probable wild progenitor is believed to be *Sesamum malabaricum* Burm. which is endemic only to India (Bedgian, 2003).

Breeding programs evaluate huge number of traits owing to the lack of reliable information on the performance of the major morphological and agronomic descriptors. In particular cases traits are used before it is known how much they contribute to

the variability. Genetic divergence is measured from the average genetic distance between cultivars or populations and is defined as genetic divergence of two varieties as a function of their ancestry, geographic separation and adaptation at different environments. Principal component analysis (PCA) is one of the multivariate statistical techniques which is a powerful tool for investigating and summarizing underlying trends in complex data structures (Legendre and Legendre, 1998). Principal component analysis reflects the importance of the traits with largest contributor to the total variation at each axis for differentiation. The Shannon Weiner's diversity index is a measure of genetic diversity among different species of a crop. It is used to summarize the distribution of alleles in a population and quantifies the richness and evenness of traits within a population (Bisht *et al.*, 1998). However, information generated is not sufficient as far as genetic diversity in sesame

genotypes is concerned. Hence, the present study was initiated to assess genetic diversity among sesame germplasm accessions according to their genetic similarities based on the phenotypic traits.

MATERIAL AND METHODS

The experiment was conducted in the summer 2024 at ICAR-Indian Institute of Oilseeds Research, Narkhoda farm, Hyderabad which is situated at 17°15'30.1608 N longitude and 78°19'11.1324 E latitude at an altitude of 569 metre above sea level (MSL).

The experimental material comprised of 60 germplasm accessions, 30 were indigenous land races of India and 30 were exotic accessions (originating from 15 countries) and three checks (Swetha, GT 10 and Jagtial Til-1). The experiment was conducted in an Augmented Block Design. Each experimental material was sown at random on a 2.7m² plot consisting of 2 rows of 3m length. The spacing adopted was 45 cm between rows and 15 cm between plant-to-plant. Three to four seeds were sown in a hill by dibbling and thinned at 3-4 leaves stage (18-20 DAS). The crop was irrigated to field capacity after thinning operation and thereafter at 15-20 days interval. All the recommended package of practices including application of fertilizers (30:30:20 N, P, K/ha) were followed uniformly. The crop was harvested when the leaves turn yellow and start drooping and the bottom capsules turn lemon yellow, by cutting out the root portion. The rest of the portion was covered in a labelled cloth bag and tied with a rope. The plants were dried in the sun for 7-10 days and beat with sticks to break open the capsules and the seeds were collected, cleaned and preserved for various post-harvest observations.

All data were collected from the two central plants of both rows for plant data. The descriptors were collected as per the descriptors of PPVFRA sesame. The quantitative data was subjected to analysis of variance (ANOVA), Principal Component Analysis and Shannon-Weiner's Diversity Index using R package (version 0.1.7.9000).

RESULTS AND DISCUSSION

Multivariate analysis of the accessions showed that the first five PCs (PC1 to PC5) having eigen values > 1.0 and cumulatively accounted for 62.79% of the total variation (Table 1). The first PC

accounted for 17.86% of the total variation, whereas the second PC explained 13.57% and the third PC accounted for 12.50% of variation, fourth PC accounted for 10.14% of variation, and fifth PC accounted for 8.73% of variation. The high level of variation in all five PC axes showed a high level of variation for these characters.

The variation in PC1 was largely correlated with oil content (0.51), seed yield (0.42), thousand seed weight (0.37), days to maturity (0.39), days to 50% flowering (-0.35) and seed coat colour (-0.31) while the variation in PC2 was mainly due to capsule width (0.53), days to maturity (0.43), number of capsules per plant (0.38), 1000-seed weight (0.33) and capsule length (0.32). PC3 variation was mainly associated with seed coat colour (0.34) and 1000-seed weight (0.20) and in the fourth PC variation was mainly correlated with plant height (0.47), seed coat colour (0.35) 1000-seed weight (0.27), and seed yield per plant (0.25). The variation in PC 5 was mainly due to plant height to first branch (0.66), capsule width (0.38) and 1000-seed weight (0.27). Similar findings have been reported by (Furat and Uzun, 2010; Singh *et al.*, 2018; Yoganjan *et al.*, 2020 and Gedifew *et al.*, 2023). These traits are important for the diversity observed in the germplasm accessions and can be relied for selecting desirable genotypes for further use in breeding programmes.

SHANNON-WEINER DIVERSITY INDEX

Estimated diversity (H_2) for individual traits ranged from 1.685 for capsule number per plant to 2.590 for 1000-seed weight closely followed by capsule width (2.520), internode length (2.474) and days to 50% flowering (2.404) (Table 2). The diversity index was classified as high ($H_2 \geq 0.60$), intermediate ($0.40 < H_2 < 0.60$), or low ($H_2 < 0.40$), as described by Eticha *et al.* (2005). According to this classification all the 12 yield and its component traits had $H' > 0.60$ indicating richness of diversity for these traits. It is interesting to note that, the 1000-seed weight which was identified as one of the key traits contributed maximum to the variation in PC1 estimated through PCA and exhibited the highest index even under Shannon-Weiner's method of assessment of diversity.

Genetic diversity assessment of sesame core collection in China by Zhang *et al.* (2012) using Shannon diversity index (H') and Nei's genetic

Table 1. The contribution of principle components and different traits towards diversity in sesame

Principal components	PC1	PC2	PC3	PC4	PC5
Eigen value	2.32	1.76	1.63	1.32	1.14
Percentage of variance	17.86	13.57	12.5	10.14	8.73
Cumulative percentage of variance	17.86	31.42	43.92	54.06	62.79
Traits	Eigenvector				
Days to 50% flowering	-0.35	0.03	-0.16	0.19	0.17
Plant height	-0.08	-0.1	-0.45	0.47	0.17
Plant height to first branch	-0.1	-0.26	-0.23	0.1	0.66
Internode length	-0.14	-0.18	0.14	0.5	-0.17
Number of capsules on main stem	0.01	-0.18	-0.46	-0.19	-0.13
Number of capsules per plant	0.01	0.38	-0.35	0.22	-0.4
Days to maturity	-0.39	0.43	-0.2	-0.01	0.05
Capsule length	0	0.32	0.26	0.27	0.06
Capsule width	0.08	0.53	-0.1	-0.18	0.38
Seed yield	0.42	0.06	-0.31	0.25	-0.23
Thousand seed weight	0.37	0.33	0.2	0.27	0.24
Seed coat colour	-0.31	-0.04	0.34	0.35	-0.04
Oil content	0.51	-0.17	0.01	0.19	0.21

Table 2. Shannon-Weiner Diversity Index in sesame

Traits	No. of classes observed	Shannon Weiner diversity index (Richness)		
		H'	Lower class limit at 95%	Upper class limit at 95%
Days to 50% flowering	7	2.4	1.235	1.946
Plant height	7	2.37	1.217	1.946
Plant height to first branch	7	2.13	1.096	1.946
Internode length	7	2.47	1.272	1.946
Capsule number on main stem	7	2.24	1.153	1.946
Capsule number per plant	7	1.69	0.94	1.792
Days to maturity	7	2.11	1.175	1.792
Capsule length	7	2.38	1.222	1.946
Capsule width	7	2.52	1.295	1.946
Seed yield/plant	7	2.36	1.214	1.946
1000-seed weight	7	2.59	1.331	1.946
Oil content	7	2.08	1.071	1.946

diversity index (h) indicated higher ($I=0.9537$, $H' = 0.5490$) diversity of the collection when calculated using phenotypic data and helped in extraction of a mini-core collection (MC) containing 184 accessions based on both phenotypic and molecular data while preserving the diversity of the original core collection. However, very few studies are available in sesame on Shannon's diversity index and more studies need to be undertaken for validation of findings.

The study also indicates that high value of phenotypic diversity index recorded by all the traits points out to the existence of more descriptors states for each trait and express diversity for the traits among the tested germplasm accessions. Further, sub-grouping of phenotypes for each trait may help in assessing and refining the diversity in sesame genetic resources. The present study showed existence of significant genetic diversity among tested genotypes indicating the presence of a huge opportunity for further improvement through selection and other breeding approaches.

CONCLUSION

A high level of genetic diversity based on agromorphological traits was observed in the present study. As the success in genetic improvement of the crop needs the availability of genetic variability and there is a great deal of genetic variability present in both indigenous and exotic accessions of sesame.

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